The role of outer membrane proteins and lipopolysaccharides for the sensitivity of Escherichia coli to antimicrobial peptides

Bacterial resistance to classical antibiotics is emerging worldwide. The number of infections caused by multidrug resistant bacteria is increasing and becoming a serious threat for human health globally. In particular, Gram-negative pathogens including multidrug resistant Escherichia coli are of serious concern being resistant to the currently available antibiotics. All Gram-negative bacteria are enclosed by an outer membrane which acts as an additional protection barrier preventing the entry of toxic compounds including antibiotics and antimicrobial peptides (AMPs). In this study we report that the outer membrane component lipopolysaccharide (LPS) plays a crucial role for the antimicrobial susceptibility of E. coli BW25113 against the cationic AMPs Cap18, Cap11, Cap11-1-18m2, melittin, indolicidin, cecropin P1, cecropin B, and the polypeptide antibiotic colistin, whereas the outer membrane protease OmpT and the lipoprotein Lpp only play a minor role for the susceptibility against cationic AMPs. Increased susceptibility toward cationic AMPs was found for LPS deficient mutants of E. coli BW25113 harboring deletions in any of the genes required for the inner part of core-oligosaccharide of the LPS, waaC, waaE, waaF, yaaG, and gmhA. In addition, our study demonstrates that the antimicrobial activity of Cap18, Cap11, Cap11-1-18m2, cecropin B, and cecropin P1 is not only dependent on the inner part of the core oligosaccharide, but also on the outer part and its sugar composition. Finally, we demonstrated that the antimicrobial activity of selected Cap18 derivatives harboring amino acid substitutions in the hydrophobic interface, are non-active against wild-type E. coli ATCC29522. By deleting waaC, waaE, waaF, or waaG the antimicrobial activity of the non-active derivatives can be partially or fully restored, suggesting a very close interplay between the LPS core oligosaccharide and the specific Cap18 derivative. Summarizing, this study implicates that the nature of the outer membrane component LPS has a big impact on the antimicrobial activity of cationic AMPs against E. coli. In particular, the inner as well as the outer part of the core oligosaccharide are important elements determining the antimicrobial susceptibility of E. coli against cationic AMPs.
Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries

Antimicrobial resistance (AMR) in bacteria and associated human morbidity and mortality is increasing. The use of antimicrobials in livestock selects for AMR that can subsequently be transferred to humans. This flow of AMR between reservoirs demands surveillance in livestock and in humans. We quantified and characterized the acquired resistance gene pools (resistomes) of 181 pig and 178 poultry farms from nine European countries, sequencing more than 5,000 Gb of DNA using shotgun metagenomics. We quantified acquired AMR using the ResFinder database and a second database constructed for this study, consisting of AMR genes identified through screening environmental DNA. The pig and poultry resistomes were very different in abundance and composition. There was a significant country effect on the resistomes, more so in pigs than in poultry. We found higher AMR loads in pigs, whereas poultry resistomes were more diverse. We detected several recently described, critical AMR genes, including mcr-1 and optrA, the abundance of which differed both between host species and between countries. We found that the total acquired AMR level was associated with the overall country-specific antimicrobial usage in livestock and that countries with comparable usage patterns had similar resistomes. However, functionally determined AMR genes were not associated with total drug use.

General information

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Organisations: Research Group for Genomic Epidemiology, National Food Institute, Department of Bio and Health Informatics, Genomic Epidemiology, Utrecht University, Wageningen University & Research, University of Geneva, Universidad Complutense, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Istituto Zooprofilattico Sperimentale del Lazio e della Toscana, Ghent University, University of Veterinary Medicine Hannover, Foundation, National Veterinary Research Institute, National Diagnostic Research Veterinary Institute, SAFOSO AG, Intomics A/S, Technical University of Denmark
Dissection of the antimicrobial and hemolytic activity of Cap18: Generation of Cap18 derivatives with enhanced specificity

Due to the rapid emergence of resistance to classical antibiotics, novel antimicrobial compounds are needed. It is desirable to selectively kill pathogenic bacteria without targeting other beneficial bacteria in order to prevent the negative clinical consequences caused by many broad-spectrum antibiotics as well as reducing the development of antibiotic resistance. Antimicrobial peptides (AMPs) represent an alternative to classical antibiotics and it has been previously demonstrated that Cap18 has high antimicrobial activity against a broad range of bacterial species. In this study we report the design of a positional scanning library consisting of 696 Cap18 derivatives and the subsequent screening for antimicrobial activity against Y. ruckeri, A. salmonicida, S. Typhimurium and L. lactis as well as for hemolytic activity measuring the hemoglobin release of horse erythrocytes. We show that the hydrophobic face of Cap18, in particular I13, L17 and I24, is essential for its antimicrobial activity against S. Typhimurium, Y. ruckeri, A. salmonicida, E. coli, P. aeruginosa, L. lactis, L. monocytogenes and E. faecalis. In particular, Cap18 derivatives harboring a I13D, L17D, L17P, I24D or I24N substitution lost their antimicrobial activity against any of the tested bacterial strains. In addition, we were able to generate species-specific Cap18 derivatives by particular amino acid substitutions either in the hydrophobic face at positions L6, L17, I20, and I27, or in the hydrophilic face at positions K16 and K18. Finally, our data showed the proline residue at position 29 to be essential for the inherent low hemolytic activity of Cap18 and that substitution of the residues K16, K23, or G21 by any hydrophobic residues enhances the hemolytic activity. This study demonstrates the potential of generating species-specific AMPs for the selective elimination of bacterial pathogens.
Direct whole-genome sequencing of Plasmodium falciparum specimens from dried erythrocyte spots

Background: Plasmodium falciparum malaria remains a major health burden and genomic research represents one of the necessary approaches for continued progress towards malaria control and elimination. Sample acquisition for this purpose is troublesome, with the majority of malaria-infected individuals living in rural areas, away from main infrastructure and the electrical grid. The aim of this study was to describe a low-tech procedure to sample P. falciparum specimens for direct whole genome sequencing (WGS), without use of electricity and cold-chain. Methods: Venous blood samples were collected from malaria patients in Bandim, Guinea-Bissau and leukocyte-depleted using Plasmodipur filters, the enriched parasite sample was spotted on Whatman paper and dried. The samples were stored at ambient temperatures and subsequently used for DNA-extraction. Ratios of parasite:human content of the extracted DNA was assessed by qPCR, and five samples with varying parasitaemia, were sequenced. Sequencing data were used to analyse the sample content, as well as sample coverage and depth as compared to the 3d7 reference genome. Results: qPCR revealed that 73% of
The 199 samples were applicable for WGS, as defined by a minimum ratio of parasite:human DNA of 2:1. WGS revealed an even distribution of sequence data across the 3d7 reference genome, regardless of parasitaemia. The acquired read depths varied from 16 to 99×, and coverage varied from 87.5 to 98.9% of the 3d7 reference genome. SNP-analysis of six genes, for which amplicon sequencing has been performed previously, confirmed the reliability of the WGS-data.

Conclusion: This study describes a simple filter paper based protocol for sampling P. falciparum from malaria patients for subsequent direct WGS, enabling acquisition of samples in remote settings with no access to electricity.

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BFI (2016): BFI-level 1
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Web of Science (2010): Indexed yes
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Prevalence and risk factors for CTX-M gram-negative bacteria in hospitalized patients at a tertiary care hospital in Kilimanjaro, Tanzania

Emergence and spread of extended spectrum beta-lactamase (ESBL)-producing gram-negative bacteria, mainly due to CTX-M, is a major global public health problem. Patients infected with ESBL-producing gram-negative bacteria have an increased risk of treatment failure and death. We investigated the prevalence and risk factors for CTX-M gram-negative bacteria isolated from clinical specimens of patients hospitalized at a tertiary care hospital in Kilimanjaro, Tanzania. Isolated gram-negative bacteria from inpatients admitted at Kilimanjaro Christian Medical Centre (KCMC) between August 2013 and August 2015 were fully genome sequenced. The prevalence of ESBL-producing gram-negative bacteria was determined based on the presence of bla_{CTX-M}. The odds ratio (OR) and risk factors for ESBL-producing gram-negative bacteria due to CTX-M were assessed using logistic regression models. The overall CTX-M prevalence (95% CI) was 13.6% (10.1–18.1). Adjusted for other factors, the OR of CTX-M gram-negative bacteria for patients previously hospitalized was 0.26 (0.08–0.88), p = 0.031; the OR for patients currently on antibiotics was 4.02 (1.29–12.58), p = 0.017; the OR for patients currently on ceftriaxone was 0.14 (0.04–0.46), p = 0.001; and the OR for patients with wound infections was 0.24 (0.09–0.61), p = 0.003. The prevalence of ESBL-producing gram-negative bacteria due to CTX-M in this setting is relatively low compared to other previous reports in similar settings. However, to properly stop further spread in the hospital, we recommend setting up a hospital surveillance system that takes full advantage of the available next-generation sequencing facility to routinely screen for all types of bacterial resistance genes.

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Organisations: Department of Bio and Health Informatics, Genomic Epidemiology, National Food Institute, Research Group for Genomic Epidemiology, Kilimanjaro Christian Medical Centre, Kilimanjaro Christian Medical University College, University of Copenhagen, East African Health Research Commission
Contributors: Sonda, T., Kumburu, H., van Zwetselaar, M., Alifrangis, M., Mmbaga, B. T., Lund, O., Møller Aarestrup, F., Kibiki, G.
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Comparative genomics of quinolone-resistant and susceptible Campylobacter jejuni of poultry origin from major poultry producing European countries (GENCAMP)

A total of 502 Campylobacter jejuni isolates from poultry in 12 different European countries (10 of them the largest poultry production countries in Europe) were whole genome sequenced to examine the genomic diversity of fluoroquinolone resistant (FQ-R) and susceptible (FQ-S) C. jejuni across the poultry producing European countries and to determine whether the emergence of fluoroquinolone resistance among C. jejuni is related to the transmission through countries or to
the selection through fluoroquinolone use in the individual countries. A high genomic diversity was observed. The isolates clustered in four main clusters. All trees revealed that the isolates were clustered according to the presence/absence of the gyrA mutations causing fluoroquinolone resistance and ST-types. The cgMLST trees of only FQ-R and FQ-S isolates showed that isolates from the same country of origin were distributed into multiple clusters similarly to the trees combining FQ-R and FQ-S isolates. The different phylogenetic methods, ranging from single nucleotide polymorphisms analysis to gene-by-gene approaches such as rMLST, cgMLST, wgMLST and core genome tree, provided concordant results, but it is not known which is the most accurate method for identifying the country of origin of the isolates. Allele frequency analysis of isolates under this study and a selection of previously published C. jejuni genomes in ENA showed association of geographical origin of poultry C. jejuni populations between Romania-Poland, Italy-Germany-England, Portugal-The Netherlands and USA-Luxemburg. Allele frequency and phylogenetic analysis indicated that the isolates from Finland were genetically different from C. jejuni populations from other European countries included in this study. Trade pattern and antimicrobial use in livestock were not significantly associated with allele frequency or populations of C. jejuni, but data available to investigate these associations were limited.

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Genomics-Based Identification of Microorganisms in Human Ocular Body Fluid
Advances in genomics have the potential to revolutionize clinical diagnostics. Here, we examine the microbiome of vitreous (intraocular body fluid) from patients who developed endophthalmitis following cataract surgery or intravitreal injection. Endophthalmitis is an inflammation of the intraocular cavity and can lead to a permanent loss of vision. As controls, we included vitreous from endophthalmitis-negative patients, balanced salt solution used during vitrectomy and DNA extraction blanks. We compared two DNA isolation procedures and found that an ultraclean production of reagents appeared to reduce background DNA in these low microbial biomass samples. We created a curated microbial genome database (>5700 genomes) and designed a metagenomics workflow with filtering steps to reduce DNA sequences originating from: (i) human hosts, (ii) ambiguousness/contaminants in public microbial reference genomes and (iii) the environment. Our metagenomic read classification revealed in nearly all cases the same microorganism that was determined in cultivation- and mass spectrometry-based analyses. For some patients, we identified the sequence type of the microorganism and antibiotic resistance genes through analyses of whole genome sequence (WGS) assemblies of isolates and metagenomic assemblies. Together, we conclude that genomics-based analyses of human ocular body fluid specimens can provide actionable information relevant to infectious disease management.

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Hospital Epidemiology of Methicillin-Resistant Staphylococcus aureus in a Tertiary Care Hospital in Moshi, Tanzania, as Determined by Whole Genome Sequencing

Objective. To determine molecular epidemiology of methicillin-resistant S. aureus in Tanzania using whole genome sequencing. Methods. DNA from 33 Staphylococcus species was recovered from subcultured archived Staphylococcus isolates. Whole genome sequencing was performed on IlluminaMiseq using paired-end 2x250 bp protocol. Raw sequence data were analyzed using online tools. Results. Full susceptibility to vancomycin and chloramphenicol was observed. Thirteen isolates (43.3%) resisted cefoxitin and other antimicrobials tested. Multilocus sequence typing revealed 13 different sequence types among the 30 S. aureus isolates, with ST-8 (n = seven, 23%) being the most common. Gene detection in S. aureus stains were as follows: mecA, 10 (33.3%); pvl, 5 (16.7%); tst, 2 (6.7%). The SNP difference among the six Tanzanian ST-8MRSA isolates ranged from 24 to 196 SNPs and from 16 to 446 SNPs when using the USA300_FPR3757 or the USA500 2395 as a reference, respectively. The mutation rate was 1.38 x 10(-11) SNPs/site/year or 1.4 x 10(-6) SNPs/site/year as estimated by USA300_FPR3757 or the USA500 2395, respectively. Conclusion. S. aureus isolates causing infections in hospitalized patients in Moshi are highly diverse and epidemiologically unrelated. Temporal phylogenetic analysis provided better resolution on transmission and introduction of MRSA and it may be
important to include this in future routines.

**General information**

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**Organisations:** National Food Institute, Research Group for Genomic Epidemiology, Department of Bio and Health Informatics, Genomic Epidemiology, KCRI Kilimanjaro Clinical Research Institute, University of Copenhagen  
**Contributors:** Kumburu, H. H., Sonda, T., Leekitcharoenphon, P., van Zwetselaar, M., Lukjancenko, O., Alifrangis, M., Lund, O., Mmbaga, B. T., Kibiki, G., Aarestrup, F. M.  
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- BFI (2016): BFI-level 1  
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- Web of Science (2016): Impact factor 2.476  
- BFI (2015): BFI-level 1  
- Scopus rating (2015): CiteScore 1.77 SJR 0.854 SNIP 0.799  
- Web of Science (2015): Impact factor 2.134  
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- BFI (2014): BFI-level 1  
- Scopus rating (2014): CiteScore 1.29 SJR 0.797 SNIP 0.777  
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- BFI (2013): BFI-level 1  
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- Scopus rating (2012): SJR 1.084 SNIP 0.872  
- Web of Science (2012): Impact factor 2.88  
- ISI indexed (2012): ISI indexed yes  
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- ISI indexed (2011): ISI indexed yes  
- Web of Science (2011): Indexed yes  
- BFI (2010): BFI-level 1  
- Scopus rating (2010): SJR 0.526 SNIP 0.488  
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- BFI (2009): BFI-level 1  
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Molecular epidemiology of virulence and antimicrobial resistance determinants in Klebsiella pneumoniae from hospitalised patients in Kilimanjaro, Tanzania

This study aimed to use whole-genome sequencing to determine virulence and antimicrobial resistance genes in K. pneumoniae isolated from patients in a tertiary care hospital in Kilimanjaro. K. pneumoniae isolates from patients attending Kilimanjaro Christian Medical Centre between August 2013 and August 2015 were fully genome-sequenced and analysed locally. Sequence analysis was done for identification of virulence and AMR genes. Plasmid and multi-locus sequence typing and capsular or capsular (K) typing were performed and phylogeny was done to ascertain K. pneumoniae relatedness. Stata 13 (College Station, TX, 77845, USA) was used to determine Cohen’s kappa coefficient of agreement between the phenotypically tested and sequence-predicted resistance. A total of 16 (47.1%) sequence types (STs) and 10 (29.4%) K types were identified in 30 (88.2%) and 17 (50.0%) of all analysed isolates, respectively. K. pneumoniae ST17 were 6 (17.6%). The commonest determinants were blaCTX-M-15 in 16 (47.1%) isolates, blashv in 30 (88.2%), blaOXA-1 in 8 (23.5%) and blatem1 in 18 (52.9%) isolates. Resistance genes for aminoglycosides were detected in 21 (61.8%) isolates, fluoroquinolones in 13 (38.2%) and quinolones 34 (100%). Ceftazidime and ceftriaxone showed the strongest agreement between phenotype- and sequence-based resistance results: 93.8%, kappa = 0.87 and p = 0.0002. Yersiniabactin determinant was detected in 12 (35.3%) of K. pneumoniae. The proportion of AMR and virulence determinants detected in K. pneumoniae is alarming. WGS-based diagnostic approach has showed promising potentials in clinical microbiology, hospital outbreak source tracing virulence and AMR detection at KCMC.
Campylobacter spp. are food- and water borne pathogens. While rather accurate estimates for these pathogens are available in industrialized countries, a lack of diagnostic capacity in developing countries limits accurate assessments of prevalence in many regions. Proficiency in the identification and susceptibility testing of these organisms is critical for surveillance and control efforts. The aim of the study was to assess performance for identification and susceptibility testing of thermo-tolerant Campylobacter among laboratories participating in the World Health Organization (WHO) Global Foodborne Infections Network (GFN) External Quality Assurance System (EQAS) over a nine year period. Participants (primarily national level laboratories) were encouraged to self-evaluate performance as part of continuous quality improvement. The ability to correctly identify Campylobacter spp. varied by year and ranged from 61.9 % (2008) to 90.7 %
(2012), and the ability to correctly perform antimicrobial susceptibility testing (AST) for Campylobacter spp. appeared to steadily increase from 91.4 % to 93.6 % in the test period (2009-2012). Poorest performance (60.0 % correct identification and 86.8 % correct AST results) was observed in African laboratories. Overall, approximately 10 % of laboratories reported either an incorrect identification or antibiogramme. As most participants were (supra)-national reference laboratories, these data raise significant concerns regarding capacity and proficiency at the local, clinical level. Addressing these diagnostic challenges is critical for both patient level management and broader surveillance and control efforts.

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BFI (2015): BFI-level 1
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Web of Science (2015): Indexed yes
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Scopus rating (2013): CiteScore 4.18 SJR 2.438 SNIP 1.63
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ISI indexed (2012): ISI indexed yes
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BFI (2011): BFI-level 1
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ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.343 SNIP 1.731
Web of Science (2010): Impact factor 4.22
Rapid and precise alignment of raw reads against redundant databases with KMA

Background: As the cost of sequencing has declined, clinical diagnostics based on next generation sequencing (NGS) have become reality. Diagnostics based on sequencing will require rapid and precise mapping against redundant databases because some of the most important determinants, such as antimicrobial resistance and core genome multilocus sequence typing (MLST) alleles, are highly similar to one another. In order to facilitate this, a novel mapping method, KMA (k-mer alignment), was designed. KMA is able to map raw reads directly against redundant databases, it also scales well for large redundant databases. KMA uses k-mer seeding to speed up mapping and the Needleman-Wunsch algorithm to accurately align extensions from k-mer seeds. Multi-mapping reads are resolved using a novel sorting scheme (ConClave scheme), ensuring an accurate selection of templates.

Results: The functionality of KMA was compared with SRST2, MGmapper, BWA-MEM, Bowtie2, Minimap2 and Salmon, using both simulated data and a dataset of Escherichia coli mapped against resistance genes and core genome MLST alleles. KMA outperforms current methods with respect to both accuracy and speed, while using a comparable amount of memory.

Conclusion: With KMA, it was possible map raw reads directly against redundant databases with high accuracy, speed and memory efficiency.

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BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.91 SJR 1.916 SNIP 1.185
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Scopus rating (2011): CiteScore 3.34 SJR 1.662 SNIP 1.19
Web of Science (2011): Impact factor 2.751
ISI indexed (2011): ISI indexed yes
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Scopus rating (2009): SJR 1.893 SNIP 1.295
Web of Science (2009): Indexed yes

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Web of Science (2008): Indexed yes

Scopus rating (2007): SJR 1.973 SNIP 1.12
Web of Science (2007): Indexed yes

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Scopus rating (2004): SJR 3.304 SNIP 1.723
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Typing of methicillin-resistant Staphylococcus aureus (MRSA) is important in infection control and surveillance. The current nomenclature of MRSA includes the genetic background of the S. aureus strain determined by multilocus sequence typing (MLST) or equivalent methods like spa typing and typing of the mobile genetic element staphylococcal cassette chromosome mec (SCCmec), which carries the mecA or mecC gene. Whereas MLST and spa typing are relatively simple, typing of SCCmec is less trivial because of its heterogeneity. Whole-genome sequencing (WGS) provides the essential data for typing of the genetic background and SCCmec, but so far, no bioinformatic tools for SCCmec typing have been available. Here, we report the development and evaluation of SCCmecFinder for characterization of the SCCmec element from S. aureus WGS data. SCCmecFinder is able to identify all SCCmec element types, designated I to XIII, with subtyping of SCCmec types IV (2B) and V (5C2). SCCmec elements are characterized by two different gene prediction approaches to achieve correct annotation, a Basic Local Alignment Search Tool (BLAST)-based approach and a k-mer-based approach. Evaluation of SCCmecFinder by using a diverse collection of clinical isolates (n = 93) showed a high typeability level of 96.7%, which increased to 98.9% upon modification of the default settings. In conclusion, SCCmecFinder can be an alternative to more laborious SCCmec typing methods and is freely available at https://cge.cbs.dtu.dk/services/SCCmecFinder. IMPORTANCE SCCmec in MRSA is acknowledged to be of importance not only because it contains the mecA or mecC gene but also for staphylococcal adaptation to different environments, e.g., in hospitals, the community, and livestock. Typing of SCCmec by PCR techniques has, because of its heterogeneity, been challenging, and whole-genome sequencing has only partially solved this since no good bioinformatic tools have been available. In this article, we describe the development of a new bioinformatic tool, SCCmecFinder, that includes most of the needs for infection control professionals and researchers regarding the interpretation of SCCmec elements. The software detects all of the SCCmec elements accepted by the International Working Group on the Classification of Staphylococcal Cassette Chromosome Elements, and users will be prompted if diverging and potential new elements are uploaded. Furthermore, SCCmecFinder will be curated and updated as new elements are found and it is easy to use and freely accessible.
The 22nd EURL-AR Proficiency Test - Enterococci, Staphylococci and E. coli 2017

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Contributors: Bortolaia, V., Karlsmose Pedersen, S., Hendriksen, R. S., Aarestrup, F. M.
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Validation of the register-based lifetime antimicrobial usage measurement for finisher batches based on comparison with recorded antimicrobial usage at farm level

Assessing the relationship between antimicrobial usage (AMU) and antimicrobial resistance (AMR) requires the accurate and precise utilisation of register data. Therefore, validation of register-based data is essential for evaluating the quality and, subsequently, the internal validity of studies based on the data. In this study, different smoothing methods for Veterinary Medicine Statistic Program database (VetStat)-records were validated by comparing these with farm-records. Comparison between measurements included accuracy as; completeness and correctness, and precision as; a relative difference of the error, correlation with Fisher's z transformation and reliability coefficient. The most valid methods of those examined were then used in re-analyses of the abundance of AMR genes in 10 finisher batches from a previous study. Improved accuracy was found when detailed smoothing methods were applied. Although the precision also increased, the effect was not as pronounced, as the usage estimate of all smoothing methods deviated moderately compared with the farm-registrations. Applying the most valid methods to the 10 finisher batches increased estimates of statistical model fit for aminoglycosides, lincosamides, tetracyclines and decreased estimates of statistical model fit for macrolides. The estimates of statistical model fit for sulfonamides and broad-spectrum penicillins remained the same. Through refined data transformation, VetStat-records can be used to calculate a daily amount of AMU per pig reflecting the true usage accurately and moderately precisely, which is the foundation for calculating lifetime AMU.

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Contributors: Dalhoff Andersen, V., Munk, P., de Knegt, L., Stengaard Jensen, M., Aarestrup, F. M., Vigre, H.
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BFI (2016): BFI-level 1
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BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.29 SJR 1.349 SNIP 1.052
Web of Science (2015): Impact factor 2.515
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.19 SJR 1.305 SNIP 1.016
Web of Science (2014): Impact factor 2.535
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BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.57 SJR 1.337 SNIP 1.113
Web of Science (2013): Impact factor 2.491
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.69 SJR 1.437 SNIP 1.17
Web of Science (2012): Impact factor 2.867
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Whole genome sequencing reveals high clonal diversity of Escherichia coli isolated from patients in a tertiary care hospital in Moshi, Tanzania

Background: Limited information regarding the clonality of circulating E. coli strains in tertiary care hospitals in low and middle-income countries is available. The purpose of this study was to determine the serotypes, antimicrobial resistance and virulence genes. Further, we carried out a phylogenetic tree reconstruction to determine relatedness of E. coli isolated from patients in a tertiary care hospital in Tanzania.

Methods: E. coli isolates from inpatients admitted at Kilimanjaro Christian Medical Centre between August 2013 and August 2015 were fully genome-sequenced at KCMC hospital. Sequence analysis was done for identification of resistance genes, Multi-Locus Sequence Typing, serotyping, and virulence genes. Phylogeny reconstruction using CSI Phylogeny was done to ascertain E. coli relatedness. Stata 13 (College Station, Texas 77,845 USA) was used to determine Cohen's kappa coefficient of agreement between the phenotypically tested and whole genome sequence predicted antimicrobial resistance.

Results: Out of 38 E. coli isolates, 21 different sequence types (ST) were observed. Eight (21.1%) isolates belonged to ST131; of which 7 (87.5%) were serotype O25:H4. Ten (18.4%) isolates belonged to ST10 clonal complex; of these, four (40.0%) were ST617 with serotype O89:H10. Twenty-eight (73.7%) isolates carried genes encoding beta-lactam resistance enzymes. On average, agreement across all drugs tested was 83.9%. Trimethoprim/sulphamethoxazole (co-trimoxazole) showed moderate agreement: 45.8%, kappa = 15% and p = 0.08. Amoxicillin-clavulanate showed strongest agreement: 87.5%, kappa = 74% and p = 0.0001. Twenty-two (57.9%) isolates carried virulence factors for host cells adherence and 25 (65.7%) for factors that promote E. coli immune evasion by increasing survival in serum. The phylogeny analysis showed that ST131 clustering close together whereas ST10 clonal complex had a very clear segregation of the
ST617 and a mix of the rest STs.

Conclusion: There is a high diversity of *E. coli* isolated from patients admitted to a tertiary care hospital in Tanzania. This underscores the necessity to routinely screen all bacterial isolates of clinical importance in tertiary health care facilities. WGS use for laboratory-based surveillance can be an effective early warning system for emerging pathogens and resistance mechanisms in LMICs.

**General information**

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Department of Biotechnology and Biomedicine, Center for Biological sequence analysis, Department of Bio and Health Informatics, Genomic Epidemiology, KCRI Kilimanjaro Clinical Research Institute, Copenhagen University Hospital, Kilimanjaro Christian Medical University College
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- Web of Science (2016): Impact factor 2.989
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**Adhesion of Escherichia coli under flow conditions reveals potential novel effects of FimH mutations**

FimH-mediated adhesion of *Escherichia coli* to bladder epithelium is a prerequisite for urinary tract infections. FimH is also essential for blood-borne bacterial dissemination, but the mechanisms are poorly understood. The purpose of this study was to assess the influence of different FimH mutations on bacterial adhesion using a novel adhesion assay, which models the physiological flow conditions bacteria are exposed to. We introduced 12 different point mutations in the mannose binding pocket of FimH in an *E. coli* strain expressing type 1 fimbriae only (MSC95-FimH). We compared the bacterial adhesion of each mutant across several commonly used adhesion assays, including agglutination of yeast, adhesion to mono- and tri-mannosylated substrates, and static adhesion to bladder epithelial and endothelial cells. We performed a comparison of these assays to a novel method that we developed to study bacterial adhesion to mammalian cells under flow conditions. We showed that *E. coli* MSC95-FimH adheres more efficiently to microvascular endothelium than to bladder epithelium, and that only endothelium supports adhesion at physiological shear stress. The results confirmed that mannose binding pocket mutations abrogated adhesion. We demonstrated that FimH residues E50 and T53 are crucial for adhesion under flow conditions. The coating of endothelial cells on biochips and modelling of physiological flow conditions enabled us to identify FimH residues crucial for adhesion. These results provide novel insights into screening methods to determine the effect of FimH mutants and potentially FimH antagonists.

**General information**

State: Published
Analysis of 28 Arcobacter genomes belonging to different species

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Universitat Rovira i Virgili
Contributors: Alba, P., Leekitcharoenphon, P., Hendriksen, R. S., Aarestrup, F. M., José, F. M.
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Analytical Profiling of Airplane Wastewater - a New Matrix for Mapping Worldwide Patterns of Drug Use and Abuse
There is limited knowledge on the global prescription and consumption patterns of therapeutic (TD) and illicit drugs (ID). Pooled urine analysis and wastewater-based epidemiology (WBE) has been used for local-based drug screening. It is, however, difficult to study the global epidemiology due to difficulties in obtaining samples. The aims of the study were to test the detectability of TD and ID in airplane wastewater samples categorized according to their geographical origin. Wastewater samples (n= 17) were collected from long-distance flights and prepared with enzymatic conjugate cleaving followed by either precipitation or solid phase extraction. Aliquots were analysed on various liquid chromatography – mass spectrometers. TDs were grouped according to their Anatomical Therapeutic Chemical (ATC) codes. Identification confidence was assigned to three levels based on variables including detection on multiple instruments and number of targets per compound. A total of 424 compounds were identified across all samples, distributed on 87 unique TD and 2 ID. Two principal components in a principal component analysis separated three clusters of wastewater samples corresponding to geographical origin of the airplanes with therapeutic subgroup ATC codes as variables. Airplane wastewater analysis is useful for identifying targets for WBE and toxicological analysis and explore drug use and abuse patterns.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen
Contributors: Mardal, M., Aarestrup, F. M., Rasmussen, B. S., Mollerup, C. B., Dalsgaard, P. W., Linnet, K.
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ISSN (Print): 1503-9552
An Assessment of Different Genomic Approaches for Inferring Phylogeny of Listeria monocytogenes

Background/objectives: Whole genome sequencing (WGS) has proven to be a powerful subtyping tool for foodborne pathogenic bacteria like L. monocytogenes. The interests of genome-scale analysis for national surveillance, outbreak detection or source tracking has been largely documented. The genomic data however can be exploited with many different bioinformatics methods like single nucleotide polymorphism (SNP), core-genome multi locus sequence typing (cgMLST), whole-genome multi locus sequence typing (wgMLST) or multi locus predicted protein sequence typing (MLPPST) on either core-genome (cgMLPPST) or pan genome (wgMLPPST). Currently, there are little comparisons studies of these different analytical approaches. Our objective was to assess and compare different genomic methods that can be implemented in order to cluster isolates of L monocytogenes.

Methods: The clustering methods were evaluated on a collection of 207 L. monocytogenes genomes of food origin representative of the genetic diversity of the Anses collection. The trees were then compared using robust statistical analyses.

Results: The backward comparability between conventional typing methods and genomic methods revealed a near-perfect concordance. The importance of selecting a proper reference when calling SNPs was highlighted, although distances between strains remained identical. The analysis also revealed that the topology of the phylogenetic trees between wgMLST and cgMLST were remarkably similar. The comparison between SNP and cgMLST or SNP and wgMLST approaches showed that the topologies of phylogenetic trees were statistically similar with an almost equivalent clustering.

Conclusion: Our study revealed high concordance between wgMLST, cgMLST, and SNP approaches which are all suitable for typing of L. monocytogenes. The comparable clustering is an important observation considering that the two approaches have been variously implemented among reference laboratories.

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Scopus rating (2017): CiteScore 4.19 SJR 1.699 SNIP 1.174
Bacterial whole genome-based phylogeny: construction of a new benchmarking dataset and assessment of some existing methods

Background
Whole genome sequencing (WGS) is increasingly used in diagnostics and surveillance of infectious diseases. A major application for WGS is to use the data for identifying outbreak clusters, and there is therefore a need for methods that can accurately and efficiently infer phylogenies from sequencing reads. In the present study we describe a new dataset that we have created for the purpose of benchmarking such WGS-based methods for epidemiological data, and also present an analysis where we use the data to compare the performance of some current methods.

Results
Our aim was to create a benchmark data set that mimics sequencing data of the sort that might be collected during an outbreak of an infectious disease. This was achieved by letting an E. coli hypermutator strain grow in the lab for 8 consecutive days, each day splitting the culture in two while also collecting samples for sequencing. The result is a data set consisting of 101 whole genome sequences with known phylogenetic relationship. Among the sequenced samples 51 correspond to internal nodes in the phylogeny because they are ancestral, while the remaining 50 correspond to leaves. We also used the newly created data set to compare three different online available methods that infer phylogenies from whole-genome sequencing reads: NDtree, CSI Phylogeny and REALPHY. One complication when comparing the output of these methods with the known phylogeny is that phylogenetic methods typically build trees where all observed sequences are placed as leafs, even though some of them are in fact ancestral. We therefore devised a method for post processing the inferred trees by collapsing short branches (thus relocating some leafs to internal nodes), and also present two new measures of tree similarity that takes into account the identity of both internal and leaf nodes.

Conclusions
Based on this analysis we find that, among the investigated methods, CSI Phylogeny had the best performance, correctly identifying 73% of all branches in the tree and 71% of all clades. We have made all data from this experiment (raw sequencing reads, consensus whole-genome sequences, as well as descriptions of the known phylogeny in a variety of formats) publicly available, with the hope that other groups may find this data useful for benchmarking and exploring the performance of epidemiological methods. All data is freely available at: https://cge.cbs.dtu.dk/services/evolution_data.php.
Characterization and genetic variation of vibrio cholerae isolated from clinical and environmental sources in Thailand

Cholera is still an important public health problem in several countries, including Thailand. In this study, a collection of clinical and environmental V. cholerae serogroup O1, O139, and non-O1/non-O139 strains originating from Thailand (1983 to 2013) was characterized to determine phenotypic and genotypic traits and to investigate the genetic relatedness. Using a combination of conventional methods and whole genome sequencing (WGS), 78 V. cholerae strains were identified.

WGS was used to determine the serogroup, biotype, virulence, mobile genetic elements, and antimicrobial resistance genes using online bioinformatics tools. In addition, phenotypic antimicrobial resistance was determined by the minimal inhibitory concentration (MIC) test. The 78 V. cholerae strains belonged to the following serogroups O1: (n = 44), O139 (n = 16) and non-O1/non-O139 (n = 18). Interestingly, we found that the typical El Tor O1 strains were the major cause of clinical cholera during 1983-2000 with two Classical O1 strains detected in 2000. In 2004-2010, the El Tor variant strains revealed genotypes of the Classical biotype possessing either only ctxB or both ctxB and rstR while they harbored tcpA of the El Tor biotype. Thirty O1 and eleven O139 clinical strains carried CTXφ (Cholera toxin) and tcpA as well four different pathogenic islands (PAIs). Beside non-O1/non-O139, the O1 environmental strains also presented chxA and Type Three Secretion System (TTSS). The in silico MultiLocus Sequence Typing (MLST) discriminated the O1 and O139 clinical strains from other serogroups and environmental strains. ST69 was dominant in the clinical strains belonging to the 7th pandemic clone. Non-O1/non-O139 and environmental strains showed various novel STs indicating genetic variation.

Multidrug-resistant (MDR) strains were observed and conferred resistance to ampicillin, azithromycin, nalidixic acid, sulfamethoxazole, tetracycline, and trimethoprim and harboured variants of the SXT elements. For the first time since 1986, the presence of V. cholerae O1 Classical was reported causing cholera outbreaks in Thailand. In addition, we found that V. cholerae O1 El Tor variant and O139 were pre-dominating the pathogenic strains in Thailand. Using WGS and bioinformatic tools to analyze both historical and contemporary V. cholerae circulating in Thailand provided a more detailed understanding of the V. cholerae epidemiology, which ultimately could be applied for control measures and management of cholera in Thailand.
Commentary: Benefits and risks of antimicrobial use in food-producing animals

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Scopus rating (2016): CiteScore 4.16 SJR 1.759 SNIP 1.161
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Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.15 SJR 1.869 SNIP 1.193
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BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.76 SJR 1.879 SNIP 1.148
Web of Science (2014): Impact factor 3.989
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BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.56 SJR 1.776 SNIP 0.949
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Web of Science (2013): Indexed yes
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Research output: Research - peer-review › Comment/debate – Annual report year: 2017
Detection of linezolid resistance due to the optrA gene in Enterococcus faecalis from poultry meat from the American continent (Colombia)

Three Enterococcus isolates obtained from retail chicken collected in 2010-11 as part of the Colombian Integrated Program for Antimicrobial Resistance Surveillance (COIPARS) showed reduced susceptibility towards linezolid (MIC 8 mg/L). This study aimed at characterizing the isolates resistant to linezolid and detecting the resistance mechanism. Strains were analysed in 2011-12 without successful detection of the resistance mechanism. All isolates were found negative for the cfr gene and no 23S rRNA mutations were detected. In 2016, with the novel resistance gene optrA being described, the WGS data were re-analysed using in silico genomic tools for confirmation of species, detection of virulence and resistance genes, MLST and SNP analyses and comparison of the genetic environment with the previously published plasmid pE349. Three Enterococcus faecalis isolates were found positive for the optrA gene encoding resistance to linezolid and phenicols. Additional screening of 37 enterococci strains from the same study did not detect any further positives. Typing showed that two of the isolates belong to ST59, while the last belongs to ST489. All isolates carry genes encoding resistance to macrolide-lincosamide-streptogramin B, tetracycline and phenicols. In addition, the ST489 isolate also carries genes conferring aminoglycoside resistance and is resistant to quinolones, but no plasmid-mediated gene was detected. The optrA gene regions of the three plasmids showed high similarity to the originally reported optrA-carrying plasmid pE349. To the best of our knowledge, this is the first description of the optrA gene in E. faecalis isolated from poultry meat in the Americas.

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Developing a framework to assess the cost-effectiveness of COMPARE - A global platform for the exchange of sequence-based pathogen data

Analysing the genomic data of pathogens with the help of next-generation sequencing (NGS) is an increasingly important part of disease outbreak investigations and helps guide responses. While this technology has already been successfully employed to elucidate and control disease outbreaks, wider implementation of NGS also depends on its cost-effectiveness. COMPARE - short for 'Collaborative Management Platform for detection and Analyses of (Re-) emerging and foodborne outbreaks’ - is a major project, funded by the European Union, to develop a global platform for sharing and analysing NGS data and thereby improve the rapid identification, containment and mitigation of emerging infectious diseases and foodborne outbreaks. This article introduces the project and presents the results of a review of the literature, composed of previous relevant cost-benefit and cost-effectiveness analyses. The authors also outline the implications for a methodological framework to assess the cost-effectiveness of COMPARE and similar systems.

General information
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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Emergence of Livestock-Associated Methicillin-Resistant Staphylococcus aureus Bloodstream Infections in Denmark

Background: Livestock-associated methicillin-resistant Staphylococcus aureus clonal complex 398 (LA-MRSA CC398) is causing an increasing number of skin and soft tissue infections (SSTIs) in Denmark and other European countries with industrial pig production. Yet, its impact on MRSA bloodstream infections (BSIs) has not been well studied. Methods: We investigated the clinical epidemiology of all human cases of LA-MRSA CC398 BSI during 2010-2015. Cases of LA-MRSA CC398 BSI were compared to cases of BSI caused by other types of MRSA and cases of SSTI caused by LA-MRSA CC398. Whole-genome sequence analysis was used to assess the phylogenetic relationship among LA-MRSA CC398 isolates from Danish pigs and cases of BSI and SSTI. Results: The number of LA-MRSA CC398 BSIs and SSTIs increased over the years, peaking in 2014, when LA-MRSA CC398 accounted for 16% (7/44) and 21% (211/985) of all MRSA BSIs and SSTIs, corresponding to 1.2 and 37.4 cases of BSI and SSTI per 1 000 000 person-years, respectively. Most patients with LA-MRSA CC398 BSI had no contact to livestock, although they tended to live in rural areas. LA-MRSA CC398 caused 24.3 BSIs per 1000 SSTIs among people with no livestock contact, which is similar to the ratio observed for other types of MRSA. Whole-genome sequence analysis showed that most of the BSI and SSTI isolates were closely related to Danish pig isolates. Conclusions: This study demonstrates that the increasing number of LA-MRSA CC398 BSIs occurred in parallel with a much larger wave of LA-MRSA CC398 SSTIs and an expanding pig reservoir.

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Web of Science (2016): Impact factor 8.216
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Epidemiology of Danish Aeromonas salmonicida subsp salmonicida in Fish Farms Using Whole Genome Sequencing

Furunculosis, a serious infection caused by the bacterium Aeromonas salmonicida subsp. salmonicida is common in sea-reared rainbow trout production in Denmark. Developing an effective control strategy requires knowledge of the epidemiology, as well as the genomic and virulent variability of the Danish A. salmonicida subsp. salmonicida isolates. To obtain this, the genomes of 101 A. salmonicida subsp. salmonicida, including 99 Danish isolates, one Scottish strain and
the type strain NCIMB 1102, were sequenced using the Illumina HiSeq platform. Isolates were de novo assembled, examined for presence of plasmids, virulence and iron acquisition proteins, genomic islands, and antibiotic resistance genes. Single Nucleotide Polymorphisms were aligned and subjected to Bayesian temporal phylogenetic and maximum likelihood tree reconstruction using the published genome of A. salmonicida subsp. salmonicida A449 as reference. Bayesian temporal phylogenetic reconstruction suggests that four major introductions of A. salmonicida subsp. salmonicida into Denmark have occurred. The introductions correlate with the freshwater and subsequent seawater expansion of rainbow trout production. Initial transmission of the bacterium could have been from seawater to freshwater or vice versa, and most minor clades include a mixture of strains from different fresh- and seawater farms. Genomic variation of A. salmonicida subsp. salmonicida mostly appeared to be associated with their plasmids and plasmid encoded virulence factors. Nine A. salmonicida subsp. salmonicida isolates harbored worldwide known antibiotic resistance genes against several antibiotics and there is an indication that 33% of the isolates contained the genomic island AsaGEI1b. These findings not only support the usefulness of whole genome sequencing for genetic studies of homogeneous bacteria in general, but provide novel information about the Danish A. salmonicida subsp. salmonicida population, with implications for vaccine development in efforts to better protect Danish rainbow trout in the future.

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Contributors: Bartkova, S., Leekitcharoenphon, P., Aarestrup, F. M., Dalsgaard, I.
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.16 SJR 1.759 SNIP 1.161
Web of Science (2016): Impact factor 4.076
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
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Web of Science (2015): Indexed yes
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Scopus rating (2014): CiteScore 3.76 SJR 1.879 SNIP 1.148
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Scopus rating (2013): CiteScore 2.63 SJR 1.106 SNIP 1.05
Web of Science (2013): Impact factor 2.544
ISI indexed (2013): ISI indexed yes
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ISI indexed (2012): ISI indexed yes
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Evaluating next-generation sequencing for direct clinical diagnostics in diarrhoeal disease

The accurate microbiological diagnosis of diarrhoea involves numerous laboratory tests and, often, the pathogen is not identified in time to guide clinical management. With next-generation sequencing (NGS) becoming cheaper, it has huge potential in routine diagnostics. The aim of this study was to evaluate the potential of NGS-based diagnostics through direct sequencing of faecal samples. Fifty-eight clinical faecal samples were obtained from patients with diarrhoea as part of the routine diagnostics at Hvidovre University Hospital, Denmark. Ten samples from healthy individuals were also included. DNA was extracted from faecal samples and sequenced on the Illumina MiSeq system. Species distribution was determined with MGmapper and NGS-based diagnostic prediction was performed based on the relative abundance of pathogenic bacteria and Giardia and detection of pathogen-specific virulence genes. NGS-based diagnostic results were compared to conventional findings for 55 of the diarrhoeal samples; 38 conventionally positive for bacterial pathogens, two positive for Giardia, four positive for virus and 11 conventionally negative. The NGS-based approach enabled detection of the same bacterial pathogens as the classical approach in 34 of the 38 conventionally positive bacterial samples and predicted the responsible pathogens in five of the 11 conventionally negative samples. Overall, the NGS-based approach enabled pathogen detection comparable to conventional diagnostics and the approach has potential to be extended for the detection of all pathogens. At present, however, this approach is too expensive and time-consuming for routine diagnostics.

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Evaluation of methods for the concentration and extraction of viruses from sewage in the context of metagenomic sequencing

Viral sewage metagenomics is a novel field of study used for surveillance, epidemiological studies, and evaluation of waste water treatment efficiency. In raw sewage human waste is mixed with household, industrial and drainage water, and virus particles are, therefore, only found in low concentrations. This necessitates a step of sample concentration to allow for sensitive virus detection. Additionally, viruses harbor a large diversity of both surface and genome structures, which makes universal viral genomic extraction difficult. Current studies have tackled these challenges in many different ways employing a wide range of viral concentration and extraction procedures. However, there is limited knowledge of the efficacy and inherent biases associated with these methods in respect to viral sewage metagenomics, hampering the development of this field. By the use of next generation sequencing this study aimed to evaluate the efficiency of four commonly applied viral concentration techniques (precipitation with polyethylene glycol, organic flocculation with skim milk, monolithic adsorption filtration and glass wool filtration) and extraction methods (Nucleospin RNA XS, QIAamp Viral RNA Mini Kit, NucliSENSTM miniMAG®) to determine the virome in a sewage sample. We found a significant influence of concentration and extraction protocols on the detected virome. The viral richness was largest in samples extracted with QIAamp Viral RNA Mini Kit or PowerViral® Environmental RNA/DNA Isolation Kit. Highest viral specificity were found in samples concentrated by precipitation with polyethylene glycol or extracted with Nucleospin RNA XS. Detection of viral pathogens depended on the method used. These results contribute to the understanding of method associated biases, within the field of viral sewage metagenomics, making evaluation of the current literature easier and helping with the design of future studies.

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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
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BFI (2015): BFI-level 1
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Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
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BFI (2013): BFI-level 1
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Global Microbial Identifier

Human and animal populations are increasingly confronted with emerging and re-emerging infections and often such infections are exchanged between these populations, e.g. through food. A more effective and uniform approach to the prevention of these microbial threats is essential. The technological advances in the next generation sequencing field and decreasing costs of these tests provide novel opportunities in understanding the dynamics of infection—even in real time—through the analysis of microbial genome diversity. The projected significant increase in whole (microbial) genome sequencing (WGS) will likely also enable a much better understanding of the pathogenesis of the infection and the molecular basis of the host response to infection. But the full potential of these advances will only transpire if the data in this area become transferable and thereby comparable, preferably in open-source systems. There is therefore an obvious need to develop a global system of whole microbial genome databases to aggregate, share, mine and use microbiological genomic data, to address global public health and clinical challenges, and most importantly to identify and diagnose infectious diseases. The global microbial identifier (GMI) initiative, aims to build a database of whole microbial genome sequencing data linked to relevant metadata, which can be used to identify microorganisms, their communities and the diseases they cause. It would be a platform for storing whole genome sequencing (WGS) data of microorganisms, for the identification of relevant genes and for the comparison of genomes to detect outbreaks and emerging pathogens. To harness the full potential of WGS, a shared global database of genomes linked to relevant metadata and the necessary software tools needs to be generated, hence the global microbial identifier (GMI) initiative. This tool will ideally be used in amongst others in the diagnosis of infectious diseases in humans and animals, in the identification of microorganisms in food and environment, and to track and trace microbial agents in all arenas globally. This will require standardization and extensive investments in computational analytical tools. In addition, the wider introduction of WGS in clinical diagnostics can accelerate developments in health care in many poor countries. This overview describes the growing network of stakeholders behind GMI, the contours of the database, and the IT structures needed to serve the GMI user community. It discusses what essentially can be done by a global GMI tool and how the GMI organization could help achieve these goals.

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Pages: 13-31
High throughput resistance profiling of Plasmodium falciparum infections based on custom dual indexing and Illumina next generation sequencing-technology

Genetic polymorphisms in P. falciparum can be used to indicate the parasite’s susceptibility to antimalarial drugs as well as its geographical origin. Both of these factors are key to monitoring development and spread of antimalarial drug resistance. In this study, we combine multiplex PCR, custom designed dual indexing and Miseq sequencing for high throughput SNP-profiling of 457 malaria infections from Guinea-Bissau, at the cost of 10 USD per sample. By amplifying and sequencing 15 genetic fragments, we cover 20 resistance-conferring SNPs occurring in pfcr, pfmdr1, pfdfhr, pfdfps, as well as the entire length of pfK13, and the mitochondrial barcode for parasite origin. SNPs of interest were sequenced with an average depth of 2,043 reads, and bases were called for the various SNP-positions with a p-value below 0.05, for 89.8-100% of samples. The SNP data indicates that artemisinin resistance-conferring SNPs in pfK13 are absent from the studied area of Guinea-Bissau, while the pfmdr1 86 N allele is found at a high prevalence. The mitochondrial barcodes are unanimous and accommodate a West African origin of the parasites. With this method, very reliable high throughput surveillance of antimalarial drug resistance becomes more affordable than ever before.
Hospital epidemiology of methicillin-resistant Staphylococcus aureus (MRSA) in a tertiary care hospital in Moshi Tanzania as determined by whole genome sequencing

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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.55 SJR 1.583 SNIP 1.182
Web of Science (2016): Impact factor 2.85
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.4 SJR 1.559 SNIP 1.256
Web of Science (2015): Impact factor 2.519
BFI (2014): BFI-level 2
Meta-analysis of proportion estimates of extended-spectrum-beta-lactamase-producing Enterobacteriaceae in East Africa hospitals

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MGmapper: Reference based mapping and taxonomy annotation of metagenomics sequence reads

An increasing amount of species and gene identification studies rely on the use of next generation sequence analysis of either single isolate or metagenomics samples. Several methods are available to perform taxonomic annotations and a previous metagenomics benchmark study has shown that a vast number of false positive species annotations are a
problem unless thresholds or post-processing are applied to differentiate between correct and false annotations. MGmapper is a package to process raw next generation sequence data and perform reference based sequence assignment, followed by a post-processing analysis to produce reliable taxonomy annotation at species and strain level resolution. An in-vitro bacterial mock community sample comprised of 8 genuses, 11 species and 12 strains was previously used to benchmark metagenomics classification methods. After applying a post-processing filter, we obtained 100% correct taxonomy assignments at species and genus level. A sensitivity and precision at 75% was obtained for strain level annotations. A comparison between MGmapper and Kraken at species level, shows MGmapper assigns taxonomy at species level using 84.8% of the sequence reads, compared to 70.5% for Kraken and both methods identified all species with no false positives. Extensive read count statistics are provided in plain text and excel sheets for both rejected and accepted taxonomy annotations. The use of custom databases is possible for the command-line version of MGmapper, and the complete pipeline is freely available as a bitbucket package (https://bitbucket.org/genomicepidemiology/mgmapper). A web-version (https://cge.cbs.dtu.dk/services/MGmapper) provides the basic functionality for analysis of small fastq datasets.

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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.32 SJR 1.427 SNIP 1.136
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.54 SJR 1.559 SNIP 1.148
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.94 SJR 1.772 SNIP 1.153
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
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ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.58 SJR 2.425 SNIP 1.233
Web of Science (2011): Impact factor 4.092
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Web of Science (2011): Indexed yes
Patterns of infections, aetiological agents, and antimicrobial resistance at a tertiary care hospital in northern Tanzania

Objective
To determine the causative agents of infections and their antimicrobial susceptibility at a tertiary care hospital in Moshi, Tanzania, to guide optimal treatment.

Methods
A total of 590 specimens (stool (56), sputum (122), blood (126) and wound swabs (286)) were collected from 575 patients admitted in the medical and surgical departments. The bacterial species were determined by conventional methods and disk diffusion was used to determine the antimicrobial susceptibility pattern of the bacteria isolates.

Results
A total of 249 (42.2%) specimens were culture-positive yielding a total of 377 isolates. A wide range of bacteria was isolated, the most predominant being Gram-negative bacteria: Proteus spp. (n=48, 12.7%), Escherichia coli (n=44, 11.7%), Pseudomonas spp. (n=40, 10.6%), and Klebsiella spp (n=38, 10.1%). Wound infections were characterised by multiple isolates (n=293, 77.7%), with the most frequent being Proteus spp. (n=44, 15%), Pseudomonas (n=37, 12.6%), Staphylococcus (n=29, 9.9%), and Klebsiella spp. (n=28, 9.6%). All S. aureus tested were resistant to penicillin (n=22, 100%) and susceptible to vancomycin. Significant resistance to cephalosporins such as cefazolin (n=62, 72.9%), ceftriaxone (n=44, 51.8%) and ceftazidime (n=40, 37.4%) was observed in Gram-negative bacteria; as well as resistance to cefoxitin (n=6, 27.3%) in Staphylococcus aureus.

Conclusion
The study has revealed a wide range of causative agents, with an alarming rate of resistance to the commonly used antimicrobial agents. Furthermore, the bacterial spectrum differs from those often observed in high-income countries. This highlights the imperative of regular generation of data on aetiological agents and their antimicrobial susceptibility patterns especially in infectious disease endemic settings. The key steps would be to ensure the diagnostic capacity at a sufficient number of sites and implement structures to routinely exchange, compare, analyse and report data. Sentinel sites (hospitals) across the country (and region) should report on a representative subset of bacterial species and their susceptibility to drugs at least annually. A central organizing body should collate the data and report to relevant national and international stakeholders.

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Contributors: Kumburu, H. H., Sonda, T., Mmbaga, B. T., Alifrangis, M., Lund, O., Kibiki, G., Aarestrup, F. M.
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Patterns of infections, aetiological agents, and antimicrobial resistance at a tertiary care hospital in northern Tanzania

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Web of Science (2017): Impact factor 2.541
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Scopus rating (2016): CiteScore 2.55 SJR 1.583 SNIP 1.182
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BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.4 SJR 1.559 SNIP 1.256
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BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.3 SJR 1.315 SNIP 1.102
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BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 2.7 SJR 1.599 SNIP 1.173
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Web of Science (2012): Impact factor 2.938
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 2.78 SJR 1.576 SNIP 1.133
Web of Science (2011): Impact factor 2.795
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BFI (2010): BFI-level 2
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Web of Science (2010): Impact factor 2.841
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.276 SNIP 1.27
BFI (2008): BFI-level 2
PointFinder: a novel web tool for WGS-based detection of antimicrobial resistance associated with chromosomal point mutations in bacterial pathogens

Background
Antibiotic resistance is a major health problem, as drugs that were once highly effective no longer cure bacterial infections. WGS has previously been shown to be an alternative method for detecting horizontally acquired antimicrobial resistance genes. However, suitable bioinformatics methods that can provide easily interpretable, accurate and fast results for antimicrobial resistance associated with chromosomal point mutations are still lacking.

Methods
Phenotypic antimicrobial susceptibility tests were performed on 150 isolates covering three different bacterial species: Salmonella enterica, Escherichia coli and Campylobacter jejuni. The web-server ResFinder-2.1 was used to identify acquired antimicrobial resistance genes and two methods, the novel PointFinder (using BLAST) and an in-house method (mapping of raw WGS reads), were used to identify chromosomal point mutations. Results were compared with phenotypic antimicrobial susceptibility testing results. Results
A total of 685 different phenotypic tests associated with chromosomal resistance to quinolones, polymyxin, rifampicin, macrolides and tetracyclines resulted in 98.4% concordance. Eleven cases of disagreement between tested and predicted susceptibility were observed: two C. jejuni isolates with phenotypic fluoroquinolone resistance and two with phenotypic erythromycin resistance and five colistin-susceptible E. coli isolates with a detected pmrB V161G mutation when assembled with Velvet, but not when using SPAdes or when mapping the reads.

Conclusions
PointFinder proved, with high concordance between phenotypic and predicted antimicrobial susceptibility, to be a user-friendly web tool for detection of chromosomal point mutations associated with antimicrobial resistance.
Prevalence and risk factors of CTX-M Enterobacteriaceae in hospitalised patients at a tertiary hospital in Kilimanjaro, Tanzania

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Scopus rating (2015): CiteScore 2.4 SJR 1.559 SNIP 1.256
Web of Science (2015): Impact factor 2.519
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Web of Science (2013): Impact factor 2.302
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The 20th EURL-AR Proficiency Test - Enterococci, Staphylococci and E. coli 2016

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Contributors: Bortolaia, V., Karlsmose Pedersen, S., Roer, L., Cavaco, L., Hendriksen, R. S., Aarestrup, F. M.
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Research output: Commissioned › Report – Annual report year: 2017

The association between measurements of antimicrobial use and resistance in the faeces microbiota of finisher batches

The objectives were to present three approaches for calculating antimicrobial (AM) use in pigs that take into account the rearing period and rearing site, and to study the association between these measurements and phenotypical resistance and abundance of resistance genes in faecal samples from 10 finisher batches. The AM use was calculated relative to the rearing period of the batches as (i) 'Finisher Unit Exposure' at unit level, (ii) 'Lifetime Exposure' at batch level and (iii) 'Herd Exposure' at herd level. A significant effect on the occurrence of tetracycline resistance measured by cultivation was identified for Lifetime Exposure for the AM class: tetracycline. Furthermore, for Lifetime Exposure for the AM classes: macrolide, broad-spectrum penicillin, sulfonamide and tetracycline use as well as Herd Unit Exposure for the AM classes: aminoglycoside, lincosamide, macrolide, β-lactam, sulfonamide and tetracycline. No effect was observed for Finisher Unit Exposure. Overall, the study shows that Lifetime Exposure is an efficient measurement of AM use in finisher batches, and has a significant effect on the occurrence of resistance, measured either by cultivation or metagenomics.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Contributors: Dalhoff Andersen, V., de Knegt, L., Munk, P., Jensen, M. S., Agersø, Y., Aarestrup, F. M., Vigre, H.
The CGE Tool Box

As whole genome sequence data of microorganisms are becoming easily accessible and cheap to produce, a transformation of the traditional methods used for typing, phenotyping and phylogenetic analysis of microorganisms is on the way. Following the anticipation that most clinical microbiological and food safety laboratories will soon have a sequencer in use on a daily basis, there is a growing need for easy-to-use bioinformatics methods that can quickly convert the sequence data into useful information on, e.g., the type of bacteria, whether it is resistant towards any types of antibiotics, and whether it is part of an outbreak. The Center for Genomic Epidemiology, which is located at the Technical University of Denmark, has since its beginning in 2010 developed such bioinformatics methods and made them freely available as web-services. These web-services and their use is the focus of this chapter.

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The role of whole genome sequencing in antimicrobial susceptibility testing of bacteria: report from the EUCAST Subcommittee
Whole genome sequencing (WGS) offers the potential to predict antimicrobial susceptibility from a single assay. The European Committee on Antimicrobial Susceptibility Testing established a subcommittee to review the current development status of WGS for bacterial antimicrobial susceptibility testing (AST). The published evidence for using WGS as a tool to infer antimicrobial susceptibility accurately is currently either poor or non-existent and the evidence /
knowledge base requires significant expansion. The primary comparators for assessing genotypic-phenotypic concordance from WGS data should be changed to epidemiological cut-off values in order to improve differentiation of wild-type from non-wild-type isolates (harbouring an acquired resistance). Clinical breakpoints should be a secondary comparator. This assessment will reveal whether genetic predictions could also be used to guide clinical decision making. Internationally agreed principles and quality control (QC) metrics will facilitate early harmonization of analytical approaches and interpretive criteria for WGS-based predictive AST. Only data sets that pass agreed QC metrics should be used in AST predictions. Minimum performance standards should exist and comparative accuracies across different WGS laboratories and processes should be measured. To facilitate comparisons, a single public database of all known resistance loci should be established, regularly updated and strictly curated using minimum standards for the inclusion of resistance loci. For most bacterial species the major limitations to widespread adoption for WGS-based AST in clinical laboratories remain the current high-cost and limited speed of inferring antimicrobial susceptibility from WGS data as well as the dependency on previous culture because analysis directly on specimens remains challenging. For most bacterial species there is currently insufficient evidence to support the use of WGS-inferred AST to guide clinical decision making. WGS-AST should be a funding priority if it is to become a rival to phenotypic AST. This report will be updated as the available evidence increases.

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- Web of Science (2017): Impact factor 5.394
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- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 3.99 SJR 2.424 SNIP 1.757
- Web of Science (2016): Impact factor 5.292
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): CiteScore 5.11 SJR 2.637 SNIP 1.996
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): CiteScore 5.49 SJR 2.73 SNIP 2.22
- Web of Science (2014): Impact factor 5.768
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): CiteScore 4.92 SJR 2.306 SNIP 1.852
- Web of Science (2013): Impact factor 5.197
- ISI indexed (2013): ISI indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): CiteScore 3.93 SJR 1.868 SNIP 1.483
- Web of Science (2012): Impact factor 4.578
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
Viral indicators for fecal contamination - a one-year viral metagenomic study of treatment efficiency in Danish waste water treatment plants

Viral pathogens in irrigation water are a major threat to public health due to their possibility to cause disease in humans. When using reclaimed water for irrigation it is therefore important to make sure that the water is free from pathogens which can contaminate the crops. In this study we are therefore using metagenomics sequencing with the aim to map the virome in different water sources. In addition we investigate the possibility to use Human Adenovirus (HAdV) or JC Polyomavirus (JCPyV) as indicator for human fecal contamination. Water has been sampled monthly throughout the treatment process from two urban waste water treatment plants in Copenhagen. All samples are investigated for their viral content and the presence of pathogens by metagenomic sequencing and analyzed specifically for HAdV, JCPyV, norovirus GI and GII (NoV GI and GII) using quantitative (q)PCR. Preliminary qPCR results showed that the average concentration for HAdV within a sample is higher than the average concentration of NoV GI and GII. HAdV could therefore be a good indicator for human fecal contamination in water. The initial analysis of the metagenomic data identifies viruses in all water sources. However, the number of identified pathogenic viral species decreases with treatment of the waste water. Further bioinformatic analyses will investigate the seasonal variations of viral composition within a sample as well as the effect of the treatment system. Updated qPCR and metagenomics data will be presented.

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Contributors: Hellmér, M., Stranddorf, K., Seidel, M., Aarestrup, F. M., Schultz, A. C.
A Bacterial Analysis Platform: An Integrated System for Analysing Bacterial Whole Genome Sequencing Data for Clinical Diagnostics and Surveillance

Recent advances in whole genome sequencing have made the technology available for routine use in microbiological laboratories. However, a major obstacle for using this technology is the availability of simple and automatic bioinformatics tools. Based on previously published and already available web-based tools we developed a single pipeline for batch uploading of whole genome sequencing data from multiple bacterial isolates. The pipeline will automatically identify the bacterial species and, if applicable, assemble the genome, identify the multilocus sequence type, plasmids, virulence genes and antimicrobial resistance genes. A short printable report for each sample will be provided and an Excel spreadsheet containing all the metadata and a summary of the results for all submitted samples can be downloaded. The pipeline was benchmarked using datasets previously used to test the individual services. The reported results enable a rapid overview of the major results, and comparing that to the previously found results showed that the platform is reliable and able to correctly predict the species and find most of the expected genes automatically. In conclusion, a combined bioinformatics platform was developed and made publicly available, providing easy-to-use automated analysis of bacterial whole genome sequencing data. The platform may be of immediate relevance as a guide for investigators using whole genome sequencing for clinical diagnostics and surveillance. The platform is freely available at: https://cge.cbs.dtu.dk/services/CGEpipeline-1.1 and it is the intention that it will continue to be expanded with new features as these become available.
A Livestock-Associated, Multidrug-Resistant, Methicillin-Resistant Staphylococcus aureus Clonal Complex 97 Lineage Spreading in Dairy Cattle and Pigs in Italy

Pandemic methicillin-resistant Staphylococcus aureus (MRSA) clonal complex 97 (CC97) lineages originated from livestock-to-human host jumps. In recent years, CC97 has become one of the major MRSA lineages detected in Italian farmed animals. The aim of this study was to characterize and analyze differences in MRSA and methicillin-susceptible S. aureus (MSSA) mainly of swine and bovine origins. Forty-seven CC97 isolates, 35 MRSA isolates, and 6 MSSA isolates from different Italian pig and cattle holdings; 5 pig MRSA isolates from Germany; and 1 human MSSA isolate from Spain were characterized by macrorestriction pulsed-field gel electrophoresis (PFGE) analysis, multilocus sequence typing (MLST), spa typing, staphylococcal cassette chromosome mec (SCCmec) typing, and antimicrobial resistance pattern analysis. Virulence and resistance genes were investigated by PCR and microarray analysis. Most of the isolates were SCCmec type V (SCCmec V), except for two German MRSA isolates (SCCmec III). Five main clusters were identified by PFGE, with the German isolates (clusters I and II) showing 60.5% similarity with the Italian isolates, most of which (68.1%) grouped into cluster V. All CC97 isolates were Panton-Valentine leukocidin (PVL) negative, and a few (n = 7) tested positive for sak or scn. All MRSA isolates were multidrug resistant (MDR), and the main features were erm(B)- or erm(C)-mediated (n = 18) macrolide-lincosamide-streptogramin B resistance, vga(A)-mediated (n = 37) pleuromutilin resistance, fluoroquinolone resistance (n = 33), tet(K) in 32/37 tet(M)-positive isolates, and blaZ in almost all MRSA isolates. Few host-associated differences were detected among CC97 MRSA isolates: their extensive MDR nature in both pigs and dairy cattle may be a consequence of a spillback from pigs of a MRSA lineage that originated in cattle as MSSA and needs further investigation. Measures should be implemented at the farm level to prevent spillover to humans in intensive farming areas.

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A sampling and metagenomic sequencing-based methodology for monitoring antimicrobial resistance in swine herds

Objectives
Reliable methods for monitoring antimicrobial resistance (AMR) in livestock and other reservoirs are essential to understand the trends, transmission and importance of agricultural resistance. Quantification of AMR is mostly done using culture-based techniques, but metagenomic read mapping shows promise for quantitative resistance monitoring.

Methods
We evaluated the ability of: (i) MIC determination for Escherichia coli; (ii) cfu counting of E. coli; (iii) cfu counting of aerobic bacteria; and (iv) metagenomic shotgun sequencing to predict expected tetracycline resistance based on known antimicrobial consumption in 10 Danish integrated slaughter pig herds. In addition, we evaluated whether fresh or manure floor samples constitute suitable proxies for intestinal sampling, using cfu counting, qPCR and metagenomic shotgun sequencing.

Results
Metagenomic read-mapping outperformed cultivation-based techniques in terms of predicting expected tetracycline resistance based on antimicrobial consumption. Our metagenomic approach had sufficient resolution to detect antimicrobial-induced changes to individual resistance gene abundances. Pen floor manure samples were found to represent rectal samples well when analysed using metagenomics, as they contain the same DNA with the exception of a few contaminating taxa that proliferate in the extraintestinal environment.

Conclusions
We present a workflow, from sampling to interpretation, showing how resistance monitoring can be carried out in swine herds using a metagenomic approach. We propose metagenomic sequencing should be part of routine livestock resistance monitoring programmes and potentially of integrated One Health monitoring in all reservoirs.
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Web of Science (2017): Impact factor 5.217
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
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Web of Science (2015): Impact factor 4.919
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Web of Science (2014): Indexed yes
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Web of Science (2011): Indexed yes
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Scopus rating (2010): SJR 2.161 SNIP 1.643
Web of Science (2010): Impact factor 4.859
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.902 SNIP 1.615
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.076 SNIP 1.506
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.744 SNIP 1.509
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.771 SNIP 1.437
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.768 SNIP 1.5
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.435 SNIP 1.465
Web of Science (2004): Indexed yes
Next generation sequencing (NGS) may be an alternative to phenotypic susceptibility testing for surveillance and clinical diagnosis. However, current bioinformatics methods may be associated with false positives and negatives. In this study, a novel mapping method was developed and benchmarked to two different methods in current use for identification of antibiotic resistance genes in bacterial WGS data. A novel method, KmerResistance, which examines the co-occurrence of k-mers between the WGS data and a database of resistance genes, was developed. The performance of this method was compared with two previously described methods; ResFinder and SRST2, which use an assembly/BLAST method and BWA, respectively, using two datasets with a total of 339 isolates, covering five species, originating from the Oxford University Hospitals NHS Trust and Danish pig farms. The predicted resistance was compared with the observed phenotypes for all isolates. To challenge further the sensitivity of the in silico methods, the datasets were also downsampled to 1% of the reads and reanalysed. The best results were obtained by identification of resistance genes by mapping directly against the raw reads. This indicates that information might be lost during assembly. KmerResistance performed significantly better than the other methods, when data were contaminated or only contained few sequence reads. Read mapping is superior to assembly-based methods and the new KmerResistance seemingly outperforms currently available methods particularly when including datasets with few reads.
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Web of Science (2015): Impact factor 4.919
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.61 SJR 2.298 SNIP 1.765
Web of Science (2014): Impact factor 5.313
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BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.7 SJR 2.479 SNIP 1.824
Web of Science (2013): Impact factor 5.439
ISI indexed (2013): ISI indexed yes
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Web of Science (2012): Impact factor 5.338
ISI indexed (2012): ISI indexed yes
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BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.24 SJR 2.341 SNIP 1.769
Web of Science (2011): Impact factor 5.068
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.161 SNIP 1.643
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Scopus rating (2009): SJR 1.902 SNIP 1.615
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.076 SNIP 1.506
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.744 SNIP 1.509
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.771 SNIP 1.437
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.768 SNIP 1.5
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.435 SNIP 1.465
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.367 SNIP 1.338
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.4 SNIP 1.284
Scopus rating (2001): SJR 1.388 SNIP 1.232
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.113 SNIP 1.248
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.111 SNIP 1.388

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Comparative genomics of toxigenic and non-toxigenic Staphylococcus hyicus

The most common causative agent of exudative epidermitis (EE) in pigs is Staphylococcus hyicus. S. hyicus can be grouped into toxigenic and non-toxigenic strains based on their ability to cause EE in pigs and specific virulence genes have been identified. A genome wide comparison between non-toxigenic and toxigenic strains has never been performed. In this study, we sequenced eleven toxigenic and six non-toxigenic S. hyicus strains and performed comparative genomic and phylogenetic analysis. Our analyses revealed two genomic regions encoding genes that were predominantly found in toxigenic strains and are predicted to encode for virulence determinants for EE. All toxigenic strains encoded for one of the exfoliative toxins ExhA, ExhB, ExhC, or ExhD. In addition, one of these regions encoded for an ADP-ribosyltransferase (EDIN, epidermal cell differentiation inhibitor) and a novel putative RNase toxin (polymorphic toxin) and was associated with the gene encoding ExhA. A clear differentiation between toxigenic and non-toxigenic strains based on genomic and phylogenetic analyses was not apparent. The results of this study support the observation that exfoliative toxins of S. hyicus and S. aureus are located on genetic elements such as pathogenicity islands, phages, prophages and plasmids.

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Contributors: Leekitcharoenphon, P., Pamp, S. J., Andresen, L. O., Aarestrup, F. M.
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Consolidating and Exploring Antibiotic Resistance Gene Data Resources

The unrestricted use of antibiotics has resulted in rapid acquisition of antibiotic resistance (AR) and spread of multidrug-resistant (MDR) bacterial pathogens. With the advent of next-generation sequencing technologies and their application in understanding MDR pathogen dynamics, it has become imperative to unify AR gene data resources for easy accessibility for researchers. However, due to the absence of a centralized platform for AR gene resources, availability, consistency, and accuracy of information vary considerably across different databases. In this article, we explore existing AR gene data resources in order to make them more visible to the clinical microbiology community, to identify their limitations, and to propose potential solutions.
Fatal septicemia linked to transmission of MRSA clonal complex 398 in hospital and nursing home, Denmark

We describe 2 fatal cases of methicillin-resistant Staphylococcus aureus (MRSA) clonal complex 398 septicemia in persons who had no contact with livestock. Whole-genome sequencing of the isolated MRSA strains strongly suggest that both were of animal origin and that the patients had been infected through 2 independent person-to-person transmission chains.

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Scopus rating (2017): CiteScore 4.78 SJR 3.278 SNIP 1.916
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.92 SJR 3.428 SNIP 2.198
Web of Science (2016): Impact factor 8.222
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.23 SJR 3.101 SNIP 2.012
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.59 SJR 3.509 SNIP 2.406
Web of Science (2014): Impact factor 6.751
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BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.68 SJR 3.254 SNIP 2.266
Web of Science (2013): Impact factor 7.327
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.25 SJR 2.858 SNIP 2.131
Web of Science (2012): Impact factor 5.993
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 4.46 SJR 2.785 SNIP 2.19
Web of Science (2011): Impact factor 6.169
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.021 SNIP 2.319
Web of Science (2010): Impact factor 6.859
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.168 SNIP 2.701
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.231 SNIP 2.277
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.709 SNIP 2.341
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.879 SNIP 2.345
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.816 SNIP 2.297
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.683 SNIP 2.562
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.267 SNIP 2.373
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 3.094 SNIP 2.545
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.346 SNIP 2.904
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.522 SNIP 2.856
Scopus rating (1999): SJR 1.71 SNIP 2.61
Global Genomic Epidemiology of *Salmonella enterica* Serovar Typhimurium DT104

It has been 30 years since the initial emergence and subsequent rapid global spread of multidrug-resistant *Salmonella enterica* serovar Typhimurium DT104 (MDR DT104). Nonetheless, its origin and transmission route have never been revealed. We used whole-genome sequencing (WGS) and temporally structured sequence analysis within a Bayesian framework to reconstruct temporal and spatial phylogenetic trees and estimate the rates of mutation and divergence times of 315 *S* Typhimurium DT104 isolates sampled from 1969 to 2012 from 21 countries on six continents. DT104 was estimated to have emerged initially as antimicrobial susceptible in ~1948 (95% credible interval [CI], 1934 to 1962) and later became MDR DT104 in ~1972 (95% CI, 1972 to 1988) through horizontal transfer of the 13-kb Salmonella genomic island 1 (SGI1) MDR region into susceptible strains already containing SGI1. This was followed by multiple transmission events, initially from central Europe and later between several European countries. An independent transmission to the United States and another to Japan occurred, and from there MDR DT104 was probably transmitted to Taiwan and Canada. An independent acquisition of resistance genes took place in Thailand in ~1975 (95% CI, 1975 to 1990). In Denmark, WGS analysis provided evidence for transmission of the organism between herds of animals. Interestingly, the demographic history of Danish MDR DT104 provided evidence for the success of the program to eradicate *Salmonella* from pig herds in Denmark from 1996 to 2000. The results from this study refute several hypotheses on the evolution of DT104 and suggest that WGS may be useful in monitoring emerging clones and devising strategies for prevention of *Salmonella* infections.

**General information**

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Division of Food Microbiology, Department of Systems Biology, Center for Biological Sequence Analysis, Institut Pasteur, Oak Ridge National Laboratory, University of Oxford


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Impact of Sample Type and DNA Isolation Procedure on Genomic Inference of Microbiome Composition

Explorations of complex microbiomes using genomics greatly enhance our understanding about their diversity, biogeography, and function. The isolation of DNA from microbiome specimens is a key prerequisite for such examinations, but challenges remain in obtaining sufficient DNA quantities required for certain sequencing approaches, achieving accurate genomic inference of microbiome composition, and facilitating comparability of findings across specimen types and sequencing projects. These aspects are particularly relevant for the genomics-based global surveillance of infectious agents and antimicrobial resistance from different reservoirs. Here, we compare in a stepwise approach a total of eight commercially available DNA extraction kits and 16 procedures based on these for three specimen types (human feces, pig feces, and hospital sewage). We assess DNA extraction using spike-in controls and different types of beads for bead beating, facilitating cell lysis. We evaluate DNA concentration, purity, and stability and microbial community composition using 16S rRNA gene sequencing and for selected samples using shotgun metagenomic sequencing. Our results suggest that inferred community composition was dependent on inherent specimen properties as well as DNA extraction method. We further show that bead beating or enzymatic treatment can increase the extraction of DNA from Gram-positive bacteria. Final DNA quantities could be increased by isolating DNA from a larger volume of cell lysate than that in standard protocols. Based on this insight, we designed an improved DNA isolation procedure optimized for microbiome genomics that can be used for the three examined specimen types and potentially also for other biological specimens. A standard operating procedure is available from https://dx.doi.org/10.6084/m9.figshare.3475406.

Investigating Salmonella Eko from Various Sources in Nigeria by Whole Genome Sequencing to Identify the Source of Human Infections

Twenty-six Salmonella enterica serovar Eko isolated from various sources in Nigeria were investigated by whole genome sequencing to identify the source of human infections. Diversity among the isolates was observed and camel and cattle were identified as the primary reservoirs and the most likely source of the human infections.
Is the Evolution of Salmonella enterica subsp. enterica Linked to Restriction-Modification Systems?

Salmonella enterica subsp. enterica bacteria are highly diverse foodborne pathogens that are subdivided into more than 1,500 serovars. The diversity is believed to result from mutational evolution, as well as intra- and interspecies recombination that potentially could be influenced by restriction-modification (RM) systems. The aim of this study was to investigate whether RM systems were linked to the evolution of Salmonella enterica subsp. enterica. The study included 221 Salmonella enterica genomes, of which 68 were de novo sequenced and 153 were public available genomes from ENA. The data set covered 97 different serovars of Salmonella enterica subsp. enterica and an additional five genomes from four other Salmonella subspecies as an outgroup for constructing the phylogenetic trees. The phylogenetic trees were constructed based on multiple alignment of core genes, as well as the presence or absence of pangenes. The topology of the trees was compared to the presence of RM systems, antimicrobial resistance (AMR) genes, Salmonella pathogenicity islands (SPIs), and plasmid replicons. We did not observe any correlation between evolution and the RM systems in S. enterica subsp. enterica. However, sublineage correlations and serovar-specific patterns were observed. Additionally, we conclude that plasmid replicons, SPIs, and AMR were all better correlated to serovars than to RM systems. This study suggests a limited influence of RM systems on the evolution of Salmonella enterica subsp. enterica, which could be due to the conjugational mode of horizontal gene transfer in Salmonella. Thus, we conclude that other factors must be involved in shaping the evolution of bacteria.
Meta-analysis of proportion estimates of Extended-Spectrum-Beta-Lactamase-producing Enterobacteriaceae in East Africa hospitals

Background: A high proportion of Extended-Spectrum-Beta-Lactamase (ESBL) producing Enterobacteriaceae is causing common infections in all regions of the world. The burden of antibiotic resistance due to ESBL in East Africa is large but information is scarce and thus it is unclear how big the problem really is. To gain insight into the magnitude and molecular epidemiology of ESBL-producing Enterobacteriaceae in East Africa a literature search was performed in PubMed on 31 July 2015 to retrieve articles with relevant information on ESBL. Methods and results: Meta-analysis was performed to determine overall proportion estimate of ESBL-producing Enterobacteriaceae. A total of 4076 bacterial isolates were included in the analysis. The overall pooled proportion of ESBL-producing Enterobacteriaceae among included surveys done in East African hospitals was found to be 0.42 (95 % CI: 0.34-0.50). Heterogeneity (I²) between countries’ proportions in ESBL was significantly high (96.95 % and p < 0.001). The frequently detected genes encoding ESBL were CTX-M, TEM, SHV and OXA while the most infrequent reported genes were KPC and NDM. Conclusion: The available studies show a very wide variation in resistance due to ESBL between countries. This highlights a need for active surveillance systems which can help understand the actual epidemiology of ESBL, aid in formulating national or regional guidelines for proper screening of ESBL, and support developing standardized approaches for managing patients colonized with ESBL.

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Contributors: Sonda, T., Kumburu, H., van Zwetselaar, M., Alifrangis, M., Lund, O., Kibiki, G., Aarestrup, F. M.
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Research output: Research - peer-review › Journal article – Annual report year: 2016
Population Genetic Structure of Listeria monocytogenes Strains as Determined by Pulsed-Field Gel Electrophoresis and Multilocus Sequence Typing

Listeria monocytogenes is a ubiquitous bacterium that may cause the foodborne illness listeriosis. Only a small amount of data about the population genetic structure of strains isolated from food is available. This study aimed to provide an accurate view of the L. monocytogenes food strain population in France. From 1999 to 2014, 1,894 L. monocytogenes strains were isolated from food at the French National Reference Laboratory for L. monocytogenes and classified according to the five risk food matrices defined by the European Food Safety Authority (EFSA). A total of 396 strains were selected on the basis of different pulsed-field gel electrophoresis (PFGE) clusters, serotypes, and strain origins and typed by multilocus sequence typing (MLST), and the MLST results were supplemented with MLST data available from Institut Pasteur, representing human and additional food strains from France. The distribution of sequence types (STs) was compared between food and clinical strains on a panel of 675 strains. High congruence between PFGE and MLST was found. Out of 73 PFGE clusters, the two most prevalent corresponded to ST9 and ST121. Using original statistical analysis, we demonstrated that (i) there was not a clear association between ST9 and ST121 and the food matrices, (ii) serotype IIc, ST8, and ST4 were associated with meat products, and (iii) ST13 was associated with dairy products. Of the two major STs, ST121 was the ST that included the fewest clinical strains, which might indicate lower virulence. This observation may be directly relevant for refining risk analysis models for the better management of food safety. This study showed a very useful backward compatibility between PFGE and MLST for surveillance. The results enabled better understanding of the population structure of L. monocytogenes strains isolated from food and management of the health risks associated with L. monocytogenes food strains. Moreover, this work provided an accurate view of L. monocytogenes strain populations associated with specific food matrices. We clearly showed that some STs were associated with food matrices, such as meat, meat products, and dairy products. We opened the way to source attribution modeling in order to quantify the relative importance of the main food matrices.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Universite Paris-Est
Contributors: Henri, C., Félix, B., Guillier, L., Leekitcharoenphon, P., Michelon, D., Mariet, J., Aarestrup, F. M., Mistou, M., Hendriksen, R. S., Roussel, S.
Number of pages: 9
Pages: 5720-5728
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Peer-reviewed: Yes

Publication information
Journal: Applied and Environmental Microbiology
Volume: 82
Issue number: 18
ISSN (Print): 0099-2240
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 3.99
Web of Science (2017): Impact factor 3.633
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.08
Web of Science (2016): Impact factor 3.807
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.14 SJR 1.891 SNIP 1.308
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.02 SJR 1.857 SNIP 1.384
Web of Science (2014): Impact factor 3.668
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.25 SJR 1.899 SNIP 1.414
Recipien determinanter påvirkende konjugatorisk promiskuitet i Enterobacteriaceae

Den globale udvikling og hurtige spredning af antibiotika resistens anses for at være et stigende problem i vores samfund, og en stor trussel for det menneskelige helbred. Det seneste slående eksempel er observationen af plasmid-båret kolistins resistens, som i Danmark blev fundet i en Escherichia coli bakterie som kun var modtagelig for meget få klasser af antibiotika. I dette tilfælde ville optaget af yderligere resistens efterlade et meget begrænset omfang af mulige behandlingsmetoder. Det er derfor af yderste vigtighed at vi tilegner os yderligere viden indenfor de mekanismer som kontrollerer spredningen af antibiotika resistens. Plasmider er et af de mobile elementer kan udveksle DNA mellem...

Sharing Data for Global Infectious Disease Surveillance and Outbreak Detection
Rapid global sharing and comparison of epidemiological and genomic data on infectious diseases would enable more rapid and efficient global outbreak control and tracking of diseases. Several barriers for global sharing exist but, in our opinion, the presumed magnitude of the problems appears larger than they are, and solutions can be found.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology
Contributors: Roer, L., Aarestrup, F. M., Hasman, H.
Number of pages: 55
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Publication information
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Publisher: National Food Institute, Technical University of Denmark
ISBN (Electronic): 978-87-93109-77-3
Original language: English
Electronic versions:
LouiseRoer_PhD_Thesis.pdf

Sharing Data for Global Infectious Disease Surveillance and Outbreak Detection
Rapid global sharing and comparison of epidemiological and genomic data on infectious diseases would enable more rapid and efficient global outbreak control and tracking of diseases. Several barriers for global sharing exist but, in our opinion, the presumed magnitude of the problems appears larger than they are, and solutions can be found.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Erasmus MC University Medical Center
Contributors: Aarestrup, F. M., Koopmans, M. G.
Number of pages: 5
Pages: 241-245
Publication date: 2016
Peer-reviewed: Yes

Publication information
Journal: Trends in Microbiology
Volume: 24
Issue number: 4
ISSN (Print): 0966-842x
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 7.97 SJR 4.639 SNIP 2.67
Web of Science (2017): Impact factor 11.776
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 7.37 SJR 4.547 SNIP 2.324
Web of Science (2016): Impact factor 11.02
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 7.77 SJR 5.249 SNIP 2.306
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 7.96 SJR 5.233 SNIP 2.399
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 9 SJR 5.24 SNIP 2.361
Web of Science (2013): Impact factor 9.808
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 8.58 SJR 4.508 SNIP 2.222
Web of Science (2012): Impact factor 8.434
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 7.73 SJR 4.322 SNIP 2.16
Web of Science (2011): Impact factor 7.91
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 4.412 SNIP 2.104
Web of Science (2010): Impact factor 7.5
BFI (2009): BFI-level 2
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 4.209 SNIP 2.013
Scopus rating (2007): SJR 3.83 SNIP 2.018
Scopus rating (2006): SJR 4.041 SNIP 1.775
Scopus rating (2005): SJR 3.505 SNIP 1.872
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 3.003 SNIP 1.965
Scopus rating (2003): SJR 3.309 SNIP 1.984
Scopus rating (2002): SJR 3.504 SNIP 1.75
Scopus rating (2001): SJR 3.458 SNIP 2.048
Scopus rating (2000): SJR 2.903 SNIP 1.854
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 2.595 SNIP 1.692
Original language: English
Keywords: Communicable Diseases, Computer Systems, Databases, Factual, Disease Notification, Disease Outbreaks, Global Health, Humans, Information Dissemination, Population Surveillance, Statistics as Topic, bacteria, genomics, infection, metagenomics, surveillance, virus, Infectious Diseases, Microbiology (medical), Microbiology, Virology, Bacteria, Genomics, Infection, Metagenomics, Surveillance, Virus, bacterial genome, bioinformatics, disease control, disease surveillance, Ebola hemorrhagic fever, epidemic, epidemiological data, health care access, health care policy, health care system, human, information processing, medical research, next generation sequencing, nonhuman, Note, priority journal, MICR
DOIs: 10.1016/j.tim.2016.01.009
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Source-ID: 2291980930
Research output: Research - peer-review; Journal article – Annual report year: 2016
The External Quality Assurance System of the WHO Global Foodborne Infections Network, 2014

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Division of Risk Assessment and Nutrition
Contributors: Roer, L., Karlsmose Pedersen, S., Frimann, J. M., Aarestrup, F. M., Hendriksen, R. S.
Number of pages: 37
Publication date: 2016

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Place of publication: Søborg
Publisher: National Food Institute, Technical University of Denmark
ISBN (Electronic): 978-87-93109-6
Original language: English
Source: PublicationPreSubmission
Source-ID: 124318143
Research output: Commissioned › Report – Annual report year: 2016

The External Quality Assurance System of the WHO Global Foodborne Infections Network, 2015

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Division of Risk Assessment and Nutrition
Contributors: Hendriksen, R. S., Karlsmose Pedersen, S., Roer, L., Frimann, J. M., Aarestrup, F. M.
Number of pages: 38
Publication date: 2016

Publication information
Place of publication: Søborg
Publisher: National Food Institute, Technical University of Denmark
Original language: English
Source: PublicationPreSubmission
Source-ID: 124318159
Research output: Commissioned › Report – Annual report year: 2016

The Lake Chad Basin, an Isolated and Persistent Reservoir of Vibrio cholerae O1: A Genomic Insight into the Outbreak in Cameroon, 2010

The prevalence of reported cholera was relatively low around the Lake Chad basin until 1991. Since then, cholera outbreaks have been reported every couple of years. The objective of this study was to investigate the 2010/2011 Vibrio cholerae outbreak in Cameroon to gain insight into the genomic make-up of the V. cholerae strains responsible for the outbreak. Twenty-four strains were isolated and whole genome sequenced. Known virulence genes, resistance genes and integrating conjugative element (ICE) elements were identified and annotated. A global phylogeny (378 genomes) was inferred using a single nucleotide polymorphism (SNP) analysis. The Cameroon outbreak was found to be clonal and clustered distant from the other African strains. In addition, a subset of the strains contained a deletion that was found in the ICE element causing less resistance. These results suggest that V. cholerae is endemic in the Lake Chad basin and different from other African strains.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Centre Pasteur du Cameroon, Mahidol University
Contributors: Kaas, R. S., Ngandjio, A., Nzouankeu, A., Siriphap, A., Fonkoua, M., Aarestrup, F. M., Hendriksen, R. S.
Number of pages: 12
The proficiency test (pilot) report of the global microbial identifier (GMI) initiative, year 2014

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Technical University of Denmark, University of Sydney, New York State Department of Health, Hvidovre Hospital, Ben-Gurion University of the Negev, National Institute of Standards and Technology, Microbiologics, Inc., Public Health England, United States Food and Drug Administration
Number of pages: 23
Publication date: 2016

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Place of publication: Kgs. Lyngby
Publisher: National Food Institute, Technical University of Denmark
ISBN (Electronic): 978-87-93109-78-0
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Research output: Research - peer-review › Report – Annual report year: 2016

Evaluation of methods for the concentration and extraction of viruses from sewage water in the context of metagenomic sequencing

General information
State: Published
Organisations: National Food Institute, Research Group for Microbial Food Safety, Research Group for Genomic Epidemiology, University of Barcelona, Technical University of Munich, SP Technical Research Institute of Sweden
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Publication date: 2016

Host publication information
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Place of publication: Copenhagen
Publisher: American Society for Microbiology
Article number: P61
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Programme & Abstracts book
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Audouin's gull, a potential vehicle of an extended spectrum beta-lactamase producing Salmonella Agona

The genome of a multidrug-resistant Salmonella Agona isolated from Larus audouinii (Audouin's gull) in Spain was examined. The isolate showed high levels of resistance to different antimicrobials, including third generation cephalosporins and fluoroquinolones, which is a public health concern as those being used to treat severe salmonellosis in humans. Whole genome sequencing revealed the strain being multilocus sequence type ST13, and eight resistance genes (aadA2, aadB, blaCTX-M-9, bla(DHA-1), qnrA1, tetA, sul1 and dfrA16) belonging to seven antimicrobial classes were confirmed, as well as the presence of two plasmids. Migratory Audouin's gulls have the ability to cover long distances during annual movements. Therefore, they have the potential to disseminate multidrug-resistant Salmonella and resistance genes in the environment and over great geographic distances, contributing to the global dissemination of resistance genes.

General information
State: Published
### Biocide Susceptibility of Staphylococcus aureus CC398 and CC30 Isolates from Pigs and Identification of the Biocide Resistance Genes, qacG and qacC

**Objectives:** Methicillin-resistant Staphylococcus aureus (MRSA), in particular clonal complex (CC) 398, is increasingly found in livestock. Recently, MRSA CC30 was identified in Danish pigs. We determined the susceptibility of porcine S. aureus isolates of CC398 and CC30 to disinfectants used in pig farming (benzalkonium chloride, hydrogen peroxide, formaldehyde, sodium hypochlorite, and caustic soda). Furthermore, efflux pump activity, antimicrobial resistance profiles, hemolysis properties, and the presence of toxic shock syndrome toxin-1 (TSST-1) and Panton-Valentine Leukocidin (PVL)-encoding virulence factors were investigated.

**Methods:** Susceptibilities to biocides and antimicrobial agents of 79 porcine S. aureus isolates were determined by the microdilution method. Isolates comprised 21 methicillin-sensitive S. aureus (MSSA) and 40 MRSA isolates belonging to CC398 and CC30. The presence of quaternary ammonium compound (QAC) resistance efflux pumps was analyzed using an ethidium bromide accumulation assay. The presence of qac resistance genes in active efflux pump positive isolates was determined by whole-genome sequencing data. All isolates were screened for lukPV and tst genes with PCR, and hemolytic activities were determined using an agar plate assay. Results: S. aureus isolates did not show reduced susceptibility to the biocides tested. However, the QAC resistance gene, qacG, was detected in three MRSA CC30 isolates and the qacC in one MRSA CC30 isolate. CC30 isolates were generally more susceptible to non-beta-lactam antibiotics than CC398. Isolates generally had low hemolytic activity and none encoded PVL or TSST-1. Conclusion: The presence of qac genes in European porcine S. aureus isolates and in livestock-associated MRSA CC30 is for the first time described in this study. This finding is concerning as it ultimately may compromise disinfection with QACs and thereby contribute to the selection and spread of MRSA CC30.

### General information

**State:** Published

**Organisations:** National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen

**Contributors:** Seier-Petersen, M. A., Nielsen, L. N., Ingmer, H., Aarestrup, F. M., Agersø, Y.

**Number of pages:** 10

**Publication date:** 2015

**Peer-reviewed:** Yes

### Publication information

**Journal:** Microbial Drug Resistance

**Volume:** 21

**Issue number:** 5

**ISSN (Print):** 1076-6294

**Ratings:**

BFI (2018): BFI-level 1
Comparative Evaluation of the Antimicrobial Activity of Different Antimicrobial Peptides against a Range of Pathogenic Bacteria

The rapid emergence of resistance to classical antibiotics has increased the interest in novel antimicrobial compounds. Antimicrobial peptides (AMPs) represent an attractive alternative to classical antibiotics and a number of different studies have reported antimicrobial activity data of various AMPs, but there is only limited comparative data available. The mode of action for many AMPs is largely unknown even though several models have suggested that the lipopolysaccharides (LPS) play a crucial role in the attraction and attachment of the AMP to the bacterial membrane in Gram-negative bacteria. We compared the potency of Cap18, Cap11, Cap11-1-18m2, Cecropin P1, Cecropin B, Bac2A, Bac2A-NH2, Sub5-NH2, Indolicidin, Melittin, Myxixinidin, Myxinidin-NH2, Pyrrhocoricin, Apidaecin and Metalnikowin I towards Staphylococcus aureus, Enterococcus faecalis, Pseudomonas aeruginosa, Escherichia coli, Aeromonas salmonicida, Listeria monocytogenes, Campylobacter jejuni, Flavobacterium psychrophilum, Salmonella typhimurium and Yersinia ruckeri by minimal inhibitory concentration (MIC) determinations. Additional characteristics such as cytotoxicity, thermo and protease stability were measured and compared among the different peptides. Further, the antimicrobial activity of a selection of cationic AMPs was investigated in various E. coli LPS mutants.

General information
State: Published
Organisations: Department of Systems Biology, National Food Institute, Research Group for Genomic Epidemiology, Research Group for Gut Microbiology and Immunology, Aalborg University
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Peer-reviewed: Yes

Publication information
Journal: P L o S One
Volume: 10
Issue number: 12
Article number: e0144611
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.32 SJR 1.427 SNIP 1.136
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.54 SJR 1.559 SNIP 1.148
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.94 SJR 1.772 SNIP 1.153
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Detection of mcr-1 encoding plasmid-mediated colistin-resistant Escherichia coli isolates from human bloodstream infection and imported chicken meat, Denmark 2015

The plasmid-mediated colistin resistance gene, mcr-1, was detected in an Escherichia coli isolate from a Danish patient with bloodstream infection and in five E. coli isolates from imported chicken meat. One isolate from chicken meat belonged to the epidemic spreading sequence type ST131. In addition to IncI2*, an incX4 replicon was found to be linked to mcr-1. This report follows a recent detection of mcr-1 in E. coli from animals, food and humans in China.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Statens Serum Institut, Copenhagen University Hospital
Number of pages: 5
Pages: 1-5
Publication date: 2015
Peer-reviewed: Yes

Publication information
Journal: Eurosurveillance (Online Edition)
Volume: 20
Issue number: 49
ISSN (Print): 1025-496X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 5.09 SJR 3.727 SNIP 2.087
Genome sequences of copper resistant and sensitive Enterococcus faecalis strains isolated from copper-fed pigs in Denmark

Six strains of Enterococcus faecalis (S1, S12, S17, S18, S19 and S32) were isolated from copper fed pigs in Denmark. These Gram-positive bacteria within the genus Enterococcus are able to survive a variety of physical and chemical challenges by the acquisition of diverse genetic elements. The genome of strains S1, S12, S17, S18, S19 and S32
contained 2,615, 2,769, 2,625, 2,804, 2,853 and 2,935 protein-coding genes, with 41, 42, 27, 42, 32 and 44 genes encoding antibiotic and metal resistance, respectively. Differences between Cu resistant and sensitive E. faecalis strains, and possible co-transfer of Cu and antibiotic resistance determinants were detected through comparative genome analysis.

**General information**

State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen, Huazhong Agricultural University, King Saud University, Chinese Academy of Sciences
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Peer-reviewed: Yes

**Publication information**

Journal: Standards in Genomic Sciences
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Article number: 35
ISSN (Print): 1944-3277
Ratings:

Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 1.69 SJR 0.768 SNIP 0.629
Web of Science (2017): Impact factor 1.6
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 1.26 SJR 0.626 SNIP 0.511
Web of Science (2016): Impact factor 1.189
Web of Science (2016): Indexed yes
Scopus rating (2015): CiteScore 2.41 SJR 1.12 SNIP 0.917
Web of Science (2015): Impact factor 1.594
Web of Science (2015): Indexed yes
Scopus rating (2014): CiteScore 1.3 SJR 0.954 SNIP 0.448
Web of Science (2014): Indexed yes
Scopus rating (2013): CiteScore 2.89 SJR 1.206 SNIP 0.819
Web of Science (2013): Impact factor 3.167
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Scopus rating (2012): CiteScore 1.81 SJR 0.847 SNIP 0.516
Web of Science (2012): Impact factor 2.007
ISI indexed (2012): ISI indexed no
Scopus rating (2011): CiteScore 1.42 SJR 0.516 SNIP 0.303
Web of Science (2011): Impact factor 1.621
ISI indexed (2011): ISI indexed no
Scopus rating (2010): SJR 0.344 SNIP 0.285
Original language: English
Keywords: Antibiotic resistance, Comparative genomics, Copper resistance, Enterococcus faecalis, Genome sequence
Electronic versions:

art_3A10.1186_2Fs40793_015_0021_1.pdf
DOIs:
10.1186/s40793-015-0021-1
Source: FindIt
Source-ID: 2279680160
Research output: Research - peer-review › Journal article – Annual report year: 2015

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**Genomic Dissection of Travel-Associated Extended-Spectrum-Beta-Lactamase-Producing Salmonella enterica Serovar Typhi Isolates Originating from the Philippines: a One-Off Occurrence or a Threat to Effective Treatment of Typhoid Fever?**

One unreported case of extended-spectrum-beta-lactamase (ESBL)-producing Salmonella enterica serovar Typhi was identified, whole-genome sequence typed, among other analyses, and compared to other available genomes of S. Typhi. The reported strain was similar to a previously published strain harboring blaSHV-12 from the Philippines and likely part of
an undetected outbreak, the first of ESBL-producing S. Typhi.

**General information**

State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Comparative Microbial Genomics, National Center for Emerging and Zoonotic Infectious Diseases, Thailand Ministry of Public Health, VU University Medical Centre, Norwegian Institute of Public Health
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Publication date: 2015
Peer-reviewed: Yes

**Publication information**

Journal: Journal of Clinical Microbiology
Volume: 53
Issue number: 2
ISSN (Print): 0095-1137
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.55 SJR 2.256 SNIP 1.443
Web of Science (2017): Impact factor 4.054
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.196 SNIP 1.4
Web of Science (2016): Impact factor 3.712
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.56 SJR 2.206 SNIP 1.431
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.84 SJR 2.231 SNIP 1.528
Web of Science (2014): Impact factor 3.993
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.18 SJR 2.438 SNIP 1.63
Web of Science (2013): Impact factor 4.232
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.11 SJR 2.148 SNIP 1.626
Web of Science (2012): Impact factor 4.068
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.27 SJR 2.346 SNIP 1.699
Web of Science (2011): Impact factor 4.153
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.343 SNIP 1.731
Web of Science (2010): Impact factor 4.22
Genomic Signature of Multidrug-Resistant Salmonella enterica Serovar Typhi Isolates Related to a Massive Outbreak in Zambia between 2010 and 2012.

Retrospectively, we investigated the epidemiology of a massive Salmonella enterica serovar Typhi outbreak in Zambia during 2010 to 2012. Ninety-four isolates were susceptibility tested by MIC determinations. Whole-genome sequence typing (WGST) of 33 isolates and bioinformatic analysis identified the multilocus sequence type (MLST), haplotype, plasmid replicon, antimicrobial resistance genes, and genetic relatedness by single nucleotide polymorphism (SNP) analysis and genomic deletions. The outbreak affected 2,040 patients, with a fatality rate of 0.5%. Most (83.0%) isolates were multidrug resistant (MDR). The isolates belonged to MLST ST1 and a new variant of the haplotype, H58B. Most
isolates contained a chromosomally translocated region containing seven antimicrobial resistance genes, catA1, blaTEM-1, dfrA7, sul1, sul2, strA, and strB, and fragments of the incompatibility group Q1 (IncQ1) plasmid replicon, the class 1 integron, and the mer operon. The genomic analysis revealed 415 SNP differences overall and 35 deletions among 33 of the isolates subjected to whole-genome sequencing. In comparison with other genomes of H58, the Zambian isolates separated from genomes from Central Africa and India by 34 and 52 SNPs, respectively. The phylogenetic analysis indicates that 32 of the 33 isolates sequenced belonged to a tight clonal group distinct from other H58 genomes included in the study. The small numbers of SNPs identified within this group are consistent with the short-term transmission that can be expected over a period of 2 years. The phylogenetic analysis and deletions suggest that a single MDR clone was responsible for the outbreak, during which occasional other S. Typhi lineages, including sensitive ones, continued to cocirculate. The common view is that the emerging global S. Typhi haplotype, H58B, containing the MDR IncHI1 plasmid is responsible for the majority of typhoid infections in Asia and sub-Saharan Africa; we found that a new variant of the haplotype harboring a chromosomally translocated region containing the MDR islands of IncHI1 plasmid has emerged in Zambia. This could change the perception of the term "classical MDR typhoid" currently being solely associated with the IncHI1 plasmid. It might be more common than presently thought that S. Typhi haplotype H58B harbors the IncHI1 plasmid or a chromosomally translocated MDR region or both.
Identification and Antimicrobial Resistance of Bacteria Isolated from Probiotic Products Used in Shrimp Culture

Probiotics are increasingly used in aquaculture to control diseases and improve feed digestion and pond water quality; however, little is known about the antimicrobial resistance properties of such probiotic bacteria and to what extent they may contribute to the development of bacterial resistance in aquaculture ponds. Concerns have been raised that the declared information on probiotic product labels are incorrect and information on bacterial composition are often missing. We therefore evaluated seven probiotics commonly used in Vietnamese shrimp culture for their bacterial species content, phenotypic antimicrobial resistance and associated transferable resistance genes. The bacterial species was established by 16S rRNA sequence analysis of 125 representative bacterial isolates. MIC testing was done for a range of antimicrobials and whole genome sequencing of six multiple antimicrobial resistant Bacillus spp. used to identify resistance genes and genetic elements associated with horizontal gene transfer. Thirteen bacterial species declared on the probiotic products could not be identified and 11 non-declared Bacillus spp. were identified. Although our culture-based isolation and identification may have missed a few bacterial species present in the tested products this would represent minor bias, but future studies may apply culture independent identification methods like pyro sequencing. Only 6/60 isolates were resistant to more than four antimicrobials and whole genome sequencing showed that they contained macrolide (ermD), tetracycline (tetL), phenicol (fexA) and trimethoprim (dfrD, dfrG and dfrK) resistance genes, but not...
known structures associated with horizontal gene transfer. Probiotic bacterial strains used in Vietnamese shrimp culture seem to contribute with very limited types and numbers of resistance genes compared to the naturally occurring bacterial species in aquaculture environments. Approval procedures of probiotic products must be strengthened through scientific-based efficacy trials and product labels should allow identification of individual bacterial strains and inform the farmer on specific purpose, dosage and correct application measures.

**General information**

State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen
Contributors: Noor Uddin, G. M., Larsen, M. H., Christensen, H., Aarestrup, F. M., Phu, T. M., Dalsgaard, A.
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Peer-reviewed: Yes

**Publication information**

Journal: *P L o S One*
Volume: 10
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.32 SJR 1.427 SNIP 1.136
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.54 SJR 1.559 SNIP 1.148
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.94 SJR 1.772 SNIP 1.153
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.15 SJR 1.982 SNIP 1.156
Web of Science (2012): Impact factor 3.73
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.58 SJR 2.425 SNIP 1.233
Web of Science (2011): Impact factor 4.092
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.705 SNIP 1.178
Web of Science (2010): Impact factor 4.411
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.614 SNIP 1.046
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Identification of a Pseudomonas aeruginosa co-producing NDM-1, VIM-5 and VIM-6 metallo-beta-lactamases in Denmark using Whole-Genome Sequencing

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Aarhus University Hospital
Contributors: Wang, M., Borris, L. C., Aarestrup, F. M., Hasman, H.
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ISSN (Print): 0924-8579
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.54 SJR 1.699 SNIP 1.397
Web of Science (2017): Impact factor 4.253
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.38 SJR 1.608 SNIP 1.316
Web of Science (2016): Impact factor 4.307
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.45 SJR 1.703 SNIP 1.541
Web of Science (2015): Impact factor 4.097
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.45 SJR 1.477 SNIP 1.64
Web of Science (2014): Impact factor 4.296
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.63 SJR 1.706 SNIP 1.566
Web of Science (2013): Impact factor 4.259
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.57 SJR 1.633 SNIP 1.496
Web of Science (2012): Impact factor 4.415
ISI indexed (2012): ISI indexed yes
Livestock-Associated Methicillin Resistant and Methicillin Susceptible Staphylococcus aureus Sequence Type (CC)1 in European Farmed Animals: High Genetic Relatedness of Isolates from Italian Cattle Herds and Humans

Methicillin-resistant Staphylococcus aureus (MRSA) Sequence Type (ST)1, Clonal Complex (CC) 1, SCCmec V is one of the major Livestock-Associated (LA-) lineages in pig farming industry in Italy and is associated with pigs in other European countries. Recently, it has been increasingly detected in Italian dairy cattle herds. The aim of this study was to analyse the differences between ST1 MRSA and methicillin-susceptible S. aureus (MSSA) from cattle and pig herds in Italy and Europe and human isolates. Sixty-three animal isolates from different holdings and 20 human isolates were characterized by pulsed-field gel electrophoresis (PFGE), spa-typing, SCCmec typing, and by micro-array analysis for several virulence, antimicrobial resistance, and strain/host-specific marker genes. Three major PFGE clusters were detected. The bovine isolates shared a high (>= 90% to 100%) similarity with human isolates and carried the same SCCmec type IVa. They often showed genetic features typical of human adaptation or present in human-associated CC1: Immune evasion cluster (IEC) genes sak and scn, or sea; sat and aphA3-mediated aminoglycoside resistance. Contrary, typical markers of porcine origin in Italy and Spain, like erm(A) mediated macrolide-lincosamide-streptograminB, and of vga(A)-mediated pleuromutilin resistance were always absent in human and bovine isolates. Most of ST(CC) 1 MRSA from dairy cattle were multidrug-resistant and contained virulence and immunomodulatory genes associated with full capability of colonizing humans. As such, these strains may represent a greater human hazard than the porcine strains. The zoonotic capacity of CC1 LA-MRSA from livestock must be taken seriously and measures should be implemented at farm-level to prevent spill-over.

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Meta-genomic analysis of toilet waste from long distance flights; a step towards global surveillance of infectious diseases and antimicrobial resistance

Human populations worldwide are increasingly confronted with infectious diseases and antimicrobial resistance spreading faster and appearing more frequently. Knowledge regarding their occurrence and worldwide transmission is important to control outbreaks and prevent epidemics. Here, we performed shotgun sequencing of toilet waste from 18 international airplanes arriving in Copenhagen, Denmark, from nine cities in three world regions. An average of 18.6 Gb (14.8 to 25.7 Gb) of raw Illumina paired end sequence data was generated, cleaned, trimmed and mapped against reference sequence databases for bacteria and antimicrobial resistance genes. An average of 106,839 (0.06%) reads were assigned to resistance genes with genes encoding resistance to tetracycline, macrolide and beta-lactam resistance genes as the most abundant in all samples. We found significantly higher abundance and diversity of genes encoding antimicrobial resistance, including critical important resistance (e.g. \textit{bla}_{CTX-M}^{\text{CTX-M}}) carried on airplanes from South Asia compared to North America. Presence of \textit{Salmonella enterica} and norovirus were also detected in higher amounts from South Asia, whereas \textit{Clostridium difficile} was most abundant in samples from North America. Our study provides a first step towards a potential novel strategy for global surveillance enabling simultaneous detection of multiple human health threatening genetic elements, infectious agents and resistance genes.

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BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.36 SJR 1.533 SNIP 1.245
Web of Science (2017): Impact factor 4.122
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.63 SJR 1.692 SNIP 1.354
Web of Science (2016): Impact factor 4.259
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 5.3 SJR 2.034 SNIP 1.597
Web of Science (2015): Impact factor 5.228
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.75 SJR 2.163 SNIP 1.554
Web of Science (2014): Impact factor 5.578
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.06 SJR 1.998 SNIP 1.57
Web of Science (2013): Impact factor 5.078
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.44 SJR 1.531 SNIP 0.962
Web of Science (2012): Impact factor 2.927
Rapid and Easy In Silico Serotyping of Escherichia coli Isolates by Use of Whole-Genome Sequencing Data

Accurate and rapid typing of pathogens is essential for effective surveillance and outbreak detection. Conventional serotyping of Escherichia coli is a delicate, laborious, time-consuming, and expensive procedure. With whole-genome sequencing (WGS) becoming cheaper, it has vast potential in routine typing and surveillance. The aim of this study was to establish a valid and publicly available tool for WGS-based in silico serotyping of E. coli applicable for routine typing and surveillance. A FASTA database of specific O-antigen processing system genes for O typing and flagellin genes for H typing was created as a component of the publicly available Web tools hosted by the Center for Genomic Epidemiology (CGE) (www.genomicepidemiology.org). All E. coli isolates available with WGS data and conventional serotype information were subjected to WGS-based serotyping employing this specific SerotypeFinder CGE tool. SerotypeFinder was evaluated on 682 E. coli genomes, 108 of which were sequenced for this study, where both the whole genome and the serotype were available. In total, 601 and 509 isolates were included for O and H typing, respectively. The O-antigen genes wzx, wzy, wzm, and wzt and the flagellin genes fliC, flkA, filA, flmA, and flnA were detected in 569 and 508 genome sequences, respectively. SerotypeFinder for WGS-based O and H typing predicted 560 of 569 O types and 504 of 508 H types, consistent with conventional serotyping. In combination with other available WGS typing tools, E. coli serotyping can be performed solely from WGS data, providing faster and cheaper typing than current routine procedures and making WGS typing a superior alternative to conventional typing strategies.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Statens Serum Institut, University of Miyazaki
Contributors: Joensen, K. G., Tetzschner, A. M. M., Iguchi, A., Aarestrup, F. M., Scheutz, F.
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BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.55 SJR 2.256 SNIP 1.443
Web of Science (2017): Impact factor 4.054
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.196 SNIP 1.4
Web of Science (2016): Impact factor 3.712
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.56 SJR 2.206 SNIP 1.431
Reads2Type: a web application for rapid microbial taxonomy identification

Identification of bacteria may be based on sequencing and molecular analysis of a specific locus such as 16S rRNA, or a set of loci such as in multilocus sequence typing. In the near future, healthcare institutions and routine diagnostic microbiology laboratories may need to sequence the entire genome of microbial isolates. Therefore we have developed Reads2Type, a web-based tool for taxonomy identification based on whole bacterial genome sequence data. Raw sequencing data provided by the user are mapped against a set of marker probes that are derived from currently available bacteria complete genomes. Using a dataset of 1003 whole genome sequenced bacteria from various sequencing platforms, Reads2Type was able to identify the species with 99.5% accuracy and on the minutes time scale. In comparison with other tools, Reads2Type offers the advantage of not needing to transfer sequencing files, as the entire computational analysis is done on the computer of whom utilizes the web application. This also prevents data privacy issues to arise. The Reads2Type tool is available at http://www.cbs.dtu.dk/~dhany/reads2type.html.

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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
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Web of Science (2017): Impact factor 2.213
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.54 SJR 1.581 SNIP 0.974
Web of Science (2016): Impact factor 2.448
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.77 SJR 1.737 SNIP 1.079
Web of Science (2015): Impact factor 2.435
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.91 SJR 1.916 SNIP 1.185
Web of Science (2014): Impact factor 2.576
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.38 SJR 1.999 SNIP 1.323
Web of Science (2013): Impact factor 2.672
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.24 SJR 1.9 SNIP 1.145
Web of Science (2012): Impact factor 3.024
ISI indexed (2012): ISI indexed yes
Reappearance of Salmonella serovar Choleraesuis var. Kunzendorf in Danish pig herds
Salmonella enterica serovar Choleraesuis is a porcine adapted serovar which may cause serious outbreaks in pigs. Here we describe outbreaks of salmonellosis due to S. Choleraesuis in four Danish pig farms in 2012–2013 by clinic, serology, and microbiology and compare the isolates to those of a previous outbreak in 1999–2000. The infection was in some herds associated with high mortality and a moderate to high sero-prevalence was found. In 2012–2013 the disease contributed to increased mortality but occurred concomitant with other disease problems in the herds, which likely delayed the diagnosis by up to several months. Nine isolates from the four farms in 2012–2013 and 14 isolates obtained from the outbreak in Denmark in 1999–2000 were subjected to typing using pulsed-field gel electrophoresis (PFGE). Seven isolates were selected for whole genome sequencing (WGS). The PFGE results of 23 isolates displayed five different profiles. The isolates from 2012 to 2013 revealed two distinct profiles, both different from the isolates recovered in 1999–2000. Two of the 2012–2013 farms shared PFGE profiles and had also transported pigs between them. The profile found in the two other 2012–2013 farms was indistinguishable but no epidemiological connection between these farms was found. Analysis of the number of single nucleotide polymorphisms (SNPs) from the WGS data indicated that the isolates from the farms in 2012–2013 were more closely related to each other than to isolates from the outbreak in 1999. It was therefore concluded that the infection was a new introduction and not a persistent infection since the outbreak in 1999. It may further be suggested that there were two or three independent rather than a single introduction. The re-introduction of S. Choleraesuis in Denmark emphasizes the importance of strict hygiene measures in the herds. Further investigations using WGS are now in progress on a larger collection of isolates to study clonality at European level and trace the origin of the infections.

General information
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Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Food Institute, Division of Food Microbiology, Comparative Microbial Genomics, Division of Epidemiology and Microbial Genomics, Danish Agriculture and Food Council
Contributors: Pedersen, K., Sørensen, G., Löfström, C., Leekitcharoenphon, P., Nielsen, B., Wingstrand, A., Aarestrup, F. M., Hendriksen, R. S., Baggesen, D. L.
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
Web of Science (2010): Impact factor 3.256
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.309 SNIP 1.466
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
The 17th EURL-AR Proficiency Test Salmonella, Campylobacter and genotypic characterisation 2014

General information
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Organisations: Division of Epidemiology and Microbial Genomics, National Food Institute, Research Group for Genomic Epidemiology
Contributors: Karlsmose Pedersen, S., Cavaco, L., Hendriksen, R. S., Aarestrup, F. M.
Number of pages: 18
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The EcoKI Type I Restriction-Modification System in Escherichia coli Affects but Is Not an Absolute Barrier for Conjugation.
The rapid evolution of bacteria is crucial to their survival and is caused by exchange, transfer, and uptake of DNA, among other things. Conjugation is one of the main mechanisms by which bacteria share their DNA, and it is thought to be controlled by varied bacterial immune systems. Contradictory results about restriction-modification systems based on phenotypic studies have been presented as reasons for a barrier to conjugation with and other means of uptake of exogenous DNA. In this study, we show that inactivation of the R.EcoKI restriction enzyme in strain Escherichia coli K-12 strain MG1655 increases the conjugational transfer of plasmid pOLA52, which carriers two EcoKI recognition sites. Interestingly, the results were not absolute, and uptake of unmethylated pOLA52 was still observed in the wild-type strain (with an intact hsdR gene) but at a reduction of 85% compared to the uptake of the mutant recipient with a disrupted hsdR gene. This leads to the conclusion that EcoKI restriction-modification affects the uptake of DNA by conjugation but is not a major barrier to plasmid transfer.

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Contributors: Roer, L., Aarestrup, F. M., Hasman, H.
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.94 SJR 1.885 SNIP 0.903
Web of Science (2017): Impact factor 3.219
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.08 SJR 1.943 SNIP 0.877
Web of Science (2016): Impact factor 3.143
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.84 SJR 2.154 SNIP 0.95
Web of Science (2015): Impact factor 3.198
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.72 SJR 2.084 SNIP 0.931
Web of Science (2014): Impact factor 2.808
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3 SJR 2.151 SNIP 1.013
Web of Science (2013): Impact factor 2.688
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.42 SJR 2.125 SNIP 1.085
Web of Science (2012): Impact factor 3.177
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.83 SJR 2.471 SNIP 1.154
Web of Science (2011): Impact factor 3.825
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.64 SNIP 1.144
Web of Science (2010): Impact factor 3.726
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.71 SNIP 1.181
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.639 SNIP 1.088
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.653 SNIP 1.148
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.665 SNIP 1.137
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.66 SNIP 1.164
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.497 SNIP 1.188
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.71 SNIP 1.148
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 2.412 SNIP 1.111
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.661 SNIP 1.182
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 2.728 SNIP 1.157
The livestock reservoir for antimicrobial resistance: a personal view on changing patterns of risks, effects of interventions and the way forward

The purpose of this review was to provide an updated overview on the use of antimicrobial agents in livestock, the associated problems for humans and current knowledge on the effects of reducing resistance in the livestock reservoir on both human health and animal production. There is still limiting data on both use of antimicrobial agents, occurrence and spread of resistance as well as impact on human health. However, in recent years, emerging issues related to methicillin-resistant Staphylococcus aureus, Clostridium difficile, Escherichia coli and horizontally transferred genes indicates that the livestock reservoir has a more significant impact on human health than was estimated 10 years ago, where the focus was mainly on resistance in Campylobacter and Salmonella. Studies have indicated that there might only be a marginal if any benefit from the regular use of antibiotics and have shown that it is possible to substantially reduce the use of antimicrobial agents in livestock production without compromising animal welfare or health or production. In some cases, this should be done in combination with other measures such as biosecurity and use of vaccines. To enable better studies on both the global burden and the effect of interventions, there is a need for global harmonized integrated and continuous surveillance of antimicrobial usage and antimicrobial resistance, preferably associated with data on production and animal diseases to determine the positive and negative impact of reducing antimicrobial use in livestock.
Analysis of the contribution of bacteriophage ST64B to in vitro virulence traits of Salmonella enterica serovar Typhimurium

Comparison of the publicly available genomes of the virulent Salmonella enterica serovar Typhimurium (S. Typhimurium) strains SL1344, 14028s and D23580 to that of the virulence-attenuated isolate LT2 revealed the absence of a full sequence of bacteriophage ST64B in the latter. Four selected ST64B regions of unknown function (sb7–sb11, sb46, sb49–sb50 and sb54) were mapped by PCR in two strain collections: (i) 310 isolates of S. Typhimurium from human blood or stool samples, and from food, animal and environmental reservoirs; and (ii) 90 isolates belonging to other serovars. The region sb49–sb50 was found to be unique to S. Typhimurium and was strongly associated with strains isolated from blood samples (100 and 28.4 % of the blood and non-blood isolates, respectively). The region was cloned into LT2 and knocked out in SL1344, and these strains were compared to wild-type isogenic strains in in vitro assays used to predict virulence association. No difference in invasion of the Int407 human cell line was observed between the wild-type and mutated strains, but the isolate carrying the whole ST64B prophage was found to have a slightly better survival in blood. The study showed a high prevalence and a strong association between the prophage ST64B and isolates of S. Typhimurium collected from blood, and may indicate that such strains constitute a selected subpopulation within this serovar. Further studies are indicated to determine whether the slight increase in blood survival observed in the strain carrying ST64B genes is of paramount importance for systemic infections.
The emergence of resistance in food animals has been associated to the consumption of antimicrobials in veterinary medicine. Consequently, monitoring programs have been designed to monitor the occurrence of antimicrobial resistant bacteria. This study analyses the amount of antimicrobial agents used in nine European countries from 2005 to 2011, and compares by univariate analysis the correlations between consumptions of each of the following antimicrobial classes; tetracycline, penicillins, cephalosporins, quinolones and macrolides. An overview of resistance in zoonotic and commensal bacteria in Europe focusing on Salmonella, Escherichia coli, Campylobacter sp. and Enterococcus sp., during the same period of time based on monitoring programs is also assessed. With the exception of cephalosporins, linear regressions showed strong positive associations between the consumption of the four different antimicrobial classes. Substantial differences between countries were observed in the amount of antimicrobials used to produce 1kg of meat. Moreover, large variations in proportions of resistant bacteria were reported by the different countries, suggesting differences in veterinary practice. Despite the withdrawn of a specific antimicrobial from "on farm" use, persistence over the years of bacteria resistant to this particular antimicrobial agent, was still observed. There were also differences in trends of resistance associated to specific animal species. In order to correlate the use of antimicrobial agents to the presence of resistance, surveillance of antimicrobial consumption by animal species should be established. Subsequently, intervention strategies could be designed to minimize the occurrence of resistance.
Benchmarking of methods for genomic taxonomy

One of the first issues that emerges when a prokaryotic organism of interest is encountered is the question of what it is—that is, which species it is. The 16S rRNA gene formed the basis of the first method for sequence-based taxonomy and has had a tremendous impact on the field of microbiology. Nevertheless, the method has been found to have a number of shortcomings. In the current study, we trained and benchmarked five methods for whole-genome sequence-based prokaryotic species identification on a common data set of complete genomes: (i) SpeciesFinder, which is based on the complete 16S rRNA gene; (ii) Reads2Type that searches for species-specific 50-mers in either the 16S rRNA gene or the gyrB gene (for the Enterobacteracae family); (iii) the ribosomal multilocus sequence typing (rMLST) method that samples up to 53 ribosomal genes; (iv) TaxonomyFinder, which is based on species-specific functional protein domain profiles; and finally (v) KmerFinder, which examines the number of cooccurring k-mers (substrings of k nucleotides in DNA sequence data). The performances of the methods were subsequently evaluated on three data sets of short sequence reads or draft genomes from public databases. In total, the evaluation sets constituted sequence data from more than 11,000 isolates covering 159 genera and 243 species. Our results indicate that methods that sample only chromosomal, core genes have difficulties in distinguishing closely related species which only recently diverged. The KmerFinder method had the overall highest accuracy and correctly identified from 93% to 97% of the isolates in the evaluations sets.

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BFI (2017): BFI-level 1
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Web of Science (2017): Impact factor 4.054
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.196 SNIP 1.4
Web of Science (2016): Impact factor 3.712
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.56 SJR 2.206 SNIP 1.431
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.84 SJR 2.231 SNIP 1.528
Web of Science (2014): Impact factor 3.993
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.18 SJR 2.438 SNIP 1.63
Web of Science (2013): Impact factor 4.232
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Characterization of Extended spectrum beta-lactamases (ESBL)-producing Escherichia coli obtained from Danish pigs, pig farmers and their families from farms with high or no consumption of 3rd or 4th generation cephalosporins

Objectives: To compare and characterize extended-spectrum b-lactamase (ESBL)-producing Escherichia coli from pigsties, pig farmers and their families on farms with previous high or no use of third- or fourth-generation cephalosporins. Methods: Twenty farms with no third- or fourth-generation cephalosporin use and 19 herds with previous frequent use were included. The ESBL-producing isolates detected in humans and pigs were characterized by ESBL genotype, PFGE, susceptibility to non-b-lactam antibiotics and phylotype, and selected isolates were characterized by multilocus sequence typing (MLST). Furthermore, transferability of blaCTX-M-1 from both human and pig isolates was studied and plasmid incompatibility groups were defined. The volunteers answered a questionnaire including epidemiological risk factors for carriage of ESBL-producing E. coli. Results: ESBL-producing E. coli was detected in pigs on 79% of the farms with high consumption of cephalosporins compared with 20% of the pigs on farms with no consumption. ESBL-producing E. coli was detected in 19 of the 195 human participants and all but one had contact with pigs. The genes found in both humans and pigs at the same farms were blaCTX-M-1 (eight farms), blaCTX-M-14 (one
farm) and blaSHV-12 (one farm). At four farms ESBL-producing E. coli isolates with the same CTX-M enzyme, phylotype, PFGE type and MLST type were detected in both pigs and farmers. The majority of the plasmids with blaCTX-M-1 were transferable by conjugation and belonged to incompatibility group IncI1, IncF, or IncN. Conclusions: The present study shows an increased frequency of ESBL-producing E. coli on farms with high consumption of third- or fourth-generation cephalosporins and indicates transfer of either ESBL-producing E. coli or plasmids between pigs and farmers.
Characterization of methicillin-resistant Staphylococcus aureus Sequence Type 398

Staphylococcus aureus is an opportunistic pathogen that colonizes the nares and skin surfaces of several animal species, including man. S. aureus can cause a wide variety of infections ranging from superficial soft tissue and skin infections to severe and deadly systemic infections. Traditionally S. aureus and methicillin-resistant Staphylococcus aureus (MRSA) have been associated with hospitals, but during the past decades MRSA has emerged in the community and now a new branch of MRSA has been found in association with livestock (LA-MRSA). A specific lineage (multilocus sequence type 398 (ST398)) has been particularly successful in colonization of pigs and ST398 has become the most frequently reported MRSA strain found in associated with livestock.

Currently the understanding of the successful colonization and transmission of LA-MRSA ST398 in pigs are limited and mainly based on observational field surveys. The aim of this work was to develop a high-throughput approach for genotypic and phenotypic characterization of LA-MRSA ST398 in the porcine reservoir.

The thesis represents three studies (manuscript I-III). In manuscript I a genome-saturated transposon mutant library was generated and Transposon Directed Inserted site Sequencing (TraDIS) was for the first time assessed in an LA-MRSA ST398 strain. Using this high-throughput approach, genes essential for LA-MRSA ST398 survival under laboratory conditions and in whole porcine blood in vitro were identified. In manuscript II, genes important for LA-MRSA ST398 survival on porcine skin and nasal epithelium ex vivo were identified. These genes could represent targets for de-colonization, which could help prevent further spread and adaption of LA-MRSA ST398. Manuscript III describes the construction of the S. aureus VirulenceFinder database. The database can be applied for identification of virulence genes in S. aureus using whole genome 5 sequence data. The S. aureus VirulenceFinder will be part of the tool package generated for the Centre for Genomic Epidemiology (CGE) (www.genomicepidemiology.org).
Effect of subinhibitory concentrations of four commonly used biocides on the conjugative transfer of Tn916 in Bacillus subtilis

Objectives Large amounts of biocides are used to reduce and control bacterial growth in the healthcare sector, food production and agriculture. This work explores the effect of subinhibitory concentrations of four commonly used biocides (ethanol, hydrogen peroxide, chlorhexidine digluconate and sodium hypochlorite) on the conjugative transposition of the mobile genetic element Tn916.

Methods Conjugation assays were carried out between Bacillus subtilis strains. The donor containing Tn916 was pre-exposed to subinhibitory concentrations of each biocide for a defined length of time, which was determined by an analysis of the transcriptional response of the promoter upstream of tet(M) using β-glucuronidase reporter assays. Results Ethanol significantly (P = 0.01) increased the transfer of Tn916 by 5-fold, whereas hydrogen peroxide, chlorhexidine digluconate and sodium hypochlorite did not significantly affect the transfer frequency.

Conclusions These results suggest that exposure to subinhibitory concentrations of ethanol may induce the transfer of Tn916-like elements and any resistance genes they contain.
Evaluation of whole genome sequencing for outbreak detection of Salmonella enterica

Salmonella enterica is a common cause of minor and large food borne outbreaks. To achieve successful and nearly ‘real-time’ monitoring and identification of outbreaks, reliable sub-typing is essential. Whole genome sequencing (WGS) shows great promises for using as a routine epidemiological typing tool. Here we evaluate WGS for typing of S. Typhimurium including different approaches for analyzing and comparing the data. A collection of 34 S. Typhimurium isolates was sequenced. This consisted of 18 isolates from six outbreaks and 16 epidemiologically unrelated background strains. In addition, 8 S. Enteritidis and 5 S. Derby were also sequenced and used for comparison. A number of different bioinformatics approaches were applied on the data; including pan-genome tree, k-mer tree, nucleotide difference tree and SNP tree. The outcome of each approach was evaluated in relation to the association of the isolates to specific outbreaks. The pan-genome tree clustered 65% of the S. Typhimurium isolates according to the pre-defined epidemiology, the k-mer tree 88%, the nucleotide difference tree 100% and the SNP tree 100% of the strains within S. Typhimurium. The resulting outcome of the four phylogenetic analyses were also compared to PFGE revealing that WGS typing achieved the greater performance than the traditional method. In conclusion, for S. Typhimurium, SNP analysis and nucleotide difference approach of WGS data seem to be the superior methods for epidemiological typing compared to other phylogenetic analytic approaches that
may be used on WGS. These approaches were also superior to the more classical typing method, PFGE. Our study also indicates that WGS alone is insufficient to determine whether strains are related or un-related to outbreaks. This still requires the combination of epidemiological data and whole genome sequencing results.

**General information**

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Organisations: Comparative Microbial Genomics, National Food Institute, Division of Epidemiology and Microbial Genomics, Department of Systems Biology, Center for Systems Microbiology, Center for Biological Sequence Analysis, Immunological Bioinformatics, Statens Serum Institut
Contributors: Leekitcharoenphon, P., Nielsen, E. M., Kaas, R. S., Lund, O., Aarestrup, F. M.
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BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.54 SJR 1.559 SNIP 1.148
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BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.614 SNIP 1.046
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Evidence-based policy for controlling antimicrobial resistance in the food chain in Denmark

Emergence of antimicrobial resistance (AMR) in the animal reservoir forms a risk for human health. The use of antimicrobials in animals is the major cause of development of AMR in animals. In the 1990s, the use of antimicrobials in animals, particularly as a growth promoter, led to alarming levels of AMR in many countries. This paper analyses the emergence of AMR in Denmark in terms of contributing factors that formed fertile ground from which AMR could develop. New technologies in combination with scientific unknowns led to the unexpected development of cross-resistance and an uncertainty about transmission to and risk for humans. Conflict of interests and varying susceptibility to risk between agriculture, health and commercial stakeholders complicated intervention. In addition, unintended economic incentives from old legislation resulted in a situation where the use of antimicrobials in general was stimulated. Complications of alarming high levels of AMR in animals, and a general discontent about this situation (including farmers and vets) demanded a solution. National surveillance in DANMAP involving all stakeholders from the farm-to-fork food chain was setup to counteract scientific unknowns and conflicts of interest; new legislation was developed; and unintended economic incentives reduced. The current analysis may help to better understand the AMR problem in general and what may be done to counteract it.

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BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.27 SJR 1.38 SNIP 1.717
Web of Science (2014): Impact factor 2.806
Genome Sequences of Three Highly Copper-Resistant Salmonella enterica subsp. I Serovar Typhimurium Strains Isolated from Pigs in Denmark.

Salmonella typhimurium is the causative agent of typhoid fever, which causes nearly 21.7 million illnesses and 217,000 deaths around the world each year. Here, we describe the draft genome sequences of the Salmonella typhimurium strains S7, S15, and S23, isolated from copper-fed pigs in Denmark and containing additional putative determinants conferring resistances to copper and other metals and metalloids.

General information
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Genome Sequences of Two Copper-Resistant Escherichia coli Strains Isolated from Copper-Fed Pigs.
The draft genome sequences of two copper-resistant Escherichia coli strains were determined. These had been isolated from copper-fed pigs and contained additional putative operons conferring copper and other metal and metalloid resistances.

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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, University of Copenhagen, King Saud University
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10.1128/genomeA.01341-14
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Source-ID: 273382351
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Genome-Wide High-Throughput Screening to Investigate Essential Genes Involved in Methicillin-Resistant Staphylococcus aureus Sequence Type 398 Survival

Livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) Sequence Type 398 (ST398) is an opportunistic pathogen that is able to colonize and cause disease in several animal species including humans. To better understand the adaptation, evolution, transmission and pathogenic capacity, further investigations into the importance of the different genes harboured by LA-MRSA ST398 are required. In this study we generated a genome-wide transposon mutant library in an LA-MRSA ST398 isolate to evaluate genes important for bacterial survival in laboratory and host-specific environments. The transposon mutant library consisted of approximately 1 million mutants with around 140,000 unique insertion sites and an average number of unique inserts per gene of 44.8. We identified LA-MRSA ST398 essential genes comparable to other high-throughput S. aureus essential gene studies. As ST398 is the most common MRSA isolated from pigs, the transposon mutant library was screened in whole porcine blood. Twenty-four genes were specifically identified as important for bacterial survival in porcine blood. Twenty-four genes were specifically identified as important for bacterial survival in porcine blood. Mutations in 23 of these genes resulted in attenuated bacterial fitness. Seven of the 23 genes were of unknown function, whereas 16 genes were annotated with functions predominantly related to carbon metabolism, pH shock and a variety of regulations and only indirectly to virulence factors. Mutations in one gene of unknown function resulted in a hypercompetitive mutant. Further evaluation of these genes is required to determine their specific relevance in blood survival.
In Silico Detection and Typing of Plasmids using PlasmidFinder and Plasmid Multilocus Sequence Typing

In the work presented here, we designed and developed two easy-to-use Web tools for in silico detection and characterization of whole-genome sequence (WGS) and whole-plasmid sequence data from members of the family Enterobacteriaceae. These tools will facilitate bacterial typing based on draft genomes of multidrug-resistant Enterobacteriaceae species by the rapid detection of known plasmid types. Replicon sequences from 559 fully sequenced plasmids associated with the family Enterobacteriaceae in the NCBI nucleotide database were collected to build a consensus database for integration into a Web tool called PlasmidFinder that can be used for replicon sequence analysis of raw, contig group, or completely assembled and closed plasmid sequencing data. The PlasmidFinder database currently consists of 116 replicon sequences that match with at least 80% nucleotide identity all replicon sequences identified in the 559 fully sequenced plasmids. For plasmid multilocus sequence typing (pMLST) analysis, a database that is updated weekly was generated from www.pubmlst.org and integrated into a Web tool called pMLST. Both databases were evaluated using draft genomes from a collection of Salmonella enterica serovar Typhimurium isolates. PlasmidFinder
identified a total of 103 replicons and between zero and five different plasmid replicons within each of 49 S. Typhimurium draft genomes tested. The pMLST Web tool was able to subtype genomic sequencing data of plasmids, revealing both known plasmid sequence types (STs) and new alleles and ST variants. In conclusion, testing of the two Web tools using both fully assembled plasmid sequences and WGS-generated draft genomes showed them to be able to detect a broad variety of plasmids that are often associated with antimicrobial resistance in clinically relevant bacterial pathogens.

**General information**

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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Center for Biological Sequence Analysis, Immunological Bioinformatics, Department of Systems Biology, Istituto Superiore di Sanità
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BFI (2017): BFI-level 1
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Web of Science (2017): Impact factor 4.255
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.45 SJR 2.361 SNIP 1.428
Web of Science (2014): Impact factor 4.476
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.67 SJR 2.423 SNIP 1.411
Web of Science (2013): Impact factor 4.451
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.88 SJR 2.363 SNIP 1.5
Web of Science (2012): Impact factor 4.565
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 5.02 SJR 2.523 SNIP 1.574
Web of Science (2011): Impact factor 4.841
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
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Scopus rating (2010): SJR 2.458 SNIP 1.54
Rapid Whole-Genome Sequencing for Detection and Characterization of Microorganisms Directly from Clinical Samples (vol 52, pg 139, 2014)

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Department of Systems Biology, Center for Biological Sequence Analysis, Metagenomics, Behavioral Phenomics, Functional Human Variation, Immunological Bioinformatics, Copenhagen University Hospital
Contributors: Hasman, H., Saputra, D., Sicheritz-Pontén, T., Lund, O., Svendsen, C. A., Frimodt-Møller, N., Aarestrup, F. M.
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BFI (2017): BFI-level 1
Rapid whole genome sequencing for the detection and characterization of microorganisms directly from clinical samples.

Whole genome sequencing (WGS) is becoming available as a routine tool for clinical microbiology. If applied directly on clinical samples this could further reduce diagnostic time and thereby improve control and treatment. A major bottle-neck is the availability of fast and reliable bioinformatics tools. This study was conducted to evaluate the applicability of WGS directly on clinical samples and to develop easy-to-use bioinformatics tools for analysis of the sequencing data. Thirty-five random urine samples from patients with suspected urinary tract infections were examined using conventional microbiology, WGS of isolated bacteria and by directly sequencing on pellets from the urine. A rapid method for analyzing the sequence data was developed. Bacteria were cultivated from 19 samples, but only in pure culture from 17. WGS improved the identification of the cultivated bacteria and almost complete agreement was observed between phenotypic and predicted antimicrobial susceptibility. Complete agreement was observed between species identification, multi-locus-sequence typing and phylogenetic relationship for the Escherichia coli and Enterococcus faecalis isolates when comparing the results of WGS of cultured isolates and directly from the urine samples. Sequencing directly from the urine enabled bacterial identification in polymicrobic samples. Additional putative pathogenic strains were observed in some culture negative samples. WGS directly on clinical samples can provide clinically relevant information and drastically reduce diagnostic time. This may prove very useful, but the need for data analysis is still a hurdle to clinical implementation. To overcome this problem a publicly available bioinformatics tool was developed in this study.

General information

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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Department of Systems Biology, Center for Biological Sequence Analysis, Copenhagen University Hospital
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Web of Science (2017): Impact factor 4.054
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.196 SNIP 1.4
Web of Science (2016): Impact factor 3.712
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.56 SJR 2.206 SNIP 1.431
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli.
Fast and accurate identification and typing of pathogens are essential for effective surveillance and outbreak detection. The current routine procedure is based on a variety of techniques, making the procedure laborious, time-consuming, and expensive. With whole-genome sequencing (WGS) becoming cheaper, it has huge potential in both diagnostics and routine surveillance. The aim of this study was to perform a real-time evaluation of WGS for routine typing and surveillance of verocytotoxin-producing Escherichia coli (VTEC). In Denmark, the Statens Serum Institut (SSI) routinely receives all suspected VTEC isolates. During a 7-week period in the fall of 2012, all incoming isolates were concurrently subjected to WGS using IonTorrent PGM. Real-time bioinformatics analysis was performed using web-tools (www.genomicepidemiology.org) for species determination, multilocus sequence type (MLST) typing, and determination of phylogenetic relationship, and a specific VirulenceFinder for detection of E. coli virulence genes was developed as part of this study. In total, 46 suspected VTEC isolates were characterized in parallel during the study. VirulenceFinder proved successful in detecting virulence genes included in routine typing, explicitly verocytotoxin 1 (vtx1), verocytotoxin 2 (vtx2), and intimin (eae), and also detected additional virulence genes. VirulenceFinder is also a robust method for assigning verocytotoxin (vtx) subtypes. A real-time clustering of isolates in agreement with the epidemiology was established from WGS, enabling discrimination between sporadic and outbreak isolates. Overall, WGS typing produced results faster and at a lower cost than the current routine. Therefore, WGS typing is a superior alternative to conventional typing strategies. This approach may also be applied to typing and surveillance of other pathogens.
Report of the 5th External Quality Assurance System on Identification and Typing of Methicillin resistant Staphylococcus aureus (MRSA), 2013

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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Contributors: Cavaco, L., Karlsmose, S., Hendriksen, R. S., Aarestrup, F. M.
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Place of publication: Kgs. Lyngby
Publisher: National Food Institute, Technical University of Denmark
Solving the Problem of Comparing Whole Bacterial Genomes across Different Sequencing Platforms

Whole genome sequencing (WGS) shows great potential for real-time monitoring and identification of infectious disease outbreaks. However, rapid and reliable comparison of data generated in multiple laboratories and using multiple technologies is essential. So far studies have focused on using one technology because each technology has a systematic bias making integration of data generated from different platforms difficult. We developed two different procedures for identifying variable sites and inferring phylogenies in WGS data across multiple platforms. The methods were evaluated on three bacterial data sets and sequenced on three different platforms (Illumina, 454, Ion Torrent). We show that the methods are able to overcome the systematic biases caused by the sequencers and infer the expected phylogenies. It is concluded that the cause of the success of these new procedures is due to a validation of all informative sites that are included in the analysis. The procedures are available as web tools.

General information
State: Published
Organisations: Comparative Microbial Genomics, National Food Institute, Division of Epidemiology and Microbial Genomics, Department of Systems Biology, Center for Biological Sequence Analysis, Immunological Bioinformatics
Contributors: Kaas, R. S., Leekitcharoenphon, P., Aarestrup, F. M., Lund, O.
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Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.32 SJR 1.427 SNIP 1.136
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Scopus rating (2012): CiteScore 4.15 SJR 1.982 SNIP 1.156
Web of Science (2012): Impact factor 3.73
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.58 SJR 2.425 SNIP 1.233
Web of Science (2011): Impact factor 4.092
Spatio-temporal analysis of Salmonella surveillance data in Thailand

This study evaluates the usefulness of spatio-temporal statistical tools to detect outbreaks using routine surveillance data where limited epidemiological information is available. A dataset from 2002 to 2007 containing information regarding date, origin, source and serotype of 29,586 Salmonella isolates from Thailand was analysed. Data was grouped into human and non-human categories and the analysis was performed for the top five occurring serovars for each year of the study period. A total of 91 human and 39 non-human significant spatio-temporal clusters were observed, accounting for 11% and 16% of the isolates, respectively. Serovar-specific associations between human and non-human clusters were also evaluated. Results show that these statistical tools can provide information for use in outbreak prevention and detection, in countries where only limited data is available. Moreover, it is suggested that monitoring non-human reservoirs can be relevant in predicting future Salmonella human cases.

General information
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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Thailand Ministry of Public Health
Contributors: Coutinho Calado Domingues, A. R., Vieira, A., Hendriksen, R. S., Pulsrikarn, C., Aarestrup, F. M.
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Web of Science (2017): Impact factor 2.044
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The 14th EURL-AR Proficiency Test - enterococci, staphylococci and E. coli 2013

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The External Quality Assurance System of the WHO Global Foodborne Infections Network, 2013

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Research output: Research - peer-review › Report – Annual report year: 2014
The Role of the st313-td Gene in Virulence of Salmonella Typhimurium ST313

Multidrug-resistant Salmonella enterica serovar Typhimurium ST313 has emerged in sub-Saharan Africa causing severe infections in humans. Therefore, it has been speculated that this specific sequence type, ST313, carries factors associated with increased pathogenicity. We assessed the role in virulence of a gene with a yet unknown function, st313-td, detected in ST313 through comparative genomics. Additionally, the structure of the genomic island ST313-GI, harbouring the gene was determined. The gene st313-td was cloned into wild type S. Typhimurium 4/74 (4/74-C) as well as knocked out in S. Typhimurium ST313 02-03/002 (Delta st313-td) followed by complementation (02-03/002-C). Delta st313-td was less virulent in mice following i.p. challenge than the wild type and this phenotype could be partly complemented in trans, indicating that st313td plays a role during systemic infection. The gene st313-td was shown not to affect invasion of cultured epithelial cells, while the absence of the gene significantly affects uptake and intracellular survival within macrophages. The gene st313-td was proven to be strongly associated to invasiveness, harboured by 92.5% of S. Typhimurium blood isolates (n = 82) and 100% of S. Dublin strains (n = 50) analysed. On the contrary, S. Typhimurium isolates of animal and food origin (n = 82) did not carry st313-td. Six human, non-blood isolates of S. Typhimurium from Belarus, China and Nepal harboured the gene and belonged to sequence types ST398 and ST19. Our data showed a global presence of the st313-td gene and in other sequence types than ST313. The gene st313-td was shown to be expressed during logarithmic phase of growth in 14 selected Salmonella strains carrying the gene. This study reveals that st313-td plays a role in S. Typhimurium ST313 pathogenesis and adds another chapter to understanding of the virulence of S. Typhimurium and in particular of the emerging sequence type ST313.
Whole Genome Epidemiological Typing of Escherichia coli

*Escherichia coli* (E. coli) is of huge importance in global health both as a commensal organism living within its host or as a pathogen causing millions of infections each year. Infections occur both sporadic and as outbreaks with sometimes up to thousands of infected people. To limit the number of infections it is important to monitor pathogenic *E. coli* in order to detect outbreaks as quickly as possible and find the source of the outbreak. The effectiveness of monitoring and tracking of pathogens is very dependent on the typing methods that are employed. Classical typing methods employed for *E. coli* is in general expensive and to some extent unreliable. Next generation sequencing has quickly become a tool widely available and has enabled even smaller laboratories to do whole genome sequencing (WGS). Having the entire genome available provides the opportunity to create the ultimate typing method. This PhD thesis attempts to take the first steps toward such a method.

In Kaas I all publicly available *E. coli* genomes sequenced (186) are analyzed. 1,702 core genes were found in all genomes. 3,051 genes were found in 95% of the genomes. The overall phylogeny was inferred from the core genome and also set into context of the *Escherichia* genus. The variance within each gene cluster was calculated in order to compare the variance between genes and possibly identify typing targets for further study. The variance scores calculated was also used to compare the three MLST schemes that exist for *E. coli*.

It quickly became clear that single nucleotide polymorphism (SNP) analysis was becoming the method of choice for inferring the phylogeny of bacterial outbreaks. However, the method remained unavailable to many people due to technical obstacles. In Kaas II we describe the SNP method and the validation behind a web server that we set up in order to overcome some of the technical obstacles faced by many people and thereby making the method more available. The method briefly, calls SNPs against a specified reference sequence, creates an alignment (pseudosequence) of all the SNPs, and uses the maximum likelihood (ML) method to create a tree. The most important detail in the method is the assumption made about “missing” SNPs. Meaning SNPs called in one strain but not in another. It was assumed that SNPs not found in a position was due to that nucleotide being identical to the one in the reference sequence. The assumption is in general valid if all the genomes compared are closely related and the sequencing data is of good quality.

In Kaas III we sought to overcome the assumption mentioned above but most important of all we wanted to create a method that could handle sequence data obtained from different sequencing technologies. The method from Kaas II was completely rewritten and a new web server (CSI Phylogeny) was published that could handle sequence data of all kinds and no longer made assumptions about missing SNPs. Very briefly, the method differs from Kaas II mainly by validating all the locations in all the genomes in which a SNP has been called in any genome. In parallel to the development of a new SNP method another method was also developed that briefly, relies on counting nucleotide differences (ND) between each genome pair, while also validating each position analyzed and ignoring the positions that cannot be validated thereby creating a distance matrix that is used as input to an UPGMA method that creates the final phylogeny. The ND method was also implemented as a web server and published.

If whole genome sequencing is to be used for routine monitoring and tracking of *E. coli* pathogens, it is crucial to have an idea of how large the difference is between isolates from the same outbreak, compared to the difference to other non-outbreak isolates, in order to do reliable distinctions. In Kaas IV we analyzed ten different outbreaks. Seven of the outbreaks were sequenced for the study and three of the outbreaks were obtained from published studies. Several background isolates that resembled the outbreak isolates were also sequenced. Five different bioinformatic methods were evaluated against the 10 outbreaks. The five different methods were based on SNP, ND, core genes, k-mers, and average nucleotide identity (ANI). Only the ANI method was not able to cluster all outbreaks correctly. The pairwise distance between all isolates were also calculated by each method and compared. Most methods showed lower distance between isolates in the same outbreak compared to the background strains, but only the SNP method was able to set one common threshold for outbreak isolates versus non-outbreak isolates for the entire dataset.

Whole genome sequencing is a powerful but also a rather new tool. This PhD thesis has hopefully shed some light on how we can continue development of whole genome sequence typing and also made WGS more available to a broader audience.

**General information**

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**Organisations:** National Food Institute, Research Group for Genomic Epidemiology, Department of Systems Biology, Center for Biological Sequence Analysis

**Contributors:** Kaas, R. S., Aarestrup, F. M., Ussery, D., Lund, O.

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Whole Genome Epidemiological Typing of Salmonella

Salmonella is one of the most common foodborne pathogens worldwide. In the US alone, salmonellosis was estimated to cause 1.4 million cases effecting 17,000 hospitalization and almost 600 deaths each year. Particularly, Salmonella enterica is a common cause of minor and large food borne outbreaks. Technological advances and effective price in high throughput genome sequencing are making whole genome sequencing (WGS) available as a routine tool for bacterial typing. Typing of Salmonella, especially sub-typing within the same serotype or even the same clone, the genetic variation of the targeted genes being used for typing is crucial for successful discrimination. The core genes or the genes that are conserved in all members of a genus or species are potentially good candidates for investigating genomic variation in phylogeny and epidemiology. A total of 2,882 core genes have been observed among 73 available Salmonella enterica genomes (accessed in April 2011). A consensus tree based on variation of the core genes gives better resolution than 16S rRNA and MLST that rarely provide separation between closely related strains. The performance of the pan-genome tree which is based on the presence/absence of all genes across genomes, is similar to the consensus tree but with higher branching confidence value. The core genes can be divided into two categories: a few highly variable genes and a larger set of conserved core genes, with low variance. These core genes are useful for investigating molecular evolution and remain useful as candidate genes for bacterial genome typing—even if they cannot be expected to differentiate highly clonal isolates e.g. outbreak cases of Salmonella [I].

To achieve successful ‘real-time’ monitoring and identification of outbreaks, rapid and reliable sub-typing is essential. A collection of thirty-four human S. Typhimurium strains from six different outbreaks together with background strains plus eight S. Enteritidis isolates from two outbreaks and five S. Derby isolates from a single outbreak were used to evaluate the strengths and drawbacks of different WGS approaches compared to the traditional typing, PFGE, for retrospectively outbreak typing of Salmonella. The resulting outcome showed that SNP analysis and nucleotide difference approach seem to be the superior methods for outbreak detection compared to other phylogenetic analytic approaches of WGS. Furthermore, WGS approaches were also superior to the more classical typing method, PFGE. Meanwhile, k-mer method constructs a tree in high speed and giving high accuracy in clade level [II].

SNP analysis has successfully applied in recent epidemiological studies of Salmonella. Currently, there are different tools and methods to identify SNPs including various cut-off values. In addition, all the tools require bioinformatics skill. In order to use WGS in routine typing, an automatic and user-friendly tool is needed. Therefor, snpTree has been developed as a server for online-automatic SNP analysis. snpTree can identify SNPs and construct phylogenetic tree from WGS raw reads as well as from assembled genomes or contigs. The tool is freely accessible at http://cge.cbs.dtu.dk/services/snpTree/ [III].

Globally, Salmonella enterica serovar Typhimurium is the most commonly isolated serovar. S. Typhimurium consists of a number of subtypes that conventionally have been divided by phagetyping. During the last three decades, S. Typhimurium phage type DT104 emerged as the most prevalent phage type and one of the best-studied because of its rapid global dissemination. Nonetheless, the origin and transmission route of this particular phage type have not been revealed. To bridge the gaps in epidemiology of DT104, WGS and temporally structured sequence analysis within Bayesian framework have been incorporated for reconstructing temporal and spatial phylogenies, estimating rate of mutation and divergence time of global and local S. Typhimurium DT104 isolates sampled from 1969 to 2012 from twenty-one countries in six continents. The DT104 was estimated to initially emerge as antimicrobial-susceptible strains in ~1946 (1931-1959) and further became multidrug-resistant (MDR) DT104 in ~1974 (1966-1981) through horizontal transfer of 13-kb SG1 MDR region into SG1-contained susceptible strains. Changes in population size over time supported global occurrences of MDR DT104. Besides, using WGS is capable to confirm local epidemiology especially the transmission between animal herds of DT104 isolates from Denmark. Interestingly, the demographic history of Danish MDR DT104 provided an evidence for the accomplishment of an eradicating program across pig herds in Denmark during 1996 to 2000 [IV].

Overall, this Ph.D. thesis has assessed the usefulness of WGS epidemiological typing in Salmonella as well as evaluated the different WGS approaches for outbreak investigation compared to the traditional typing, PFGE. An online tool to construct phylogenetic tree based on SNPs has also been developed. Furthermore, it has revealed the application of WGS in epidemiological study of global and local occurrences of S. Typhimurium DT104.

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State: Published
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A Danish Salmonella Bareilly outbreak investigated by the use of whole genome sequencing

In 2012, we saw an increase of the Salmonella serotype Bareilly isolated from human infections. Bareilly is a rare serotype in Denmark, isolated from human infections between 2 and 9 times annually over the last 10 years. As a routine in rare serotypes, we use PFGE as the molecular method for cluster analysis, outbreak investigations, comparison with food and animal isolates as well as making international inquiries. In this case, we found Bareilly with the same PFGE profile from 8 patients. Seven of the cases could be traced back to an unknown food source served at a specific restaurant. At the same time four broiler flocks flocks were tested positive for Bareilly. Bareilly is also rare in the Danish food production, and it was the first time in more than 10 years that Bareilly was isolated in broiler flocks. PFGE was performed on these isolates as well and the profiles from humans and broilers differed by two bands.

When using PFGE in outbreak investigation there are some interpretative implications that have to be considered. There are differences on how important band changes are when defining clusters of different serotypes. Some outbreaks have been reported to include PFGE profiles with several band changes and others are defined by one PFGE profile thereby excluding closely related profiles. We decided to investigate whether whole genome sequencing (WGS) could resolve this issue and be useful in outbreak investigations.

Several analyses were performed, including a SNP tree based on the core genome, MLST profiles and detection of phages in the genome. The human cluster and the broiler isolates belonged to the same ST, but the isolates were divided into two groups, 9 SNPs apart, according to an MP phylogeny. When using PHAST, we found that two phage regions were 100% similar and present in both groups, whereas a third phage region was only present in the human isolates. These data indicate a close common ancestor between the two groups. However, the positive broiler flocks does not seem to be the direct source of the human outbreak.

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Animal and public health surveillance of infectious diseases

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KNO2* - Keynote Lectures
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Comparison of proficiency testing results on antimicrobial susceptibility testing of Salmonella and Campylobacter obtained by laboratories from the ECDC FWD network (public health) and the EURL-AR network (veterinary/food) 2012

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Contributors: Karlsmose, S., Cavaco, L., Hendriksen, R. S., Aarestrup, F. M.
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Comparison of typing by whole genome sequencing (WGS) and pulsed field gel electrophoresis (PFGE) of isolates from a hospital outbreak with a CTX-M-15 producing Klebsiella pneumoniae

Objective: Klebsiella pneumoniae (KP) is the archetype of a Gram negative outbreak organism with acquired antibiotic resistance. Reference epidemiology typing method have for many years been PFGE. The ultimate typing tool must however be knowing the entire variation within the genomes of the involved organisms. Recent technological development and pricing have made this possible. Our objective was to compare typing by WGS with PFGE on nosocomial KP outbreak isolates.

Methods: 44 KP isolates from 2006 (pre-outbreak) through 2007/8 (outbreak) to 2011 (endemic) from 33 patients and 5 KP reference strains, were investigated. The 44 isolates were phenotypic similar; ESBL-producers with reduced susceptibility to gentamicin and ciprofloxacin. PFGE was performed using XbaI; data handling in BioNumeric. For WGS a reference genome (outbreak isolate 2006-1-264) was assembled to a single scaffold using data from two platforms, Illumina (200x) and 454 (10x) and the program Consed (v23). Reads were trimmed (AdapterRemoval v1.1.) and mapped to the reference genome using Bowtie (v2.0). Single Nucleotide Polymorphisms (SNPs) were called using Samtools. To be considered valid the depth of each SNP position was ≥ 10, and mapping quality was ≥ 20. Pruning of all SNPs within 10bp of each other were done. All SNPs were concatenated into a multiple alignment and phylogeny was inferred using FastTree; tree was visualized using FigTree (v1.4.0).

Results: Both WGS and PFGE divided the 44 KP isolates in a group of 37 outbreak isolates and 7 singletons. Number of SNPs between outbreak isolates and reference strains, and within the outbreak isolates, were up to 23096 and 64 (range: 2-64), respectively. Band differences within outbreak group were 0-5. For single PFGE event no clear correlation to number of SNPs were seen; one pair of isolates differed by 4 band and 2 SNPs, while another pair differed by 0 band and 11 SNPs. The relation over time for consecutive isolates from the same patients were complex, but with a trend towards more SNPs over time.

Conclusion: In general full agreement between WGS and PFGE was seen. WGS has higher resolution and are able to discriminate between isolates of same PFGE type.

Development of bacterial resistance to biocides and antimicrobial agents as a consequence of biocide usage

Biocides are chemical compounds with antimicrobial properties and they are widely used for disinfection, antiseptic and preservation purposes. Biocides have been applied for centuries due to early empirical approaches, such as cleansing of wounds with wine, vinegar and honey and salting of fish and meat. Today, large amounts of biocides are used for disinfection to achieve a satisfactory level of hygiene in various settings and use of biocides has become an integrated part of the industrialized world.
Despite the widespread use and application of biocides knowledge about their exact mechanisms of action, especially at sub-inhibitory concentrations, and the bacterial response to such exposure, is relatively limited. The increasing use of biocides has within recent years lead to concerns about development and emergence of biocide resistant microorganisms that might make the task of eradication of pathogenic bacteria more difficult. Furthermore, it has been suggested that use of biocides may contribute to the development of resistance in bacteria to antimicrobial agents used in human and animal therapy. So far, it is evident that cross- and co-resistance mechanisms to antimicrobials agents and biocides exist.

However, much less is known about the potential effect of biocides on development of antimicrobial resistance in bacteria by promoting the horizontal transfer of resistance genes or by inducing the mutation rate. Even though biocides are commonly used at working concentrations way above the lethal bacterial dose, the efficacy of these compounds can be significantly reduced by incorrect use or the presence of residual concentrations hence, bacterial exposure to sub-inhibitory concentrations of biocides is likely to occur.

The overall objective of this study was to examine if natural bacterial isolates become less susceptible to biocides used in their environment and if this can lead to spread of antimicrobial resistant clones due to co-selection. Furthermore, the objective was to examine if exposure to subinhibitory concentrations of biocides induce development of resistance to antimicrobial agents.

So far, only few studies have investigated the susceptibility of livestock-associated isolates to biocides used in their environment. Pigs are increasingly recognised as a potential reservoir of community-acquired methicillin resistant Staphylococcus aureus (CA-MRSA), especially clones belonging to clonal complex (CC) 398. Recently, methicillin resistant S. aureus (MRSA) isolates belonging to CC30 was for the first time detected among Danish pigs. The susceptibility of 79 porcine S. aureus isolates belonging to CC398 or CC30 to commonly used biocides in pig farming was therefore determined (Manuscript III). The biocides comprised benzalkonium chloride (BC), hydrogen peroxide (HP), sodium hypochlorite (SH), formaldehyde (FH), and caustic soda (NaOH). S. aureus isolates did in general not show reduced susceptibility to the biocides tested. However, a quaternary ammonium compound (QAC) resistance gene, qacG, was detected in MRSA CC30 isolates. The presence of qacG in MRSA CC30 is worrying, since use of QACs may contribute to the selection and spread of these isolates. MRSA CC30 is often associated with MRSA types giving rise to clinical infections in Denmark and porcine MRSA CC30 may be prone to adapt to humans.

Residues or inaccurate use of biocides may lead to bacterial exposure to sub-inhibitory concentrations. The bacterial response to such exposure is however unclear. It has been suggested that the SOS response contribute to antimicrobial resistance development in bacteria by inducing mutagenesis. Therefore, the effect of sub-inhibitory concentrations of the five common biocides; BC, CHX, HP, PAA, and SH on the SOS response, indicated by the use of a recA-lacZ expression assay, and mutagenesis in S. aureus isolates was studied (Manuscript II). BC, CHX, and HP was found to induce the SOS response. In addition, HP and PAA were found to significantly (p = 0.05) increase the mutation rate by 5-15 and 3-8 fold, respectively. These results suggest that exposure to sub-inhibitory concentrations of HP and PAA may contribute to emergence of antimicrobial resistance in S. aureus. This may be of potential risk for human health, since these disinfectants are widely used at hospitals and in the food industry.

Mobile genetic elements such as conjugative transposons are important vectors in the dissemination of antibiotic resistance determinants. Tn916 including the tetracycline resistance gene tet(M) is a conjugative transposon and the prototype of a large family of related elements. They have an extremely broad host range and have been found in both pathogenic and commensal bacteria. In the study of Manuscript I, the effect of sub-inhibitory concentrations of ETOH, HP, CHX, and SH on the conjugative transposition of the mobile genetic element Tn916 was investigated. ETOH was found to significantly (p < 0.05) increase transfer of Tn916 by an average of 5-fold, whereas an increase of 4-fold on Tn916 conjugation frequency was observed (p = 0.12) when donors were exposed to hydrogen peroxide. These results suggest that exposure to sub-inhibitory concentrations of ETOH and HP may induce the spread of Tn916-like elements and their resistance genes, which is clinically important since these biocides are frequently used in hospitals.

In conclusion, no widespread selection for reduced susceptibility to commonly used disinfectants in pig farming was detected in porcine S. aureus isolates. However, a biocide resistance gene, qacG, was identified in several of the MRSA isolates, which has also been found in other animal related staphylococci. Surveillance of the occurrence and emergence of reduced susceptibility to biocides in bacteria are however, still encouraged, since this will provide important data to determine if decreased susceptibility to biocides happen over time. Importantly, the data from this thesis demonstrated a potential of certain biocides to contribute to antimicrobial resistance development and emergence in bacteria through increased mutagenesis and transfer of the antimicrobial resistance gene tet(M). On the short term these results emphasises that correct use of biocides are of outmost importance and should not be compromised. On the long term, more studies are needed to elucidate the actual risk of biocide use on generating antimicrobial resistant bacteria in practice.
External quality assurance system (EQAS) for identification of mastitis pathogens in Denmark from 2006 to 2011

Bovine mastitis is the most common and costly dairy cattle disease. Mastitis is most frequently caused by bacterial species, and to ensure optimal treatment and control strategies, proper quality assured diagnosis and identification of the causative agent is important. With the aim to assess the capacity to isolate and identify mastitis pathogens at veterinary clinics, an external quality assurance system (EQAS) was annually (from 2006 to 2011) provided for the identification of mastitis pathogens. This study presents the setup of the proficiency test and the obtained results that enabled the organizers to pinpoint areas for improvement and thereby to assist veterinary practices at strengthening their mastitis diagnostics. The proficiency test consisted of 15 milk samples spiked with a pure culture of a mastitis pathogen and distributed to veterinary practices for identification. Applying an internal quality control strain, i.e. including the same strain of Streptococcus agalactiae in all iterations of the proficiency test, served to gauge the bias caused by the year-to-year variation in the selection of test strains. A total of 73% of all uploaded results over the years were correct, with the internal quality control strain exhibiting a statistically significant ascending trend from 54% correct identifications in 2006 to 91% in 2011 (p-value=0.0082; n=13). Even if specifics were not recorded as regards the laboratory methods employed at the veterinary clinics for identification of mastitis pathogens, the results from this study indicate that the practices' application of basic biochemical analyses in this context could be optimized. In addition, dissemination of information on new methods and updated nomenclature appeared to be an area which future efforts with advantage could aim at.

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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Impact factor 1.987
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.1 SJR 1.282 SNIP 1.177
Web of Science (2015): Impact factor 2.182
Web of Science (2015): Indexed yes
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Scopus rating (2014): CiteScore 2.37 SJR 1.27 SNIP 1.407
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ISI indexed (2013): ISI indexed yes

Two cases of extremely drug-resistant Salmonella enterica serovar Senftenberg isolated from patients in Zambia were investigated by utilizing MIC determinations and whole-genome sequencing. The isolates were resistant to, and harbored genes toward, nine drug classes, including fluoroquinolones and extended-spectrum cephalosporins, contained two plasmid replicons, and differed by 93 single-nucleotide polymorphisms.

General information
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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, University Teaching Hospital, Pathology and Microbiology Department
Genomics of an emerging clone of Salmonella serovar Typhimurium ST313 from Nigeria and the Democratic Republic of Congo.

We showed in a limited number of isolates that S. Typhimurium ST313 is a prevalent sequence-type causing gastrointestinal diseases and septicemia in patients from Nigeria and DRC. We found three distinct phylogenetic clusters based on the origin of isolation suggesting some spatial evolution. Comparative genomics showed an interesting putative virulence fragment (ST313-TD) unique to S. Typhimurium ST313 and invasive S. Dublin.

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Web of Science (2015): Impact factor 1.139
Genotyping using whole-genome sequencing is a realistic alternative to surveillance based on phenotypic antimicrobial susceptibility testing

Objectives: Antimicrobial susceptibility testing of bacterial isolates is essential for clinical diagnosis, to detect emerging problems and to guide empirical treatment. Current phenotypic procedures are sometimes associated with mistakes and may require further genetic testing. Whole-genome sequencing (WGS) may soon be within reach even for routine surveillance and clinical diagnostics. The aim of this study was to evaluate WGS as a routine tool for surveillance of antimicrobial resistance compared with current phenotypic procedures.

Methods: Antimicrobial susceptibility tests were performed on 200 isolates originating from Danish pigs, covering four bacterial species. Genomic DNA was purified from all isolates and sequenced as paired-end reads on the Illumina platform. The web servers ResFinder and MLST (www.genomicepidemiology.org) were used to identify acquired antimicrobial resistance genes and MLST types (where MLST stands for multilocus sequence typing). ResFinder results were compared with phenotypic antimicrobial susceptibility testing results using EUCAST epidemiological cut-off values and MLST types.

Results: A total of 3051 different phenotypic tests were performed; 482 led to the categorizing of isolates as resistant and 2569 as susceptible. Seven cases of disagreement between tested and predicted susceptibility were observed, six of which were related to spectinomycin resistance in Escherichia coli. Correlation between MLST type and resistance profiles was only observed in Salmonella Typhimurium, where isolates belonging to sequence type (ST) 34 were more resistant than ST19 isolates.

Conclusions: High concordance (99.74%) between phenotypic and predicted antimicrobial susceptibility was observed. Thus, antimicrobial resistance testing based on WGS is an alternative to conventional phenotypic methods.

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Web of Science (2016): Impact factor 5.071
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Scopus rating (2015): CiteScore 4.06 SJR 2.259 SNIP 1.516
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Scopus rating (2014): CiteScore 4.61 SJR 2.298 SNIP 1.765
Web of Science (2014): Impact factor 5.313
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Scopus rating (2010): SJR 2.161 SNIP 1.643
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Scopus rating (2009): SJR 1.902 SNIP 1.615
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.076 SNIP 1.506
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.744 SNIP 1.509
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.771 SNIP 1.437
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.768 SNIP 1.5
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.435 SNIP 1.465
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.367 SNIP 1.338
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.4 SNIP 1.284
Scopus rating (2001): SJR 1.388 SNIP 1.232
Livestock Origin for a Human Pandemic Clone of Community-Associated Methicillin-Resistant Staphylococcus aureus

ABSTRACT The importance of livestock as a source of bacterial pathogens with the potential for epidemic spread in human populations is unclear. In recent years, there has been a global increase in community-associated methicillin-resistant Staphylococcus aureus (CA-MRSA) infections of healthy humans, but an understanding of the different evolutionary origins of CA-MRSA clones and the basis for their recent expansion is lacking. Here, using a high-resolution phylogenetic approach, we report the discovery of two emergent clones of human epidemic CA-MRSA which resulted from independent livestock-to-human host jumps by the major bovine S. aureus complex, CC97. Of note, one of the new clones was isolated from human infections on four continents, demonstrating its global dissemination since the host jump occurred over 40 years ago. The emergence of both human S. aureus clones coincided with the independent acquisition of mobile genetic elements encoding antimicrobial resistance and human-specific mediators of immune evasion, consistent with an important role for these genetic events in the capacity to survive and transmit among human populations. In conclusion, we provide evidence that livestock represent a reservoir for the emergence of new human-pathogenic S. aureus clones with the capacity for pandemic spread. These findings have major public health implications highlighting the importance of surveillance for early identification of emergent clones and improved transmission control measures at the human-livestock interface. IMPORTANCE Animals are the major source of new pathogens affecting humans. However, the potential for pathogenic bacteria that originally were found in animals to switch hosts and become widely established in human populations is not clear. Here, we report the discovery of emergent clones of methicillin-resistant Staphylococcus aureus (MRSA) that originated in livestock and switched to humans, followed by host-adaptive evolution and epidemic spread in global human populations. Our findings demonstrate that livestock can act as a reservoir for the emergence of new human bacterial clones with potential for pandemic spread, highlighting the potential role of surveillance and biosecurity measures in the agricultural setting for preventing the emergence of new human pathogens.
PathogenFinder - Distinguishing Friend from Foe Using Bacterial Whole Genome Sequence Data.

Although the majority of bacteria are harmless or even beneficial to their host, others are highly virulent and can cause serious diseases, and even death. Due to the constantly decreasing cost of high-throughput sequencing there are now many completely sequenced genomes available from both human pathogenic and innocuous strains. The data can be used to identify gene families that correlate with pathogenicity and to develop tools to predict the pathogenicity of newly sequenced strains, investigations that previously were mainly done by means of more expensive and time consuming experimental approaches. We describe PathogenFinder (http://cge.cbs.dtu.dk/services/PathogenFinder/), a web-server for the prediction of bacterial pathogenicity by analysing the input proteome, genome, or raw reads provided by the user. The method relies on groups of proteins, created without regard to their annotated function or known involvement in pathogenicity. The method has been built to work with all taxonomic groups of bacteria and using the entire training-set, achieved an accuracy of 88.6% on an independent test-set, by correctly classifying 398 out of 449 completely sequenced bacteria. The approach here proposed is not biased on sets of genes known to be associated with pathogenicity, thus the approach could aid the discovery of novel pathogenicity factors. Furthermore the pathogenicity prediction web-server could be used to isolate the potential pathogenic features of both known and unknown strains.
Real-Time WGS-based Typing of VTEC Isolates for Surveillance and Outbreak Detection

Objectives: Fast and accurate typing of foodborne pathogens is essential for effective surveillance and the ability to detect and prevent outbreaks. Current routine typing is based on a variety of different typing techniques, making the complete typing procedure laborious, time-consuming and expensive. With whole-genome sequencing (WGS) becoming continuously cheaper and more available, it has huge potential in both diagnostics and routine surveillance. The aim of this study was to evaluate WGS-based typing, in a real-time setup, for routine typing and surveillance of verocytotoxin-producing E.coli (VTEC) infections.

Methods: As part of the routine surveillance in Denmark, suspected VTEC isolates are sent to Statens Serum Institut (SSI) for phenotypic and molecular characterisation by a range of methods. During 7 weeks in the fall 2012, the isolates were simultaneously subjected to WGS using the IonTorrent PGM benchtop sequencing technology. WGS-based typing was carried out using web-based tools, developed by the Center for Genomic Epidemiology (www.genomicepidemiology.org),
for determination of MLST types, virulence genes and phylogenetic relationship between the isolates. The WGS-based
typing was compared to the routine typing and surveillance, with regard to typing results, time consumption and price.
Results: In total, 47 suspected VTEC isolates were typed during the 7 weeks, both by the routine procedures and in
parallel by the WGS-approach, and during the period of the study a small outbreak occurred. For all isolates, apart from
one resulting in poor sequence output, the WGS-based typing led to detection of the same virulence gene variants as the
routine typing, and was also able to detect many other possible virulence features, and in most instances produce a useful
typing result faster than routine typing. Also, the WGS-approach was able to correctly detect, according to the routine
typing, the isolates belonging to the outbreak.
Conclusion: The real-time WGS-based typing was able to produce typing results comparable to the routine typing, at least
as fast as the routine typing. Thus, the benchtop WGS-based typing approach is a reasonable alternative to conventional
typing strategies, and could be applicable to typing and surveillance of other pathogens.

General information
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Report of the 4th External Quality Assurance System on Isolation, Identification and Typing of Methicillin resistant
Staphylococcus aureus (MRSA) from Swab Samples, year 2012

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Contributors: Cavaco, L., Karlsmose, S., Hendriksen, R. S., Aarestrup, F. M.
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Resistance in bacteria of the food chain: epidemiology and control strategies
Antimicrobial agents are widely used for treatment of animals and humans as well as for production purposes in livestock
production in several countries. This is exerting a major selective pressure on bacterial populations, and is selecting for
populations resistant to the antimicrobials used. The emergence and spread of resistant bacteria in the food chain is a
major concern as food-producing animals may constitute a huge reservoir for antimicrobial resistance. Furthermore, food
animals and food of animal origin is traded worldwide, which means that the occurrences of antimicrobial resistance in the
food supply of one country is currently potentially a problem for all countries.

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Staphylococcus aureus CC398: Host Adaptation and Emergence of Methicillin Resistance in Livestock

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Scopus rating (2015): CiteScore 4.93
Web of Science (2015): Impact factor 6.975
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.23
Web of Science (2014): Impact factor 6.786
Web of Science (2014): Indexed yes
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ISI indexed (2013): ISI indexed yes
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The 12th EURL-AR Proficiency Test - enterococci, staphylococci and E. coli 2012

General information
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Contributors: Cavaco, L., Karlsmose, S., Hendriksen, R. S., Aarestrup, F. M.
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The 13th EURL-AR Proficiency Testing Salmonella, Campylobacter and genotypic characterization 2012

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Contributors: Karlsmose, S., Cavaco, L., Hendriksen, R. S., Aarestrup, F. M.
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The first attempt of an active integrated laboratory-based Salmonella surveillance programme in the north-eastern region of Nigeria
To identify the sources of Salmonella contamination, distribution, prevalence and antimicrobial susceptibility patterns, which have significant impact on public and animal health, and international trade. A total of 1888 samples were collected by stratified random sampling from 2009 to 2011 from cattle, camels, poultry, fish, vegetables and humans. All identified Salmonella isolates were serotyped and tested for antimicrobial susceptibility by MIC determinations. A total of 149 Salmonella isolates comprising 17 different serovars were obtained (7.9% prevalence). Salmonella Hadar (37%), S. Eko (17%), S. Enteritidis (10%), S. Kentucky (7%) and S. Uganda (7%) were isolated from different sources. The occurrence of antimicrobial resistance was generally low, but S. Enteritidis and S. Eko showed variable antimicrobial resistance patterns, while all S. Kentucky isolates were resistant to seven of 17 tested antimicrobials, including ciprofloxacin and nalidixic acid.
Three S. Hadar isolates revealed reduced susceptibility to ciprofloxacin and susceptibility to nalidixic acid and harboured the plasmid-mediated quinolone resistance gene qnrS1. Salmonella serovars Hadar, Enteritidis and the previously very rarely reported Eko were the major serovars associated with human infections, animal and environmental contamination in the north-eastern region of Nigeria. These serovars constitute a health risk to poultry, environment and human population in the region.

General information
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Scopus rating (2017): CiteScore 2.41
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.41
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BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.57
Web of Science (2015): Impact factor 1.579
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.56
Web of Science (2014): Impact factor 1.659
Web of Science (2014): Indexed yes
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Scopus rating (2013): CiteScore 2.69
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ISI indexed (2013): ISI indexed yes
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BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.51
Web of Science (2012): Impact factor 1.629
ISI indexed (2012): ISI indexed yes
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Scopus rating (2011): CiteScore 2.55
Web of Science (2011): Impact factor 1.622
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Web of Science (2010): Impact factor 1.647
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Voluntary ban on cephalosporin use in Danish pig production has effectively reduced extended-spectrum cephalosporinase-producing Escherichia coli in slaughter pigs

Objectives To measure the effect of a voluntary ban on cephalosporin usage in the Danish pig production on the prevalence of extended-spectrum cephalosporinase (ESC)-producing Escherichia coli in pigs and pork.Methods Data on cephalosporin consumption were obtained from the VetStat database. For detection of ESC-producing E. coli, three sampling types were included: at slaughter, caecal samples were collected from pigs in 2009 and 2010 (June) before and in two periods (2010 and 2011) after a voluntary ban on cephalosporins was effected (July 2010); at farm level, pools of five stool samples from different pigsties were collected in 2010 and in 2011; and samples from pork were collected randomly at retail stores and outlets from 2009 to 2011. ESC-producing E. coli was isolated after selective enrichment in MacConkey broth with 1 mg/L ceftriaxone. ESC genes were detected using PCR, microtube array and sequencing.Results From July 2010 the consumption of cephalosporins approximated zero. The occurrence of ESC-producing E. coli in pigs at slaughter was not significantly different (P = 0.7) between 2009 [10.8% (85/786)] and 2010 [11.8% (48/407)], but in 2011 the occurrence [3.6% (28/777)] decreased significantly (P <0.001). A significant decrease (P = 0.002) in occurrence of ESC-producing E. coli at pig farm level from 2010 [11% (11/99)] to 2011 (0/78) was also observed. The blaCTX-M-1 gene was most often detected (63%), but blaCTX-M-14 and blaCTX-M-15 were also found. Occurrence in pork was between 1.3% and 0.9%.Conclusions The discontinuation of an already low use of cephalosporins in pig production has significantly reduced the occurrence of ESC-producing E. coli.

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Contributors: Agerø, Y., Aarestrup, F. M.
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Web of Science (2018): Indexed yes
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Web of Science (2017): Impact factor 5.217
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Impact factor 5.071
Antimicrobial resistance in Salmonella spp. recovered from patients admitted to six different hospitals in Tehran, Iran from 2007 to 2008

The objective of this study was to assess the genotypic diversity associated with antimicrobial susceptibility of Salmonella serovars isolated from patients arriving with diarrhoea to six hospitals of Tehran, Iran. During 2007–2008, a cross-sectional convenience study was performed. Stool samples were screened for the presence of Salmonella, serotyped, tested for antimicrobial susceptibility using disk diffusion and examined for the presence of relevant resistance genes and integrons by PCR. A total of 1,120 patients were screened for the presence of Salmonella. Out of 71 Salmonella isolates recovered, the following serovars were identified: 17 Typhi, 14 Paratyphi C, 13 Enteritidis, 11 Paratyphi B, 10 Paratyphi A and six Infantis. Most resistance was observed towards sulfamethoxazole (30%), tetracyclines (25%), nalidixic acid (22%), spectinomycin (17%), trimethoprim (15%), ampicillin (14%) and kanamycin (14%). The tetracycline resistance genes tet(A), tet(B), and tet(G) were found in 28%, 14% and 6% of the tetracycline resistant isolates, respectively. The genes aadA, aadB, strA, strB and aphA1-lab were present in 83%, 55%, 34%, 1% and 17% of the aminoglycoside resistant isolates, respectively. Additionally, blaPSE and blaTEM β-lactamase genes were detected in 63% and 18% of the ampicillin-resistant isolates. The 23 sulfonamide resistant isolates harboured sul1 and intI1 genes, typical to class 1 integrons. Nine of these isolates also yielded amplicons for intI2 (class 2 integrons). The presence of multi-drug resistant Salmonella may compromise the successful treatment of enteric infection diseases. The enforcement of strict prescription practices will help to minimise the emergence of resistance.

General information
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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Shahid Beheshti University of Medical Sciences, CReSA - Centre for Animal Health Research
Contributors: Tajbakhsh, M., Hendriksen, R. S., Nochi, Z., Zali, M. R., Aarestrup, F. M., Garcia-Migura, L.
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Web of Science (2017): Impact factor 1.311
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.38 SJR 0.558 SNIP 0.574
Web of Science (2016): Impact factor 1.521
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.22 SJR 0.472 SNIP 0.558
Web of Science (2015): Impact factor 1.335
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.11 SJR 0.425 SNIP 0.576
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Web of Science (2014): Indexed yes
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Scopus rating (2013): CiteScore 1.15 SJR 0.436 SNIP 0.563
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Scopus rating (2012): CiteScore 0.89 SJR 0.338 SNIP 0.517
Antimicrobial-resistant Shigella infections from Iran: an overlooked problem?

Objectives: In this study, we wanted to assess the level of antimicrobial resistance, the presence of genes encoding resistance to cephalosporins and plasmid-mediated quinolone resistance (PMQR), and genetic relatedness among Shigella isolates obtained from Iranian patients. Methods: A total of 44 Shigella isolates were collected from Iranian patients admitted to Milad Hospital, Tehran, Iran, during 2008–10. Of these, 37 were serotyped and characterized by MIC determination. A subset of eight suspected extended-spectrum β-lactamase (ESBL) producers (six Shigella sonnei phase II and two Shigella flexneri type 1b) were examined for the presence of genes encoding cephalosporin resistance. The presence of PMQR was assessed in one S. flexneri isolate exhibiting low-level resistance to ciprofloxacin and susceptibility to nalidixic acid. PFGE was performed on 25 S. sonnei phase II isolates. Results: Of the isolates, 25 (68%) were S. sonnei phase II, with 5 (14%) S. flexneri, 5 (14%) Shigella dysenteriae type 2, and 2 (5%) Shigella boydii type 2. Resistance to at least three classes of antimicrobials was detected in all species. The presence of blaCTX-M-15 and the AmpC β-lactamase producer blaCMY-2 was confirmed in five and one S. sonnei phase II isolates, respectively. One of the two S. flexneri type 1b that contained blaCTX-M-15 also harboured a qnrS1 gene. PFGE identified seven PFGE profiles; the main cluster included 15 of the strains, suggesting low genetic diversity between isolates or the presence of an endemic clone in Iran. Conclusions: This is the first known description of ESBL-producing and AmpC β-lactamase-producing Shigella and of PMQR Shigella in Iran. The emergence of CTX-15, CMY-2 and qnrS1 genes may compromise the treatment of shigellosis. Strategies to minimize the spread of ESBL-producing and AmpC-β-lactamase-producing Shigella should be implemented.

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, Shahid Beheshti University of Medical Sciences, Centre de Reserca en Sanitat Animal, Iranian Reference Health Laboratory, Milad Hospital
Contributors: Tajbakhsh, M., García Migura, L., Rahbar, M., Svendsen, C. A., Mohammazadeh, M., Zali, M. R., Aarestrup, F. M., Hendriksen, R. S.
Pages: 1128-1133
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Salmonella enterica serovar Stanley (S. Stanley) is a common serovar in Southeast Asia and was the second most common serovar implicated in human salmonellosis in Thailand in the years 2002 to 2007. In contrast, this serovar is relatively uncommon in Europe. The objective of this study was to characterize a collection of S. Stanley strains isolated from Thai (n = 62), Danish (n = 39), and French (n = 24) patients to gain a broader understanding of the genetic diversity, population dynamics, and susceptibility to antimicrobials. All isolates were characterized by pulsed-field gel electrophoresis and antimicrobial susceptibility testing. The molecular mechanisms of resistance to extended-spectrum cephalosporins and plasmid-mediated resistance to quinolones were characterized by PCR and sequencing. Plasmid profiling, replicon typing, and microarray analysis were used to characterize the genetic mechanisms of antimicrobial resistance in 10 extended-spectrum cephalosporinase-producing isolates. Considerable genetic diversity was observed among the isolates characterized with 91 unique XbaI pulsed-field gel electrophoresis (PFGE) patterns, including 17 distinct clusters consisting of two to seven indistinguishable isolates. We found some of the S. Stanley isolates isolated from patients in Europe were acquired during travel to Southeast Asia, including Thailand. The presence of multiple plasmid lineages carrying the extended-spectrum cephalosporinase-encoding bla<sub>CMY-2</sub> gene in S. Stanley isolates from the central part of Thailand was confirmed. Our results emphasize that Thai authorities, as well as authorities in other countries lacking prudent use of antimicrobials, should improve the ongoing efforts to regulate antimicrobial use in agriculture and in clinical settings to limit the spread of multidrug-resistant Salmonella isolates and plasms among humans and pigs in Thailand and abroad.
Clonal diversity of *Staphylococcus aureus* originating from the small ruminants goats and sheep

*Staphylococcus aureus* is an important pathogen in humans and many animal species. The prevalence of different clonal types in animal species remains largely unknown. We analyzed 267 *S. aureus* from intramammary infections in goats (47) and sheep (220) by spa typing, multi-locus sequence typing (MLST) and antimicrobial susceptibility. The most frequent spa types in goats were t337 (N = 9), t759 (N = 6) and t1534 (N = 5). Sheep isolates mainly belonged to spa types t1534 (N = 72), t2678 (N = 29) and t3576 (N = 20). Eighteen novel spa-types were observed; two from goat strains, 13 from sheep and three in both species. The majority of the goat strains grouped in MLST CC133 (N = 10) and ST522 (N = 10), followed by CC9 (N = 9), while the majority of the sheep strains were of ST522 (N = 108) followed by CC133 (N = 86) and CC130 (N = 11). Nine new MLST types were detected; three in goat and sheep isolates (ST1739, ST1758 and ST1780), two identified in goats only (ST1740 and ST2061) and four in sheep only (ST1742, ST1743, ST1781 and ST2011). Strains showed resistance below 20% against penicillin and tetracycline; a strong association between CC-types and penicillin resistance was observed. No resistance was detected to cefoxitin, quinupristin-dalfopristin, rifampicin and vancomycin. This study suggests that ST522 is the most common *S. aureus* clone associated with small ruminants followed by CC133.

General information

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Comparison between Livestock and Community associated MRSA in Europe

General information
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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, NOVA University Lisbon
Contributors: Cavaco, L., Miragaia, M., Rolo, J., Conceicao, T., Hasman, H., Aarestrup, F. M., de Lencastre, H.
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Comparison of proficiency testing results on antimicrobial susceptibility testing of Salmonella and Campylobacter obtained by laboratories from the ECDC FWD network (public health) and the EURL-AR network (veterinary/food) 2011.

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Diversity and epidemiology of plasmids from Enterobacteriaceae from human and non-human reservoirs
The family of Enterobacteriaceae is comprised of Gram negative bacteria found in a variety of natural environments as well as in the gastrointestinal (GI) tracts of humans and many animals including diverse mammals, birds and reptiles. Three species of the enteric bacteria are largely responsible for causing infections both in humans and animals worldwide; these are Escherichia coli, Salmonella enterica and Klebsiella pneumoniae; ß-lactams are antimicrobials commonly prescribed to treat uncomplicated as well as severe infections caused by these Enterobacteriaceae and other Gram negative and also Gram positive bacteria. In particular, aminopenicillins, cephalosporins and carbapenems found broad
application in treatment of infections caused by the aforementioned enteric species. Recently however, increasing levels of resistance to β-lactams is observed in these key infectious agents as well as in many other previously susceptible species. This phenomenon has become a major public concern. Antimicrobials including β-lactams have been often used in heavy amounts in farming, not only to treat the diagnosed infections in individual animals but also as prophylaxis, metaphylaxis and growth promotion. It is believed that these practices lead to the generation of reservoirs of antimicrobial resistance genes in the GI tracts of intensively reared food production animals like pigs, poultry and cattle. Moreover, it has been previously shown that the bla genes (e.g. genes encoding resistance to β-lactams) could be transmitted between different bacteria on mobile genetic elements (MGEs) like plasmids and variety of transposons. Evidences were also published indicating that zoonotic bacteria like E. coli or S. enterica resistant to diverse antimicrobials and harbouring plasmids might have been transmitted from farm animals to humans (farm workers, animal caretakers etc.). It has been therefore speculated whether the plasmids with the bla genes found in Enterobacteriaceae in humans could actually originate from the animal sources.

The overall aim of this thesis was to verify if indeed related resistance plasmids can circulate between enteric bacteria from humans and food production animals; and if so, then which of these plasmid species are specifically associated with the epidemic types of blaTEM genes in Enterobacteriaceae. Furthermore, the association of the plasmid encoded blaTEM genes with transposable elements is also studied in order to get a broader perspective of which MGEs are involved in mobilization and spread of these bla genes in the diverse reservoirs. Finally, an attempt is made to encompass ecological aspects of plasmid driven transmission of resistance among the enteric bacteria.

In the first study the relationship between plasmids harbouring blaTEM-52 genes isolated from humans, poultry and also meat products was examined. Twenty- two plasmids from a collection of E. coli and different serovars of S. enterica were characterized. The study delivered molecular evidences that epidemiologically related plasmids circulated in the diverse species of enteric bacteria and between humans and animals, and the possible transmission route could have been contaminated food products like meat. Two types of epidemic plasmids were detected in isolates of E. coli and S. enterica; namely undistinguishable Inc11 blaTEM-52 plasmids were found in human and poultry isolates of E. coli and S. enterica; also undistinguishable IncX1 plasmids were isolated from E. coli and S. enterica from human infections, poultry and meat products (from poultry, broiler and beef). The strains harbouring these plasmids were confirmed not to be clonally related, hence indicating the transmission of the plasmids between the different bacteria from humans and animals rather than isolation of the same bacterial clones from the different reservoirs.

With relation to the study I, a range of other observations was made. On majority of the examined plasmids, the blaTEM-52 genes resided on the Tn3-related transposons. Further analysis of the genetic environment of these blaTEM genes resulted in the conclusion, that it was a defined type of Tn3-like element that harboured the blaTEM-52, namely the Tn2 transposon. This knowledge was later used in the second study to design more discriminatory PCR method that would allow for distinction of which transposon types (Tn1, 2 or 3) or insertion sequences (IS26) could be linked to the blaTEM genes of interest. Moreover, the initial typing of – as realized later the IncX1 –blaTEM-52 plasmids with the use of available standard PCR-based methods for replicon typing (PBRT) was unsuccessful. In the course of this study the whole plasmid from E. coli 2161 was sequenced and deposited in GenBank as plasmid pE001. It became apparent that the standard PBRT method targeted another group of IncX family of replicons, namely the IncX2 plasmids, which so far have been rather rarely detected in humans or animals. The replicon of the pE001 was designated in the published Manuscript I as an IncX1A. The reason to that was the discovery of dissimilarities between the replicon of pE001 and the replicon of an IncX1 plasmid called pOLA52. The latter was published before pE001 and was considered to carry a classical IncX1 replicon. In the study I, an incompatibility assay for the pE001 and the pOLA52 (variant with the deletion in blaTEM gene) was performed. The two plasmids turned out to be compatible, which was surprising considering the high degree of overall similarities between the two sequenced scaffolds. Based on these results it was concluded that the standard incompatibility assays may in some cases give a false reflection of the real relatedness of the examined plasmids. Combining this experience with the knowledge that the PBRT method is often sensitive to the sequence substitutions within the replicon scaffolds, another idea was generated. It was previously reported that the plasmids from Klebsiella pneumoniae often escaped the detection by the classical PBRT methods, which was originally designed based on E. coli replicons. Therefore in the third study, which will be described later in this summary, a novel method was elaborated for rapid detection and sub-classification of plasmids from this species. The blaTEM-52 genes that were the focus of the first sub-project are in fact evolutionary descendants of blaTEM-1 genes. The second study aimed therefore at verifying on which plasmids scaffolds these blaTEM predecessors are usually located in Enterobacteriaceae found in humans and food production animals like pigs, poultry and cattle. In this sub-project the focus was shifted to the plasmids from E. coli, which is known to be either an indicator organism colonizing (as a commensal) both the human and animal GI tracts; or it may cause infections to its hosts. Evidences were found in the study II that either undistinguishable or similar blaTEM-1 plasmids circulated in different E. coli from humans and from animal sources in Denmark. Possibly epidemic blaTEM-1 Inc11 and IncB/O plasmids were found in humans and the diverse animals (pigs, poultry and cattle). Moreover, a larger variation of the transposable elements linked to the blaTEM-1 genes was detected on plasmids in the second study compared to blaTEM-52 plasmids. In the second study usually specific alleles of the blaTEM-1 genes resided on either the Tn2 (blaTEM-1b and blaTEM-1c) or Tn3 (blaTEM-1a) transposons. In many cases the insertions of IS26 elements upstream of the blaTEM-1 genes were detected by PCR. These results gave important clues not only regarding which plasmids but also which specific transposons might have served as platforms for mobilization and evolution of the blaTEM-1 to blaTEM-52 genes.

In the third sub-project plasmids from K. pneumoniae from human infections and from surface waters (designated as environmental isolates) were typed. In this study the strains were not pre-selected based on the defined resistance markers. The results allowed for evaluating if there are differences in the replicons normally found on plasmids from humans and from the environment in this bacterial species. Additionally, these potentially host specific replicons could have been compared to the replicons of plasmids previously shown to be specifically associated with the resistance genes...
in the clinically relevant K. pneumoniae.

At the time when this project was initiated the standard PBRT method often failed to detect the replicons from K. pneumoniae. Therefore a novel multiplex PCR (mPCR) was designed for detection of these otherwise untypable plasmids. While this was pursued, updated protocols for PBRT were published by other authors and many of the sequenced plasmids from K. pneumoniae used as references for designing of the mPCR turned out to be the IncFIIk types. However, an interesting observation was made. Namely, in one of the previously sequenced K. pneumoniae strain MGH78578 apparently multiple plasmids with the similar incompatibility determinants IncFIIk were detected; this was opposing to the theory that the plasmids from the same incompatibility groups typically would not be able to co-exist in the same bacterium. In fact, a similar pattern was seen in study III in some of the examined K. pneumoniae strains from human infections and from the environment, where also multiple IncFIIk plasmids were present in the same isolates simultaneously, but these plasmids harboured diverse secondary replicons detected by the mPCR. The conclusion from the third study was that plasmids may acquire secondary replicons in order to persist in the given bacterium and to overcome the incompatibility phenomenon and this seems to be fairly common in K. pneumoniae. Analysis of literature data against the data from the study III resulted also in a conclusion, that the same replicons that are generally predominant in K. pneumoniae (IncFIIk, likely also IncR and yet unknown replicons) are often associated with a variety of the bla genes in the clinical strains of this species.

In summary, the combined data from the three studies suggested that often the blaTEM plasmids are generally host specific to the species they were detected in. This is exemplified by IncFII, IncFI, IncB/O and IncI1 replicons in E. coli, IncI1 and likely IncX1 in S. enterica or IncFIIk in K. pneumoniae. Many of the broad host range replicons (IncP, IncA/C, IncR, IncL/M, IncN) were found rather occasionally in these hosts. Although some exceptions were seen, namely the IncP were often found with blaTEM-1 genes in particular in cattle, while IncA/C were often associated with blaTEM variants encoding Extended Spectrum ß-Lactamases in the diverse reservoirs. Evidences presented above indicate that the transmission of plasmids between animal and human Enterobacteriaceae is possible and it is likely that in some cases the resistance plasmids might have been delivered from animal to human strains via food chain.

Further studies are needed to determine the chromosomal progenitors of the resistance genes like blaTEM-1. Determination of the very origins of resistance genes is crucial if further mobilization of these genes from the given source is to be prevented. Plasmids undoubtedly play a major role in transmission of bla genes also across the reservoirs. Solutions like whole genome sequencing should be preferentially applied in the future in order to efficiently detect, classify and tract the epidemiology of resistance plasmids in populations of Enterobacteriaceae.

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Estimating variation within the genes and inferring the phylogeny of 186 sequenced diverse Escherichia coli genomes

Background

Escherichia coli exists in commensal and pathogenic forms. By measuring the variation of individual genes across more than a hundred sequenced genomes, gene variation can be studied in detail, including the number of mutations found for any given gene. This knowledge will be useful for creating better phylogenies, for determination of molecular clocks and for improved typing techniques.

Results

We find 3,051 gene clusters/families present in at least 95% of the genomes and 1,702 gene clusters present in 100% of the genomes. The former 'soft core' of about 3,000 gene families is perhaps more biologically relevant, especially considering that many of these genome sequences are draft quality. The E. coli pan-genome for this set of isolates contains 16,373 gene clusters.

A core-gene tree, based on alignment and a pan-genome tree based on gene presence/absence, maps the relatedness of the 186 sequenced E. coli genomes. The core-gene tree displays high confidence and divides the E. coli strains into the observed MLST type clades and also separates defined phylogenotypes.

Conclusion

The results of comparing a large and diverse E. coli dataset support the theory that reliable and good resolution phylogenies can be inferred from the core-genome. The results further suggest that the resolution at the isolate level may,
subsequently be improved by targeting more variable genes. The use of whole genome sequencing will make it possible to eliminate, or at least reduce, the need for several typing steps used in traditional epidemiology.
Expansion of a plasmid classification system for Gram-positive bacteria and determination of the diversity of plasmids in Staphylococcus aureus strains of human, animal, and food origins.

An expansion of a previously described plasmid classification was performed and used to reveal the plasmid content of a collection of 92 Staphylococcus aureus strains of different origins. rep genes of other genera were detected in Staphylococcus. S1 pulsed-field gel electrophoresis (PFGE) hybridizations were performed with 18 representative S. aureus strains, and a high number of plasmids of different sizes and organizations were detected. Copyright © 2012, American Society for Microbiology. All Rights Reserved.

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Genetic and phenotypic characteristics of importance for clonal success and diversity in Salmonella

Salmonella are zoonotic pathogens that cause food-borne illness and that are widely disseminated in nature. An estimated number of 93.8 million human cases of gastroenteritis caused by Salmonella occur annually throughout the world. The epidemic success of Salmonella is characterized by a temporal dominance of certain clones. These epidemically successful clones are often resistant to antibiotics and associated with severe human illness. They pose a major threat to public health and lead to heavy economic losses. So far, little is known about the environmental and bacterial factors leading to the emergence of successful clones. However, resistance to multiple antimicrobial drugs and quinolones seems to contribute to the epidemic success of Salmonella as it is associated with an increased severity of illness and epidemicity. In order to predict and prevent future outbreaks and epidemics, research should focus on the evolutionary mechanisms of emerging success clones.

The ability to spread in different food production sectors and to cause human disease seems critical for a clone to become successful. The aim of this PhD study was to identify common phenotypic and genetic traits of success clones that may have an epidemic importance with respect to the survival in the food chain and to human infection. Non-typhoid Salmonella isolates from food, production animals and humans were carefully selected and characterized as successful or non-successful based on epidemiological data. In addition, the isolates were categorized based on their antibiotic resistance pattern into quinolone resistant (Q; at least low level resistance to one fluoroquinolone), multidrug resistant (MR; resistant to four or more antibiotic agents), resistant (R; resistant to less than four antibiotic agents) and sensitive (S; fully susceptible to the tested antibiotics).

The ability to survive and grow after physical stress experienced in the food chain is likely to contribute to a successful spread of Salmonella. Thus, the response of Salmonella isolates in exponential and stationary growth state to freezing in minced meat and to drying at two combinations of temperature and humidity was investigated. The results of this study are presented in Manuscript I. Stationary phase cells survived freezing for up to one year without major decline and initiated growth with a short lag time of 1.7 hours on average. Exponential phase cells showed reduced survival and a tendency to exhibit shorter lag times. Dehydration at 82 % relative humidity (RH) and 10 °C was less harmful for Salmonella than 49 % RH and 25 °C. Dehydration, in contrast to freezing, was differently tolerated by the Salmonella isolates but neither the tolerance to freezing nor to dehydration appears to contribute to the epidemic success of Salmonella.

MR and Q Salmonella seem to have a virulence or fitness advantage apart from the effect posed by the antibiotic resistance phenotype. Manuscript II describes a study aiming to identify genes and genetic structures in Q and MR isolates that might confer fitness or virulence attributes by the use of array-based comparative genomic hybridizations and PCR screenings. The largest fraction of the genes dominating in Q and MR Salmonella were single genes and gene clusters belonging to prophages, among these the virulence genes sopE (STY4609) and gipA (STM2599) and the genes recT (SG1183), sugR (STM3753) and trh (AF261825_S012). The latter three genes were knocked out and the mutants were used in functional analyses. The mutants were not significantly different from the wildtype but RecT knockout mutants seemed to be more susceptible to the early defense of macrophages and exhibited increased spontaneous mutation rates. The largest group of genes dominating in sensitive isolates were related to metabolism indicating that many of these genes are typically absent or diverged in Q and MR Salmonella. The acquisition and maintenance of bacteriophages conferring fitness and virulence attributes may be part of the evolution of successful MR and Q Salmonella.

The bacterial and host factors leading to an increased severity of illness caused by quinolone resistant Salmonella were investigated as they are largely unknown. Quinolone resistance is mostly caused by point mutations and can develop in Salmonella during infection. As described in Manuscript III, the spontaneous mutations rates and virulence potential of ciprofloxacin (CIP) resistant Salmonella in presence and absence of CIP were assessed using cell cultures. The rate at which CIP sensitive isolates can experience a reduction in their CIP susceptibility after macrophage infection and in presence and absence of CIP was investigated. Strain dependent differences in the mutation rate, the ability to invade intestinal epithelial cells and to replicate within macrophages were found, but there was no correlation between virulence, mutation rate and resistance pattern. The presence of clinically relevant CIP concentrations decreased but failed to eliminate the number of CIP resistant intraphagocytic Salmonella. During macrophage infection, Salmonella adapted to higher CIP concentrations (to at least 2 – 8 fold the initial MIC). When CIP was added to the extracellular medium, the frequency of intraphagocytic bacteria exhibiting reduced CIP susceptibilities increased markedly. Thus virulent Salmonella strains that are likely to persist in macrophages for prolonged times might become resistant to quinolones and the administration of quinolones may increase the rate of resistant mutants.

In conclusion, the emergence of successful clones is likely to be the result of a combination of factors including the acquisition and maintenance of bacteriophages encoding genes that increase the fitness or virulence of their bacterial host. Marker genes related to bacteriophages might be useful in the future for the early detection of these clones. Macrophages might play a role in the evolution of quinolone resistance in invasive Salmonella strains. Both in absence of antimicrobial drugs and when quinolones are administered, intraphagocytic Salmonella may become quinolone resistant and simultaneously may acquire other advantageous mutations. This highlights the importance of an antibiotic therapy that is effective in eliminating intracellular pathogens.
Genomic variation in Salmonella enterica core genes for epidemiological typing

Background: Technological advances in high throughput genome sequencing are making whole genome sequencing (WGS) available as a routine tool for bacterial typing. Standardized procedures for identification of relevant genes and of variation are needed to enable comparison between studies and over time. The core genes—the genes that are conserved in all (or most) members of a genus or species—are potentially good candidates for investigating genomic variation in phylogeny and epidemiology. Results: We identify a set of 2,882 core genes clusters based on 73 publicly available Salmonella enterica genomes and evaluate their value as typing targets, comparing whole genome typing and traditional methods such as 16S and MLST. A consensus tree based on variation of core genes gives much better resolution than 16S and MLST; the pan-genome family tree is similar to the consensus tree, but with higher confidence. The core genes can be divided into two categories: a few highly variable genes and a larger set of conserved core genes, with low variance. For the most variable core genes, the variance in amino acid sequences is higher than for the corresponding nucleotide sequences, suggesting that there is a positive selection towards mutations leading to amino acid changes. Conclusions: Genomic variation within the core genome is useful for investigating molecular evolution and providing candidate genes for bacterial genome typing. Identification of genes with different degrees of variation is important especially in trend analysis.
Identification of acquired antimicrobial resistance genes

Objectives
Identification of antimicrobial resistance genes is important for understanding the underlying mechanisms and the epidemiology of antimicrobial resistance. As the costs of whole-genome sequencing (WGS) continue to decline, it becomes increasingly available in routine diagnostic laboratories and is anticipated to substitute traditional methods for resistance gene identification. Thus, the current challenge is to extract the relevant information from the large amount of generated data.

Methods
We developed a web-based method, ResFinder, that uses BLAST for identification of acquired antimicrobial resistance genes in whole-genome data. As input, the method can use both pre-assembled, complete or partial genomes, and short sequence reads from four different sequencing platforms. The method was evaluated on 1862 GenBank files containing 1411 different resistance genes, as well as on 23 de-novo-sequenced isolates.

Results
When testing the 1862 GenBank files, the method identified the resistance genes with an ID = 100% (100% identity) to the genes
in ResFinder. Agreement between in silico predictions and phenotypic testing was found when the method was further tested on 23 isolates of five different bacterial species, with available phenotypes. Furthermore, ResFinder was evaluated on WGS chromosomes and plasmids of 30 isolates. Seven of these isolates were annotated to have antimicrobial resistance, and in all cases, annotations were compatible with the ResFinder results. Conclusions A web server providing a convenient way of identifying acquired antimicrobial resistance genes in completely sequenced isolates was created. ResFinder can be accessed at www.genomicepidemiology.org. ResFinder will continuously be updated as new resistance genes are identified.

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Integrating genome-based informatics to modernize global disease monitoring, information sharing, and response.

The rapid advancement of genome technologies holds great promise for improving the quality and speed of clinical and public health laboratory investigations and for decreasing their cost. The latest generation of genome DNA sequencers can provide highly detailed and robust information on disease-causing microbes, and in the near future these technologies will be suitable for routine use in national, regional, and global public health laboratories. With additional improvements in instrumentation, these next- or third-generation sequencers are likely to replace conventional culture-based and molecular typing methods to provide point-of-care clinical diagnosis and other essential information for quicker and better treatment of patients. Provided there is free-sharing of information by all clinical and public health laboratories, these genomic tools could spawn a global system of linked databases of pathogen genomes that would ensure more efficient detection, prevention, and control of endemic, emerging, and other infectious disease outbreaks worldwide.

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In vitro susceptibility testing of fluoroquinolone activity against Salmonella: recent changes to CLSI standards.

Fluoroquinolone (FQ) resistance in Salmonella enterica is a significant clinical concern. Recognition of resistance by the clinical laboratory is complicated by the multiple FQ resistance mechanisms found in Salmonella. The Clinical Laboratory Standards Institute (CLSI) recently addressed this issue by revising the ciprofloxacin break points for Salmonella species. It is critical for clinicians and laboratory workers to be aware of the multiple technical issues surrounding these revised break points. In this article, we review FQ resistance mechanisms in Salmonella, their clinical significance, and data supporting the revised ciprofloxacin break points. We encourage clinical laboratories to adopt the revised CLSI ciprofloxacin break points for all Salmonella isolates in which susceptibility testing is indicated and discuss the technical issues for laboratories using commercial antimicrobial susceptibility systems. © The Author 2012. Published by Oxford University Press on behalf of the Infectious Diseases Society of America. All rights reserved.

**General information**

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ISI indexed (2013): ISI indexed yes
Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria

Accurate strain identification is essential for anyone working with bacteria. For many species, multilocus sequence typing (MLST) is considered the “gold standard” of typing, but it is traditionally performed in an expensive and time-consuming manner. As the costs of whole-genome sequencing (WGS) continue to decline, it becomes increasingly available to scientists and routine diagnostic laboratories. Currently, the cost is below that of traditional MLST. The new challenges will be how to extract the relevant information from the large amount of data so as to allow for comparison over time and between laboratories. Ideally, this information should also allow for comparison to historical data. We developed a Web-based method for MLST of 66 bacterial species based on WGS data. As input, the method uses short sequence reads from four sequencing platforms or preassembled genomes. Updates from the MLST databases are downloaded monthly, and the best-matching MLST alleles of the specified MLST scheme are found using a BLAST-based ranking method. The sequence type is then determined by the combination of alleles identified. The method was tested on preassembled genomes from 336 isolates covering 56 MLST schemes, on short sequence reads from 387 isolates covering 10 schemes, and on a small test set of short sequence reads from 29 isolates for which the sequence type had been determined by traditional methods. The method presented here enables investigators to determine the sequence types of their isolates on the basis of WGS data. This method is publicly available at www.cbs.dtu.dk/services/MLST.
Prevalence and Characterization of Cephalosporin Resistance in Nonpathogenic Escherichia coli from Food-Producing Animals Slaughtered in Poland

The prevalence of Escherichia coli with putative extended-spectrum cephalosporin resistance was assessed in cattle, pigs, broilers, layers, and turkey slaughtered in Poland. The occurrence of random E. coli isolates recovered from MacConkey agar plates with non–wild-type minimal inhibitory concentrations for cefotaxime and ceftazidime reached 0.6% in layers, 2.3% in turkey, and 4.7% in broilers, whereas all cattle and pigs isolates fell into the wild-type subpopulation. The use of MacConkey agar supplemented with cefotaxime (2 mg/L) increased the recovery of resistant strains up to 33.3% of samples from pigs, 42.3% from layers, 48.0% from turkey, and 54.5% from broilers. Still, no cephalosporin-resistant E. coli was found in cattle. E-test identified extended-spectrum beta-lactamase (ESBL) and ampC-type resistance phenotypes in 15 and 33 strains, respectively. Molecular characterization identified CTX-M-1 gene in 13 ESBL strains, 5 of which possessed also TEM-1b. One strain harbored SHV-12 gene. CMY-2 was found in all of 20 tested ampC-type cephalosporinase-positive strains either alone (n = 14) or in combination with mutations in ampC promoter region (n = 6). CTX-M-1 and CMY-2 genes were noted also in five strains from laying hens and broilers originated from Belgium and Germany. Nosocomial infections in Poland are caused by E. coli carrying other determinants than those found in our study. Thus, our results indicate that animals colonized with cephalosporin-resistant strains might not be the major source of human infections in Poland. However, the contribution to community-acquired infections by spread of resistant clones or resistance genes may not be excluded.
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
Web of Science (2017): Impact factor 2.344
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
Web of Science (2016): Impact factor 2.306
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
Web of Science (2015): Impact factor 2.529
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
Web of Science (2014): Impact factor 2.49
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.87 SJR 1.265 SNIP 1.118
Web of Science (2013): Impact factor 2.524
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.45 SJR 0.963 SNIP 0.9
Web of Science (2012): Impact factor 2.364
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.76 SJR 1.163 SNIP 1.14
Web of Science (2011): Impact factor 2.153
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.054 SNIP 0.8
Web of Science (2010): Impact factor 1.936
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.915 SNIP 0.838
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.038 SNIP 0.73
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.042 SNIP 0.764
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.319 SNIP 0.908
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.364 SNIP 0.983
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.998 SNIP 0.968
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.303 SNIP 1.029
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.42 SNIP 0.918
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.791 SNIP 1.006
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.902 SNIP 1.36
Prevalence of extended-spectrum cephalosporinase (ESC)-producing Escherichia coli in Danish slaughter pigs and retail meat identified by selective enrichment and association with cephalosporin usage

OBJECTIVES: To investigate the prevalence of extended-spectrum cephalosporinase (ESC)-producing Escherichia coli in pigs at slaughter and retail meat, and possible associations with the consumption of third- and fourth-generation cephalosporins.

METHODS: During 2009, faecal samples from Danish pigs (n = 786) were collected at slaughter, and 866 meat samples [Danish: pork (153), broiler meat (121) and beef (142); and imported: pork (173), broiler meat (193) and beef (84)] were randomly collected in retail stores and outlets. E. coli was isolated after enrichment in MacConkey broth with ceftriaxone (1 mg/L). ESC genotypes were detected using PCR, microtube array and sequencing. The MIC of cefotaxime was determined for 150 E. coli from the pigs and 606 E. coli from meat isolated without selective enrichment.

RESULTS: Eleven percent (86/786) of slaughter pigs contained ESC E. coli and a significantly higher prevalence was observed among pigs originating from farms with registered cephalosporin consumption in slaughter pigs (P = 0.034). Among ESC E. coli from pigs, 66% contained blaCTX-M-1. From meat, a high prevalence of ESC E. coli was found in imported broiler meat (36%) compared with 0.7%–3.3% in other meat types. ESC E. coli from imported broiler meat (n = 69) contained blaCMY-2 (48%), blaCTX-M-1 (25%) and blaSHV-12 (16%). Without selective enrichment, no ESC E. coli from pigs and only 4.1% from imported broiler meat were found. CONCLUSIONS: The usage of cephalosporins for slaughter pigs may increase the prevalence of ESC E. coli in slaughter pigs. Meat may be a source of ESCs in humans, especially imported broiler meat. Selective enrichment should be considered as a supplementary surveillance method.
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.7 SJR 2.479 SNIP 1.824
Web of Science (2013): Impact factor 5.439
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.35 SJR 2.283 SNIP 1.718
Web of Science (2012): Impact factor 5.338
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.24 SJR 2.341 SNIP 1.769
Web of Science (2011): Impact factor 5.068
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.161 SNIP 1.643
Web of Science (2010): Impact factor 4.659
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.902 SNIP 1.615
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.076 SNIP 1.506
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.744 SNIP 1.509
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.771 SNIP 1.437
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.768 SNIP 1.5
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.435 SNIP 1.465
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.367 SNIP 1.338
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.4 SNIP 1.284
Scopus rating (2001): SJR 1.388 SNIP 1.232
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.113 SNIP 1.248
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.111 SNIP 1.388
Original language: English
Keywords: Swine, Meat, CTX-M, CMY-2, ESBLs
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Source: orbit
Source-ID: 318574
Research output: Research - peer-review › Journal article – Annual report year: 2012


General information
State: Published
SCCmec Type IX Element in Methicillin Resistant Staphylococcus aureus spa Type t337 (CC9) Isolated from Pigs and Pork in Thailand

Methicillin resistant Staphylococcus aureus (MRSA) have emerged among livestock in several countries. In this study, we describe the results of a screening performed in pigs and raw pork samples in Thailand. Ten pork samples and 15 nasal swabs from pigs were collected from 2 markets and 1 pig farm in the Samuth Songkhram province in Thailand. MRSA were isolated using selective isolation procedures and confirmed by mecA PCR. The MRSA were characterized by antimicrobial susceptibility testing, pulsed field gel electrophoresis (PFGE), spa typing, SCCmec typing, and MLST. Resistance and virulence markers were screened using a microarray. Five of the pork samples and six pig nasal swabs were positive for MRSA. All 11 isolates belonged to spa type t337 but showed diversity in antimicrobial resistance patterns and PFGE profiles. Additionally, the isolates were sequence-typed; ST9, ST2136, ST2278 belonging to the clonal complex; CC9. All isolates harbored SCCmec IX and were resistant to 7 out of 14 tested antimicrobials; additional resistances to all antimicrobials tested were found in some of the pork and pig isolates and 1 pork isolate was resistant to 13 antimicrobials tested. Microarray analysis identified blaZ, aac-aphD, vga(A), tetM, and a tet efflux marker, in all strains and additionally ermB and aadD, cat and fex(A) in the pork isolates. None of the isolates were found PVL-positive, but enterotoxins were identified in all isolates. To our knowledge, only a few descriptions of MRSA in livestock and food products in Thailand have been observed but this is the first observation of MRSA CC9 associated with SCCmec IX in pork. This study indicates a likely widespread distribution of MRSA in pig and pork in Thailand and further investigation on the prevalence and importance of livestock associated MRSA in Thailand is needed.

General information
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Organisations: Department of Systems Biology, National Food Institute, Division of Microbiology and Risk Assessment, Regional Medical Sciences Center, Thailand Ministry of Public Health
Contributors: Vestergaard, M., Cavaco, L. M., Sirichote, P., Unahalekhaka, A., Dangsakul, W., Svendsen, C. A., Aarestrup, F. M., Hendriksen, R. S.
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snpTree - a web-server to identify and construct SNP trees from whole genome sequence data.

Background
The advances and decreasing economical cost of whole genome sequencing (WGS), will soon make this technology available for routine infectious disease epidemiology. In epidemiological studies, outbreak isolates have very little diversity and require extensive genomic analysis to differentiate and classify isolates. One of the successfully and broadly used methods is analysis of single nucleotide polymorphisms (SNPs). Currently, there are different tools and methods to identify SNPs including various options and cut-off values. Furthermore, all current methods require bioinformatic skills. Thus, we lack a standard and simple automatic tool to determine SNPs and construct phylogenetic tree from WGS data.

Results
Here we introduce snpTree, a server for online-automatic SNPs analysis. This tool is composed of different SNPs analysis suites, perl and python scripts. snpTree can identify SNPs and construct phylogenetic trees from WGS as well as from assembled genomes or contigs. WGS data in fastq format are aligned to reference genomes by BWA while contigs in fasta format are processed by Nucmer. SNPs are concatenated based on position on reference genome and a tree is constructed from concatenated SNPs using FastTree and a perl script. The online server was implemented by HTML, Java and python script.
The server was evaluated using four published bacterial WGS data sets (V. cholerae, S. aureus CC398, S. Typhimurium and M. tuberculosis). The evaluation results for the first three cases was consistent and concordant for both raw reads and assembled genomes. In the latter case the original publication involved extensive filtering of SNPs, which could not be repeated using snpTree.

Conclusions
The snpTree server is an easy to use option for rapid standardised and automatic SNP analysis in epidemiological studies also for users with limited bioinformatic experience. The web server is freely accessible at http://www.cbs.dtu.dk/services/snpTree-1.0/.

General information
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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Center for Systems Microbiology, Department of Systems Biology, Center for Biological Sequence Analysis, Division of Microbiology and Risk Assessment
Contributors: Leekitcharoenphon, P., Kaas, R. S., Thomsen, M. C. F., Rundsten, C. F., Rasmussen, S., Aarestrup, F. M.
Number of pages: 8
Pages: S6
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Volume: 13
Issue number: Suppl 7
ISSN (Print): 1471-2164
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.08 SJR 2.11 SNIP 1.151
Web of Science (2017): Impact factor 3.73
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.05 SJR 2.163 SNIP 1.096
Web of Science (2016): Impact factor 3.729
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.3 SJR 2.348 SNIP 1.159
Web of Science (2015): Impact factor 3.867
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.18 SJR 2.327 SNIP 1.199
Web of Science (2014): Impact factor 3.986
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.39 SJR 2.195 SNIP 1.188
Web of Science (2013): Impact factor 4.041
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.61 SJR 2.236 SNIP 1.243
Web of Science (2012): Impact factor 4.397
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.38 SJR 2.307 SNIP 1.191
Web of Science (2011): Impact factor 4.073
ISI indexed (2011): ISI indexed yes
Staphylococcus aureus CC398: Host Adaptation and Emergence of Methicillin Resistance in Livestock

Since its discovery in the early 2000s, methicillin-resistant Staphylococcus aureus (MRSA) clonal complex 398 (CC398) has become a rapidly emerging cause of human infections, most often associated with livestock exposure. We applied whole-genome sequence typing to characterize a diverse collection of CC398 isolates (n = 89), including MRSA and methicillin-susceptible S. aureus (MSSA) from animals and humans spanning 19 countries and four continents. We identified 4,238 single nucleotide polymorphisms (SNPs) among the 89 core genomes. Minimal homoplasy (consistency index = 0.9591) was detected among parsimony-informative SNPs, allowing for the generation of a highly accurate phylogenetic reconstruction of the CC398 clonal lineage. Phylogenetic analyses revealed that MSSA from humans formed the most ancestral clades. The most derived lineages were composed predominantly of livestock-associated MRSA possessing three different staphylococcal cassette chromosome mec element (SCCmec) types (IV, V, and VII-like) including nine subtypes. The human-associated isolates from the basal clades carried phages encoding human innate immune modulators that were largely missing among the livestock-associated isolates. Our results strongly suggest that livestock-associated MRSA CC398 originated in humans as MSSA. The lineage appears to have undergone a rapid radiation in conjunction with the jump from humans to livestock, where it subsequently acquired tetracycline and methicillin resistance. Further analyses are required to estimate the number of independent genetic events leading to the methicillin-resistant sublineages, but the diversity of SCCmec subtypes is suggestive of strong and diverse antimicrobial selection associated with food animal production. IMPORTANCE Modern food animal production is characterized by densely concentrated animals and routine antibiotic use, which may facilitate the emergence of novel antibiotic-resistant zoonotic pathogens. Our findings strongly support the idea that livestock-associated MRSA CC398 originated in humans. The jump of CC398 from humans to livestock was accompanied by the loss of phage-carried human virulence genes, which likely attenuated its zoonotic potential, but it was also accompanied by the acquisition of tetracycline and methicillin resistance. Our findings exemplify a bidirectional zoonotic exchange and underscore the potential public health risks of widespread antibiotic use in food animal production. IMPORTANCE Modern food animal production is characterized by densely concentrated animals and routine antibiotic use, which may facilitate the emergence of novel antibiotic-resistant zoonotic pathogens. Our findings strongly support the idea that livestock-associated MRSA CC398 originated in humans. The jump of CC398 from humans to livestock was accompanied by the loss of phage-carried human virulence genes.
genes, which likely attenuated its zoonotic potential, but it was also accompanied by the acquisition of tetracycline and methicillin resistance. Our findings exemplify a bidirectional zoonotic exchange and underscore the potential public health risks of widespread antibiotic use in food animal production.

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, University Paris Diderot - Paris 7, Statens Serum Institut, Northern Arizona University, Österreichische Agentur für Gesundheit und Ernährungssicherheit GmbH, University of Ljubljana, Istituto Zooprofilattico Sperimentale delle Regioni Lazio e Toscana, National Veterinary Research Institute, Friedrich-Loeffler-Institute, Ghent University, Interdisciplinary Centre of Research in Animal Health, Universidad Complutense, University of Iowa, University of Guelph, National University of San Marcos, First Affiliated Hospital of Wenzhou Medical College, National Reference Center for Staphylococci, University of Mississippi, Translational Genomics Research Institute
Pages: e00305
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Publication information
Journal: mBio
Volume: 3
Issue number: 1
ISSN (Print): 2150-7511
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 6.08
Web of Science (2017): Impact factor 6.689
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 5.79
Web of Science (2016): Impact factor 6.956
Scopus rating (2015): CiteScore 4.93
Web of Science (2015): Impact factor 6.975
Web of Science (2015): Indexed yes
Scopus rating (2014): CiteScore 4.23
Web of Science (2014): Impact factor 6.786
Web of Science (2014): Indexed yes
Scopus rating (2013): CiteScore 4.26
Web of Science (2013): Impact factor 6.875
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
Scopus rating (2012): CiteScore 4.08
Web of Science (2012): Impact factor 5.621
ISI indexed (2012): ISI indexed no
Scopus rating (2011): CiteScore 4.33
Web of Science (2011): Impact factor 5.311
ISI indexed (2011): ISI indexed no
Web of Science (2010): Impact factor
Original language: English
DOIs: 10.1128/mBio.00305-11
Source: dtu
Source-ID: n::oai:DTIC-ART:highwire/321028251::15095
Research output: Research - peer-review ; Journal article – Annual report year: 2012

Study of methicillin resistant Staphylococcus aureus (MRSA) in Danish pigs at slaughter and in imported retail meat reveals a novel MRSA type in slaughter pigs
Methicillin-resistant Staphylococcus aureus (MRSA), especially CC398, have emerged in livestock worldwide. We investigated the occurrence of MRSA in pigs at slaughter and in retail meat. During 2009, nasal swabs (n=789) were taken...
from pigs at slaughter. Moreover, 866 meat samples [Danish: pork (153), broiler meat (121), beef (142) and; imported: pork (173), broiler meat (193), and beef (84)] were randomly collected in retail stores and outlets. MRSA was isolated from nasal swabs or from meat samples after preenrichment (Mueller Hinton broth with 6.5% NaCl), selective enrichment (tryptone soya broth with 4mg/L cefoxitine and 75mg/L aztreonam) and selective plating on Brilliance Chromogenic MRSA agar. The presence of meca was confirmed by PCR and the MRSA isolates were spa typed. Novel MRSA spa types were characterized by MLST, PFGE and SCCmec typing. Thirteen percent (101/789) of the pigs had MRSA. Based on spa types 93% corresponded to CC398 (spa t011, t034, t1451, t2876, t2974), 4% to CC30 (t1333) and one isolate to CC1 (t0127). The spa type t1333 (CC30), which is common among methicillin susceptible S. aureus (MSSA) from pigs in Denmark, contained a SCCmec cassette type V and czrC zinc resistance gene. Imported broiler meat had the highest occurrence (18%) of MRSA, followed by imported pork (7.5%) and Danish pork (4.6%). MRSA ST398 was found for the first time in Danish beef (1.4%). The finding of MRSA CC30 (spa t1333) suggest possible spread of the SCCmec cassette normally associated with ST398 into another S. aureus lineage common in pigs.

General information
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Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Agersø, Y., Hasman, H., Cavaco, L. M., Pedersen, K., Aarestrup, F. M.
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Volume: 157
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BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
Sustainable farming: Get pigs off antibiotics

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State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Contributors: Aarestrup, F. M.
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BFI (2018): BFI-level 3
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 14.59
Web of Science (2017): Impact factor 19.181
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 13.33
Web of Science (2016): Impact factor 19.304
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 14.38
Web of Science (2015): Impact factor 17.184
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 14.22
Web of Science (2014): Impact factor 14.547
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 14.96
Web of Science (2013): Impact factor 15.295
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 14.01
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 13.96
Web of Science (2011): Impact factor
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
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Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes
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10.1038/486465a
Source: dtu
Source-ID: n::oai:DTIC-ART:npg/366239203::17631
Research output: Research - peer-review \ Journal article – Annual report year: 2012

The 10th EURL-AR Proficiency Test enterococci, staphylococci and E. coli 2011.: European Union Reference Laboratory – Antimicrobial Resistance

General information

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Contributors: Karlsmose, S., Cavaco, L., Hendriksen, R. S., Aarestrup, F. M.
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Research output: Research - peer-review › Report – Annual report year: 2012

The External Quality Assurance System of the WHO Global Foodborne Infections Network, 2011

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Contributors: Hendriksen, R. S., Karlsmose, S., Jensen, A. B., Aarestrup, F. M.
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Contributors: Hendriksen, R. S., Karlsmose, S., Jensen, A. B., Aarestrup, F. M.
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Report of the 2nd External Quality Assurance System on Isolation, Identification and Typing of Methicillin resistant Staphylococcus aureus (MRSA) from Swab Samples, year 2010

General information
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Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Cavaco, L., Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M.
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The 8th EURL-AR Proficiency Testing enterococci, staphylococci and E. coli 2010

General information
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Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Migura, L. G., Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M.
Number of pages: 57
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The 9th EURL-AR Proficiency Testing Salmonella and Campylobacter 2010

General information
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Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Karlsmose, S., Hendriksen, R. S., Bortolaia, V., Aarestrup, F. M.
Adjustment of pH of enrichment media might improve selective isolation of MRSA from pig samples

Methicillin resistant Staphylococcus aureus (MRSA) have emerged in livestock in several countries worldwide in recent years. MRSA may colonise in low numbers which makes both epidemiological studies and the implementation of control programmes difficult. Methods for selective isolation of MRSA from animal samples have been developed. However, obtaining sufficient sensitivity has been a challenge. Staphylococcus aureus is normally found on the skin, surviving and growing under extreme conditions: dry environment with high salt and low pH. In the selective isolation so far used high salt concentrations has been the main selection. We hypothesized that also pH adjustment could be used for selection of this species. In this study we compared the growth of MRSA and back ground flora in enrichment media at several different combinations of salt and pH. Background flora isolates were obtained from pig swabs. Initially a total of seven strains, including: two MRSA, two enterococci, two CNS one Aerococcus viridans and one Proteus spp. strains, were tested for growth in Mueller Hinton II broth with pH ranging from 4 to 5.5 and salt addition of 4% to 7%. In the next step, these strains were tested for growth in 12 different combinations of salt (5%- 6.5%) and pH (4.5-5.5). For assessment of the growth of S. aureus in pH adjusted media, further 14 MRSA and 13 MSSA were tested in a similar way. In a preliminary study using reference strains (data not shown) it was observed that pH ≤5.5 as well as salt concentrations ≥4% did allow growth of S. aureus but was inhibiting the growth of enterococci. Subsequent growth experiments with isolates from background flora showed an inhibitory effect of pH below 5 for Aerococcus spp and enterococci, whereas less effect was observed on CNS and Proteus spp. In the assays using different combinations of pH and salt, the pH showed, in general, a larger effect than the salt concentration on growth. MRSA and MSSA strains were partially inhibited by pH below 4.5 and grew with a moderate growth rate at pH 5.5 with lower salt concentration (5%). The growth of enterococci strains was completely inhibited by pH ≤5.5 at any salt concentrations tested (5- 6.5%), whereas the growth of Proteus spp. was only inhibited totally at pH of 4.5, but the growth rate could be reduced combining pH at 5 or 5.5 with high salt concentrations. In conclusion, pH adjustment of enrichment media might improve sensitivity of methods for detection of S. aureus by reducing background flora growth. Moreover, the combination of pH adjustment with reduction of the currently used salt enrichment concentration migth increase the sensitivity of the detection of MRSA. For screening purposes it will still be necessary to have further steps for the selective enrichment and isolation of MRSA. Further studies are underway to evaluate the value of this under field conditions.
Antimicrobials in livestock - Excessive use promotes resistance in human pathogens

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Contributors: Schlundt, J., Wegener, H. C., Aarestrup, F. M.
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Antimicrobial susceptibility and tetracycline resistance determinant genotyping of Gallibacterium anatis
The present investigation was undertaken to assess the antimicrobial susceptibility of a collection of 58 Gallibacterium isolates. All strains were tested by the broth dilution method using the veterinary fastidious medium. A total of 46 field strains were tested, whereof 23 were clinical isolates from 10 Mexican layer flocks and another 23 isolates originated from 13 clinically healthy poultry flocks in Denmark. In addition, 12 Gallibacterium reference strains that had been isolated some 30–40 years ago were included. The 58 strains were tested against 23 compounds of different classes. Multidrug resistance (resistance towards≥three drugs) was observed for 65% of the field strains and only two strains were susceptible to all compounds. Most prominently, resistance to tetracycline and sulfamethoxazole was observed in 92% and 97% of the field strains, respectively. For comparison these figures were 67% and 42%, respectively, for the reference strains. Genotyping of tetracycline resistance determinants was performed with primers specific for tet(A–E, H, K–M, O). Strains positive for tet(B), tet(H) and tet(L) were identified, however, in 20 out of 49 tetracycline resistant strains no determinant was identified. This is the first study to determine the antimicrobial susceptibility of Gallibacterium anatis by MIC revealing that multidrug resistance is very common among G. anatis field isolates. tet(B) was by far the most common determinant identified but future work should aim at identifying the tetracycline resistance determinants in the remaining 41% of strains where no determinant was assigned.

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Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Lohmann Animal Health International, Boehringer Ingelheim Vetmedica, Inc., University of Copenhagen
Contributors: Bojesen, A. M., Vazquez, M. E., Bager, R. J., Ifrah, D., Gonzalez, C., Aarestrup, F. M.
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Association Between Antimicrobial Resistance in Escherichia coli Isolates from Food Animals and Blood Stream Isolates from Humans in Europe: An Ecological Study

Background: In addition to medical antimicrobial usage, the use of antimicrobials in food animals contributes to the occurrence of resistance among some bacterial species isolated from infections in humans. Recently, several studies have indicated that a large proportion of Escherichia coli causing infections in humans, especially those resistant to antimicrobials, have an animal origin.

Methods: We analyzed the correlation between the prevalence of antimicrobial resistance in E. coli isolates from blood stream infections in humans and in E. coli isolates from poultry, pigs, and cattle between 2005 and 2008 for 11 countries, using available surveillance data. We also assessed the correlation between human antimicrobial usage and the occurrence of resistance in E. coli isolates from blood stream infections.

Results: Strong and significant correlations between prevalences of resistance to ampicillin (r=0.94), aminoglycosides (r=0.72), third-generation cephalosporins (r=0.76), and fluoroquinolones (r=0.68) were observed for human and poultry E. coli isolates. Similar significant correlations were observed for ampicillin (r=0.91), aminoglycosides (r=0.73), and fluoroquinolone resistance (r=0.74) in pig and human isolates. In cattle isolates, only ampicillin resistance (r=0.72) was significantly correlated to human isolates. When usage of antimicrobials in humans was analyzed with antimicrobial resistance among human isolates, only correlations between fluoroquinolones (r=0.90) and third-generation cephalosporins (r=0.75) were significant.

Conclusions: Resistance in E. coli isolates from food animals (especially poultry and pigs) was highly correlated with resistance in isolates from humans. This supports the hypothesis that a large proportion of resistant E. coli isolates causing blood stream infections in people may be derived from food sources.
Characterization of Salmonella Occurring at High Prevalence in a Population of the Land Iguana Conolophus subcristatus in Galapagos Islands, Ecuador

The aim of the study was to elucidate the association between the zoonotic pathogen Salmonella and a population of land iguana, Conolophus subcristatus, endemic to Galapagos Islands in Ecuador. We assessed the presence of Salmonella subspecies and serovars and estimated the prevalence of the pathogen in that population. Additionally, we investigated the genetic relatedness among isolates and serovars utilising pulsed field gel electrophoresis (PFGE) on XbaI-digested DNA and determined the antimicrobial susceptibility to a panel of antimicrobials. The study was carried out by sampling cloacal swabs from animals (n = 63) in their natural environment on the island of Santa Cruz. A high prevalence (62/63, 98.4%) was observed with heterogeneity of Salmonella subspecies and serovars, all known to be associated with reptiles and with reptile-associated salmonellosis in humans. Serotyping revealed 14 different serovars among four Salmonella enterica subspecies: S. enterica subsp. enterica (n = 48), S. enterica subsp. salamae (n = 2), S. enterica subsp. diarizonae (n = 1), and S. enterica subsp. houtenae (n = 7). Four serovars were predominant: S. Poona (n = 18), S. Pomona (n = 10), S. Abaetetuba (n = 8), and S. Newport (n = 5). The S. Poona isolates revealed nine unique XbaI PFGE patterns, with 15 isolates showing a similarity of 70%. Nine S. Pomona isolates had a similarity of 84%. One main cluster with seven (88%) indistinguishable isolates of S. Abaetetuba was observed. All the Salmonella isolates were pan-susceptible to antimicrobials representative of the most relevant therapeutic classes. The high prevalence and absence of clinical signs suggest a natural interaction of the different Salmonella serovars with the host species. The interaction may have been established before any possible exposure of the iguanas and the biocenosis to direct or indirect environmental factors influenced by the use of antimicrobials in agriculture, in human medicine or in veterinary medicine.
Epidemiological Investigation of Salmonella enterica Serovar Kedougou in Thailand

Objective: Salmonella enterica serovar Kedougou is among the top 10 serovars reported in northern Thailand. The objective of this study was to identify risk factors associated with Salmonella Kedougou infection in Thailand and to compare the molecular types and antimicrobial resistance with Salmonella Kedougou isolates of human origin from United States and of animal origin from the United Kingdom. Methods: Data from 13,976 Salmonella infections of which 253 were Salmonella Kedougou collected in Thailand between 2002 and 2008 were analyzed by logistic regression. Antimicrobial susceptibility testing and pulsed-field gel electrophoresis (PFGE) were performed on selected Salmonella Kedougou strains causing infections in Thailand (n = 66), and compared to isolates from the United States (n = 5) and the United Kingdom (n = 20). Results: Logistic analysis revealed season (hot/dry; p = 0.023), region (northern Thailand; p < 0.001), and specimen (stool; p < 0.001) as significant risk factors associated with Salmonella Kedougou infection compared to other nontyphoid Salmonella. Of the Salmonella Kedougou isolates of human origin, 84% exhibited resistance to at least three antimicrobial classes. Three strains recovered from human stool in Thailand were resistant to third-generation cephalosporins: two harbored \textit{bla}_{CTX-M-63} and one \textit{bla}_{CMY-2}. PFGE revealed 45 unique clusters. Isolates obtained from humans in Thailand and the United States presented identical PFGE profiles suggesting a travel association, whereas the majority of the animal isolates from United Kingdom clustered separately. Conclusions: This study reveals Salmonella Kedougou as a major cause of human infections in northern Thailand especially during the hot period and suggests a global spread probably due to travel. The clonal types causing infections in humans differed from those observed in animals in United Kingdom, which suggests the absence of an epidemiological link and could suggest differences in virulence. The high frequency of antimicrobial resistance, including emergence of resistance to fluoroquinolones and third-generation cephalosporins, might pose problems for treatment of infections.

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Contributors: Pornruangwong, S., Hendriksen, R. S., Pulsrikarn, C., Bangstrakulnonth, A., Mikoleit, M., Davies, R. H., Aarestrup, F. M., Migura, L. G.
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BFI (2015): BFI-level 1
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Web of Science (2015): Impact factor 2.27
BFI (2014): BFI-level 1
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Establishing Streptomycin Epidemiological Cut-Off Values for Salmonella and Escherichia coli

This study was conducted to elucidate the accuracy of the current streptomycin epidemiological cut-off value (ECOFF) for Escherichia coli and Salmonella spp. A total of 236 Salmonella enterica and 208 E. coli isolates exhibiting MICs between 4 and 32 mg/L were selected from 12 countries. Isolates were investigated by polymerase chain reaction for aadA, strA, and strB streptomycin resistance genes. Out of 236 Salmonella isolates, 32 (13.5%) yielded amplicons for aadA (n = 23), strA (n = 9), and strB (n = 11). None of the 60 Salmonella isolates exhibiting MIC 4 mg/L harbored resistance genes. Of the Salmonella isolates exhibiting MICs 8 mg/L, 16 mg/L, and 32 mg/L, 1.6%, 15%, and 39%, respectively, tested positive for one or more genes. For most monitoring programs, the streptomycin ECOFF for Salmonella is wild type (WT) ≤32 or ≤16 mg/L. A cut-off value of WT ≤32 mg/L would have misclassified 13.5% of the strains as belonging to the WT population, since this proportion of strains harbored resistance genes and exhibited MICs ≤32 mg/L. Out of 208 E. coli strains, 80 (38.5%) tested positive for aadA (n = 69), strA (n = 18), and strB (n = 31). Of the E. coli isolates exhibiting MICs of 4 mg/L, 8 mg/L, 16 mg/L, and 32 mg/L, 3.6%, 17.6%, 53%, and 82.3%, respectively, harbored any of the three genes. Based on the European Committee on Antimicrobial Susceptibility Testing guidelines (ECOFF ≤16 mg/L), 25% of the E. coli strains presenting MIC ≤16 mg/L would have been incorrectly categorized as belonging to the WT population. The authors recommend an ECOFF value of WT ≤16 mg/L for Salmonella and WT ≤8 mg/L for E. coli.

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Global Food Safety Portal: A visualisation tool to promote new research into data relations and assess trends, patterns and risk factors for foodborne pathogens

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Salmonella enterica is commonly acquired from contaminated food and is an important cause of illness worldwide. Interventions are needed to control Salmonella; subtyping Salmonella by serotyping is useful for targeting such interventions. We, therefore, analyzed the global distribution of the 15 most frequently identified serovars of Salmonella isolated from humans from 2001 to 2007 in laboratories from 37 countries that participated in World Health Organization Global Foodborne Infections Network and demonstrated serotyping proficiency in the Global Foodborne Infections Network External Quality Assurance System. In all regions throughout the study period, with the exception of the Oceania and North American regions, Salmonella serovars Enteritidis and Typhimurium ranked as the most common and second most common serovar, respectively. In the North American and Oceania (Australia and New Zealand) regions, Salmonella serovar Typhimurium was the most common serovar reported, and Salmonella serovar Enteritidis was the second most common serovar. During the study period, the proportion of Salmonella isolates reported from humans that were Salmonella serovar Enteritidis was 43.5% (range: 40.6% [2007] to 44.9% [2003]), and Salmonella serovar Typhimurium was 17.1% (range: 15% [2007] to 18.9% [2001]). Salmonella serovars Newport (mainly observed in Latin and North American and European countries), Infantis (dominating in all regions), Virchow (mainly observed in Asian, European, and Oceanic countries), Hadar (profound in European countries), and Agona (intense in Latin and North American and European countries) were also frequently isolated with an overall proportion of 3.5%, 1.8%, 1.5%, 1.5%, and 0.8%, respectively. There were large differences in the most commonly isolated serovars between regions, but lesser differences
between countries within the same region. The results also highlight the complexity of the global epidemiology of Salmonella and the need and importance for improving monitoring data of those serovars of highest epidemiologic importance.

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BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.41 SJR 1.064 SNIP 1.035
Web of Science (2015): Impact factor 2.27
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.16 SJR 0.953 SNIP 1.051
Web of Science (2014): Impact factor 1.905
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.41 SJR 1.184 SNIP 1.129
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ISI indexed (2013): ISI indexed yes
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BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.55 SJR 1.185 SNIP 1.144
Web of Science (2012): Impact factor 2.283
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Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.33 SJR 1.118 SNIP 1.037
Web of Science (2011): Impact factor 2.26
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.86 SNIP 0.94
Web of Science (2010): Impact factor 2.134
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.864 SNIP 1.088
Web of Science (2009): Indexed yes
Scopus rating (2008): SJR 0.72 SNIP 0.682
Web of Science (2008): Indexed yes
Increasing transmission of antibiotic resistance from animals to humans

The importance of the animal reservoir for emergence of antimicrobial resistance in bacteria in humans is difficult to estimate. In this article we give our estimate of the importance and also highlight on which points we have become wiser during recent years. We conclude that it still is the human usage of antibiotics which contributes most to resistance observed in humans, but also that the contribution from animals is large and larger than estimated just a few years ago. This indicates the need to implement restriction on antimicrobial usage for both humans and animals.

General information
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Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Statens Serum Institut
Contributors: Aarestrup, F. M., Frimodt-Møller, N.
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BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 0.04 SJR 0.115 SNIP 0.02
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.02 SJR 0.118 SNIP 0.056
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.03 SJR 0.124 SNIP 0.082
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 0.05 SJR 0.134 SNIP 0.121
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 0.06 SJR 0.142 SNIP 0.125
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 0.08 SJR 0.147 SNIP 0.151
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 0.1 SJR 0.144 SNIP 0.162
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.161 SNIP 0.17
Web of Science (2010): Indexed yes
Indications and patterns of therapeutic use of antimicrobial agents in the Danish pig production from 2002 to 2008
This study describes trends in the use and indications for prescriptions of antimicrobial agents in the Danish pig production in the period between 2002 and 2008 and is the first description of a complete prescription pattern for one animal species in an entire country. Data on all prescription for pigs in Denmark were retrieved from the VetStat database. Antimicrobial use was measured in defined animal daily doses (ADD) for the specific age-group and in ADDkg as a measure of amounts used. According to the results of the ADDkg data, 26% of all antimicrobials were prescribed for sows, 38% for weaner pigs, and 33% for finisher pigs. In weaner and finisher pigs, gastrointestinal infections accounted for 74–83% and 56–65% of the use, while respiratory infections accounted for 9–17% and 18–24%, respectively. From 2002 to 2008, prescription for respiratory disease increased by 145% for sows/piglets, by 141% for weaning pigs, and by 81% for finisher pig. The most commonly used class of antibiotics was tetracycline for all age-groups, replacing the previously used macrolide/lincosamide group. The use of pleuromutilin increased in 2008 to the level of macrolides. In sow/piglets, the second most used class was penicillins. The switch in choice of antimicrobial classes prescribed seems to be related primarily to changes in the price of the drugs.
Scopus rating (2015): CiteScore 1.14 SJR 0.651 SNIP 0.85
Web of Science (2015): Impact factor 1.279
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 1.31 SJR 0.823 SNIP 0.845
Web of Science (2014): Impact factor 1.189
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 1.27 SJR 0.693 SNIP 0.869
Web of Science (2013): Impact factor 1.323
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BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 0.96 SJR 0.535 SNIP 0.795
Web of Science (2012): Impact factor 1.349
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 0.91 SJR 0.583 SNIP 0.809
Web of Science (2011): Impact factor 1.181
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.556 SNIP 0.657
Web of Science (2010): Impact factor 1.675
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.648 SNIP 1.141
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.631 SNIP 0.842
Scopus rating (2007): SJR 0.805 SNIP 1.068
Scopus rating (2006): SJR 0.675 SNIP 1.114
Scopus rating (2005): SJR 0.584 SNIP 0.921
Scopus rating (2004): SJR 0.411 SNIP 0.762
Scopus rating (2003): SJR 0.465 SNIP 0.788
Scopus rating (2002): SJR 0.327 SNIP 0.807
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.423 SNIP 0.93
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.714 SNIP 1.099
Scopus rating (1999): SJR 0.624 SNIP 1.128
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International collaborative study on the occurrence of plasmid-mediated quinolone resistance in Salmonella enterica and Escherichia coli isolated from animals, humans, food and the environment in 13 European countries

OBJECTIVES: This study was initiated to collect retrospective information on the occurrence of plasmid-mediated quinolone resistance (PMQR) in Salmonella enterica and Escherichia coli isolates in Europe and to identify the responsible genes. METHODS: Databases of national reference laboratories containing MIC values for Salmonella and E. coli isolated between 1994 and 2009 in animals, humans, food and the environment from 13 European countries were screened for isolates exhibiting a defined quinolone resistance phenotype, i.e. reduced susceptibility to fluoroquinolones and nalidixic acid. PCR and sequence analysis were performed to identify the responsible PMQR genes. RESULTS: Screening of databases of 13 European countries resulted in a selection of 1215 Salmonella and 333 E. coli isolates. PMQR genes were identified in 59% of the Salmonella isolates and 15% of the E. coli isolates selected. In Salmonella, qnrS1 (n = 125) and variants of qnrB (n = 138) were frequently identified, whereas qnrA1 (n = 3) and aac(6')-1b-cr (n = 3) were rarely found. qnrD was detected in 22 Salmonella isolates obtained from humans and animals. In E. coli, qnrS1 was identified in 19 isolates and qnrB19 was found in one isolate. No qnrC or qepA genes were detected in either Salmonella or E. coli. CONCLUSIONS: This study shows the occurrence and dissemination of PMQR genes in Salmonella and E. coli
in Europe with a defined quinolone resistance phenotype. We also report the first detection of qnrD in Salmonella collected in Europe.

**General information**

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Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Central Veterinary Institute, Istituto Zooprofilattico Sperimentale delle Regioni Lazio e Toscana, Scientific Institute of Public Health Safety, State Veterinary Institute, Laboratorio Central de Veterinaria de Algete, Federal Institute for Risk Assessment, Central Veterinary Research Laboratory, Health Protection Agency, Finnish Food Safety Authority, National Veterinary Institute, National Veterinary Research Institute
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Impact factor 5.071
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Web of Science (2015): Impact factor 4.919
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Scopus rating (2014): CiteScore 4.61 SJR 2.298 SNIP 1.765
Web of Science (2014): Impact factor 5.313
Web of Science (2014): Indexed yes
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Scopus rating (2013): CiteScore 4.7 SJR 2.479 SNIP 1.824
Web of Science (2013): Impact factor 5.439
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BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.35 SJR 2.283 SNIP 1.718
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BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.24 SJR 2.341 SNIP 1.769
Web of Science (2011): Impact factor 5.068
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
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Scopus rating (2010): SJR 2.161 SNIP 1.643
International Spread of an Epidemic Population of Salmonella enterica Serotype Kentucky ST198 Resistant to Ciprofloxacin

National Salmonella surveillance systems from France, England and Wales, Denmark, and the United States identified the recent emergence of multidrug-resistant isolates of Salmonella enterica serotype Kentucky displaying high-level resistance to ciprofloxacin. A total of 489 human cases were identified during the period from 2002 (3 cases) to 2008 (174 cases). These isolates belonged to a single clone defined by the multilocus sequence type ST198, the XbaI-pulsed-field gel electrophoresis cluster X1, and the presence of the Salmonella genomic island 1 variant SGI1-K. This clone was probably selected in 3 steps in Egypt during the 1990s and the early 2000s and has now spread to several countries in Africa and, more recently, in the Middle East. Poultry has been identified as a potential major vehicle for infection by this clone. Continued surveillance and appropriate control measures should be implemented by national and international authorities to limit the spread of this strain.

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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.86 SJR 3.931 SNIP 1.62
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.88 SJR 3.958 SNIP 1.711
Web of Science (2015): Impact factor 6.344
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.84 SJR 3.836 SNIP 1.74
Web of Science (2014): Impact factor 5.997
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 5.21 SJR 3.64 SNIP 1.687
Web of Science (2013): Impact factor 5.778
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 5.43 SJR 3.361 SNIP 1.702
Web of Science (2012): Impact factor 5.848
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 5.79 SJR 3.559 SNIP 1.934
Web of Science (2011): Impact factor 6.41
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 3.482 SNIP 1.772
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 3.121 SNIP 1.768
BFI (2008): BFI-level 2
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 3.059 SNIP 1.784
Scopus rating (2006): SJR 3.004 SNIP 1.677
Scopus rating (2005): SJR 2.695 SNIP 1.686
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.58 SNIP 1.691
Scopus rating (2003): SJR 2.25 SNIP 1.665
Scopus rating (2002): SJR 2.361 SNIP 1.577
Scopus rating (2001): SJR 2.457 SNIP 1.581
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 2.257 SNIP 1.757
Scopus rating (1999): SJR 2.395 SNIP 1.849
Molecular Characterization and Antimicrobial Susceptibility Testing of Escherichia coli Isolates from Patients with Urinary Tract Infections in 20 Chinese Hospitals

A total of 222 urinary Escherichia coli isolates from 20 tertiary hospitals in 15 different provinces and 4 municipalities in mainland China were characterized by antimicrobial susceptibility, phylogrouping, and the presence of plasmid-mediated quinolone resistance genes. A subset of 138 suspected extended-spectrum cephalosporinase (ESC) producers were examined for genes encoding cephalosporin resistance. Forty-three isolates harboring blaCTX-M-14 or blaCTX-M-15 were analyzed by pulsed-field gel electrophoresis (PFGE), and plasmids containing these genes were typed using PCR-based replicon typing (PBRT). Thirteen phylogroup B2 blaCTX-M-14- and blaCTX-M-15-positive isolates were analyzed by multilocus sequence typing (MLST). A frequent occurrence of resistance (>46%) was observed toward cephalosporins, gentamicin, and fluoroquinolones. Among the 222 isolates, 4 qnrS1, 4 qepA, and 16 aac(6')-Ib-cr genes were confirmed. Four major phylogroups (A, B1, B2, and D) and nontypeable isolates (NTs) were found among the isolates, with phylogroup D (54%) being the most common phylogroup. A total of 110 (80%) of the 138 screened isolates harbored blaCTX-M genes, with blaCTX-M-14 (71%) and blaCTX-M-15 (24%) being the most prevalent of these genes. Nine of the 13 CTX-M-15- or CTX-M-14-containing B2 isolates belonged to ST131. PFGE typing showed a high level of diversity, and plasmid analysis indicated a very large pool of different resistance plasmids mediating the spread of blaCTX-M genes in mainland China. An equally very high frequency of resistance and equally high levels of diversity in phylogroups, PFGE types, and plasmids were observed among community- and hospital-acquired E. coli isolates, indicating the presence of a large reservoir in the community and a long-term spread of cephalosporin resistance in China.

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BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.55 SJR 2.256 SNIP 1.443
Web of Science (2017): Impact factor 4.054
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.196 SNIP 1.4
Web of Science (2016): Impact factor 3.712
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.56 SJR 2.206 SNIP 1.431
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.84 SJR 2.231 SNIP 1.528
Web of Science (2014): Impact factor 3.993
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.18 SJR 2.438 SNIP 1.63
Web of Science (2013): Impact factor 4.232
ISI indexed (2013): ISI indexed yes
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Scopus rating (2012): CiteScore 4.11 SJR 2.148 SNIP 1.626
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ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.27 SJR 2.346 SNIP 1.699
Web of Science (2011): Impact factor 4.153
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.343 SNIP 1.731
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BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.199 SNIP 1.691
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Scopus rating (2008): SJR 2.265 SNIP 1.608
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.224 SNIP 1.688
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.212 SNIP 1.641
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.037 SNIP 1.65
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.699 SNIP 1.701
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.854 SNIP 1.853
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.976 SNIP 1.724
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.066 SNIP 1.804
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**Perspectives of a global, real-time microbiological genomic identification system - implications for national and global detection and control of infectious diseases: Consensus report of an expert meeting 1-2 September 2011, Bruxelles, Belgium**

**General information**
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Contributors: Hendriksen, R. S., Aarestrup, F. M.
Phenotypic, Proteomic, and Genomic Characterization of a Putative ABC-Transporter Permease Involved in Listeria monocytogenes Biofilm Formation

The foodborne pathogen Listeria monocytogenes is able to form biofilms in food processing environments. Previously, we have reported that an lm.G_1771 gene (encoding a putative ABC-transporter permease) was involved in negative regulation of L. monocytogenes biofilm formation using LM-49, a biofilm-enhanced mutant isolated on Tn917 mutagenesis (AEM 2008 p.7675–7683). Here, the possible action of this ABC-transporter permease in L. monocytogenes biofilm formation was characterized by phenotypic, proteomic, and genomic analyses using an lm.G_1771 gene deletant (Δ1771). The Δ1771 mutant exhibited the same enhanced ability for biofilm formation as the LM-49 strain using a crystal violet staining assay. DNA microarrays and two-dimensional gel electrophoresis revealed 49 and 11 differentially expressed (twofold or more) genes or proteins in Δ1771, respectively. The transcriptomics study indicated that lm.G_1771 could play a vital role in regulating candidate genes involved in biofilm formation such as genes encoding cell surface proteins (Dlt), cell surface anchor proteins (SrtA), and transcriptional regulators (GntR) contributing to negative regulation of biofilm formation by L. monocytogenes. The mutant Δ1771 was more sensitive to Triton X-100 and less resistant to cationic antibiotics, which might be explained by the down-regulation of dlt operon in this deletant and the fact that dlt involves the incorporation of D-alanine residues into lipoteichoic acids, resulting in a positive net charge on the teichoic acids. Therefore, lm.G_1771 is considered to be involved in negative regulation of biofilm formation, and the results from this work provide a possible molecular mechanism of biofilm formation regulated by lm.G_1771 in L. monocytogenes.
Population Genetics of Vibrio cholerae from Nepal in 2010: Evidence on the Origin of the Haitian Outbreak

ABSTRACT: Cholera continues to be an important cause of human infections, and outbreaks are often observed after natural disasters, such as the one following the 2010 earthquake in Haiti. Once the cholera outbreak was confirmed, rumors spread that the disease was brought to Haiti by a battalion of Nepalese soldiers serving as United Nations peacekeepers. This possible connection has never been confirmed. We used whole-genome sequence typing (WGST), pulsed-field gel electrophoresis (PFGE), and antimicrobial susceptibility testing to characterize 24 recent Vibrio cholerae isolates from Nepal and evaluate the suggested epidemiological link with the Haitian outbreak. The isolates were obtained from 30 July to 1 November 2010 from five different districts in Nepal. We compared the 24 genomes to 10 previously sequenced V. cholerae isolates, including 3 from the Haitian outbreak (began July 2010). Antimicrobial susceptibility and PFGE patterns were consistent with an epidemiological link between the isolates from Nepal and Haiti. WGST showed that all 24 V. cholerae isolates from Nepal belonged to a single monophyletic group that also contained isolates from Bangladesh and Haiti. The Nepalese isolates were divided into four closely related clusters. One cluster contained three Nepalese isolates and three Haitian isolates that were almost identical, with only 1- or 2-bp differences. Results in this study are consistent with Nepal as the origin of the Haitian outbreak. This highlights how rapidly infectious diseases might be transmitted globally through international travel and how public health officials need advanced molecular tools along with standard epidemiological analyses to quickly determine the sources of outbreaks. IMPORTANCE Cholera is one of the ancient classical diseases and particularly prone to cause major outbreaks following major natural disasters, such as earthquakes and hurricanes, where the normal separation between sewage and drinking water is destroyed. This was the case following the 2010 earthquake in Haiti. Rumors spread that the disease was brought to Haiti by a battalion of Nepalese soldiers serving as United Nations peacekeepers. This possible connection has never been confirmed. Sequencing the genomes of bacteria can give detailed information on whether isolates from different sites share a common origin. We used this technology to sequence isolates of Vibrio cholerae from Nepal, identify single-nucleotide polymorphisms (SNPs), and compare these high-resolution genotypes to the complete genome sequences of isolates from the Haiti outbreak. We provide support for the hypothesis that the isolates were brought to Haiti from Nepal.

IMPORTANCE: Cholera is one of the ancient classical diseases and particularly prone to cause major outbreaks following major natural disasters, such as earthquakes and hurricanes, where the normal separation between sewage and drinking water is destroyed.
water is destroyed. This was the case following the 2010 earthquake in Haiti. Rumors spread that the disease was brought to Haiti by a battalion of Nepalese soldiers serving as United Nations peacekeepers. This possible connection has never been confirmed. Sequencing the genomes of bacteria can give detailed information on whether isolates from different sites share a common origin. We used this technology to sequence isolates of Vibrio cholerae from Nepal, identify single-nucleotide polymorphisms (SNPs), and compare these high-resolution genotypes to the complete genome sequences of isolates from the Haiti outbreak. We provide support for the hypothesis that the isolates were brought to Haiti from Nepal.

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Scopus rating (2015): CiteScore 4.93
Web of Science (2015): Impact factor 6.975
Web of Science (2015): Indexed yes
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Source-ID: 282520
Research output: Research - peer-review > Journal article – Annual report year: 2011
Prevalence and characterization of human Shigella infections in Henan Province, China, in 2006.

In 2006, 3531 fecal samples were collected from patients with diarrhea in Henan Province, China. A total of 467 (13.2%) Shigella strains were isolated and serotyped. Seventy-one Shigella flexneri strains were characterized by MIC determination, pulsed-field gel electrophoresis (PFGE), and detection of genes encoding cephalosporin resistance. Most infections were caused by S. flexneri variant X [IV:(7),8] (27.6%), S. sonnei (24.2%), and S. flexneri 2a (20.8%). However, large regional differences were observed. Significantly higher odds (2.0) of females compared to males were infected with S. flexneri 2a. Untypeable S. flexneri (–:6) isolates were absent among males, as were untypeable S. flexneri [I:(7),8] isolates among females. Patient ages ranged from 2 months to 82 years, with 231 subjects (49.7%).

General information
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Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Xia, S., Xu, B., Huang, L., Zhao, J. Y., Ran, L., Zhang, J., Chen, H., Pulsrikarn, C., Pornruangwong, S., Aarestrup, F. M., Hendriksen, R. S.
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.196 SNIP 1.4
Web of Science (2016): Impact factor 3.712
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.56 SJR 2.206 SNIP 1.431
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.84 SJR 2.231 SNIP 1.528
Web of Science (2014): Impact factor 3.993
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.18 SJR 2.438 SNIP 1.63
Web of Science (2013): Impact factor 4.232
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.11 SJR 2.148 SNIP 1.626
Web of Science (2012): Impact factor 4.068
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.27 SJR 2.346 SNIP 1.699
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Reply to "South Asia Instead of Nepal May Be the Origin of the Haitian Cholera Outbreak Strain"

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Scopus rating (2016): CiteScore 5.79
Risk assessment of antimicrobial usage in Danish pig production on the human exposure to antimicrobial resistant bacteria from pork

During the last decades, bacteria with resistance to all commonly used antimicrobial agents have been detected, thereby posing a major threat to public health. In worst case, infections with resistant bacteria can lead to treatment failure and death of humans. The evolution of bacteria resistant to antimicrobials are influenced by the use of antimicrobial agents, and the prudence of antimicrobial use have been emphasized since the Swann report in 1969 recommended that antibiotics used in human medicine should not be used as growth promoters in food-producing animals. In 2007, the World Health Organisation (WHO) pronounced a list of the antimicrobial classes critically important for the treatment of infectious
diseases in humans. On this list occurred among others the third and fourth generation cephalosporins. Cephalosporins have been used increasingly worldwide throughout the recent years to treat various infections in veterinary and human medicine and the occurrence of resistance to this antimicrobial class have been detected with increasing frequency.

The purpose of this thesis was to perform a quantitative assessment of the association between the use of antimicrobial agents for treatment of slaughter pigs and the occurrence of extended-spectrum cephalosporinases (ESC) producing E. coli in pigs and pork. The thesis addresses this purpose by estimating the effect of the antimicrobial usage on the occurrence of resistance. And by using the obtained results in a risk assessment model where the human exposure to cephalosporin resistance from pork purchased in retail shops was assessed using different scenarios for the amount of antimicrobial used in the primary production. Also, farm-related factors affecting the antimicrobial usage were investigated as a part of this thesis.

The thesis addresses this in the following sections:

Objective 1: Estimating the association between antimicrobial usage and the detection of ESC producing E. coli

Objective 2: Quantifying the effect of antimicrobial usage on the proportion of ESC producing E. coli

Objective 3: Identification of management factors in the Danish finishing pig production important for antimicrobial usage

In Objective 1, the occurrence (presence/non-passage) of ESC producing E. coli in samples from healthy pigs at slaughter was investigated using selective agar plates supplemented with ceftriaxone. The occurrence of ESC producing E. coli was used as the outcome in the data analysis, where the effect of using cephalosporins, extended spectrum penicillins and tetracyclines was estimated using regression analysis.

In Objective 2, the samples collected for Objective 1 were diluted in 10 fold and spread on selective plates in two set of triplicates (one set containing three MacConkey agar plates, and one set containing three MacConkey agar plates supplemented with ceftriaxone). This provided quantitative data for the ESC producing E. coli and total concentration of E. coli in each sample. The proportion of ESC producing E. coli was thereafter estimated using a Poisson regression adjusting for applied dilution factor. The resistance proportion was subsequently used as outcome in a regression model to estimate the effect of the antimicrobial usage on the proportion of ESC producing E. coli.

The prevalence, concentration and proportion of ESC producing E. coli obtained in Objective 1 and Objective 2 was used as input in a human exposure assessment model. In Objective 2, a significant effect on the resistance proportion was found from the quantitative use of tetracyclines one year prior to the sampling date. This effect was used in the exposure assessment model. This model also used data from additional sources to estimate the human exposure to ESC producing E. coli from the purchase of Danish pork chops. By using the ESC producing E. coli prevalence of 41 % (obtained in Objective 1), the resulting prevalence in pork chops was found to vary from 19.70 % to 21.80 %. The prevalence of ESC producing E. coli was increasing as the usage of tetracyclines increased. However, this prevalence was found in pork chops originating from the study population, which was chosen based on their usage of cephalosporin.

In an attempt to check the validity of the model, the data from a national survey was used as input. This survey also used selective enrichment, but did not estimate the concentration of E. coli or the proportion of ESC producing E. coli, therefore the prevalence obtained from the healthy pigs at slaughter was used as input in the model, whereas the remaining steps of the model were not changed. The resulting effect on the estimated prevalence of ESC producing E. coli in 100,000 pork chops was compared to the observed prevalence from the national survey. This analysis estimated the prevalence to 5.3 % ESC producing E. coli, which is 2.6 times higher than the observed prevalence on 2 %. However, the data from the national survey was obtained at retail, whereas the model was not considering the growth or inactivation taking place under the transport and storage of the meat.

In Objective 3, the risk factors for a high usage of tetracycline were investigated by assessing the effect of tetracycline usage on the occurrence of tetracycline resistance in pigs originating from three different production types. The effect of the tetracycline usage and the effect of the production type was estimated using logistic regression. The results of this objective showed a highly significant effect of the production type, where the organic production had significantly lower occurrence of tetracycline resistance, and also had a much lower average usage of tetracycline. No significant difference in the tetracycline resistance could be found between the conventional and free range productions. When estimating the effect of the tetracycline usage in general using all the production types, a significant effect on the occurrence of resistance was found on the quantitative usage of tetracycline.

Data in this study unfortunately did not have enough power to point out single factors within the production types that could be responsible for the size of the tetracycline usage.

The overall conclusion of this thesis is that there is a significant effect of the quantitative antimicrobial usage (i.e. the amount of antimicrobial used) on the occurrence of ESC producing E. coli. A high antimicrobial usage gives an increased prevalence of resistance, but also an increased proportion of resistance. Furthermore, the occurrence of cephalosporin resistance appears to be influenced by a generic use of antimicrobial agents rather than the effect of a single antimicrobial class. The exposure assessment indicate that human exposure to ESC producing E. coli is to some degree affected by the generic use of antimicrobial agents in the primary pig production. However, this thesis also found big differences in the occurrence of resistance and antimicrobial usage, when comparing conventional and free range production to organic production. There seems to be a huge potential to lower the generic antimicrobial usage in the conventional and free range productions. Future studies evaluating the effect of specific risk factors in the organic production could lead to useful recommendations on how to lower the antimicrobial usage in the other production types. However, welfare issues need to be investigated to rule out the possibility of untreated diseases in the organic production.

General information
Susceptibility of Clostridium difficile Toward Antimicrobial Agents Used as Feed Additives for Food Animals
A total of 65 toxigenic Clostridium difficile strains isolated from patients with antibiotic-associated diarrhea were tested for susceptibility to avilamycin, flavomycin, monensin, and salinomycin. Except for flavomycin the substances showed in vitro efficacy comparable to reports of the currently most commonly used drugs for treatment of C. difficile. This indicates that these old compounds may be useful for the treatment of C. difficile infections in man and perhaps for other bacterial causes of diarrhea.
The rarely reported tet(31) tetracycline resistance determinant is common in Gallibacterium anatis

The present investigation was undertaken to identify and characterize the tetracycline resistance determinant in 22 Gallibacterium anatis strains for which no determinant was identified using primers specific for tet(A, B, C, D, E, G, H, K, L, M, O). A recent study found tet(B) to be the most prevalent tetracycline resistance determinant in a larger collection of G. anatis field strains from Mexico and Denmark. However, in 41% of the tetracycline resistant strains no determinant could be assigned. Here we demonstrate that tet(31) is a common determinant in G. anatis originating from chickens from very different production systems and localities. In addition, tet(31) was identified in strains isolated over a 30-year period. This is the first report on tet(31) since its original identification in Aeromonas salmonicida.

General information
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Contributors: Bojesen, A. M., Bager, R. J., Ifrah, D., Aarestrup, F. M.
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The Salmonella enterica Pan-genome

Salmonella enterica is divided into four subspecies containing a large number of different serovars, several of which are important zoonotic pathogens and some show a high degree of host specificity or host preference. We compare 45 sequenced S. enterica genomes that are publicly available (22 complete and 23 draft genome sequences). Of these, 35 were found to be of sufficiently good quality to allow a detailed analysis, along with two Escherichia coli strains (K-12 substr. DH10B and the avian pathogenic E. coli (APEC O1) strain). All genomes were subjected to standardized gene finding, and the core and pan-genome of Salmonella were estimated to be around 2,800 and 10,000 gene families, respectively. The constructed pan-genomic dendrograms suggest that gene content is often, but not uniformly correlated to serotype. Any given Salmonella strain has a large stable core, whilst there is an abundance of accessory genes, including the Salmonella pathogenicity islands (SPIs), transposable elements, phages, and plasmid DNA. We visualize conservation in the genomes in relation to chromosomal location and DNA structural features and find that variation in gene content is localized in a selection of variable genomic regions or islands. These include the SPIs but also encompass phage insertion sites and transposable elements. The islands were typically well conserved in several, but not all, isolates—a difference which may have implications in, e.g., host specificity.

General information

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Organisations: Department of Chemical and Biochemical Engineering, Division of Microbiology and Risk Assessment, National Food Institute, Center for Biological Sequence Analysis, Department of Systems Biology
Contributors: Jacobsen, A., Hendriksen, R. S., Aarestrup, F. M., Ussery, D., Friis, C.
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Scopus rating (2016): CiteScore 3.55 SJR 1.325 SNIP 1.108
Web of Science (2016): Impact factor 3.63
Web of Science (2016): Indexed yes
General information

WHO Global Foodborne Infections Network external quality assurance system (EQAS) for antimicrobial susceptibility testing of Salmonella isolates
Zinc resistance of Staphylococcus aureus of animal origin is strongly associated with methicillin resistance

This study was conducted to determine the occurrence of zinc and copper resistances in methicillin-resistant Staphylococcus aureus (MRSA) from swine and veal calves in a global strain collection. The test population consisted of 476 porcine MRSA isolates from ten European countries, 18 porcine MRSA isolates from Canada and seven MRSA from China, 92 MRSA and 60 methicillin-susceptible S. aureus (MSSA) isolates from veal calves in the Netherlands and 88 porcine MSSA isolates from four European countries. Most porcine MRSA (n=454) and all bovine MRSA belonged to clonal complex (CC) 398 whereas 37 of the pig MRSA from Europe and the seven Chinese isolates belonged to other CCs and 3 isolates were not classified into a CC. All isolates were tested for susceptibility to zinc chloride and copper sulphate using agar dilution and tested by PCR for the czrC gene encoding zinc resistance. Phenotypic zinc resistance (MIC > 2 mM) was observed in 74% (n=324) and 42% (n=39) of European MRSA CC398 from pigs and veal calves, respectively, and in 44% of the Canadian isolates (n=8), but not among the Chinese isolates. Almost all (99%) zinc-resistant MRSA carried czrC. Of the 37 European non-CC398 MRSA, 62% were resistant to zinc, but only 46% of them carried czrC. The MICs of the MSSA isolates to zinc chloride ranged from 1 to 4 mM and none carried czrC. The MICs of copper sulphate were associated neither with methicillin resistance nor with the detection of czrC. This study showed that zinc resistance and the czrC gene are widespread among CC398 MRSA isolates. This suggests that the use of zinc in feed might have contributed to the emergence of MRSA.

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Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
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Contributors: Hendriksen, R. S., Karlsmose, S., Bortolaia, V., Jensen, A. B., Aarestrup, F. M.
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The 6th EURL-AR Proficiency Testing enterococci, staphylococci and E. coli 2009

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Migura, L. G., Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M.
Number of pages: 68
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Publisher: National Food Institute
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Original language: English
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Source-ID: 271028
Research output: Research › Report – Annual report year: 2010

The 7th EURL-AR Proficiency Testing Salmonella and Campylobacter 2009

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Karlsmose, S., Hendriksen, R. S., Migura, L. G., Aarestrup, F. M.
Number of pages: 68
Publication date: May 2010

Publication information
Place of publication: Lyngby, Denmark
Publisher: National Food Institute
Edition: 1
ISBN (Print): 978-87-92158-74-1
Original language: English
Source: orbit
Source-ID: 271027
Research output: Research › Report – Annual report year: 2010

Global epidemiology of non-typhoidal Salmonella infections in humans

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
A classification system for plasmids from Enterococci and other Gram-positive bacteria

A classification system for plasmids isolated from enterococci and other Gram-positive bacteria was developed based on 111 published plasmid sequences from enterococci and other Gram-positive bacteria; mostly staphylococci. Based on PCR amplification of conserved areas of the replication initiating genes (rep), alignment of these sequences and using a cut off value of 80% identity on both protein and DNA level, 19 replicon families (rep-families) were defined together with several unique sequences. The prevalence of these rep-families was tested on 79 enterococcal isolates from a collection of isolates of animal and human origin. Difference in prevalence of the designed rep-families were detected with rep9 being most prevalent in Enterococcus faecalis and rep2 in Enterococcus faecium. In 33 % of the tested E. faecium and 32% of the tested E. faecalis no positive amplicons were detected. Furthermore, conjugation experiments were performed obtaining 30 transconjugants when selecting for antimicrobial resistance. Among them 19 gave no positive amplicons indicating presence of rep-families not tested for in this experimental setup.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Emborg, H., Vieira, A., Mazzolini, F., Aarestrup, F. M., Christiansen, P., Bielak, E. M., Beloeil, P.
Number of pages: 168
Publication date: 2010

Host publication information
Title of host publication: Proceeding of the 2nd ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens in Animals, Humans and the Environment, Source: orbit
Source-ID: 264768
Research output: Research › Conference abstract in proceedings – Annual report year: 2010

Antimicrobial-resistant faecal Escherichia coli in wild mammals in central Europe: multiresistant Escherichia coli producing extended-spectrum β-lactamases in wild boars

Aims: To determine the presence of antibiotic-resistant faecal Escherichia coli in populations of wild mammals in the Czech Republic and Slovakia. Methods and Results: Rectal swabs or faeces collected during 2006-2008 from wild mammals were spread on MacConkey agar and MacConkey agar containing 2 mg/l of cefotaxime. From plates with positive growth, one isolate was recovered and identified as E. coli. Susceptibility to 12 antibiotics was tested using the disk diffusion method. Resistance genes, class 1 and 2 integrons and gene cassettes were detected in resistant isolates by polymerase chain reaction (PCR). Extended-spectrum beta-lactamases (ESBL) were further characterized by DNA sequencing, macrorestriction profiling and determination of plasmid sizes. Plasmid DNA was subjected to EcoRV digestion, transferability by conjugation and incompatibility grouping by multiplex PCR. The prevalence of resistant isolates was 2% in small terrestrial mammals (rodents and insectivores, n(E. coli) = 242), 12% in wild ruminants and foxes (n(E. coli) = 290), the prevalence of resistant isolates was 6%. Class 1 and 2 integrons with various gene cassettes were recorded in resistant isolates. From wild boars, five (2%, n(rectal smears) = 293) multiresistant isolates producing ESBL were recovered: one isolate with bla(CTX-M-1) + bla(TEM-1), three with bla(CTX-M-1) and one with bla(TEM-52b). The bla(CTX-M-1) genes were carried on approx. 90 kb IncI1 conjugative plasmids. Conclusions: Antibiotic-resistant E. coli occurred in populations of wild mammals in various prevalences. Significance and Impact of the Study: Wild mammals are reservoirs of antibiotic-resistant E. coli including ESBL-producing strains which were found in wild boars.

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Literak, I., Dolejska, M., Radimersky, T., Klimes, J., Friedman, M., Aarestrup, F. M., Hasman, H., Cizek, A.
Pages: 1702-1711
Publication date: 2010
Peer-reviewed: Yes

Publication information
Journal: Journal of Applied Microbiology
Volume: 108
Issue number: 5
ISSN (Print): 1364-5072
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.41
Web of Science (2017): Impact factor 1.471
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.41
Web of Science (2016): Impact factor 1.575
BFI (2015): BFI-level 1
Antimicrobial susceptibility and serovars of Salmonella from chickens and humans in Ibadan, Nigeria

BACKGROUND: This study determines the prevalence and antibiotic resistance of Salmonella serovars from humans and chickens in Ibadan, Nigeria, in 2004-2007. METHODOLOGY: A total of 991 blood samples were collected from patients in 2004 to 2005 and 641 fecal samples were collected from poultry farms in 2007. All Salmonella isolates were serotyped and tested for antimicrobial susceptibility. RESULTS: Thirty-nine (4%) Salmonella isolates were obtained from human blood and 70 (11%) from chicken fecal samples. The human isolates revealed nine different serovars; 82% were non-typhoidal Salmonella and 18% were (S. Typhi). The majority of serovars from humans were S. Enteritidis (33%), S. Dublin (18%), and S. Typhimurium (18%). Resistance to chloramphenicol, sulfamethoxazole, trimethoprim, and ampicillin ranged from 36% to 59% for the human isolates. Eight different serovars were obtained from chickens; S. Virchow (71%) predominated. A high frequency (87%) of reduced susceptibility to ciprofloxacin was observed among the chicken isolates. A high frequency of resistance to tetracycline (93%), nalidixic acid (81%), and sulfamethoxazole (87%) was observed. Rare serovars such as S. Apapa, S. Mouschaui, S. Jukestown, S. Oritamerin, and S. Onireke were isolated from both...
humans and chickens. Identical serovars were not found among human and chicken isolates. CONCLUSIONS: This study indicates that chickens are not a reservoir of Salmonella causing bacteraemia among humans in Ibadan, Nigeria. Studies locating the reservoirs responsible for invasive salmonellosis in humans are needed. Controls and targeted interventions against S. Virchow and the frequent occurrence of antimicrobial resistance in chickens should be initiated to prevent the spread of this serovar.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Fashae, K., Ogunsola, F., Aarestrup, F. M., Hendriksen, R. S.
Pages: 484-494
Publication date: 2010
Peer-reviewed: Yes

Publication information
Journal: Journal of Infection in Developing Countries
Volume: 4
Issue number: 8
ISSN (Print): 1972-2680
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.53 SJR 0.704 SNIP 0.768
Web of Science (2017): Impact factor 1.33
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 1.56 SJR 0.755 SNIP 0.9
Web of Science (2016): Impact factor 1.353
Scopus rating (2015): CiteScore 1.34 SJR 0.675 SNIP 0.912
Web of Science (2015): Impact factor 1.139
Scopus rating (2014): CiteScore 1.44 SJR 0.674 SNIP 1.107
Web of Science (2014): Impact factor 1.138
Web of Science (2014): Indexed yes
Scopus rating (2013): CiteScore 1.65 SJR 0.707 SNIP 1.151
Web of Science (2013): Impact factor 1.267
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Scopus rating (2012): CiteScore 1.55 SJR 0.575 SNIP 1.018
Web of Science (2012): Impact factor 0.996
ISI indexed (2012): ISI indexed no
Scopus rating (2011): CiteScore 1.54 SJR 0.618 SNIP 1.086
Web of Science (2011): Impact factor 1.191
ISI indexed (2011): ISI indexed no
Scopus rating (2010): SJR 0.327 SNIP 0.48
Scopus rating (2009): SJR 0.163
Scopus rating (2008): SJR 0.101
Original language: English
Source: orbit
Source-ID: 267331
Research output: Research - peer-review › Journal article – Annual report year: 2010

A tool to investigate new data relations and track trends, patterns and risk factors for foodborne pathogens.

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Coutinho Calado Domingues, A. R., Hendriksen, R. S., Aarestrup, F. M.
Publication date: 2010
Peer-reviewed: No
Broiler chickens, broiler chicken meat, pigs and pork as sources of ExPEC related virulence genes and resistance in Escherichia coli isolates from community-dwelling humans and UTI patients.

Urinary tract infection (UTI) is one of the most common bacterial infections. UTI is primarily caused by extraintestinal pathogenic Escherichia coli (ExPEC) from the patients’ own fecal flora. The ExPEC often belong to phylogroups B2 and D, the groups which include potent human ExPEC isolates causing UTI, bacteremia, and meningitis. The external sources of these ExPEC in the human intestine are unknown. The food supply may transmit ExPEC to humans. However, evidence of this hypothesis is limited. To assess this hypothesis, the objective of our study was to investigate the presence of ExPEC related virulence genes in E. coli isolates from UTI patients, community-dwelling humans, meat, and production animals. Accordingly, we included 964 geographically and temporally matched E. coli isolates from UTI patients (n=102), community-dwelling humans (n=109), fresh Danish (n=197) and imported broiler chicken meat (n=86), broiler chickens (n=138), fresh Danish (n=177) and imported pork (n=10), and pigs (n=145) in the study. All isolates were investigated for the presence of eight ExPEC related genes (kpsM II, papA, papC, iutA, sfaS, focG, afa, hlyD) using PCR. To investigate any similarities between isolates from the different origins, we performed a cluster analysis including antimicrobial resistance data previously published. We detected seven of the eight ExPEC related genes in isolates from broiler chicken meat, broiler chickens, pork and pigs. Our findings suggest that broiler chicken meat, broiler chickens, pork and pigs could be the source of strains with these ExPEC related virulence genes in community-dwelling humans and UTI patients. Especially detection of ExPEC related virulence genes in isolates belonging to phylogroups B2 and D is very concerning and may have a significant medical impact. The cluster analysis of virulence gene and antimicrobial resistance profiles showed strong similarities between UTI patient, community-dwelling human isolates, meat, and production animal isolates. Thus, these strains from meat and production animals may pose a zoonotic risk.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Microbiology
Pages: 264-272
Publication date: 2010
Peer-reviewed: Yes

Publication information
Journal: International Journal of Food Microbiology
Volume: 142
Issue number: 1-2
ISSN (Print): 0168-1605
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 3.76 SJR 1.366 SNIP 1.436
Web of Science (2017): Impact factor 3.451
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.97 SJR 1.481 SNIP 1.553
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.02 SJR 1.614 SNIP 1.683
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.62 SJR 1.493 SNIP 1.695
Web of Science (2014): Impact factor 3.082
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Changes in the use of antimicrobials and the effects on productivity of swine farms in Denmark

Objective-To evaluate changes in antimicrobial consumption and productivity by Danish swine farms during 1992 to 2008.

Sample Population-All Danish swine farms for antimicrobial consumption data and a representative sample of Danish swine herds for productivity data. Procedures-Antimicrobial consumption by Danish swine farms from 1992 to 2008 was determined and evaluated in light of policies to regulate antimicrobial consumption, changes in disease patterns, and productivity data. Trend analyses of productivity data were conducted before and after a ban on use of antimicrobial growth promoters (AGPs). Results-Antimicrobial consumption peaked at 100 mg/kg of swine produced in 1992, decreased...
to 31 mg/kg in 1999, and increased to 49 mg/kg in 2008. Key factors for changes were regulations banning subtherapeutic use of antimicrobials and veterinary profits from the prescription and sale of antimicrobials in 1994 and termination of AGP use by January 2000. Pig production increased from 18.4 to 271 million pigs, and the mean number of pigs per sow per year raised for slaughter increased from 21 in 1992 to 25 in 2007 Average daily gain for weaning (<35 kg) and finishing (>35 kg) pigs was higher in 2008 than in 1992, but mortality rates for weaning and finishing pigs were similar in 1992 and 2008. Conclusions and Clinical Relevance—From 1992 to 2008, antimicrobial consumption per kilogram of pig produced in Denmark decreased by >50%. Furthermore, there was improvement in productivity, suggesting that long-term swine productivity was not negatively impacted by a ban on AGP use.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Jensen, V. F., Emborg, H., Jacobsen, E., Wegener, H. C.
Pages: 726-733
Publication date: 2010
Peer-reviewed: Yes

Publication information
Journal: American Journal of Veterinary Research
Volume: 71
Issue number: 7
ISSN (Print): 0002-9645
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 1.17 SJR 0.567 SNIP 0.773
Web of Science (2017): Impact factor 0.833
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.08 SJR 0.641 SNIP 0.769
Web of Science (2016): Impact factor 1.004
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 1.3 SJR 0.829 SNIP 0.884
Web of Science (2015): Impact factor 1.124
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 1.6 SJR 1.01 SNIP 1.059
Web of Science (2014): Impact factor 1.335
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 1.4 SJR 0.936 SNIP 0.876
Web of Science (2013): Impact factor 1.214
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 1.48 SJR 0.829 SNIP 1.03
Web of Science (2012): Impact factor 1.348
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 1.48 SJR 0.922 SNIP 1.03
Web of Science (2011): Impact factor 1.269
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.905 SNIP 1.003
Web of Science (2010): Impact factor 1.413
Web of Science (2010): Indexed yes

Ninety-three Salmonella isolates recovered from commercial foods and exotic animals in Colombia were studied. The serotypes, resistance profiles and where applicable the quinolone resistance genes were determined. Salmonella Anatum (n=14), Uganda (19), Braenderup (10) and Newport (10) were the most prevalent serovars, and resistance to tetracycline (18.3%), ampicillin (17.2%) and nalidixic acid (14%) was most common. Nalidixic acid-resistant isolates displayed minimum inhibitory concentrations ranging from 32 to 1024 μg mL⁻¹. A Thr57→Ser substitution in ParC was the most frequent (12 of the 13 isolates). Six isolates possessed an Asp87→Tyr substitution in GyrA. No alterations in GyrA in a further seven nalidixic acid-resistant isolates were observed. Of these, four serovars including two Uganda, one Infantis and a serovar designated 6,7:d:-, all carried qnrB19 genes associated with 2.7 kb plasmids, two of which were completely sequenced. These exhibited 97% (serovar 6,7:d:- isolate) and 100% (serovar Infantis isolate) nucleotide sequence identity with previously identified ColE-like plasmids. This study demonstrates the occurrence of the qnrB19 gene associated with small ColE plasmids hitherto unrecognized in various Salmonella serovars in Colombia. We also report unusual high-level quinolone resistance in the absence of any DNA gyrase mutations in serovars S. Carrau, Muenchen and Uganda.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 10-19
Publication date: 2010
Peer-reviewed: Yes

Publication information
Journal: F E M S Microbiology Letters
Volume: 313
Issue number: 1
ISSN (Print): 0378-1097
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.8 SJR 0.79 SNIP 0.58
Web of Science (2017): Impact factor 11.392
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.76 SJR 0.842 SNIP 0.615
Web of Science (2016): Impact factor 12.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.08 SJR 1.156 SNIP 0.756
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.17 SJR 1.136 SNIP 0.767
Web of Science (2014): Impact factor 13.244
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.25 SJR 1.053 SNIP 0.719
Web of Science (2013): Impact factor 13.806
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.25 SJR 1.073 SNIP 0.804
Web of Science (2012): Impact factor 13.231
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.26 SJR 1.105 SNIP 0.764
Web of Science (2011): Impact factor 10.96
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.081 SNIP 0.754
Web of Science (2010): Impact factor 11.796
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.13 SNIP 0.834
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.084 SNIP 0.834
Scopus rating (2007): SJR 1.103 SNIP 0.864
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.105 SNIP 0.86
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1 SNIP 0.8
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.005 SNIP 0.725
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.018 SNIP 0.866
Scopus rating (2002): SJR 0.902 SNIP 0.791
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.944 SNIP 0.752
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.936 SNIP 0.739
Web of Science (2000): Indexed yes
Cloning and occurrence of czrC, a gene conferring cadmium and zinc resistance in MRSA CC398 Isolates

We recently reported a phenotypic association between reduced susceptibility to zinc and methicillin resistance in Staphylococcus aureus CC398 isolates from Danish swine (F. M. Aarestrup, L. M. Cavaco, and H. Hasman, Vet. Microbiol. 142:455-457, 2009). The aim of this study was to identify the genetic determinant causing zinc resistance in CC398 and examine its prevalence in isolates of animal and human origin. Based on the sequence of the staphylococcal cassette chromosome mec (SCCmec) element from methicillin-resistant S. aureus (MRSA) CC398 strain SO385, a putative metal resistance gene was identified in strain 171 and cloned in S. aureus RN4220. Furthermore, 81 MRSA and 48 methicillin-susceptible S. aureus (MSSA) strains, isolated from pigs (31 and 28) and from humans (50 and 20) in Denmark, were tested for susceptibility to zinc chloride and for the presence of a putative resistance determinant, czrC, by PCR. The cloning of czrC confirmed that the zinc chloride and cadmium acetate MICs for isogenic constructs carrying this gene were increased compared to those for S. aureus RN4220. No difference in susceptibility to sodium arsenate, copper sulfate, or silver nitrate was observed. Seventy-four percent (n = 23) of the animal isolates and 48% (n = 24) of the human MRSA isolates of CC398 were resistant to zinc chloride and positive for czrC. All 48 MSSA strains from both human and pig origins were found to be susceptible to zinc chloride and negative for czrC. Our findings showed that czrC is encoding zinc and cadmium resistance in CC398 MRSA isolates, and that it is widespread both in humans and animals. Thus, resistance to heavy metals such as zinc and cadmium may play a role in the coselection of methicillin resistance in S. aureus.

General information

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Statens Serum Institut, University Medical Centre Utrecht, Juntendo University
Contributors: Cavaco, L., Hasman, H., Stegger, M., Andersen, P. S., Skov, R., Fluit, A. C., Ito, T., Aarestrup, F. M.
Pages: 3605-3608
Publication date: 2010
Peer-reviewed: Yes

Publication information

Journal: Antimicrobial Agents and Chemotherapy
Volume: 54
Issue number: 9
ISSN (Print): 0066-4804
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.15 SJR 2.291 SNIP 1.263
Web of Science (2017): Impact factor 4.255
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.45 SJR 2.361 SNIP 1.428
Web of Science (2014): Impact factor 4.476
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Decreased susceptibility to zinc chloride is associated with methicillin resistant Staphylococcus aureus CC398 in Danish swine

A total of 31 MRSA and 60 MSSA isolated from different swine farms in Denmark were examined for their susceptibility to zinc chloride, erythromycin, penicillin and tetracycline, as well as their spa-type. mecA positive isolates were examined for their SCCmec type. The isolates were assigned to a CC-type based on their spa-type and supportive multi-locus sequence typing (MLST). No difference in susceptibility to erythromycin, penicillin or tetracycline could be observed between methicillin resistant and susceptible isolates of CC398. Twenty-three (74%) of the MRSA CC398 isolates had
reduced susceptibility to ZnCl2 (MIC 4-12 mM), whereas all MSSA had MICs from 0.5 to 2 mM. Thirty MRSA, including all 23 zinc resistant isolates harboured SCCmec type V. This provides biological evidence to suggest that the use of zinc compounds may be partly implicated in the emergence of some MRSA clones among swine in Denmark. (C) 2009 Elsevier B.V. All rights reserved.
Escherichia coli Isolates from Broiler Chicken Meat, Broiler Chickens, Pork, and Pigs Share Phylogroups and Antimicrobial Resistance with Community-Dwelling Humans and Patients with Urinary Tract Infection

Escherichia coli is the most common cause of urinary tract infection (UTI). Phylogroup B2 and D isolates are associated with UTI. It has been proposed that E. coli causing UTI could have an animal origin. The objective of this study was to investigate the phylogroups and antimicrobial resistance, and their possible associations in E. coli isolates from patients with UTI, community-dwelling humans, broiler chicken meat, broiler chickens, pork, and pigs in Denmark. A total of 964 geographically and temporally matched E. coli isolates from UTI patients (n = 102), community-dwelling humans (n = 109), Danish (n = 197) and imported broiler chicken meat (n = 86), Danish broiler chickens (n = 138), Danish (n = 177) and imported pork (n = 10), and Danish pigs (n = 145) were tested for phylogroups (A, B1, B2, D, and nontypeable [NT] isolates) and antimicrobial susceptibility. Phylogroup A, B1, B2, D, and NT isolates were detected among all groups of isolates except for imported pork isolates. Antimicrobial resistance to three (for B2 isolates) or five antimicrobial agents (for A, B1, D, and NT isolates) was shared among isolates regardless of origin. Using cluster analysis to investigate antimicrobial resistance data, we found that UTI isolates always grouped with isolates from meat and/or animals. We detected B2 and D isolates, that are associated to UTI, among isolates from broiler chicken meat, broiler chickens, pork, and pigs. Although B2 isolates were found in low prevalences in animals and meat, these sources could still pose a risk for acquiring uropathogenic E. coli. Further, E. coli from animals and meat were very similar to UTI isolates with respect to their antimicrobial resistance phenotype. Thus, our study provides support for the hypothesis that a food animal and meat reservoir might exist for UTI-causing E. coli.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 537-547
Publication date: 2010
Peer-reviewed: Yes

Publication Information
Journal: Foodborne Pathogens and Disease
Volume: 7
Issue number: 5
ISSN (Print): 1535-3141
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.47 SJR 1.063 SNIP 1.016
Web of Science (2017): Impact factor 2.476
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.46 SJR 1.062 SNIP 1.08
Web of Science (2016): Impact factor 2.12
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.41 SJR 1.064 SNIP 1.035
Web of Science (2015): Impact factor 2.27
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.16 SJR 0.953 SNIP 1.051
Web of Science (2014): Impact factor 1.905
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.41 SJR 1.184 SNIP 1.129
Web of Science (2013): Impact factor 2.092
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.55 SJR 1.185 SNIP 1.144
Web of Science (2012): Impact factor 2.283
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.33 SJR 1.118 SNIP 1.037
Web of Science (2011): Impact factor 2.26
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.86 SNIP 0.94
Web of Science (2010): Impact factor 2.134
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.864 SNIP 1.088
Web of Science (2009): Indexed yes
Scopus rating (2008): SJR 0.72 SNIP 0.682
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.611 SNIP 0.621
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.399 SNIP 0.318
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.198 SNIP 0.45
Original language: English
DOIs:
10.1089/fpd.2009.0409
Source: orbit
Source-ID: 263276
Research output: Research - peer-review › Journal article – Annual report year: 2010
Establishing streptomycin epidemiological cut-off values for Salmonella and Escherichia coli.

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Publication date: 2010
Peer-reviewed: No
Source: orbit
Source-ID: 269011
Research output: Research › Poster – Annual report year: 2010

Evaluation of ceftiofur and cefquinome for phenotypic detection of methicillin resistance in Staphylococcus aureus using disk diffusion testing and MIC-determinations
Methicillin-resistant Staphylococcus aureus (MRSA) have emerged in animals. Testing 98 mecA negative and 71 mecA positive S. aureus we compared the usefulness of ceftiofur and cefquinome to cefoxitin, for detection of MRSA and found that these cephalosporins are not as efficient as cefoxitin.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Skov, R. L.
Pages: 176-179
Publication date: 2010
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
Volume: 140
Issue number: 1-2
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
This study evaluates the efficacy of eight different cephalosporins for detection of cephalosporin resistance mediated by extended spectrum beta-lactamases (ESBL) and plasmidic AmpC beta-lactamases in Salmonella and Escherichia coli. A total of 138 E. coli and 86 Salmonella isolates with known beta-lactamase genes were tested for susceptibility toward cefoperazone, cefotaxime, cefpodoxime, cefquinome, ceftazidime, ceftiofur, ceftriaxone, and cefuroxime using minimum inhibitory concentration determinations and disc diffusion. The collection consisted of 84 ampicillin-susceptible, 57 ampicillin-resistant but cephalosporin-susceptible, 56 ESBL isolates and 19 isolates with plasmidic AmpC, as well as 10 ampC hyper-producing E. coli. The minimum inhibitory concentration distributions and zone inhibitions varied with the tested compound. Ampicillin-resistant isolates showed reduced susceptibility to the cephalosporins compared to ampicillin-susceptible isolates. Cefoperazone, cefquinome, and cefuroxime were not useful in detecting isolates with ESBL or...
plasmidic AmpC. The best substances for detection were cefotaxime, cefpodoxime, and ceftriaxone, whereas ceftazidime and ceftiofur were not as efficient. Ceftriaxone may be the recommended substance for monitoring because of some ability in separating ampC hyper-producing E. coli from ESBL and plasmidic AmpC isolates.

**General information**

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Hasman, H., Veldman, K., Mevius, D.
Pages: 253-261
Publication date: 2010
Peer-reviewed: Yes

**Publication information**

Journal: Microbial Drug Resistance
Volume: 16
Issue number: 4
ISSN (Print): 1076-6294
Ratings:
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
- Web of Science (2017): Impact factor 2.344
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
- Web of Science (2016): Impact factor 2.306
- BFI (2015): BFI-level 1
- Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
- Web of Science (2015): Impact factor 2.529
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
- Web of Science (2014): Impact factor 2.49
- BFI (2013): BFI-level 1
- Scopus rating (2013): CiteScore 2.87 SJR 1.265 SNIP 1.118
- Web of Science (2013): Impact factor 2.524
- ISI indexed (2013): ISI indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): CiteScore 2.45 SJR 0.963 SNIP 0.9
- Web of Science (2012): Impact factor 2.364
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): CiteScore 2.76 SJR 1.163 SNIP 1.14
- Web of Science (2011): Impact factor 2.153
- ISI indexed (2011): ISI indexed yes
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 1.054 SNIP 0.8
- Web of Science (2010): Impact factor 1.936
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 0.915 SNIP 0.838
- BFI (2008): BFI-level 1
- Scopus rating (2008): SJR 1.038 SNIP 0.73
- Web of Science (2008): Indexed yes

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Carlson, V. P., Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M., Lo Fo Wong, D. M. A., Weill, F., Angulo, F. J.
Publication date: 2010
Peer-reviewed: No
Event: Poster session presented at International Conference on Emerging Infectious Diseases, Atlanta, GA, United States.
Source: orbit
Source-ID: 269021
Research output: Research › Poster – Annual report year: 2010

First European External Quality Assurance System (EQAS) for isolation, identification and typing of methicillin-resistant Staphylococcus aureus (MRSA) from dust samples, year 2009

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Cavaco, L., Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M.
Publication date: 2010
Peer-reviewed: No
Event: Poster session presented at 2nd ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens in Animals, Huamns and Environment, Toronto, Canada.
Source: orbit
Source-ID: 263855
Research output: Research › Poster – Annual report year: 2010

Heterogeneity among methicillin-resistant Staphylococcus aureus from Italian pig finishing holdings
A survey for methicillin-resistant Staphylococcus aureus (MRSA) in finishing pig holdings was carried out in Italy in 2008. MRSA isolates were characterised by spa- SCCmec- and antimicrobial susceptibility typing. A prevalence of 38% (45/118, 95% CI 29.4-46.9%) positive holdings was observed. Eleven different spa-types were found among 102 MRSA isolates, clustering in lineages associated with farm animals (ST398, ST9, ST(CC)97 in 36 holdings) and humans (ST1, 7 holdings). Nine (7.6%) holdings were positive for two, three or four different and unrelated spa-types in various combinations. ST398 was the most prevalent lineage (33 positive holdings). The most prevalent spa-type was t899
(ST398), detected in 22 positive holdings. Three novel spa-types (t4794 of ST9: t4795 of ST97; t4838 of ST398) were detected. Ten holdings were positive for spa-type 11730, that proved to be a new single-locus variant of ST97, within the CC97 (ST1476). The most prevalent SCCmec was Type V (79 isolates), while Type IVb was found in 10 isolates. None of the isolates was positive for Panton-Valentine Leukocidin, while most of the t127 and t1730 isolates, one t4794, one t4795, and one t2922 were positive for LukE-LukD genes. All 64 antimicrobial susceptibility tested isolates were resistant to tetracyclines, with high resistance rates to trimethoprim (68.8%), erythromycin (60.9%), and ciprofloxacin (35.4%). All t127, ST1 isolates were resistant to tetracycline-ciprofloxacin-erythromycin. This survey provides the first report of MRSA ST1 and ST(CC)97 among pigs and the first report of MRSA ST9 from pigs in Europe. The presence of human-associated CA-MRSA (t127, ST1, SCCmec type V) in 6% holdings surveyed can represent an additional MRSA reservoir for infections in humans.
In Silico Prediction of Human Pathogenicity in the gamma-Proteobacteria

In Background: Although the majority of bacteria are innocuous or even beneficial for their host, others are highly infectious pathogens that can cause widespread and deadly diseases. When investigating the relationships between bacteria and other living organisms, it is therefore essential to be able to separate pathogenic organisms from non-pathogenic ones. Using traditional experimental methods for this purpose can be very costly and time-consuming, and also uncertain since animal models are not always good predictors for pathogenicity in humans. Bioinformatics-based methods are therefore strongly needed to mine the fast growing number of genome sequences and assess in a rapid and reliable way the pathogenicity of novel bacteria.

Methodology/Principal Findings: We describe a new in silico method for the prediction of bacterial pathogenicity, based on the identification in microbial genomes of features that appear to correlate with virulence. The method does not rely on identifying genes known to be involved in pathogenicity (for instance virulence factors), but rather it inherently builds families of proteins that, irrespective of their function, are consistently present in only one of the two kinds of organisms, pathogens or non-pathogens. Whether a new bacterium carries proteins contained in these families determines its prediction as pathogenic or non-pathogenic. The application of the method on a set of known genomes correctly classified the virulence potential of 86% of the organisms tested. An additional validation on an independent test-set assigned correctly 22 out of 24 bacteria.

Conclusions: The proposed approach was demonstrated to go beyond the species bias imposed by evolutionary relatedness, and performs better than predictors based solely on taxonomy or sequence similarity. A set of protein families that differentiate pathogenic and non-pathogenic strains were identified, including families of yet uncharacterized proteins that are suggested to be involved in bacterial pathogenicity.
International Collaborative study on the prevalence of plasmid mediated quinolone resistance (PMQR) in Salmonella and E. coli isolated from humans and animals in Europe

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Central Veterinary Institute, Instituto Zooprofilattico Sperimentale delle Venezie, Veterinary Institute Prague, Prague, Czech Republic, Laboratorio Central de Veterinaria de Algete, Bundesinstitut für Risikobewertung, Central Veterinary Research Laboratory, Institute of Public Health, Food Microbiology Laboratory, Health Protection Agency, Finnish Food Safety Authority, Agence Française de Sécurité Sanitaire des Aliments, National Veterinary Institute, National Veterinary Research Institute
Publication date: 2010

Event information
Event: ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens in Animals, Humans and Environment
Location: Toronto, Canada
Source: orbit
Source-ID: 263803
Research output: Research - peer-review → Journal article – Annual report year: 2010

International Collaborative study on the prevalence of plasmid mediated quinolone resistance (PMQR) in Salmonella and E. coli isolated from humans and animals in Europe

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Instituto Zooprofilattico Sperimentale delle Venezie, Veterinary Institute Prague, Prague, Czech Republic, Laboratorio Central de Veterinaria de Algete, Bundesinstitut für Risikobewertung, Central Veterinary Research Laboratory, Institute of Public Health, Food Microbiology Laboratory, Health Protection Agency, Finnish Food Safety Authority, Agence Française de Sécurité Sanitaire des Aliments, National Veterinary Institute, National Veterinary Research Institute, Wageningen University & Research
Pages: 118-119
Publication date: 2010

Peer-reviewed: Yes

Invited speaker: Global emergence of antimicrobial resistance.
IS6100-mediated genetic rearrangement within the complex class 1 integron In104 of the Salmonella genomic island 1

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Targant, H., Doublet, B., Aarestrup, F. M., Cloeckaert, A., Madec, J.
Pages: 1543-1545
Publication date: 2010
Peer-reviewed: Yes

Publication information
Journal: Journal of Antimicrobial Chemotherapy
Volume: 65
Issue number: 7
ISSN (Print): 0305-7453
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.34 SJR 2.419 SNIP 1.568
Web of Science (2017): Impact factor 5.217
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Impact factor 5.071
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.06 SJR 2.259 SNIP 1.516
Web of Science (2015): Impact factor 4.919
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.61 SJR 2.298 SNIP 1.765
Web of Science (2014): Impact factor 5.313
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.7 SJR 2.479 SNIP 1.824
Web of Science (2013): Impact factor 5.439
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.35 SJR 2.283 SNIP 1.718
Web of Science (2012): Impact factor 5.338
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.24 SJR 2.341 SNIP 1.769
Web of Science (2011): Impact factor 5.068
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.161 SNIP 1.643
Microbiologic and Clinical Features of Salmonella Species Isolated From Bacteremic Children In Eastern Democratic Republic of Congo

Background: The morbidity of Salmonella bloodstream infections is unacceptably high in Africa. In 2000, the WHO Global Salmonella-Surveillance (GSS) program was founded to reduce the health burden of foodborne diseases. The incorporation, in 2002, of the Democratic Republic of Congo (DRC) in this program allowed the improvement of laboratory capacities. In this retrospective study, we describe the first signs of impact the GSS program has had in DRC in the management of bacteremia. Methods: Between 2002 and 2006, we evaluated, in one pediatric hospital, the microbiologic and clinical features of Salmonella isolated from children suspected of having bacteremia. A random selection of isolates was typed by pulsed field gel electrophoresis (PFGE). Results: Among the 1528 children included in the study, 26.8% were bacteremic. Salmonella accounted for 59% of all bloodstream infections. Salmonella typhimurium (60.5%) and Salmonella enteritidis (22.3%) were the most common Salmonella serotypes. In total, 92.4% were resistant to at least 3 antimicrobials with the following proportion of strains resistant to: ampicillin (86%), chloramphenicol (92%), trimethoprim/sulfamethoxazole (95%), and tetracycline (34%). In 2002, 32.1% of children received an appropriate empiric antimicrobial treatment. In 2006, with the restoration of the confidence in the results provided by the laboratory, we observed an increase of the proportion of patients appropriately (82.9%) treated with antimicrobials (P <0.01) without any decrease in the overall mortality rates associated with salmonellae bacteremia. Conclusions: Our findings indicate the benefit to strengthen laboratory capacities in Africa, allowing the development of management guidelines of bloodstream infection.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Vandenberg, O., Nyarukweba, D. Z., Ndeba, P. M., Hendriksen, R. S., Barzilay, E. J., Schirvel, C., Bisimwa, B. B., Collard, J., Kane, A. A., Aarestrup, F. M.
Pages: 504-510
Publication date: 2010
Peer-reviewed: Yes
Publication information
Journal: Pediatric Infectious Disease Journal
Volume: 29
Issue number: 6
ISSN (Print): 0891-3668
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.01 SJR 1.392 SNIP 1.005
Web of Science (2017): Impact factor 2.305
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.09 SJR 1.557 SNIP 1.054
Web of Science (2016): Impact factor 2.486
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.1 SJR 1.478 SNIP 1.063
Web of Science (2015): Impact factor 2.587
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.48 SJR 1.846 SNIP 1.171
Web of Science (2014): Impact factor 2.723
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 2.81 SJR 1.654 SNIP 1.231
Web of Science (2013): Impact factor 3.135
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.23 SJR 1.847 SNIP 1.355
Web of Science (2012): Impact factor 3.569
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.08 SJR 1.756 SNIP 1.365
Web of Science (2011): Impact factor 3.577
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.728 SNIP 1.374
Web of Science (2010): Impact factor 3.064
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.466 SNIP 1.399
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.676 SNIP 1.304
Scopus rating (2007): SJR 1.599 SNIP 1.428
Scopus rating (2006): SJR 1.485 SNIP 1.428
Scopus rating (2005): SJR 1.412 SNIP 1.34
Scopus rating (2004): SJR 1.418 SNIP 1.46
Scopus rating (2003): SJR 1.296 SNIP 1.471
Scopus rating (2002): SJR 1.15 SNIP 1.305
Scopus rating (2001): SJR 1.125 SNIP 1.383
Scopus rating (2000): SJR 0.921 SNIP 1.53
Scopus rating (1999): SJR 0.939 SNIP 1.302
Original language: English
Keywords: Africa, children, bacteremia, Salmonella
Molecular Characterization of Extended-Spectrum Cephalosporinase-Producing Salmonella enterica Serovar Choleraesuis Isolates from Patients in Thailand and Denmark

The objective of this study was to characterize extended-spectrum cephalosporinase (ESC)-producing isolates of Salmonella enterica serovar Choleraesuis recovered from patients in Thailand and Denmark. Twenty-four blood culture isolates from 22 patients were included in the study, of which 23 isolates were recovered from 21 Thai patients during 2003, 2007, or 2008 and one isolate was recovered from a Danish traveler to Thailand. ESC production was confirmed in 13 out of the 24 isolates by MIC testing. Microarray and plasmid profiling (replicon typing and restriction fragment length polymorphism [RFLP]) were used to characterize the genetic mechanisms of antimicrobial resistance in the 13 ESC-producing isolates. Pulsed-field gel electrophoresis (PFGE) and MIC testing were used to compare the clonality between the 13 ESC-producing isolates and the 11 non-ESC-producing isolates. Based on susceptibility patterns, the ESC-producing isolates were more closely related than non-ESC-producing isolates. Microarray, PCR, plasmid profiling, and replicon typing revealed that the 13 ESC-producing isolates harbored either bla(CMY-2) containing incA/C or bla(CTX-M-14) containing incFIIA, incFrepB, and an unknown replicon located on plasmids ranging in size from 75 to 200 kb. The RFLP and replicon typing clustered the isolates into four distinct groups. PFGE revealed 16 unique patterns and five clusters; each cluster contained two or three of the 24 isolates. The isolate from the Danish patient was indistinguishable from two Thai clinical isolates by PFGE. This study revealed the emergence of the bla(CTX-M-14) gene among several clones of Salmonella serovar Choleraesuis. Numerous plasmids were identified containing up to two different ESC genes and four distinct replicons. A "travel-associated" spread was confirmed. Overall, a high degree of clonal diversity between isolates resistant and susceptible to cephalosporins was observed. The findings represent a serious threat to public health for the Thai people and tourists.
Possible association between usage of zinc compounds in pig production and emergence of methicillin resistant Staphylococcus aureus CC398 in pigs

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Possible association between usage of zinc compounds in pig production and emergence of methicillin resistant Staphylococcus aureus CC398 in pigs

Prevalence and Characterization of Sephalosporin resistance in non-pathogenic Escherichia coli from food producing animals in Poland

Reference testing performed as part of the WHO Global Foodborne Infections Network activities

Ringtesten for identifikation og resistensbestemmelse af mastitispatakger 2010
Ringtesten for identifikation og resistensbestemmelse af mastitispatogener - uddrag af mastitistingtest rapporten 2010

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Dianova
Contributors: Hendriksen, R. S., Karlsmose, S., Jensen, J. D., Aarestrup, F. M., Jensen, A. B., Krogh, K., Østergaard Heinesen, H.
Pages: 9-13
Publication date: 2010
Peer-reviewed: No

Publication information
Journal: Dansk Veterinærtidsskrift
Issue number: 19
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 267324
Research output: Research › Journal article – Annual report year: 2010

Screening for Zinc Resistance and czrC genes in methicillin-resistant and methicillin-susceptible Staphylococcus aureus from animal origin in Europe

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Faculty of Veterinary Medicine, Central Veterinary Institute, Bundesinstitut für Risikobewertung, Universität Complutense, Agence Française de Sécurité Sanitaire des Aliments, Ghent University, Central Agricultural Office, National Veterinary Research Institute, Instituto Zooprofilattico Sperimentale delle Venezie, Friedrich-Loeffler-Institute, Central Veterinary Research Laboratory
Pages: 19-20
Publication date: 2010

Host publication information
Title of host publication: ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens in Animals, Humans and Environment
Publisher: ASM International
Source: orbit
Source-ID: 263804
Research output: Research › peer-review › Conference abstract in proceedings – Annual report year: 2010
spa type distribution in Staphylococcus aureus originating from pigs, cattle and poultry

Methicillin-resistant S. aureus (MRSA) of clonal complex 398 (CC398) is emerging globally among production animals such as cattle, pigs and poultry as well as among humans. However, little is known about the prevalence of CC398 among methicillin sensitive S. aureus (MSSA) or the relative clonal distribution of S. aureus isolated from these three animal reservoirs. To study this, we have analyzed a random sample of S. aureus consisting of 296 epidemiologically unrelated isolates from infections and colonisation of pigs, cattle and poultry. These were examined and compared by spa and multi-locus sequence typing (MIST) and the result was compared to the most common spa types found among human blood isolates. Little overlap in spa types was seen between isolates from the three animal reservoirs or between animals and humans. Most of the porcine isolates had the spa types t034 (CC398), t1333 (COO) and 037 (CC9), while the bovine isolates mainly had spa types t518 (CC50), t524 (CC97) and t529 (CC151). None of these spa types are common among human blood isolates in Denmark. Surprisingly, almost all of the poultry isolates (96%) belonged to CC5 (spa types t002 and 006), which is also known to be commonly found among human blood isolates and subsequent pulsed-field gel electrophoresis (PFGE) analysis identified indistinguishable PFGE patterns among a poultry isolate and selected human isolates. In conclusion, strains of MSSA CC398 were commonly present in pigs but not present at all in the other reservoirs tested.
Upsurge of infections caused by Salmonella Concord among Ethiopian adoptees in Denmark, 2009

Multidrug-resistant (MDR) Salmonella Concord has been associated with adoptees from Ethiopia. In 2009, Denmark saw an increase in MDR S. Concord infections among Ethiopian adoptees.
WHO Global Foodborne Infections Network External Quality Assurance System (EQAS) for serotyping and antimicrobial susceptibility testing of Salmonella isolates

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, World Health Organization
Contributors: Karlsmose, S., Hendriksen, R. S., Mikoleit, M., Jensen, A., DeLong, S., Weill, F., Aidara-Kane, A., Lo Fo Wong, D., Aarestrup, F. M.
Publication date: 2010
Peer-reviewed: Yes
Event: Poster session presented at International Conference on Emerging Infectious Diseases, Atlanta, GA, United States.
Source: orbit
Source-ID: 269009
Research output: Research - peer-review › Poster – Annual report year: 2010

Report of the 1st External Quality Assurance System on Isolation, Identification and Typing of Methicillin resistant Staphylococcus aureus (MRSA) from Dust Samples, year 2009: Community Reference Laboratory – Antimicrobial Resistance

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Contributors: Cavaco, L., Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M.
Number of pages: 36
Publication date: Dec 2009

Publication information
Publisher: The National Food Institute, Technical University of Denmark
Edition: 1
ISBN (Print): 978-87-92158-66-6
Original language: English
Research output: Research › Report – Annual report year: 2009

The External Quality Assurance System of the WHO Global Salm-Surv Year 2008

To support laboratories participating in WHO GSS an External Quality Assurance System (EQAS) was established in 2000. The EQAS supports the assessment of the quality of serotyping and antimicrobial susceptibility testing of Salmonella in participating laboratories. In 2003, the program was extended to include other foodborne pathogens as well, and the number of participants has increased from 44 laboratories in 2000, to 187 laboratories in 2008. The serotyping results indicate a continuous need for improving skills in Salmonella serotyping. Future training efforts should be aimed at enhancing the capability to detect the flagella phases and disseminating protocols for preparing high quality swarm agar plates. Harmonising the methodology and providing adequate guidelines for antimicrobial susceptibility testing is crucial for improving the results. Clearly, there is a need to disseminate the latest breakpoint guidelines, to strengthen awareness of performing and interpreting internal QC, as well as to identify the barriers for antimicrobial susceptibility testing in each individual laboratory. This year’s data also show that many of the laboratories were able to conduct a satisfactory confirmatory test on the ESBL producing strain. It is important to draw attention to this in the future as we have to recognise the increase of resistance to 3rd and 4th generation of cephalosporins. Many of this year’s participants had difficulties identifying Campylobacter lari. These results indicate a need for additional training modules on identification procedures for Campylobacter spp. Given the growing concerns over increasing macrolide resistance in Campylobacter spp., participants in the 2009 EQAS will also be offered the opportunity to perform susceptibility testing of Campylobacter spp.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Karlsmose, S., Jensen, A. B., Aarestrup, F. M.
Number of pages: 54
Publication date: Sep 2009
Antimicrobial Susceptibilities, Phage Types, and Molecular Characterization of Salmonella enterica Serovar Enteritidis from Chickens and Chicken Meat in Turkey

Thirty-eight Salmonella Enteritidis isolates from chickens and chicken meat in Turkey were examined for antimicrobial susceptibility, XbaI pulsed-field gel electrophoresis (PFGE) patterns, phage types, plasmid profiles, and resistance genes. Seven different PFGE patterns were observed, with the most common accounting for 71% (X1). The most common phage type was PT4, followed by PT7, PT16, PT1, PT6, and PT35. Different phage types shared the same PFGE pattern. Twenty-one isolates were susceptible to all antimicrobial agents tested whereas eight were resistant to two or more antimicrobials. Six isolates were resistant to gentamicin, spectinomycin, streptomycin, and sulphamethoxazole and one of these in addition to nalidixic acid. Two isolates were resistant to ampicillin and nalidixic acid. An additional nine isolates were resistant to nalidixic acid only. All six streptomycin-resistant isolates had aadA located in an integron class 1 structure. Both ampicillin-resistant isolates had the bla(TEM) gene. Five different plasmid profiles were found among the isolates. Sixty-five percent of isolates contained a single plasmid with an approximate size of 55-60 kb. Plasmid profiling confirmed the PFGE pattern.
Association between resistance to zinc and methicillin resistance in Staphylococcus aureus - Results of a comparative study of MRSA and MSSA CC398 strains isolated from pigs in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Cavaco, L., Hasman, H., Aarestrup, F. M.
Publication date: 2009
Association between resistance to zinc and methicillin resistance in Staphylococcus aureus- Results of a comparative study of MRSA and MSSA CC398 strains isolated from pigs in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Cavaco, L., Hasman, H., Aarestrup, F. M.
Publication date: 2009

Event information
Event: ASM conference- Methicillin –resistant Staphylococci in animals
Location: London, United Kingdom
Source: orbit
Source-ID: 250550
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2009

Bedre identifikation af mastitis patogener

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M., Krogh, K., Voss, H.
Publication date: 2009
Peer-reviewed: No

Publication information
Journal: Dyrlægen
Volume: 4
Original language: Danish
Source: orbit
Source-ID: 255320
Research output: Research › Sound/Visual production (digital) – Annual report year: 2009

Comment on: Causal regulations vs. political will: Why human zoonotic infections increase despite precautionary bans on animal antibiotics

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Pires, S. M.
Pages: 760-761
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Environment International
Volume: 35
Issue number: 4
ISSN (Print): 0160-4120
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 7.32 SJR 2.568 SNIP 2.211
Web of Science (2017): Impact factor 7.297
Web of Science (2017): Indexed yes
Diversity of the tetracycline resistance gene tet(M) and identification of Tn916- and Tn5801-like (Tn6014) transposons in Staphylococcus aureus from humans and animals

To analyse the sequence diversity of the tetracycline resistance gene tet(M) in Staphylococcus aureus from humans and animals and to determine mobile elements associated with tet(M) in S. aureus. In total, 205 tetracycline-resistant isolates were screened for tet(M) by PCR. tet(M) genes were sequenced and compared with tet(M) deposited in GenBank. Based on phylogenetic analysis isolates were screened for Tn916- and Tn5801-like xis/int genes, and transposons were confirmed by linking PCR. spa typing was performed and selected isolates were used as donors in a filter mating experiment. Forty-one isolates (21.3%, 60.7%, 2.6% and 4.4% of the human, pig, poultry and cattle isolates, respectively) were tet(M) positive. tet(M) was located on Tn5801-like and Tn916-like transposons in humans and on a specific Tn916-like element in animals. Human isolates were of different spa types (t034, t008, t037, t051, t065, t078, t318 and t964) corresponding to different clonal complexes (CC398, CC8, CC25 and CC30). Animal isolates were of spa type t034, t011 or t0571 corresponding to CC398. tet(M) sequence types correlated with CC types. Tn916-like and Tn5801-like (Tn6014) transposons were able to transfer to S. aureus recipients. S. aureus of human origin contained diverse tet(M) located on Tn916- and Tn5801-like (Tn6014) transposons, and S. aureus of animal origin contained Tn916-like tet(M) genes. This suggests that conjugative transposition plays an important role in the evolution and horizontal spread of tet(M) in S. aureus. This is the first study showing horizontal transfer of Tn5801 (Tn6014).

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: de Vries, L. E., Christensen, H., Skov, R. L., Aarestrup, F. M., Agersø, Y.
Pages: 490-500
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Journal of Antimicrobial Chemotherapy
Volume: 64
Issue number: 3
ISSN (Print): 0305-7453
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.34 SJR 2.419 SNIP 1.568
Web of Science (2017): Impact factor 5.217
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Impact factor 5.071
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.06 SJR 2.259 SNIP 1.516
Web of Science (2015): Impact factor 4.919
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.61 SJR 2.298 SNIP 1.765
Web of Science (2014): Impact factor 5.313
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.7 SJR 2.479 SNIP 1.824
Web of Science (2013): Impact factor 5.439
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.35 SJR 2.283 SNIP 1.718
Web of Science (2012): Impact factor 5.338
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.24 SJR 2.341 SNIP 1.769
Web of Science (2011): Impact factor 5.068
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.161 SNIP 1.643
Web of Science (2010): Impact factor 4.659
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.902 SNIP 1.615
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.076 SNIP 1.506
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.744 SNIP 1.509
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.771 SNIP 1.437
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.768 SNIP 1.5
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.435 SNIP 1.465
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.367 SNIP 1.338
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.4 SNIP 1.284
Scopus rating (2001): SJR 1.388 SNIP 1.232
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.113 SNIP 1.248
Web of Science (2000): Indexed yes
Emergence of Multidrug-Resistant Salmonella Concord Infections in Europe and the United States in Children Adopted From Ethiopia, 2003-2007

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 814-818
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Pediatric Infectious Disease Journal
Volume: 28
Issue number: 9
ISSN (Print): 0891-3668
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.01 SJR 1.392 SNIP 1.005
Web of Science (2017): Impact factor 2.305
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.09 SJR 1.557 SNIP 1.054
Web of Science (2016): Impact factor 2.486
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.1 SJR 1.478 SNIP 1.063
Web of Science (2015): Impact factor 2.587
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.48 SJR 1.848 SNIP 1.171
Web of Science (2014): Impact factor 2.723
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 2.81 SJR 1.654 SNIP 1.231
Web of Science (2013): Impact factor 3.135
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.23 SJR 1.847 SNIP 1.355
Web of Science (2012): Impact factor 3.569
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.08 SJR 1.756 SNIP 1.365
Web of Science (2011): Impact factor 3.577
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Evaluation of Quinolones for use in detection of determinants of acquired quinolone resistance, including the new transmissible resistance mechanisms (qnrA, qnrB, qnrS and aac(6’)Ib-cr) in Escherichia coli and Salmonella enterica and determinations of wild type distributions

General information
- State: Published
- Organisations: Division of Microbiology and Risk Assessment, National Food Institute
- Contributors: Cavaco, L., Aarestrup, F. M.
- Pages: 2751-2758
- Publication date: 2009
- Peer-reviewed: Yes

Publication information
- Journal: Journal of Clinical Microbiology
- Volume: 47
- Issue number: 9
- ISSN (Print): 0095-1137
- Ratings:
  - BFI (2018): BFI-level 1
  - Web of Science (2018): Indexed yes
  - BFI (2017): BFI-level 1
  - Scopus rating (2017): CiteScore 3.55 SJR 2.256 SNIP 1.443
  - Web of Science (2017): Impact factor 4.054
  - Web of Science (2017): Indexed yes
  - BFI (2016): BFI-level 1
  - Scopus rating (2016): CiteScore 3.57 SJR 2.196 SNIP 1.4
  - Web of Science (2016): Impact factor 3.712
  - Web of Science (2016): Indexed yes
  - BFI (2015): BFI-level 1
  - Scopus rating (2015): CiteScore 3.56 SJR 2.206 SNIP 1.431
  - Web of Science (2015): Indexed yes
  - BFI (2014): BFI-level 1
First description of an MRSA skin infection in a dog and attending veterinarian in Portugal
First description of meticillin-resistant Staphylococcus aureus (MRSA) CC30 and CC398 from swine in Portugal

Publication information
Journal: International Journal of Antimicrobial Agents
Volume: 34
Issue number: 2
ISSN (Print): 0924-8579
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.54 SJR 1.699 SNIP 1.397
Web of Science (2017): Impact factor 4.253
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.38 SJR 1.608 SNIP 1.316
Web of Science (2016): Impact factor 4.307
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.45 SJR 1.703 SNIP 1.541
Web of Science (2015): Impact factor 4.097
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.45 SJR 1.477 SNIP 1.64
Web of Science (2014): Impact factor 4.296
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.63 SJR 1.706 SNIP 1.566
Web of Science (2013): Impact factor 4.259
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.57 SJR 1.633 SNIP 1.496
Web of Science (2012): Impact factor 4.415
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.15 SJR 1.388 SNIP 1.316
Web of Science (2011): Impact factor 4.128
ISI indexed (2011): ISI indexed yes
Molecular Characterization and Antimicrobial Susceptibility of Salmonella Isolates from Infections in Humans in Henan Province, China

We characterized 208 human Salmonella isolates from 2006 to 2007 and 27 human Salmonella enterica serovar Typhimurium isolates from 1987 to 1993 from Henan Province, China, by serotyping, by antimicrobial susceptibility testing, and, for the most common serovars, by pulsed-field gel electrophoresis (PFGE). The most common serovars among the 2006-2007 isolates were S. enterica serovar Typhimurium (27%), S. enterica serovar Enteritidis (17%), S. enterica serovar Derby (10%), S. enterica serovar Indiana (6%), and S. enterica serovar Litchfield (6%). A high percentage of the isolates were multiple-drug resistant, and 54% were resistant to both nalidixic acid and ciprofloxacin. Of these, 42% were resistant...
to a high level of ciprofloxacin (MIC > 4 μg/ml), whereas for the remaining isolates, the MICs ranged from 0.125 to 2 μg/ml. Five isolates (2%) were ceftiofur resistant and harbored bla(CTX-M14) or bla(CTX-M15). With the possible exception of the quinolones and cephalosporins, the 1987-1993 S. enterica serovar Typhimurium isolates were almost as resistant as the recent isolates. PFGE typing of S. enterica serovar Typhimurium showed that the most common cluster predominated over time. Two other clusters have emerged, and another cluster has disappeared.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Xia, S., Hendriksen, R. S., Xie, Z., Huang, L., Zhang, J., Guo, W., Xu, B., Ran, L., Aarestrup, F. M.
Pages: 401-409
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Journal of Clinical Microbiology
Volume: 47
Issue number: 2
ISSN (Print): 0095-1137
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.55 SJR 2.256 SNIP 1.443
Web of Science (2017): Impact factor 4.054
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.196 SNIP 1.4
Web of Science (2016): Impact factor 3.712
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.56 SJR 2.206 SNIP 1.431
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.84 SJR 2.231 SNIP 1.528
Web of Science (2014): Impact factor 3.993
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.18 SJR 2.438 SNIP 1.63
Web of Science (2013): Impact factor 4.232
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.11 SJR 2.148 SNIP 1.626
Web of Science (2012): Impact factor 4.068
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.27 SJR 2.346 SNIP 1.699
Web of Science (2011): Impact factor 4.153
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.343 SNIP 1.731
Web of Science (2010): Impact factor 4.22
Web of Science (2010): Indexed yes
Occurrence and characterization of Salmonella enterica subspecies enterica serovar 9,12:l,v:- strains from Bulgaria, Denmark, and the United States

In 2006, Salmonella enterica serovar I 9,12:l,v:- emerged in Bulgaria. The aim of this study was to characterize Salmonella serovar I 9,12:l,v:- isolates from Bulgaria, Denmark, and the United States. We compared isolates of Salmonella I 9,12:l,v:- and diphasic serovars with similar antigenic formulas by pulsed-field gel electrophoresis (PFGE) and antimicrobial susceptibility. The phase 2 flagellin gene (fljB) was also sequenced for selected isolates. By PFGE, the Salmonella I 9,12:l,v:- isolates from Bulgaria were indistinguishable from the isolate from the United States and distinct from isolates from Denmark; furthermore, several Salmonella I 9,12:l,v:- were indistinguishable from an isolate of Salmonella serovar Goettingen. Sequence analysis showed 100% sequence identity with known H:e,n,z15 sequences of Salmonella Goettingen, which has the antigenic formula I 9,12:l,v:e,n,z15. The study indicated that Salmonella I 9,12:l,v:- is a monophasic variant of Salmonella Goettingen and is present in different countries and on different continents.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 473-479
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: European Journal of Clinical Microbiology & Infectious Diseases
Volume: 28
Issue number: 5
ISSN (Print): 0934-9723
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
The objective of this study was to determine the prevalence of Salmonella serovars and the antimicrobial susceptibility in chickens and poultry meat products in rural areas in Nigeria. The study was an observational cross-sectional investigation
in which the target population included exotic and local chickens in Maiduguri main markets, chickens from farms, and free-range local chickens. A total of 865 samples were collected from feces, kidney, lungs, cecum, intestine, liver, heart, gizzard, and cloacal swabs from 525 different chickens. Salmonella was isolated from 130 of the samples. A stratified random sampling technique was used to select 41 isolates out of the 130 strains for serotyping, pulsed-field gel electrophoresis (PFGE), and antimicrobial susceptibility testing. Thirty-nine out of the 41 samples serotyped yielded Salmonella Hiduddify; two yielded a rough Salmonella serovar. The 39 Salmonella Hiduddify isolates and the two rough isolates were highly similar by PFGE typing, indicating that all of the isolates were of the same serovar. A low frequency of resistance was found among the isolates, except for resistance to ciprofloxacin for which 23 (56%) of the isolates tested exhibited resistance. This study documents for the first time the isolation of Salmonella Hiduddify in chickens and shows that this serovar is widespread in rural areas in Nigeria. It also documents a high frequency of fluoroquinolone resistance in the isolates indicating the presence of selective pressure in the environment. Further studies should be conducted to reveal if the serovar is present in eggs and causes salmonellosis among the general population.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Raufu, I., Hendriksen, R. S., Ameh, J., Aarestrup, F. M.
Pages: 425-430
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Foodborne Pathogens and Disease
Volume: 6
Issue number: 4
ISSN (Print): 1535-3141
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.47 SJR 1.063 SNIP 1.016
Web of Science (2017): Impact factor 2.476
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.46 SJR 1.062 SNIP 1.08
Web of Science (2016): Impact factor 2.12
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.41 SJR 1.064 SNIP 1.035
Web of Science (2015): Impact factor 2.27
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.16 SJR 0.953 SNIP 1.051
Web of Science (2014): Impact factor 1.905
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.41 SJR 1.184 SNIP 1.129
Web of Science (2013): Impact factor 2.092
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.55 SJR 1.185 SNIP 1.144
Web of Science (2012): Impact factor 2.283
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.33 SJR 1.118 SNIP 1.037
Web of Science (2011): Impact factor 2.26
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1  
Scopus rating (2010): SJR 0.86 SNIP 0.94  
Web of Science (2010): Impact factor 2.134  
BFI (2009): BFI-level 1  
Scopus rating (2009): SJR 0.864 SNIP 1.088  
Web of Science (2009): Indexed yes  
Scopus rating (2008): SJR 0.72 SNIP 0.682  
Web of Science (2008): Indexed yes  
Scopus rating (2007): SJR 0.611 SNIP 0.621  
Web of Science (2007): Indexed yes  
Scopus rating (2006): SJR 0.399 SNIP 0.318  
Web of Science (2006): Indexed yes  
Scopus rating (2005): SJR 0.198 SNIP 0.45  

Original language: English  
DOIs:  
10.1089/fpd.2008.0150  
Source: orbit  
Source-ID: 243677  
Research output: Research - peer-review › Journal article – Annual report year: 2009  

Patterns of antimicrobial use in the Danish pig production.

**General information**  
State: Published  
Organisations: Division of Microbiology and Risk Assessment, National Food Institute  
Contributors: Jensen, V. F., Vieira, A., Emborg, H., Aarestrup, F. M.  
Number of pages: 714  
Publication date: 2009  

**Host publication information**  
Title of host publication: Proceeding of the 12th Symposium of the International Society for Veterinary Epidemiology and Economics, Durban, South Africa:  
Source: orbit  
Source-ID: 264763  
Research output: Research › Conference abstract in proceedings – Annual report year: 2009  

qnrD, a Novel Gene Conferring Transferable Quinolone Resistance in Salmonella enterica Serovar Kentucky and Bovismorbificans Strains of Human Origin  
In a previous study, four Salmonella isolates from humans in the Henan province of China showed reduced susceptibility to ciprofloxacin (MIC, 0.125 to 0.25 μg/ml) but were susceptible to nalidixic acid (MIC, 4 to 8 μg/ml). All isolates were negative for known qnr genes (A, B, and S), aac(6')Ib-cr, and mutations in gyrA and parC. Plasmid DNA was extracted from all four isolates and transformed into Escherichia coli TG1 and DH10B cells by electroporation, and transformants were selected on 0.06 μg/ml ciprofloxacin containing brain heart infusion agar plates. Resistance to ciprofloxacin could be transferred by electroporation, and a similar 4,270-bp plasmid was found in all transformants. By sequence analysis, the plasmid was found to carry an open reading frame that had similarities to other qnr genes and that encoded a 214-amino-acid pentapeptide repeat protein. This gene, designated qnrD, showed 48% similarity to qnrA1, 61% similarity to qnrB1, and 41% similarity to qnrS1. Further subcloning of the qnrD coding region into the constitutively expressed tetA gene of vector pBR322 showed that the gene conferred an increase in the MIC of ciprofloxacin by a factor of 32 (from an MIC of 0.002 to an MIC of 0.06 μg/ml). For comparison, qnrA1 and qnrS1 were also subcloned into pBR322 and transformed into DH10B cells, conferring MICs of 0.125 and 0.5 μg/ml, respectively. A phylogenetic analysis of all known qnr sequences was performed and showed that qnrD was more closely related to the qnrB variants but formed an independent cluster. To our knowledge, this is the first description of this qnrD gene.

**General information**  
State: Published  
Organisations: Division of Microbiology and Risk Assessment, National Food Institute  
Contributors: Cavaco, L., Hasman, H., Xia, S., Aarestrup, F. M.  
Pages: 603-608  
Publication date: 2009  
Peer-reviewed: Yes
Results of Use of WHO Global Salm-Surv External Quality Assurance System for Antimicrobial Susceptibility Testing of Salmonella Isolates from 2000 to 2007

An international External Quality Assurance System (EQAS) for antimicrobial susceptibility testing of Salmonella was initiated in 2000 by the World Health Organization (WHO) Global Salm-Surv in order to enhance the capacities of national reference laboratories to obtain reliable data for surveillance purposes worldwide. Seven EQAS iterations have been conducted from 2000 to 2007. In each iteration, participating laboratories submitted susceptibility results from 10 to 15 antimicrobial agents for eight Salmonella isolates and an Escherichia coli reference strain (ATCC 25922). A total of 287 laboratories in 102 countries participated in at least one EQAS iteration. A large number of laboratories reported results for the E. coli ATCC 25922 reference strain which were outside the quality control ranges. Critical deviations for susceptibility testing of the Salmonella isolates varied from 4% in 2000 to 3% in 2007. Consistent difficulties were observed in susceptibility testing of amoxicillin-clavulanic acid, cefotaxime, ceftazidime, streptomycin, sulfonamides, and tetracycline.

Regional variations in performance were observed, with laboratories in central Asia, Africa, and the Middle East not performing as well as those in other regions. Results from the WHO Global Salm-Surv EQAS show that most laboratories worldwide are capable of correctly performing antimicrobial susceptibility testing of Salmonella isolates, but they also indicate that further improvement for some laboratories is needed. In particular, further training and dissemination of information on quality control, appropriate interpretive criteria (breakpoints), and harmonization of the methodology worldwide through WHO Global Salm-Surv and other programs will contribute to the generation of comparable and reliable antimicrobial susceptibility data (D. M. A. Lo Fo Wong, R. S. Hendriksen, D. J. Mevius, K. T. Veldman, and F. M. Aarestrup, Vet. Microbiol. 115: 128-139, 2006).

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Pages: 79-85
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Journal of Clinical Microbiology
Volume: 47
Issue number: 1
ISSN (Print): 0095-1137
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.55 SJR 2.256 SNIP 1.443
Web of Science (2017): Impact factor 4.054
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.196 SNIP 1.4
Web of Science (2016): Impact factor 3.712
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.56 SJR 2.206 SNIP 1.431
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.84 SJR 2.231 SNIP 1.528
Web of Science (2014): Impact factor 3.993
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.18 SJR 2.438 SNIP 1.63
Web of Science (2013): Impact factor 4.232
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.11 SJR 2.148 SNIP 1.626
Web of Science (2012): Impact factor 4.068
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.27 SJR 2.346 SNIP 1.699
Web of Science (2011): Impact factor 4.153
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.343 SNIP 1.731
Web of Science (2010): Impact factor 4.22
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.199 SNIP 1.691
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.265 SNIP 1.608
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.224 SNIP 1.688
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.212 SNIP 1.641
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.037 SNIP 1.65
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.699 SNIP 1.701
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.854 SNIP 1.853
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.976 SNIP 1.724
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.066 SNIP 1.804
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.783 SNIP 1.935
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.886 SNIP 2.024
Risk Factors and Epidemiology of the Ten Most Common Salmonella Serovars from Patients in Thailand: 2002-2007

We conducted a retrospective observational study to assess epidemiological trends and risk factors associated with the 10 most common Salmonella serovars isolated from humans in Thailand between 2002 and 2007. A total of 11,656 Salmonella isolates covering all 6 years were included in the study. The top 10 Salmonella serovars identified during the course of this study were Enteritidis, Stanley, Weltevreden, Rissen, I [1],[4],[5],[12]:i:-, Choleraesuis, Anatum, Typhimurium, Corvallis, and Panama, which accounted for 8108 (69.6%) of the isolates. Most isolates were from patients 5 years; S. Choleraesuis was recovered with a higher frequency from patients in Bangkok and the central region, whereas S. Enteritidis was recovered predominantly from patients in the southern region. This study also indicates a shift in prevalence of the most common Salmonella serovars responsible for human infections in Thailand compared to previous studies. Notably, there was an increase in human infections with S. Stanley, S. Corvallis, and S. Choleraesuis, three serovars that have previously been associated with swine, and a decrease in infections due to S. Weltevreden and S. Anatum. The study also revealed differences in the epidemiology among the different serovars, suggesting that serovar-specific interventions are needed. We recommend initiating targeted interventions for the two serovars associated with a high odds ratio for submitted blood samples, S. Enteritidis and S. Choleraesuis. The authors also recommend additional epidemiologic studies to investigate the observed increase in swine associated serovars (S. Stanley, S. Corvallis, and S. Choleraesuis) and determine interventions to reduce the burden of disease from these serovars.
Risk factors for salmonellosis caused by the most common Salmonella serovars in patients from Thailand

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Bangtrakulnonth, A., Pornreongwong, S., Pulsrikarn, C., Aarestrup, F. M.
Pages: 1009-1019
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Foodborne Pathogens and Disease
We report the first outbreak of salmonellosis caused by consumption of contaminated marlin mousse. Between 29 October and 5 November 2008, at least 53 persons developed diarrheal illness, all with a history of eating marlin mousse. Salmonella spp. that did not produce gas from glucose was isolated from stools of 26 affected patients and blood culture from one patient. Salmonella sp. isolates with the same phenotype were isolated in three samples of marlin mousse manufactured on 27 October 2008. The constituents of the mousse were smoked marlin, raw eggs, bovine gelatin, oil, and cream. A laboratory investigation of one sample of marlin mousse manufactured 3 days later, and the individual ingredients sampled a week after production of the contaminated batch were all negative for Salmonella. Serotyping and minimum inhibitory concentration determination were performed on 12 patient isolates related to the outbreak and two mousse isolates. All isolates belonged to Salmonella serovar Typhimurium and were pansusceptible to all antimicrobials tested. Pulsed-field gel electrophoresis revealed that all the isolates were indistinguishable, thus implicating the mousse as the vehicle of the outbreak.
The 1st External Quality Assurance System on isolation, identification and typing of methicillin resistant Staphylococcus aureus (MRSA) from dust samples, Year 2009

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Cavaco, L., Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M.
Publication date: 2009

Publication information
Edition: 1st
ISBN (Print): 978-87-92158-66-6
Original language: English
Source: orbit
Source-ID: 255666
Research output: Research - peer-review › Report – Annual report year: 2009

The 4th CRL-AR Proficiency Testing enterococci, staphylococci and E. coli 2008: Community Reference Laboratory – Antimicrobial Resistance

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Migura, L. G., Krause, M., Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M.
Number of pages: 82
Publication date: 2009

Publication information
Publisher: The National Food Institute, Technical University of Denmark
Edition: 1
ISBN (Print): 978-87-92158-52-9
Original language: English
Source: orbit
Source-ID: 245081
Research output: Research › Report – Annual report year: 2009

The effect of pH and storage on copper speciation and bacterial growth in complex growth media
In this paper we examine how the bacterial growth is influenced by the availability of copper ions in complex Mueller Hinton growth media. The data shows that the free copper concentration is seven to eight orders of magnitude lower the total copper concentration and that there seems to be a better correlation between the free copper concentration and bacterial growth, than for the total copper concentration and growth. Furthermore, it is shown that the initial pH influences the amount of free copper ions in the media and that this has a direct effect on the ability of bacterial cultures to grow.
However, there still remains an effect of pH on bacterial growth which cannot be attributed to the influence of the Cu2+ concentration alone. The study also shows that the sterilization treatment can have some effect on the availability of copper ions in the media over time. Freshly autoclaved and sterile filtered media contain the same level of free copper ions and perform equally well in the biological assay. However, storage in the refrigerator influences the free copper contents in media, which have been autoclaved, but not in media, which were sterile filtered. Therefore, the latter method is to be recommended, when working with bacterial copper testing.
The in vitro fitness cost of antimicrobial resistance in Escherichia coli varies with the growth conditions

The objective of this study was to investigate the influence of stressful growth conditions on the fitness cost of antimicrobial resistance in Escherichia coli BJ4 caused by chromosomal mutations and plasmid acquisition. The fitness cost of chromosomal streptomycin resistance increased significantly when the bacteria were grown under all stress conditions tested, while the cost in 1/3 Luria–Bertani was not significantly changed in a streptomycin+rifampicin mutant. The increase in the fitness cost depended in a nonregular manner on the strain/stress combination. The fitness cost of plasmid-encoded resistance on R751 did not differ significantly, and was generally less under stressful growth conditions than in rich media. The fitness cost associated with R751 with the multiple drug resistance cassette from Salmonella Typhimurium DT104 increased significantly only under stressful conditions at low pH and at high-salt concentrations. Strains with an impaired rpoS demonstrated a reduced fitness only during growth in a high-salt concentration. In conclusion, it was demonstrated that bacterial fitness cost in association with antimicrobial resistance generally increases under stressful growth conditions. However, the growth potential of bacteria with antimicrobial resistances did not increase in a straightforward manner in these in vitro experiments and is therefore probably even more difficult to predict in vivo.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Petersen, A., Aarestrup, F. M., Olsen, J. E.
Pages: 53-59
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: F E M S Microbiology Letters
Volume: 299
Issue number: 1
ISSN (Print): 0378-1097
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.8 SJR 0.79 SNIP 0.58
Web of Science (2017): Impact factor 11.392
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.76 SJR 0.842 SNIP 0.615
Web of Science (2016): Impact factor 12.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.08 SJR 1.156 SNIP 0.756
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.17 SJR 1.136 SNIP 0.767
Web of Science (2014): Impact factor 13.244
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.25 SJR 1.053 SNIP 0.719
Web of Science (2013): Impact factor 13.806
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.25 SJR 1.073 SNIP 0.804
Web of Science (2012): Impact factor 13.231
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.26 SJR 1.105 SNIP 0.764
Web of Science (2011): Impact factor 10.96
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.081 SNIP 0.754
Web of Science (2010): Impact factor 11.796
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.13 SNIP 0.834
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.084 SNIP 0.834
Scopus rating (2007): SJR 1.103 SNIP 0.864
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.105 SNIP 0.86
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1 SNIP 0.8
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.005 SNIP 0.725
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.018 SNIP 0.866
Scopus rating (2002): SJR 0.902 SNIP 0.791
Web of Science (2002): Indexed yes
WHO Global Salm-Surv External Quality Assurance System for Serotyping of Salmonella Isolates from 2000 to 2007

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Pages: 2729-2736
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Journal of Clinical Microbiology
Volume: 47
Issue number: 9
ISSN (Print): 0095-1137
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.55 SJR 2.256 SNIP 1.443
Web of Science (2017): Impact factor 4.054
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.196 SNIP 1.4
Web of Science (2016): Impact factor 3.712
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.56 SJR 2.206 SNIP 1.431
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.84 SJR 2.231 SNIP 1.528
Web of Science (2014): Impact factor 3.993
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.18 SJR 2.438 SNIP 1.63
Web of Science (2013): Impact factor 4.232
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.11 SJR 2.148 SNIP 1.626
Web of Science (2012): Impact factor 4.068
The use of antimicrobials in food animals creates an important source of antimicrobial-resistant bacteria that can spread to humans through the food supply. Improved management of the use of antimicrobials in food animals, particularly reducing the usage of those that are "critically important" for human medicine, is an important step toward preserving the benefits of antimicrobials for people. The World Health Organization has developed and applied criteria to rank antimicrobials according to their relative importance in human medicine. Clinicians, regulatory agencies, policy makers, and other stakeholders can use this ranking when developing risk management strategies for the use of antimicrobials in food production animals. The ranking allows stakeholders to focus risk management efforts on drugs used in food animals that are the most important to human medicine and, thus, need to be addressed most urgently, such as fluoroquinolones, macrolides, and third-and fourth-generation cephalosporins.
Antimicrobial resistance and molecular epidemiology of Salmonella Rissen from animals, food products, and patients in Thailand and Denmark

Recently we reported increases in both the number of Salmonella infections due to Salmonella Rissen in Thailand and the isolation of this serovar from pork products in Thailand. The objectives of the present study were to determine the genetic diversity and antimicrobial resistance of Salmonella Rissen isolates recovered from humans, food products, and animals in Denmark and Thailand. Additionally, risk factors due to travel and consumption of specific food products were analyzed and evaluated. A total of 112 Salmonella Rissen isolates were included in this study from Thailand and Denmark. Thai isolates were recovered from humans, uncooked food, and ready-to-eat food. Danish isolates were obtained from humans (with and without a history of travel to Thailand prior to the infection), Danish pig or pork products, imported pig or pork products, turkeys, and animal feed. A total of 63 unique XbaI-PFGE patterns were observed. The predominant pattern was shared by 22 strains. Limited antimicrobial resistance was observed in the Danish strains, and a higher degree of resistance was observed in strains originating from Thailand. Virtually all isolates were resistant to tetracycline. The tetA gene was detected in tetracycline-resistant isolates. Statistical analysis and molecular subtyping identified the combination of travel to Thailand and consumption of imported pig or pork products as well consumption of as pig or pork products produced in Denmark as risk factors for Salmonella Rissen infection among the Danish patients. The outcome of this study might be used as a supplement for future Salmonella Rissen investigations and outbreak detection.
Antimicrobial resistance and UTI virulence genes of Escherichia coli obtained from pigs, Danish and imported pork and healthy humans in Denmark
General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 2008
Peer-reviewed: Yes
Event: Poster session presented at 1st ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens, Copenhagen, Denmark.
Source: orbit
Source-ID: 233950
Research output: Research - peer-review » Poster – Annual report year: 2008

Antimicrobial resistance in swine production

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Oliver Duran, C., Burch, D.
Pages: 135-148
Publication date: 2008
Peer-reviewed: Yes

Publication information
Journal: Animal Health Research Reviews
Volume: 9
Issue number: 2
ISSN (Print): 1466-2523
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 1.61 SJR 0.69 SNIP 0.788
Web of Science (2017): Impact factor 2.406
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 1.73 SJR 0.831 SNIP 0.535
Web of Science (2016): Impact factor 1.886
Scopus rating (2015): CiteScore 1.72 SJR 0.898 SNIP 0.397
Web of Science (2015): Impact factor 1.5
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.74 SJR 1.271 SNIP 1.628
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.87 SJR 1.327 SNIP 0.486
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.58 SJR 1.067 SNIP 0.012
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.97 SJR 1.253 SNIP 4.361
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.862 SNIP 2.227
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.666
Scopus rating (2007): SJR 0.762 SNIP 1.073
Scopus rating (2006): SJR 0.62 SNIP 1.074
Scopus rating (2005): SJR 0.302 SNIP 0.083
Scopus rating (2004): SJR 0.871 SNIP 3.044
Development of a miniaturised microarray-based assay for the rapid identification of antimicrobial resistance genes in Gram-negative bacteria

We describe the development of a miniaturised microarray for the detection of antimicrobial resistance genes in Gram-negative bacteria. Included on the array are genes encoding resistance to aminoglycosides, trimethoprim, sulphonamides, tetracyclines and beta-lactams, including extended-spectrum beta-lactamases. Validation of the array with control strains demonstrated a 99% correlation between polymerase chain reaction and array results. There was also good correlation between phenotypic and genotypic results for a large panel of Escherichia coli and Salmonella isolates. Some differences were also seen in the number and type of resistance genes harboured by E. coli and Salmonella strains. The array provides an effective, fast and simple method for detection of resistance genes in clinical isolates suitable for use in diagnostic laboratories, which in future will help to understand the epidemiology of isolates and to detect gene linkage in bacterial populations. (C) 2008 Published by Elsevier B.V. and the International Society of Chemotherapy.
Diversity of plasmids carrying the blaTem-52 gene

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Bergenholtz, R., Jørgensen, M. J., Hasman, H., Jensen, L. B., Aarestrup, F. M.
Publication date: 2008
Peer-reviewed: Yes
Event: Poster session presented at Plasmid Biology’08, Gdansk, Poland.
Source: orbit
Source-ID: 236414
Research output: Research - peer-review › Poster – Annual report year: 2008

Eleven years of antimicrobial susceptibility testing of Salmonella from Danish pig farms

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Emborg, H., Baggesen, D. L., Aarestrup, F. M.
Publication date: 2008
Peer-reviewed: Yes
Event: Poster session presented at 1st ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens, Copenhagen, Denmark.
Source: orbit
Source-ID: 233904
Research output: Research - peer-review › Poster – Annual report year: 2008

Epidemier skal bremses før de når forbrugeren

General information
State: Published
Organisations: Division of Food Production Engineering, National Food Institute, National Institute of Aquatic Resources, Division of Microbiology and Risk Assessment, Communications and Management Secretariat, Center for Biological Sequence Analysis, Department of Systems Biology
Publication date: 2008
Peer-reviewed: Unknown

Publication information
Journal: FoodDTU Midt i Ugen
Original language: Danish
Source: orbit
Source-ID: 258262
Research output: Communication › Journal article – Annual report year: 2008
Evaluation of quinolones for detection of quinolone resistance, including the new transmissible resistance mechanism (qnrA, qnrB, qnrS and aac(6’)-1B-CR) in Escherichia coli and Salmonella enterica and determinations of wild type distributions

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Cavaco, L., Aarestrup, F. M.
Publication date: 2008
Peer-reviewed: Yes
Event: Poster session presented at 1st ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens, Copenhagen, Denmark.
Source: orbit
Source-ID: 233872
Research output: Research - peer-review › Poster – Annual report year: 2008

Fremskridt - med plads til forbedring

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, National Veterinary Institute
Contributors: Hendriksen, R. S., Aarestrup, F. M., Krogh, K., Voss, H.
Publication date: 2008
Peer-reviewed: Unknown
Publication information
Journal: Dyrlægen
Volume: 4
Original language: English
Source: orbit
Source-ID: 233703
Research output: Communication › Journal article – Annual report year: 2008

Guidelines for antimicrobial use in swine

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Burch, D. G. S., Oliver, D. C., Aarestrup, F. M.
Pages: 102-125
Publication date: 2008
Publication information
Title of host publication: Guide to antimicrobial use in animals
Place of publication: Oxford, United Kingdom
Publisher: Blackwell Publishing
ISBN (Print): 1405150793
Source: orbit
Source-ID: 233845
Research output: Research - peer-review › Book chapter – Annual report year: 2008

Harmonised monitoring of antimicrobial resistance in Salmonella and Campylobacter among food animals in the European Union

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 522-533
Publication date: 2008
Peer-reviewed: Yes
Publication information
Identifikation og resistensbestemmelse af mastitis patogener

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, National Veterinary Institute
Contributors: Hendriksen, R. S., Aarestrup, F. M., Krogh, K., Voss, H.
Publication date: 2008

Publication information
Original language: Danish
Source: orbit
Source-ID: 233823
Research output: Research › Report – Annual report year: 2008

Mechanisms and selection of resistance to quinolones and cephalosporins in Escherichia coli

General information
State: Published
Organisations: Unknown
Contributors: Cavaco, L., Guardabassi, L., Aarestrup, F. M., Frimodt-Møller, N.
Publication date: 2008

Publication information
Original language: English
Source: orbit
Source-ID: 235355
Research output: Research › Ph.D. thesis – Annual report year: 2008

Multi drug resistant Salmonella Concord in adoptee from Ethiopia: A collaborative international investigation

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Kornschober, C., Mikoleit, M., Cormican, M., Hasman, H., Threlfall, J., Mevius, D., Biggerstaff, M., Angulo, F., Kjelsø, C., Aarestrup, F. M.
Publication date: 2008
Peer-reviewed: No
Event: Abstract from International Conference on Emerging Infectious Diseases, Atlanta, GA, United States.
Source: orbit
Source-ID: 235844
Research output: Research › Conference abstract for conference – Annual report year: 2008
Needs Assessment of the WHO Global Salm-Surv External Quality Assurance System for Evaluating Microbiological Testing Proficiency: An internal CDC conference for fellowship programs

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Carlson, V. P., Hendriksen, R. S., Karlsnose, S., Aarestrup, F. M.
Publication date: 2008
Peer-reviewed: No
Event: 1st ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens
Location: Copenhagen, Denmark
Source: orbit
Source-ID: 235849
Research output: Research › Sound/Visual production (digital) – Annual report year: 2008

Occurrence of antimicrobial resistance among bacterial pathogens and indicator bacteria in pigs in different European countries from year 2002 – 2004: the ARBAO-II study

Background: The project "Antibiotic resistance in bacteria of animal origin - II" (ARBAO-II) was funded by the European Union (FAIR5-QLK2-2002-01146) for the period 2003-05. The aim of this project was to establish a program for the continuous monitoring of antimicrobial susceptibility of pathogenic and indicator bacteria from food animals using validated and harmonized methodologies. In this report the first data on the occurrence of antimicrobial resistance among bacteria causing infections in pigs are reported.

Methods: Susceptibility data from 17,642 isolates of pathogens and indicator bacteria including Actinobacillus pleuropneumoniae, Streptococcus suis and Escherichia coli isolated from pigs were collected from fifteen European countries in 2002-2004.

Results: Data for A. pleuropneumoniae from infected pigs were submitted from five countries. Most of the isolates from Denmark were susceptible to all drugs tested with the exceptions of a low frequency of resistance to tetracycline and trimethoprim - sulphonamide. Data for S. suis were obtained from six countries. In general, a high level of resistance to tetracycline (48.0 - 92.0%) and erythromycin (29.1 - 75.0%) was observed in all countries whereas the level of resistance to ciprofloxacin and penicillin differed between the reporting countries. Isolates from England (and Wales), France and The Netherlands were all susceptible to penicillin. In contrast the proportion of strains resistant to ciprofloxacin ranged from 12.6 to 79.0% (2004) and to penicillin from 8.1 - 13.0% (2004) in Poland and Portugal. Data for E. coli from infected and healthy pigs were obtained from eleven countries. The data reveal a high level of resistance to tetracyclines, streptomycin and ampicillin among infected pigs whereas in healthy pigs the frequency of resistance was lower. Conclusion: Bacterial resistance to some antimicrobials was frequent with different levels of resistance being observed to several antimicrobial agents in different countries. The occurrence of resistance varied distinctly between isolates from healthy and diseased pigs, with the isolates from healthy pigs generally showing a lower level of resistance than those from diseased pigs. The study suggests that the choice of antimicrobials used for the treatment of diseased animals should preferably be based on knowledge of the local pattern of resistance.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 19
Publication date: 2008
Peer-reviewed: Yes

Publication information
Journal: Acta Veterinaria Scandinavica (Online Edition)
Volume: 50
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
Web of Science (2017): Indexed yes
Pigs as an Important source of Methicillin-Resistant Staphylococcus aureus CC398 Infections in humans in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Lewis, H. C., Mølbak, K., Reese, C., Aarestrup, F. M., Smørum, M., Skov, R.
Publication date: 2008
Peer-reviewed: Yes
Event: Poster session presented at 1st ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens, Copenhagen, Denmark.

Pigs as source of methicillin-resistant Staphylococcus aureus CC398 infections in humans, Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Lewis, H. C., Mølbak, K., Reese, C., Aarestrup, F. M., Selchau, M., Sorum, M., Skov, R. L.
Pages: 1383-1389
Publication date: 2008
Peer-reviewed: Yes

Publication information
Journal: Emerging Infectious Diseases
Volume: 14
Issue number: 9
ISSN (Print): 1080-6040
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 4.78 SJR 3.278 SNIP 1.916
Web of Science (2017): Impact factor 7.422
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.92 SJR 3.428 SNIP 2.198
Web of Science (2016): Impact factor 8.222
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.23 SJR 3.101 SNIP 2.012
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.59 SJR 3.509 SNIP 2.406
Web of Science (2014): Impact factor 6.751
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.68 SJR 3.254 SNIP 2.266
Web of Science (2013): Impact factor 7.327
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Plasmid-mediated quinolone resistance due to qnrB5 and qnrS1 genes in Salmonella enterica serovars Newport, Hadar and Saintpaul isolated from turkey meat in Denmark

General information
State: Published
Organisations: National Food Institute
Contributors: Cavaco, L., Korsgaard, H., Sørensen, G., Aarestrup, F. M.
Pages: 632-634
Publication date: 2008
Peer-reviewed: Yes

Publication information
Journal: Journal of Antimicrobial Chemotherapy
Volume: 62
Issue number: 3
Prevalence of antimicrobial resistance among bacterial pathogens isolated from cattle in different European countries: 2002–2004

Background: The project "Antibiotic resistance in bacteria of animal origin - II" (ARBAO-II) was funded by the European Union (FAIR5-QLK2-2002-01146) for the period 2003 - 2005, with the aim to establish a continuous monitoring of antimicrobial susceptibility among veterinary laboratories in European countries based on validated and harmonised methodologies. Available summary data of the susceptibility testing of the bacterial pathogens from the different laboratories were collected. Method: Antimicrobial susceptibility data for several bovine pathogens were obtained over a three year period (2002-2004). Each year the participating laboratories were requested to fill in excelfile templates with national summary data on the occurrence of antimicrobial resistance from different bacterial species. A proficiency test (EQAS - external quality assurance system) for antimicrobial susceptibility testing was conducted each year to test the accuracy of antimicrobial susceptibility testing in the participating laboratories. The data from this testing demonstrated that for the species included in the EQAS the results are comparable between countries. Results: Data from 25,241 isolates were collected from 13 European countries. For Staphylococcus aureus from bovine mastitis major differences were apparent in the occurrence of resistance between countries and between the different antimicrobial agents tested. The highest frequency of resistance was observed for penicillin. For Mannheimia haemolytica resistance to ampicillin, tetracycline and trimethoprim/sulphonamide were observed in France, the Netherlands and Portugal. All isolates of Pasteurella multocida isolated in Finland and most of those from Denmark, England (and Wales), Italy and Sweden were susceptible to the majority of the antimicrobials. Streptococcus dysgalactiae and Streptococcus uberis isolates from Sweden were fully susceptible. For the other countries some resistance was observed to tetracycline, gentamicin and erythromycin. More resistance and variation of the resistance levels between countries were observed for Escherichia coli compared to the other bacterial species investigated. Conclusion: In general, isolates from Denmark, England (and Wales), the Netherlands, Norway, Sweden and Switzerland showed low frequencies of resistance, whereas many isolates from Belgium, France, Italy, Latvia and Spain were resistant to most antimicrobials tested. In the future, data on the prevalence of resistance should be used to develop guidelines for appropriate antimicrobial use in veterinary medicine.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 28
Publication date: 2008
Peer-reviewed: Yes

Publication information
Journal: Acta Veterinaria Scandinavica (Online Edition)
Volume: 50
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Prevalence of quinolone resistance mechanisms and associations to minimum inhibitory concentrations in quinolone-resistant Escherichia coli isolated from humans and swine in Denmark

Prevalence of quinolone resistance mechanisms and associations to minimum inhibitory concentrations (MICs) of nalidixic acid (NAL) and ciprofloxacin (CIP) were investigated in 124 Escherichia coli isolated from humans (n = 85) and swine (n = 39) in Denmark. The collection included 59 high-level CIP-resistant isolates (MIC >= 4) from human (n = 51) and pig origin (n = 8) and 65 low-level CIP-resistant isolates (MIC >= 0.125) from human (n = 34) and pig origin (n = 31). Resistance by target modification was screened by PCR amplification and sequencing, of the quinolone resistance determining regions (QRDRs) of gyrA, gyrB, parC, and parE. QRDR mutations occurred in all except two isolates (98%). All high-level CIP-resistant E. coli had one or two mutations in gyrA in combination with mutations in parC or parE. Mutations in parC and parE were only found in combination with gyrA mutations, and no mutations were observed in gyrB. Efflux pump mechanisms were detected in 10 human (11.8%) and 29 porcine (74.4%) isolates by an efflux pump inhibitor (EPI) agar dilution assay. The aac(6')-Ib-cr gene mediating resistance by enzymatic modification was found in 12 high-level CIP-resistant human isolates. The qnrA and qnrS genes conferring quinolone resistance by target protection were detected in two human low-level CIP-resistant isolates that did not display NAL resistance. As expected, target mutation in QRDRs was the most prevalent mechanism of quinolone resistance. This mechanism was complemented by efflux mechanisms in most porcine isolates. Transferable resistance by target protection or enzymatic modification was less common (10%) and restricted to human isolates.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Cavaco, L., Frimodt-Møller, N., Hasman, H., Guardabassi, L., Nielsen, L., Aarestrup, F. M.
Pages: 163-169
Publication date: 2008
Peer-reviewed: Yes

Publication information
Journal: Microbial Drug Resistance
Volume: 14
Issue number: 2
ISSN (Print): 1076-6294
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
Web of Science (2017): Impact factor 2.344
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
Web of Science (2016): Impact factor 2.306
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
Web of Science (2015): Impact factor 2.529
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
Web of Science (2014): Impact factor 2.49
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.87 SJR 1.265 SNIP 1.118
Web of Science (2013): Impact factor 2.524
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.45 SJR 0.963 SNIP 0.9
Web of Science (2012): Impact factor 2.364
Report from the Task Force on Zoonoses Data Collection including guidance for harmonized monitoring and reporting of antimicrobial resistance in commensal Escherichia coli and Enterococcus spp. from food animals: Question No EFSA-Q-2007-131

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: EFSA Publication
Number of pages: 44
Publication date: 2008

Publication information
Publisher: European Food Safety Authority
Original language: English
(The EFSA Journal; No. 141).
Source: orbit
Source-ID: 235876
Resistance in bacteria of the food chain: epidemiology and control strategies

Bacteria have evolved multiple mechanisms for the efficient evolution and spread of antimicrobial resistance. Modern food production facilitates the emergence and spread of resistance through the intensive use of antimicrobial agents and international trade of both animals and food products. The main route of transmission between food animals and humans is via food products, although other modes of transmission, such as direct contact and through the environment, also occur. Resistance can spread as resistant pathogens or via transferable genes in different commensal bacteria, making quantification of the transmission difficult. The exposure of humans to antimicrobial resistance from food animals can be controlled by either limiting the selective pressure from antimicrobial usage or by limiting the spread of the bacteria genes. A number of control options are reviewed, including drug licensing, removing financial incentives, banning or restricting the use of certain drugs, altering prescribers behavior, improving animal health, improving hygiene and implementing microbial criteria for certain types of resistant pathogens for use in the control of trade of both food animals and food.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Wegener, H. C., Collignon, P.
Pages: 733-750
Publication date: 2008
Peer-reviewed: Yes

Publication information
Journal: Expert Review of Anti-infective Therapy
Volume: 6
Issue number: 5
ISSN (Print): 1478-7210
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 2.97 SJR 1.264 SNIP 1.057
Web of Science (2017): Impact factor 3.141
Web of Science (2016): Indexed yes
Scopus rating (2016): CiteScore 2.95 SJR 1.392 SNIP 1.054
Web of Science (2015): Impact factor 3.139
Scopus rating (2015): CiteScore 2.74 SJR 1.406 SNIP 1.099
Web of Science (2014): Impact factor 3.542
Scopus rating (2014): CiteScore 2.81 SJR 1.38 SNIP 1.232
Web of Science (2013): Impact factor 3.461
Scopus rating (2013): CiteScore 2.74 SJR 1.109 SNIP 1.102
Web of Science (2012): Impact factor 3.063
ISI indexed (2013): ISI indexed yes
Scopus rating (2012): CiteScore 2.86 SJR 1.257 SNIP 1.203
Web of Science (2012): Impact factor 3.218
ISI indexed (2012): ISI indexed yes
Scopus rating (2011): CiteScore 2.84 SJR 1.121 SNIP 1.155
Web of Science (2011): Impact factor 3.283
ISI indexed (2011): ISI indexed no
Scopus rating (2010): SJR 0.963 SNIP 1.081
Web of Science (2010): Impact factor 3.09
Scopus rating (2009): SJR 0.953 SNIP 0.836
Scopus rating (2008): SJR 0.788 SNIP 0.741
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.686 SNIP 0.887
Scopus rating (2006): SJR 0.616 SNIP 0.715
Scopus rating (2005): SJR 0.493 SNIP 0.579
Scopus rating (2004): SJR 0.281 SNIP 0.246
Original language: English
Keywords: Antimicrobial resistance, Control, Food, Global epidemiology, Intervention
Results of the Community Reference Laboratory on antimicrobial resistance External Quality Assurance System (EQAS) for Salmonella and Campylobacter in 2006 and 2007

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Krause, M., Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M.
Publication date: 2008
Peer-reviewed: Yes
Event: Poster session presented at ASM Conference of Antimicrobial Resistance in Zoontic Bacteria and Foodborne Pathogens, Copenhagen, Denmark.
Source: orbit
Source-ID: 234035
Research output: Research - peer-review › Poster – Annual report year: 2008

Results of the Community Reference Laboratory's External Quality Assurance System for antimicrobial resistance for Salmonella and Campylobacter in 2006 and 2007

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Krause, M., Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M.
Publication date: 2008
Peer-reviewed: No
Event: Abstract from 1st ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens, Copenhagen, Denmark.
Source: orbit
Source-ID: 235847
Research output: Research › Conference abstract for conference – Annual report year: 2008

Ringtesten for identifikation og resistensbestemmelse af mastitispatogener 2008

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Contributors: Hendriksen, R. S., Aarestrup, F. M., Krogh, K., Voss, H.
Number of pages: 11
Publication date: 2008

Publication information
Publisher: Danmarks Tekniske Universitet, Fødevareinstituttet
ISBN (Print): 978-87-92158-56-7
Original language: Danish
Research output: Research › Report – Annual report year: 2008

Scientific Opinion of the Panel on Biological Hazards on a request from DG SANCO on the assessment of the possible effect of the four antimicrobial treatment substances on the emergence of antimicrobial resistance: Question No EFSA-Q-2007-203

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: EFSA Publication
Number of pages: 26
Publication date: 2008

Publication information
Scientific Opinion of the Panel on Biological Hazards on a request from the European Food Safety Authority on foodborne antimicrobial resistance as a biological hazard: Question No EFSA-Q-2007-089

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: EFSA Publication
Number of pages: 87
Publication date: 2008

Selection and persistence of CTX-M-producing Escherichia coli in the intestinal flora of pigs treated with amoxicillin, ceftiofur, or ceftquinome

Extended-spectrum beta-lactamases (ESBLs), mainly of the CTX-M family, have been associated with Escherichia coli strains of animal origin in Europe. An in vivo experiment was performed to study the effects of veterinary beta-lactam drugs on the selection and persistence of ESBL-producing E. coli in the intestinal flora of pigs. Twenty pigs were randomly allocated into three treatment groups and one control group. All pigs were inoculated intragastrically with 10(10) CFU of a nalidixic acid (NAL)-resistant mutant derived from a CTX-M-1-producing E. coli strain of pig origin. Treatment with amoxicillin, ceftiofur, or ceftquinome according to the instructions on the product label was initiated immediately after bacterial inoculation. Feces were collected from the rectum before inoculation and on days 4, 8, 15, 22, and 25 after the start of treatment. The total and resistant coliforms were counted on MacConkey agar with and without cefotaxime (CTX). Furthermore, MacConkey agar with CTX and NAL was used to count the number of CFU of the inoculated strain. Significantly higher counts of CTX-resistant coliforms were observed in the three treatment groups than in the control group for up to 22 days after the discontinuation of treatment. Ceftiofur and ceftquinome exerted larger selective effects than amoxicillin, and the effects persisted beyond the withdrawal times recommended for these cephalosporins. The inoculated strain was detected in only nine animals on day 25. The increase in the number of CTX-resistant coliforms was mainly due to the proliferation of indigenous CTX-M-producing strains and the possible emergence of strains that acquired CTX-M genes by horizontal transfer. The study provides evidence that the cephalosporins used in pig production select for CTX-M-producing E. coli strains. Their use in animals should be carefully considered in view of the critical importance of cephalosporins and the zoonotic potential of ESBL-producing bacteria.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Cavaco, L., Abatih, E., Aarestrup, F. M., Guardabassi, L.
Pages: 3612-3616
Publication date: 2008
Peer-reviewed: Yes

Publication information
Journal: Antimicrobial Agents and Chemotherapy
Volume: 52
Issue number: 10
ISSN (Print): 0066-4804
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.15 SJR 2.291 SNIP 1.263
Serotypes, antimicrobial susceptibility and molecular characterization of Salmonella from infections in humans in Henan province, China

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Xia, S., Hendriksen, R. S., Guo, W., Xu, B., Lu, R., Aarestrup, F. M.
Publication date: 2008
Peer-reviewed: No
Event: Abstract from International Conference on Emerging Infectious Diseases, Atlanta, GA, United States.

Shigella from humans in Thailand during 1993 to 2006: spatial-time trends in species and serotype distribution

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 2008
Peer-reviewed: No
Event: Abstract from International Conference on Emerging Infectious Diseases, Atlanta, GA, United States.

Shigella from Humans in Thailand During 1993 to 2006: Spatial-Time Trends in Species and Serotype Distribution
In Thailand during 1993-2006, a total of 9063 Shigella isolates from different medical centers were serotyped and trends over time and. spatial clustering analyzed. Of 3583 cases with age information, 1315 (37%) cases were from children between 0 and 4 years and 684 (1.9%) from children between 5 and 8 years. Most infections were recorded during 1993-1994 (> 1500 per year), decreasing to <200 in 2006. The relative species distribution also changed. During 1993-1994, Shigella flexneri accounted for 2241 (65%) of 3474 isolations. This proportion decreased to 64 (36%) of 176 infections in 2006. Most infections occurred during July and August, and fewest in December. S. flexneri clustered around Bangkok, and Shigella sonnei in southern Thailand. Most S. flexneri infections were caused by serotype 2a (1590 of 4035) followed by serotype var X (1249). For both serotypes, a pronounced decrease in the number of isolates occurred over time. A Much smaller decrease was observed for serotype 3a isolates. Phase I S. sonnei was initially most common, but shifted gradually over phase I, II, to only phase II. No differences in spatial distribution were found. The three most common S. flexneri serotypes all clustered in, around, and west of Bangkok. Serotypes 2a and 3a also clustered in southern Thailand, whereas var X clustered north and northeast of Bangkok. In conclusion, looking at Shigella species, Thailand changed from being a developing country to a developed country between 1995 and 1996. In addition, major shifts in the types of S. sonnei were observed as were differences in spatial clustering of S. flexneri and S. sonnei and S. flexneri serotypes.

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Pages: 773-784
Publication date: 2008
Peer-reviewed: Yes
Simulation Study for Transfer of Antibiotic Resistance via Mutator Subpopulation

Evolution of antibiotic resistance in bacterial populations is an increasing problem having fatal consequences for treatment of diseases. Therefore it is very important to understand this evolution. Traditionally evolution is considered to happen by single point mutations, where each mutant must have a growth advantage over the parent strain and grow to a sufficient number before a second mutation can occur. However, when multiple mutations are necessary for development of resistance, single mutations occurring with a normal mutation rate can not always explain the observed resistance. We introduce an alternative hypothesis by which a subpopulation of mutators drives the evolution process. Resistance is acquired by a subpopulation of mutators, for which the mutation rate is much higher than the wild-type. If the resistance is located on a transferable plasmid it can subsequently be transferred to the wild-type population by conjugation. To examine whether this pathway will in fact speed up evolution, we perform a simulation study, where bacteria are simulated to grow in a chemostat environment, such as the intestine of a human. Since mutation events are stochastic processes, we model the system by a discrete Markov process with the possibility of changes in each state given by a Poisson distribution. Parameters for growth, mutation and conjugation rates used in the simulation study resemble those of E.coli with a mutator obtained with the XL1-red mutator strain having a 5000 times higher mutation rate than the wild-type. We simulate the process for 24 hours and perform 1000 repetitions, which correspond to considering 1000 people with the same initial bacterial population in the intestine. In none of the repetitions a double mutation occurs in the wild-type population, but in almost 300 cases a double mutated strain has been conjugated to the wild-type bacterial population. To confirm these results future work should include an experimental study of the hypothesis.

Ten years of antimicrobial susceptibility testing of Salmonella from Danish pig farms

Objectives: This study analysed the trends in antimicrobial resistance in Salmonella serovars and phage types from pigs in Denmark from 1997 to 2006. Methods: Salmonella isolates collected through the Salmonella surveillance programme in pigs were serotyped and phage-typed, and susceptibility to the following antimicrobials were determined: ampicillin, chloramphenicol, gentamicin, nalidixic acid, colistin, streptomycin, sulphonamide, tetracycline and trimethoprim. Results: No significant development of resistance occurred within the most important serovars, except Salmonella Typhimurium. A major decrease in Salmonella Typhimurium DT12 occurred from 46.5% in 1998 to 16.8% in 2006 while DT120, DT170 and DT104 increased. Throughout the study period, 80.9% of the DT12 isolates remained susceptible to the antimicrobials tested despite an increase in antimicrobial consumption in pigs during the period. In DT120, DT170 and DT104, only 20.1%, 33.1% and 23.0%, respectively, remained fully susceptible. Conclusions: The results support that the use of antimicrobial agents might select for multiple resistant clones and that this might be the driver of changes in antimicrobial resistance within a serovar, rather than an emergence of resistance within clones. The results of this study also support that susceptible serovars only slowly become resistant to the antimicrobials tested.
The 3rd CRL Proficiency Testing Salmonella and Campylobacter 2007: Community Reference Laboratory – Antimicrobial Resistance

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Contributors: Karlsmose, S., Hendriksen, R. S., Krause, M., Aarestrup, F. M.
Number of pages: 86
Publication date: 2008

Publication information
Publisher: The National Food Institute, Technical University of Denmark
ISBN (Print): 978-87-92158-39-0
Original language: English
Research output: Research - Report – Annual report year: 2008

The attribution of human infections with antimicrobial resistant Salmonella bacteria in Denmark to sources of animal origin

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hald, T., Wong, D. L. F., Aarestrup, F. M.
Publication date: 2008
Peer-reviewed: Yes
Event: Poster session presented at 1st ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens, Copenhagen, Denmark.
Source: orbit
Source-ID: 233912
Research output: Research - peer-review » Poster – Annual report year: 2008

The second CRL Proficiency Testing enterococci, staphylococci and E. coli 2007: Community Reference Laboratory – Antimicrobial Resistance

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Contributors: Krause, M., Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M.
Use of Antimicrobials in Food Animal Production

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, L. B.
Pages: 405-417
Publication date: 2008

Host publication information
Title of host publication: Foodborne Diseases
Place of publication: New Jersey, USA
Publisher: Humana Press
ISBN (Print): 978-1-58829-518-7
Source: orbit
Source-ID: 235971
Research output: Research - peer-review › Book chapter – Annual report year: 2008

Using free-cost spatial technology as a tool for assessment of antimicrobial consumption data and spatial distribution of pig herds

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, National Veterinary Institute, Communications and Management Secretariat
Number of pages: 12
Publication date: 2008

Host publication information
Title of host publication: The ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens: Copenhagen, Denmark
Publisher: ASM Press
Source: orbit
Source-ID: 238729
Research output: Research › Article in proceedings – Annual report year: 2008

Vancomycin-resistant Enterococcus faecalis isolates from a Danish patient and two healthy human volunteers are possibly related to isolates from imported turkey meat

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Microbiology
Pages: 844-845
Publication date: 2008
Peer-reviewed: Yes

Publication information
Journal: Journal of Antimicrobial Chemotherapy
Volume: 62
WHO Global Salm-Surv external quality assurance system (EQAS) for antimicrobial susceptibility testing of Salmonella isolates, 2000-2007

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Publication date: 2008
Peer-reviewed: Yes
Event: Poster session presented at 1st ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens, Copenhagen, Denmark.
Source-ID: 233948
Research output: Research - peer-review > Poster – Annual report year: 2008

Antimicrobial drug resistance of Salmonella isolates from meat and humans, Denmark

We compared 8,144 Salmonella isolates collected from meat imported to or produced in Denmark, as well as from Danish patients. Isolates from imported meat showed a higher rate of antimicrobial drug resistance, including multidrug resistance, than did isolates from domestic meat. Isolates from humans showed resistance rates lower than those found in imported meat but higher than in domestic meat. These findings indicate that programs for controlling resistant Salmonella spp. are a global issue.

General information
State: Published
Organisations: Risø National Laboratory for Sustainable Energy, Department of Informatics and Mathematical Modeling, Division of Microbiology and Risk Assessment, National Food Institute, Section of Poultry Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Contributors: Skov, M., Andersen, J. S., Aabo, S., Ethelberg, S., Aarestrup, F. M., Sørensen, A. M. H., Sørensen, G., Pedersen, K., Nordentoft, S., Olsen, K. E. P., Gerner-Smidt, P., Baggesen, D. L.
Pages: 638-641
Publication date: 2007
Peer-reviewed: Yes
Web of Science (2017): Impact factor 7.422
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.92 SJR 3.428 SNIP 2.198
Web of Science (2016): Impact factor 8.222
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.23 SJR 3.101 SNIP 2.012
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.59 SJR 3.509 SNIP 2.406
Web of Science (2014): Impact factor 6.751
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.68 SJR 3.254 SNIP 2.266
Web of Science (2013): Impact factor 7.327
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.25 SJR 2.858 SNIP 2.131
Web of Science (2012): Impact factor 5.993
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 4.46 SJR 2.785 SNIP 2.19
Web of Science (2011): Impact factor 6.169
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.021 SNIP 2.319
Web of Science (2010): Impact factor 6.859
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.168 SNIP 2.701
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.231 SNIP 2.277
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.709 SNIP 2.341
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.879 SNIP 2.345
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.816 SNIP 2.297
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.683 SNIP 2.562
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.267 SNIP 2.373
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 3.094 SNIP 2.545
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.346 SNIP 2.904
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.522 SNIP 2.856
Antimicrobial susceptibility of *Listeria monocytogenes* from food products

This study was conducted to determine the susceptibility of *Listeria monocytogenes* isolated from food products to antimicrobial agents commonly used for treatment of infections with gram-positive bacteria, and to disinfectants. A total of 114 *L. monocytogenes* retail isolates were tested for susceptibility to ceftiofur, chloramphenicol, ciprofloxacin, erythromycin, florfenicol, penicillin, spectinomycin, streptomycin, tetracycline, tiamulin, trimethoprim, and co-trimoxazole, and the disinfectants benzalkonium chloride and triclosan, by determination of minimum inhibitory concentrations (MICs). All isolates were resistant to ceftiofur, but susceptible to the other antibiotics. A single isolate had a MIC of 4 mg/L for ciprofloxacin. For tiamulin, the MIC values were around the breakpoint used. Most isolates had MICs for triclosan at 16 mg/L. The MICs for benzalkonium chloride formed a bimodal distribution, with 105 isolates having a MIC of 4 mg/L and 9 isolates MICs of 16 and 32 mg/L. This study showed that Danish isolates of *L. monocytogenes* have not developed or acquired resistance to antimicrobial agents used for treatment or disinfection, except for benzalkonium chloride. The MICs for triclosan was high compared to other gram-positive bacteria, suggesting that triclosan might not be useful against *L. monocytogenes* if incorporated in materials in the food industry.

**General information**

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Knöchel, S., Hasman, H.
Pages: 216-221
Publication date: 2007
Peer-reviewed: Yes

**Publication information**

Journal: Foodborne Pathogens and Disease
Volume: 4
Issue number: 2
ISSN (Print): 1535-3141
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.47 SJR 1.063 SNIP 1.016
Web of Science (2017): Impact factor 2.476
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.46 SJR 1.062 SNIP 1.08
Web of Science (2016): Impact factor 2.12
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.41 SJR 1.064 SNIP 1.035
Web of Science (2015): Impact factor 2.27
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.16 SJR 0.953 SNIP 1.051
Web of Science (2014): Impact factor 1.905
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.41 SJR 1.184 SNIP 1.129
Web of Science (2013): Impact factor 2.092
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.55 SJR 1.185 SNIP 1.144
Antimicrobial susceptibility testing – clinical break points and epidemiological cut-off values

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., McDermott, P. F., Kahlmeter, G.
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: The Community Reference Laboratory for Antimicrobial Resistance
Original language: English
Source: orbit
Source-ID: 236111
Research output: Research - peer-review › Journal article – Annual report year: 2007

Breakpoints

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: The Community Reference Laboratory for Antimicrobial Resistance
Original language: English
Source: orbit
Source-ID: 236108
Research output: Research - peer-review › Journal article – Annual report year: 2007
Danish integrated antimicrobial in resistance monitoring and research program

Resistance to antimicrobial agents is an emerging problem worldwide. Awareness of the undesirable consequences of its widespread occurrence has led to the initiation of antimicrobial agent resistance monitoring programs in several countries. In 1995, Denmark was the first country to establish a systematic and continuous monitoring program of antimicrobial drug consumption and antimicrobial agent resistance in animals, food, and humans, the Danish Integrated Antimicrobial Resistance Monitoring and Research Program (DANMAP). Monitoring of antimicrobial drug resistance and a range of research activities related to DANMAP have contributed to restrictions or bans of use of several antimicrobial agents in food animals in Denmark and other European Union countries.

General information
State: Published
Organisations: Department of Microbiology, National Food Institute, Division of Microbiology and Risk Assessment, Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Communications and Management Secretariat
Pages: 1632-1639
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: Emerging Infectious Diseases
Volume: 13
Issue number: 11
ISSN (Print): 1080-6040
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 4.78 SJR 3.278 SNIP 1.916
Web of Science (2017): Impact factor 7.422
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.92 SJR 3.428 SNIP 2.198
Web of Science (2016): Impact factor 8.222
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.23 SJR 3.101 SNIP 2.012
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.59 SJR 3.509 SNIP 2.406
Web of Science (2014): Impact factor 6.751
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.68 SJR 3.254 SNIP 2.266
Web of Science (2013): Impact factor 7.327
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.25 SJR 2.858 SNIP 2.131
Web of Science (2012): Impact factor 5.993
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 4.46 SJR 2.785 SNIP 2.19
Danish Integrated Antimicrobial Resistance Monitoring and Research Programme

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Communications and Management Secretariat
Pages: 1632-1639
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: Emerging Infectious Diseases
Volume: 13
Issue number: 11
ISSN (Print): 1080-6040
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 4.78 SJR 3.278 SNIP 1.916
Web of Science (2017): Impact factor 7.422
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.92 SJR 3.428 SNIP 2.198
Web of Science (2016): Impact factor 8.222
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.23 SJR 3.101 SNIP 2.012
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.59 SJR 3.509 SNIP 2.406
Web of Science (2014): Impact factor 6.751
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.68 SJR 3.254 SNIP 2.266
Web of Science (2013): Impact factor 7.327
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.25 SJR 2.858 SNIP 2.131
Web of Science (2012): Impact factor 5.993
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 4.46 SJR 2.785 SNIP 2.19
Web of Science (2011): Impact factor 6.169
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.021 SNIP 2.319
Web of Science (2010): Impact factor 6.859
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.168 SNIP 2.701
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.231 SNIP 2.277
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.709 SNIP 2.341
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.879 SNIP 2.345
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.816 SNIP 2.297
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.683 SNIP 2.562
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.267 SNIP 2.373
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 3.094 SNIP 2.545
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.346 SNIP 2.904
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.522 SNIP 2.856
Scopus rating (1999): SJR 1.71 SNIP 2.61
DANMAP – 10 years of monitoring antimicrobial resistance among indicator bacteria in food animals

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Hendriksen, R. S., Seyfarth, A. M., Pedersen, K., Emborg, H., Wegener, H. C.
Publication date: 2007
Peer-reviewed: No
Event: Abstract from 5th International Conference on Emerging Infectious Diseases, Atlanta, GA, United States.
Source: orbit
Source-ID: 239768
Research output: Research - peer-review › Journal article – Annual report year: 2007

Den mulige selektion af antibiotikaresistens ved anvendelse af desinfektionsmidler til kyllinger

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2007

**Publication information**
Publisher: DG Sanco
Original language: Danish
Source: orbit
Source-ID: 236546
Research output: Research › Conference abstract for conference – Annual report year: 2007

ESBL's, foods and cephalosporin use in food animals

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Collignon, P., Aarestrup, F. M.
Pages: 1391-1392
Publication date: 2007
Peer-reviewed: Yes

**Publication information**
Journal: Clinical Infectious Diseases
Volume: 44
ISSN (Print): 1058-4838
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 5.42 SJR 5.051 SNIP 2.795
Web of Science (2017): Impact factor 9.117
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.88 SJR 4.614 SNIP 2.56
Web of Science (2016): Impact factor 8.216
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 5.47 SJR 4.827 SNIP 3.001
ESBL’s, foods and cephalosporin use in food animals

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Collignon, P., Aarestrup, F. M.
Pages: 1632-1639
Publication date: 2007
Peer-reviewed: Yes

Publication information
Extended-spectrum beta-lactamases, food, and cephalosporin use in food animals

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Collignon, P., Aarestrup, F. M.
Pages: 1391-1392
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: Clinical Infectious Diseases
Volume: 44
Issue number: 10
ISSN (Print): 1058-4838
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 5.42 SJR 5.051 SNIP 2.795
Web of Science (2017): Impact factor 9.117
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.88 SJR 4.614 SNIP 2.56
Web of Science (2016): Impact factor 8.216
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 5.47 SJR 4.827 SNIP 3.001
Web of Science (2015): Impact factor 8.736
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 6.11 SJR 5.258 SNIP 3.415
Web of Science (2014): Impact factor 8.886
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 6.37 SJR 4.751 SNIP 3.298
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 6.25 SJR 4.573 SNIP 3.193
Web of Science (2012): Impact factor 9.374
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 6.09 SJR 4.292 SNIP 3.233
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 4.05 SNIP 3.129
First Cases Of Infection With Escherichia Coli Containing Plasmid Mediated Quinolone Resistance (qnrA and qnrS) In Scandinavia

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Cavaco, L., Hansen, D. S., Aarestrup, F. M., Frimodt-Møller, N.
Publication date: 2007
Peer-reviewed: No
Event: Poster session presented at The 17th ECCMID, Munich,
Source: orbit
Source-ID: 214353
Research output: Research › peer-review › Journal article – Annual report year: 2007

First detection of plasmid-mediated quinolone resistance (qnrA and qnrS) in Escherichia coli strains isolated from humans in Scandinavia

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Cavaco, L., Hansen, D., Friis-Møller, A., Aarestrup, F. M., Hasman, H., Frimodt-Møller, N.
Pages: 804-805
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: Journal of Antimicrobial Chemotherapy
Volume: 59
Issue number: 4
ISSN (Print): 0305-7453
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
First detection of transmissible quinolone resistance genes in Escherichia coli isolates from humans in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Cavaco, L., Hansen, D., Friis-Møller, A., Aarestrup, F. M., Hasman, H., Frimodt-Møller, N.
Publication date: 2007

Host publication information
Title of host publication: DANMAP 2006: Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, foods and humans in Denmark
Source: orbit
Source-ID: 244448
Research output: Research › Book chapter – Annual report year: 2007

Fødevaresikkerhed skal løses globalt

General information
State: Published
Organisations: Division of Food Production Engineering, National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Jørgensen, S. B. (ed.), Aarestrup, F. M.
Publication date: 2007
Peer-reviewed: Unknown

Publication information
Journal: FoodDTU Midt i Ugen
Original language: Danish
Source: orbit
Source-ID: 258723
Research output: Communication › Journal article – Annual report year: 2007

International spread of multidrug-resistant Salmonella Schwarzengrund in food products
We compared 581 Salmonella enterica serotype Schwarzengrund isolates from persons, food, and food animals in Denmark, Thailand, and the United States by antimicrobial drug susceptibility and pulsed-field gel electrophoresis (PFGE) typing. Resistance, including resistance to nalidixic acid, was frequent among isolates from persons and chickens in Thailand, persons in the United States, and food imported from Thailand to Denmark and the United States. A total of 183 PFGE patterns were observed, and 136 (23.4%) isolates had the 3 most common patterns. Seven of 14 isolates from persons in Denmark had patterns found in persons and chicken meat in Thailand; 22 of 390 human isolates from the United States had patterns found in Denmark and Thailand. This study suggests spread of multidrug-resistant S. Schwarzengrund from chickens to persons in Thailand, and from imported Thai food products to persons in Denmark and the United States.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 726-731
Publication date: 2007
Peer-reviewed: Yes
IS21-558 insertion sequences are involved in the mobility of the multiresistance gene cfr

During a study of florfenicol-resistant porcine staphylococci from Denmark, the genes cfr and fexA were detected in the chromosomal DNA or on plasmids of Staphylococcus hyicus, Staphylococcus warneri, and Staphylococcus simulans. A novel variant of the phenicol resistance transposon Tn558 was detected on the ca. 43-kb plasmid pSCFS6 in S. warneri and S. simulans isolates. Sequence analysis of a 22,010-bp segment revealed that the new Tn558 variant harbored an additional resistance gene region integrated into the tnpC reading frame. This resistance gene region consisted of the clindamycin exporter gene lsa(B) and the gene cfr for combined resistance to phenicols, lincosamides, oxazolidinones, pleuromutilins, and streptogramin A antibiotics bracketed by IS21-558 insertion sequences orientated in the same direction. A 6-bp target site duplication was detected at the integration site within tnpC. Transpositionally active forms of the IS21-558 element, known as minicircles, were detected by PCR and suggest that this insertion sequence is involved in the mobility of the multiresistance gene cfr. Based on the knowledge of the transposition pathways of IS21-like insertion sequences and the sequence features detected, the resistance gene region of plasmid pSCFS6 is believed to have developed via IS21-558-mediated cointegrate formation. The data obtained in this study identified the multiresistance gene cfr not only in three novel host species but also in a novel genetic context whose further analysis suggested that insertion sequences of the type IS21-558 are likely to be involved in the dissemination of cfr.
Methicillin-resistant Staphylococcus aureus in animals

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2007
Peer-reviewed: Yes

Methods for testing Salmonella and campylobacter

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., McDermott, P. F.
Publication date: 2007
Peer-reviewed: Yes

Molecular characterisation of multidrug-resistant Salmonella enterica serovar Typhimurium isolates from Gomel region, Belarus

This study describes the characterisation by pulsed-field gel electrophoresis (PFGE), multilocus variable number tandem repeat analysis (MLVA) typing and antimicrobial resistance profiles of 35 Salmonella enterica serovar Typhimurium isolates, mostly from infections in children who acquired an infection outside hospitals in the Gomel region of Belarus. Thirty-one isolates were highly similar according to PFGE and MLVA typing, were multidrug-resistant, including resistance to ceftiofur, and harboured the bla(CTX-M-5) gene. These results indicate that a common source may have been responsible for most of the infections.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, National Veterinary Institute
Contributors: Tapalski, D., Hendriksen, R. S., Hasman, H., Ahrens, P., Aarestrup, F. M.
Pages: 1030-1033
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: Clinical Microbiology and Infection
Volume: 13
Issue number: 10
ISSN (Print): 1198-743X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.57 SJR 2.569 SNIP 1.854
Web of Science (2017): Impact factor 5.394
Web of Science (2017): Indexed yes
Nucleoside analogues are activated by bacterial deoxyribonucleoside kinases in a species-specific manner

To investigate the bactericidal activity of antiviral and anticancer nucleoside analogues against a variety of pathogenic bacteria and characterize the activating enzymes, deoxyribonucleoside kinases (dNKs). Several FDA-approved nucleoside analogue drugs were screened for their potential bactericidal activity against several clinical bacterial isolates and type strains. We identified and subcloned the genes coding for putative deoxyribonucleoside kinases in Escherichia coli, Pasteurella multocida, Salmonella enterica, Yersinia enterocolitica, Bacillus cereus, Clostridium perfringens and Listeria monocytogenes. These genes were tested for their ability to increase the susceptibility of a dNK-deficient E. coli strain to various analogues. We overexpressed, purified and characterized the substrate specificity and kinetic properties of the recombinant enzymes from S. enterica and B. cereus. The tested Gram-negative bacteria were susceptible to 3″-azido-3″-deoxythymidine (AZT) in the concentration range 0.032-31.6 µM except for a single E. coli isolate and two Pseudomonas aeruginosa isolates which were resistant to the tested AZT concentrations. Purified recombinant S. enterica thymidine kinase phosphorylated AZT efficiently with a Km of 73.3 µM and kcat/Km of 6.6 × 10^4 s⁻¹ M⁻¹ and is the activator of this drug in vivo. 2″,2″-Difluoro-2″-deoxycytidine (gemcitabine) was a potent antibiotic against Gram-positive bacteria in the concentration range between 0.001 and 1.0 µM. The B. cereus deoxyadenosine kinase had a Km for gemcitabine of 33.5 µM and kcat/Km of 5.1 × 10^3 s⁻¹ M⁻¹ and activates gemcitabine in vivo. S. enterica and B. cereus are now amongst the first bacteria with a completely characterized set of dNK enzymes. Bacterial dNKs efficiently activate nucleoside analogues in a species-specific manner. Therefore, nucleoside analogues have a potential to be employed as antibiotics in the fight against emerging multiresistant bacteria.
Oxytetracyclin overskridelse af ADI

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2007

Publication information
Publisher: Fødevarestyrelsen
Original language: Danish
Source: orbit
Source-ID: 215379
Research output: Research › Report – Annual report year: 2007
Plasmid-mediated quinolone resistance determinant qnrS1 detected in Salmonella enterica serovar Corvallis strains isolated in Denmark and Thailand

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Cavaco, L., Hendriksen, R. S., Aarestrup, F. M.
Pages: 704-706
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: Journal of Antimicrobial Chemotherapy
Volume: 60
Issue number: 3
ISSN (Print): 0305-7453
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.34 SJR 2.419 SNIP 1.568
Web of Science (2017): Impact factor 5.217
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Impact factor 5.071
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.06 SJR 2.259 SNIP 1.516
Web of Science (2015): Impact factor 4.919
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.61 SJR 2.298 SNIP 1.765
Web of Science (2014): Impact factor 5.313
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.7 SJR 2.479 SNIP 1.824
Web of Science (2013): Impact factor 5.439
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.35 SJR 2.283 SNIP 1.718
Web of Science (2012): Impact factor 5.338
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.24 SJR 2.341 SNIP 1.769
Web of Science (2011): Impact factor 5.068
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.161 SNIP 1.643
Web of Science (2010): Impact factor 4.659
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Prevalence and antibiotic resistance of Salmonella isolated from a poultry farm and processing plant environment in the state of Kuwait

The prevalence of Salmonella isolated from a poultry farm and from the poultry processing plant environment were evaluated from August 2004 to July 2005 along with microbial antibiotic resistance. In total, 3242 samples were collected from the farm and processing plant. Samples collected from the farm included hatching eggs, paper liners, litter, feed, water, drinkers, air, bird rinse, and ceca. While samples collected from the processing plant included carcass rinse and ceca. Out of 2882 samples collected from the farm, the overall percentage prevalence of Salmonella was 5.4% with prevalence rates of 10%, 1.5%, 0.7%, 0.2%, 13.5%, and 12.6% for hatching eggs, litter, feed, drinkers, bird rinse and ceca, respectively. No Salmonella were detected in any of the paper liner, water, or air samples. Out of 360 samples collected from the processing plant, the overall percentage prevalence of Salmonella was 4.7% with prevalence rates of 6.1% and 3.3% for carcass rinse and ceca samples, respectively. Salmonella Enteritidis was the most prevalent serotype. All of the isolates were resistant to at least one antibiotic and 10 different resistance profiles were found among 173 isolates of Salmonella Enteritidis. Resistance to ampicillin, nalidixic acid, and tetracycline were the most common. The widespread occurrence of multiple resistant Salmonella Enteritidis is a cause for concern, and local regulatory enforcement agencies should ensure prudent use of antibiotics.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 367-373
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: Foodborne Pathogens and Disease
Volume: 4
Issue number: 3
ISSN (Print): 1535-3141
Ratings:
BFI (2018): BFI-level 1
Proposal for a baseline monitoring of methicillin resistant Staphylococcus aureus in the EU

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Relativ klassifikation af veterinære antibiotika

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2007

Ringtesten for identifikation og resistensbestemmelse af mastitispatogener

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Aarestrup, F. M., Krogh, K.
Publication date: 2007

Ringtesten for identifikation og resistensbestemmelse af mastitispatogener 2007

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Contributors: Hendriksen, R. S., Aarestrup, F. M., Krogh, K.
Number of pages: 11
Publication date: 2007

Salmonella krefeld isolates in Serbia

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Grego, E., Galic, N., Hendriksen, R. S., Aarestrup, F. M.
Publication date: 2007
Peer-reviewed: No
Short report on the assessment of risks posed by use of disinfectants to DG-Sanco

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2007

Publication information
Original language: English
Source: orbit
Source-ID: 247757
Research output: Research › Report – Annual report year: 2007

Ten Years of DANMAP: How Integrated Monitoring Contributed to Combat Antimicrobial Resistance in Denmark

General information
State: Published
Organisations: Department of Microbiology, National Food Institute, Division of Microbiology and Risk Assessment, Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Pages: 1632-1639
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: Emerging Infectious Diseases
Volume: 13
ISSN (Print): 1080-6040
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 4.78 SJR 3.278 SNIP 1.916
Web of Science (2017): Impact factor 7.422
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.92 SJR 3.428 SNIP 2.198
Web of Science (2016): Impact factor 8.222
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.23 SJR 3.101 SNIP 2.012
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.59 SJR 3.509 SNIP 2.406
Web of Science (2014): Impact factor 6.751
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.68 SJR 3.254 SNIP 2.266
Web of Science (2013): Impact factor 7.327
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Tetracycline consumption and occurrence of tetracycline resistance in Salmonella typhimurium phage types from Danish pigs

The aims of the present study were to investigate at the farm-owner level the effect of prescribed tetracycline consumption in pigs and different Salmonella Typhimurium phage types on the probability that the S. Typhimurium was resistant to tetracycline. In this study, 1,307 isolates were included, originating from 877 farm owners, and data were analyzed using logistic regression. The analysis showed that both the S. Typhimurium phage type (p <0.0001) and an increase in tetracycline consumption (p = 0.0007) were significantly associated with tetracycline resistance. In particular, the phage type was strongly associated with tetracycline resistance. A further analysis of data from the Danish Integrated Antimicrobial Resistance Monitoring and Research Programme (DANMAP) indicates that the tetracycline-susceptible phage types only slowly become tetracycline resistant, although tetracycline consumption more than doubled at the national level from 12,000-13,000 kg of active compound in 1996-1998 to 29,000 kg of active compound in 2004. Instead, tetracycline-resistant S. Typhimurium phage types became more prevalent. This suggests that the spread of already established or new resistant clones, rather than conversion of "old" well-established susceptible clones to resistant clones by uptake of resistance genes, explains most of the increased levels of tetracycline resistance in S. Typhimurium in Danish swine production in response to increased tetracycline consumption.

General information
The 1st proficiency testing - 2006 Salmonella and Campylobacter: Community Reference Laboratory – Antimicrobial Resistance

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M.
Number of pages: 102
Publication date: 2007

Publication information
Place of publication: Copenhagen, Denmark
Publisher: National Food Institute
ISBN (Print): 978-87-92158-49-9
Original language: English
URLs:
http://www.crl-ar.eu/203-reports.htm
Source: orbit
Source-ID: 243387
Research output: Research › Report – Annual report year: 2007

The 2nd Proficiency Testing, 2007: – Enterococci, staphylococci and E. coli

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Krause, M., Hendriksen, R. S., Karlsmose, S., Aarestrup, F. M.
Publication date: 2007

Publication information
Publisher: DTU Food
ISBN (Print): 978-87-92158-47-5
Original language: English
URLs:
http://www.crl-ar.eu/203-reports.htm
Source: orbit
Source-ID: 235068
Research output: Research › Report – Annual report year: 2007
The assessment of risks posed by use of disinfectants

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2007

Publication information
Publisher: DG Sanco
Original language: English
Source: Orbit
Source-ID: 236552
Research output: Research › Report – Annual report year: 2007

The attribution of human infections with antimicrobial resistant Salmonella bacteria in Denmark to sources of animal origin

Based on the Danish Salmonella surveillance in 2000-2001, we developed a mathematical model for quantifying the contribution of each major animal-food sources to human salmonellosis caused by antimicrobial resistant bacteria. Domestic food products accounted for 53.1% of all cases, mainly caused by table eggs (37.6%). A large proportion (19%) of cases were travel related, while 18% could not be associated with any source. Imported food products accounted for 9.5% of all cases; the most important source being imported chicken. Multidrug and quinolone resistance was rarely found in cases acquired from Danish food, but was common in cases related to imported products (49.7% and 35.6% of attributable cases) and travelling (26.5% and 38.3% of attributable cases). For most serovars, the quinolone-resistant isolates were found to be associated with relatively more human infections than that of resistant isolates, which in turn was higher than that of susceptible isolates. This may be due to quinolone-resistant isolates having a higher ability to survive food processing and/or cause disease. This study showed domestic food to be the most important source of Salmonella infections in Denmark, but infections with multidrug- and quinolone-resistant isolates were more commonly caused by imported food products and travelling, emphasizing the need for a global perspective on food safety and antimicrobial usage.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hald, T., Lo Fo Wong, D. M. A., Aarestrup, F. M.
Pages: 313-326
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: Foodborne Pathogens and Disease
Volume: 4
Issue number: 3
ISSN (Print): 1535-3141
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.47 SJR 1.063 SNIP 1.016
Web of Science (2017): Impact factor 2.476
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.46 SJR 1.062 SNIP 1.08
Web of Science (2016): Impact factor 2.12
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.41 SJR 1.064 SNIP 1.035
Web of Science (2015): Impact factor 2.27
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.16 SJR 0.953 SNIP 1.051
Web of Science (2014): Impact factor 1.905
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
The External Quality Assurance System of the WHO Global Salm-Surv: Year 2006

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Seyfarth, A. M., Karlsmose, S., Aarestrup, F. M.
Publication date: 2007

Publication information
Place of publication: Copenhagen, Denmark
Publisher: National Food Institute
Original language: English
Source: orbit
Source-ID: 243389
Research output: Research › Report – Annual report year: 2007

The External Quality Assurance System of the WHO Global Salm-Surv Year 2007

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Karlsmose, S., Krause, M., Aarestrup, F. M.
Number of pages: 38
Publication date: 2007
Transferable low-level resistance fluoroquinolone resistance in Enterobacteriaceae - recent developments

Use of Antimicrobials in Food Animal Production

Antibiotic Resistance

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2006

Publication information
Publisher: Teknologirådet
Original language: English
Source: orbit
Source-ID: 236545
Research output: Research › Report – Annual report year: 2006

Antimicrobial consumption and occurrence of resistance in Salmonella Typhimurium from Danish pigs

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Publication date: 2006
Peer-reviewed: No
Event: Abstract from 11th International Symposium on Veterinary Epidemiology and Economics, Cairns, Australia.
Source: orbit
Source-ID: 232423
Research output: Research › Conference abstract for conference – Annual report year: 2006

Anvendelse af antibiotika til dyr – bruger danske dyrlæger for meget eller for lidt?

General Information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Wegener, H. C.
Pages: 19-23
Publication date: 2006
Peer-reviewed: No
Beta-lactamases among Extended spectrum Beta-lactamase resistant (ESBL) Salmonella from poultry, poultry products and human patients in the Netherlands

Objectives: The purpose of this work was to study the genetic determinants responsible for extended-spectrum beta-lactamase (ESBL) resistance of Salmonella isolated from Dutch poultry, poultry meat and hospitalized humans. Methods: Thirty-four ESBL-resistant Salmonella isolates from The Netherlands were tested towards 21 antimicrobial agents. PCR and sequencing were used to determine the underlying genetic determinants responsible for the ESBL phenotypes. The transferability of the ESBL phenotypes was tested by conjugation to a susceptible Salmonella enterica serovar Dublin and plasmid purification, restriction fragment length polymorphism (RFLP) and pulsed-field gel electrophoresis (PFGE) were employed to further characterize a subset of the isolates. Results: A great genetic diversity was seen among the isolates. The bla(TEM-52) gene was most predominant and was found among Salmonella enterica serovars Blockley, Thomson, London, Enteritidis phage type 14b, Paratyphi B, Virchow and Typhimurium phage types 11 and 507. We also found the bla(TEM-20) gene in S. Paratyphi B var. Java and the bla(TEM-63) gene in S. Isangi. Furthermore, we detected the blaCTX-M-28 gene in S. Isangi and the blaCTX-M-3 gene in S. Typhimurium phage type 507. The blaCTX-M-2 gene was identified in S. Virchow, which also contained a copy of the blaSHV-2 gene and a copy of the blaTEM-1 gene. The blaSHV-12 gene was found alone in S. Concord and together with the blaTEM-52 gene in S. Typhimurium. Finally, the blaACC-1 gene was cloned from a S. Bareilly isolate and was found to be present on indistinguishable plasmids in all S. Bareilly isolates examined as well as in a S. Braenderup isolate and a S. Infantis isolate. Conclusions: Our data underscore the diversity of ESBL genes in Salmonella enterica isolated from animals, food products and human patients.
Copper resistance in Enterococcus faecium, mediated by the tcrB gene, is selected by supplementation of pig feed with copper sulfate

The tcr gene cluster mediates in vitro copper resistance in Enterococcus faecium. Here we describe the selection of tcr-mediated copper resistance in E. faecium in an animal feeding experiment with young pigs fed 175 mg copper/kg feed (ppm), which is the concentration commonly used for piglets in European pig production. tcr-mediated copper resistance was not selected for in a control group fed low levels of copper (6 ppm). We also show coselection of macrolide- and glycopeptide-resistant E. faecium in the animal group fed the high level of copper. Finally, we identify the tcr genes in the enterococcal species E. mundtii, E. casseliflavus, and E. gallinarum for the first time.
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.14 SJR 1.891 SNIP 1.308
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.02 SJR 1.857 SNIP 1.384
Web of Science (2014): Impact factor 3.668
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.25 SJR 1.899 SNIP 1.414
Web of Science (2013): Impact factor 3.952
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.29 SJR 1.975 SNIP 1.429
Web of Science (2012): Impact factor 3.678
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 4.12 SJR 1.914 SNIP 1.455
Web of Science (2011): Impact factor 3.829
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.887 SNIP 1.436
Web of Science (2010): Impact factor 3.778
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.972 SNIP 1.528
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 2.156 SNIP 1.572
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.043 SNIP 1.647
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.054 SNIP 1.602
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.074 SNIP 1.653
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.108 SNIP 1.648
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.097 SNIP 1.821
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 2.046 SNIP 1.754
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.989 SNIP 1.736
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.957 SNIP 1.758
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 2.3 SNIP 1.732
Original language: English
Source: orbit
Source-ID: 236693
DANMAP – 10 years of monitoring antimicrobial resistance among indicator bacteria in food animals

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Hendriksen, R. S., Seyfarth, A. M., Pedersen, K., Emborg, H., Wegener, H. C.
Publication date: 2006
Peer-reviewed: No
Event: Poster session presented at 5th International Conference on Emerging Infectious Diseases, Atlanta, GA, United States.
Source: orbit
Source-ID: 236349

Research output: Research - peer-review › Journal article – Annual report year: 2006

dfrA25, a novel trimethoprim resistance gene from Salmonella Agona isolated from a human urine sample in Brazil

Objectives: To describe a novel trimethoprim resistance gene, designated dfrA25, which was detected as a gene cassette within a class 1 integron in Salmonella Agona. Methods: The gene was cloned into Escherichia coli MT102 and resistance to 10 different antimicrobial drugs was measured. A phylogenetic tree was constructed based on representative trimethoprim-resistance-mediating DfrA proteins retrieved from GenBank. Filter-mating experiments and Southern blots of plasmid preparations were performed with the donor and selected transconjugants. Results and conclusions: dfrA25 encodes a dihydrofolate reductase of 157 amino acids with closest identity (85%) to dfrA5 dihydrofolate reductase. dfrA25 was located on a transferable plasmid (similar to 150 kb) that also harboured the tetracycline resistance gene tet(A).

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Agersø, Y., Peirano, G., Aarestrup, F. M.
Pages: 1044-1047
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: Journal of Antimicrobial Chemotherapy
Volume: 58
Issue number: 5
ISSN (Print): 0305-7453
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.34 SJR 2.419 SNIP 1.568
Web of Science (2017): Impact factor 5.217
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Impact factor 5.071
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.06 SJR 2.259 SNIP 1.516
Web of Science (2015): Impact factor 4.919
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.61 SJR 2.298 SNIP 1.765
Web of Science (2014): Impact factor 5.313
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.7 SJR 2.479 SNIP 1.824
Diversity and evolution of blaZ from Staphylococcus aureus and coagulase-negative staphylococci

Objectives: To elucidate the diversity and evolutionary history of plasmid- and chromosomally-located blaZ, to detect indications of frequent exchange of blaZ between human and bovine staphylococci and to estimate the frequency of transfer of blaZ between coagulase-negative staphylococci (CoNS) and Staphylococcus aureus of bovine origin. Methods: blaZ was detected in 143 strains of penicillin-resistant S. aureus and CoNS from five Danish cattle herds (n = 25/23), random CoNS isolates from Denmark (n = 37), a collection of S. aureus from six different countries (n = 52), humans in Denmark (n = 3) and beta-lactamase control strains (n = 3). The sequence was determined in 105 strains and compared to published sequences by pairwise and multiple alignments. Maximum likelihood analysis was performed including bootstrap analysis. Parsimony, neighbour joining and consensus comparisons were performed for recombination. The localization of blaZ was determined by Southern blotting in 108 isolates. Results: All penicillin-resistant strains carried blaZ and showed a similar organization of blaR1 and blaZ. The blaZ gene was localized to a plasmid in only 16 of the resistant strains. Sixty-nine sequences representing 105 isolates and sequences retrieved from public databases were compared. A
phylogenetic tree showed that blaZ exists in three evolutionary lines: one group was of plasmid origin, one group was of chromosomal origin and one intermediate group. Sixty-nine sequence types were demonstrated. They translated into 11 BlaZ protein types. The major types all contained strains of both human and bovine origin, and more than one Staphylococcus species, demonstrating a shared gene pool. In a comparison of S. aureus and CoNS obtained from five Danish cattle herds, the same type of blaZ was only detected in one case. Conclusions: Results indicated a separate evolution for plasmid- and chromosomally-encoded blaZ. Although a common gene pool seems to exist among staphylococci, exchange of blaZ between strains and species is judged to be an extremely rare event.
**External quality assurance system for antibiotic resistance in bacteria of animal origin in Europe (ARBAO-II), 2003**

**General information**
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Wong, D. L. F., Hendriksen, R. S., Mevius, D. J., Veldman, K. T., Aarestrup, F. M.
Pages: 128-139
Publication date: 2006
Peer-reviewed: Yes

**Publication information**
Journal: VETERINARY MICROBIOLOGY
Volume: 115
Issue number: 1-3
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
Web of Science (2010): Impact factor 3.256
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.309 SNIP 1.466
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.164 SNIP 1.29
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.048 SNIP 1.315
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.03 SNIP 1.396
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.089 SNIP 1.259
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.873 SNIP 1.248
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.905 SNIP 1.181
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.905 SNIP 1.13
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.828 SNIP 1.051
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.699 SNIP 1.066
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.714 SNIP 1.089
Original language: English
DOIs:
First description of an oxyimino-cephalosporin-resistant, ESBL-carrying Escherichia coli isolated from meat sold in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Jensen, L. B., Hasman, H., Agersø, Y., Emborg, H., Aarestrup, F. M.
Pages: 793-794
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: JOURNAL OF ANTIMICROBIAL CHEMOTHERAPY
Volume: 57
Issue number: 4
ISSN (Print): 0305-7453
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.34 SJR 2.419 SNIP 1.568
Web of Science (2017): Impact factor 5.217
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Impact factor 5.071
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.06 SJR 2.259 SNIP 1.516
Web of Science (2015): Impact factor 4.919
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.61 SJR 2.298 SNIP 1.765
Web of Science (2014): Impact factor 5.313
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.7 SJR 2.479 SNIP 1.824
Web of Science (2013): Impact factor 5.439
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.35 SJR 2.283 SNIP 1.718
Web of Science (2012): Impact factor 5.338
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.24 SJR 2.341 SNIP 1.769
Web of Science (2011): Impact factor 5.068
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.161 SNIP 1.643
First description of bla(CTX-M-1)-carrying Escherichia coli isolates in Danish primary food production

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Hasman, H., Agersø, Y., Jensen, L. B., Harksen, S., Svensmark, B.
Pages: 1258-1259
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: Journal of Antimicrobial Chemotherapy
Volume: 57
Issue number: 6
ISSN (Print): 0305-7453
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.34 SJR 2.419 SNIP 1.568
Web of Science (2017): Impact factor 5.217
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Impact factor 5.071
Web of Science (2016): Indexed yes
Heterologous expression of glycopeptide resistance vanHAX gene clusters from soil bacteria in Enterococcus faecalis

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hasman, H., Aarestrup, F. M., Dalsgaard, A., Guardabassi, L.
Pages: 648-653
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: JOURNAL OF ANTIMICROBIAL CHEMOTHERAPY
Volume: 57
Issue number: 4
ISSN (Print): 0305-7453
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.34 SJR 2.419 SNIP 1.568
Web of Science (2017): Impact factor 5.217
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Impact factor 5.071
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.06 SJR 2.259 SNIP 1.516
Web of Science (2015): Impact factor 4.919
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.61 SJR 2.298 SNIP 1.765
Web of Science (2014): Impact factor 5.313
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.7 SJR 2.479 SNIP 1.824
Web of Science (2013): Impact factor 5.439
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.35 SJR 2.283 SNIP 1.718
Web of Science (2012): Impact factor 5.338
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.24 SJR 2.341 SNIP 1.769
Web of Science (2011): Impact factor 5.068
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.161 SNIP 1.643
Web of Science (2010): Impact factor 4.659
Identification of the first ESBL (oxyimono-cephalosporin) resistant Escherichia coli isolated from meat sold in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Jensen, L. B., Hasman, H., Emborg, H. D., Aarestrup, F. M.
Pages: 793-794
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: Journal of Antimicrobial Chemotherapy
Volume: 57
ISSN (Print): 0305-7453
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.34 SJR 2.419 SNIP 1.568
Web of Science (2017): Impact factor 5.217
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Impact factor 5.071
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.06 SJR 2.259 SNIP 1.516
Web of Science (2015): Impact factor 4.919
Identification of Tn5397-like and Tn916-like transposons and diversity of the tetracycline resistance gene tet(M) in enterococci from humans, pigs and poultry
Matitis: ringtesten 2006

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Aarestrup, F. M., Krogh, K.
Pages: 20-23
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 18
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Methicillinresistente stafylokokker fra dyr

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Pages: 30-31
Publication date: 2006
Peer-reviewed: No

Publication information
Journal: Dansk Veterinær Tidsskrift
Volume: 89
Issue number: 3
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 236448
Research output: Research › Journal article – Annual report year: 2006

Microbiological and epidemiological aspects of the antibiotic resistance of Typhimurium

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Tapalsky, D. V., Hendriksen, R. S., Aarestrup, F. M.
Pages: 39-39
Publication date: 2006
Peer-reviewed: No

Publication information
Journal: Clinical microbiology and antimicrobic chemotherapy
Volume: 8
Issue number: 2
Original language: Russian
Source: orbit
Source-ID: 236412
Research output: Research › Journal article – Annual report year: 2006

Molecular characterisation of multiple drug resistant Salmonella Typhimurium from Gomel region, Belarus
Molecular characterization and occurrence of extended-spectrum beta-lactamase resistance genes among Salmonella enterica serovar Corvallis from Thailand, Bulgaria and Denmark

Fifty nine Salmonella Corvallis isolates from humans and food products in Bulgaria, Denmark, and Thailand were examined for antimicrobial susceptibility and characterized by pulsed-field gel electrophoresis (PFGE). Cephalosporin-resistant isolates were examined for the presence of genes encoding beta-lactamases by PCR and sequencing. Ten different PFGE types were observed. One type (30 isolates) was recovered in all three countries; three types were found only in Bulgaria, two only in Denmark, two only in Thailand, and two both in Denmark and Thailand. Ten isolates were susceptible to all antimicrobial agents tested, whereas 41 were resistant to three or more antimicrobials. Most resistance was observed among the isolates from Bulgaria. Of the 25 isolates from Bulgaria, 20 displayed resistance to ampicillin and the cephalosporins cefotiofur and cephalothin. All 20 isolates tested negative for bla(CMY-1), bla(CMY-2), and bla(ACC), but positive for bla(SHV), of which five were sequenced to bla(SHV-2). Plasmid profiling and hybridization revealed that the bla(SHV) gene was located on plasmids of approximately 70 kb. Five plasmid profiles were found among these 20 isolates. The plasmid profiling confirmed the PFGE-type and was able to further subdivide the strains. Seventeen of these 20 isolates contained also bla(TEM), of which nine representatives were sequenced to bla(TEM-1B), or bla(TEM-1H). One isolate contained bla(CTX-M-15), bla(SHV-2), and bla(TEM-1H), with the bla(CTX-M-15), and bla(TEM-1H) genes located on a 63-kb transferable plasmid. This study showed a high frequency of resistance among S. Corvallis isolated from humans and food products in Bulgaria, with a lower frequency in Thailand and Denmark. The clonal relatedness among the isolates from three countries could indicate a recent spread of this serovar.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Archambault, M., Petrov, P., Hendriksen, R. S., Asseva, G., Bangtrakulnonth, A., Hasman, H., Aarestrup, F. M.
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: Microbial Drug Resistance
Volume: 12
Issue number: 3
ISSN (Print): 1076-6294
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
Web of Science (2017): Impact factor 2.344
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
Web of Science (2016): Impact factor 2.306
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
Web of Science (2015): Impact factor 2.529
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
Monitoring of antimicrobial resistance in animals: principles and practices

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: McEwan, S. A., Aarestrup, F. M., Jordan, D.
Pages: 397-413
Multidrug resistance among different serotypes of clinical Salmonella isolates in Taiwan

Of the 798 clinical Salmonella isolates collected from multiple hospitals in Taiwan, resistance to ampicillin (48.5%), chloramphenicol (55.3%), streptomycin (59.0%), sulfamethoxazole (68.0%), and tetracycline (67.8%) was high, whereas resistance to all 5 antimicrobials (ACSSuT R-type) comprised 327 (41%) and was highly prevalent in Salmonella enterica serotype Typhimurium (72.7%, 176/242) the most common serotype. Additional resistance to trimethoprim was present in 155 (19.4% overall) of the ACSSuT R-type isolates from several serotypes. Reduced susceptibility to fluoroquinolone (FQ) (ciprofloxacin MIC > 0.125-1 μg/mL and nalidixic acid-resistant) was detected in 223 (27.9%) isolates including 117 (14.7% overall) that were also ACSSuT-resistant. Full resistance to FQ was detected in Salmonella Choleraesuis (35.5%, 6/17) and Salmonella Schwarzengrund (16.7%, 10/60); both serotypes were also multiresistant to other antimicrobials. Studies are needed to determine the sources of different multidrug-resistant serotypes. Continued national surveillance is underway to monitor changes in resistance trends and to detect further emergence of resistant Salmonella serotypes in Taiwan. (c) 2006 Elsevier Inc. All rights reserved.
Occurrence of integrons and antimicrobial resistance genes among Salmonella enterica from Brazil

Objectives: To determine the occurrence of antimicrobial resistance genes and role of integrons among 135 anti microbial-resistant Salmonella enterica from Brazil. Methods: The presence of antimicrobial resistance genes, class 1 and 2 integrons and gene cassettes was analysed by PCR and sequencing. The genetic location of class 1 integrons was determined in 25 isolates by hybridization and plasmid transfer experiments. Results: Fifty-five of the isolates were positive for class I integrons. Integron-positive isolates represented 17 different serovars and were mainly from human (n = 28) and animal (n = 13) sources. The gene cassette arrangements could be determined in 51 of the positive isolates, which harboured one [dfrA22, aadA1 or orf3 (putative trimethoprim resistance)], two [aadA1-dfrA1, aac(6)-lb-orf1 (unknown function) or aacA4-aadA1], three [dfrA15b-cmlA4-aadA2, orf2 (unknown function)-dfrA5-orfD] or four [orf4-
aacA4-bla(OXA-30) (interrupted by an IS1 element)-aadA1] cassettes in their variable region. Only one isolate harboured a class 2 integron with the gene cassette array dfrA1-sat-aadA1. Several integron unrelated resistance genes were also detected in the isolates. Sulphonamide resistance was primarily mediated by sul2 and sul3, tetracycline resistance by tet(B) and tet(A), chloramphenicol resistance by catA1, streptomycin resistance by strA and ampicillin resistance by bla(TEM). bla(CTX) and bla(CMY-2) were found in cephalosporin-resistant isolates. Mating and hybridization experiments demonstrated that a high-molecular-weight plasmid mediated the gene transfer of integrons and additional resistance determinants. Conclusions: The present study revealed that integron-mediated resistance genes contributed to the multiresistance phenotype observed in the isolates, but most resistance genes were located outside the integron structure, as independent genes. However, they might be located on the same conjugative plasmid.
Occurrence of Salmonella, Campylobacter spp. and antimicrobial resistance in imported and Danish poultry meat sold in retail stores in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Agersø, Y., Munkholm, N., Emborg, H., Larsen, P. B., Aarestrup, F. M.
Publication date: 2006
Peer-reviewed: No
Event: Poster session presented at 5th International Conference on Emerging Infectious Diseases, Atlanta, GA, United States.
Source: orbit
Source-ID: 239856
Research output: Research - peer-review › Journal article – Annual report year: 2006

Origin, evolution, and local and global dissemination of antimicrobial resistance

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Aarestrup, F. M. (ed.)
Pages: 339-360
Publication date: 2006

Host publication information
Title of host publication: Antimicrobial resistance in bacteria of animal origin
Overskudsmælk til kalve - godt or not

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Engelbrecht, R., Aarestrup, F. M.
Pages: 6-9
Publication date: 2006
Peer-reviewed: No

Publication information
Journal: Bovologisk
Volume: 20
Issue number: 11
ISSN (Print): 0906-009X
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: orbit
Source-ID: 236413
Research output: Research › Journal article – Annual report year: 2006

Pheno- and genotyping of Staphylococcus epidermidis isolated from bovine milk and human skin
The purpose of this study was to improve our knowledge concerning the epidemiology and strain diversity of Staphylococcus epidermidis isolated from bovine milk in commercial dairy herds. A total of 341 S. epidermidis isolates obtained from cows' milk (317), farmers (17) and patients (7) were characterized. Of these 105 isolates were from cows' milk in two farms, where also 17 isolates were sampled from farmers. The remaining 212 isolates from cows' milk were from 170 farms. All isolates were examined by antimicrobial susceptibility, whereas 202 were examined by pulsed-field gel electrophoresis (PFGE) and 122 by ribotyping. PFGE showed single patterns in the human strains with one exception; one strain was categorised as the same clone as four of the milk strains. PFGE divided 73 of the milk strains into 62 different patterns. The PFGE method had high discriminatory power and shows that many different S. epidermidis types exist in milk samples. Antibiotic resistance patterns matched the SmaI profiles closely in the two herds, but poorly in the routinely collected milk samples. Isolates from herd 1 showed one to five patterns, depending on the typing method used. Isolates from the milker's skin showed one pattern, which was identical to the most common pattern found in the milk isolates. Isolates from herd 2 showed three to four patterns, two of these being identical to skin isolates from the milker. As dairy cows are not a natural host for S. epidermidis the results suggest a human source of these udder infections. (c) 2006 Elsevier B.V. All rights reserved.
Priorities for antibiotic resistance surveillance in Europe
Antibiotic resistance is an increasing global problem. Surveillance studies are needed to monitor resistance development, to guide local empirical therapy, and to implement timely and adequate countermeasures. To achieve this, surveillance studies must have standardised methodologies, be longitudinal, and cover a sufficiently large and representative population. However, many fall short of these requirements that define good surveillance studies. Moreover, current efforts are dispersed among many, mostly small, initiatives with different objectives. These studies must be tailored to the various reservoirs of antibiotic-resistant bacteria, such as hospitalised patients, nursing homes, the community, animals and food. Two studies that could serve as examples of tailored programmes are the European Antimicrobial Resistance Surveillance System (EARSS), which collects resistance data during the diagnosis of hospitalised patients, and the DANMAP programme, which collects data in the veterinary sector. As already noted by the WHO, genetic studies that include both the typing of isolates and the characterisation of resistance determinants are necessary to understand fully the spread and development of antibiotic resistance.
Quality-control ranges for antimicrobial susceptibility testing by broth dilution of the Brachyspira hyodysenteriae type strain (ATCC 27164(T))

There are no approved standards for antimicrobial susceptibility testing of the fastidious spirochete Brachyspira hyodysenteriae. An interlaboratory study was performed to establish MIC quality control ranges for six antimicrobial agents for the type strain of B. hyodysenteriae using broth dilution. The results showed that B. hyodysenteriae B78(T) ATCC 27164(T) is a suitable quality control strain. This is a first step toward standardization of methods regarding this anaerobe.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 219-221
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: MICROBIAL DRUG RESISTANCE
Volume: 12
Issue number: 3
ISSN (Print): 1076-6294
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
Web of Science (2017): Impact factor 2.344
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
Web of Science (2016): Impact factor 2.306
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
Web of Science (2015): Impact factor 2.529
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
Web of Science (2014): Impact factor 2.49
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.87 SJR 1.265 SNIP 1.118
Web of Science (2013): Impact factor 2.524
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.45 SJR 0.963 SNIP 0.9
Web of Science (2012): Impact factor 2.364
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.76 SJR 1.163 SNIP 1.14
Web of Science (2011): Impact factor 2.153
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.054 SNIP 0.8
Web of Science (2010): Impact factor 1.936
Web of Science (2010): Indexed yes
Resistance to penicillin of Staphylococcus aureus isolates from cows with high somatic cell counts in organic and conventional dairy herds in Denmark

Background: Quarter milk samples from cows with high risk of intramammary infection were examined to determine the prevalence of Staphylococcus aureus (SA) and penicillin resistant SA (SAr) in conventional and organic dairy herds and herds converting to organic farming in a combined longitudinal and cross-sectional study. Methods: 20 conventional herds, 18 organic herds that converted before 1995, and 19 herds converting to organic farming in 1999 or 2000 were included in the study. Herds converting to organic farming were sampled three times one year apart; the other herds were sampled once. Risk of infection was estimated based on somatic cell count, milk production, breed, age and lactation stage. Results: The high-risk cows represented about 49% of the cows in the herds. The overall prevalence of SA and SAr among these cows was 29% (95% confidence interval: 24%-34%) and 4% (95% confidence interval: 2%-5%) respectively. The prevalence of penicillin resistance among SA infected cows was 12% (95% confidence interval: 6%-19%) when calculated from the first herd visits. No statistically significant differences were observed in the prevalence of SAr or the proportion of isolates resistant to penicillin between herd groups. Conclusion: The proportion of isolates resistant to penicillin was low compared to studies in other countries except Norway and Sweden. Based on the low prevalence of penicillin resistance of SA, penicillin should still be the first choice of antimicrobial agent for treatment of bovine intramammary infection in Denmark.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Bennedsgaard, T. W., Thamsborg, S. M., Aarestrup, F. M., Enevoldsen, C., Vaarst, M., Christoffersen, A.
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: Acta Veterinaria Scandinavica
Volume: 48
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Impact factor 1.472
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.98 SJR 0.644 SNIP 1.641
Web of Science (2015): Impact factor 1.23
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.54 SJR 0.753 SNIP 1.21
Web of Science (2014): Impact factor 1.377
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.41 SJR 0.539 SNIP 1.11
Web of Science (2013): Impact factor 1.382
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.26 SJR 0.591 SNIP 0.789
Web of Science (2012): Impact factor 1.345
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 1.42 SJR 0.664 SNIP 0.997
Web of Science (2011): Impact factor 1.367
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.551 SNIP 1.005
Web of Science (2010): Impact factor 1.196
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.409 SNIP 0.716
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.338 SNIP 0.588
Scopus rating (2007): SJR 0.207 SNIP 1.86
Scopus rating (2006): SJR 0.184 SNIP 0.963
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.131 SNIP 0.191
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.114 SNIP 0
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.214 SNIP 0
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.486 SNIP 0.454
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.318 SNIP 0.757
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.015 SNIP 0.912
Web of Science (2000): Indexed yes
Ringtest for identifikation og resistensbestemmelse af mastitispagogener 2006

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Aarestrup, F. M., Krogh, K.
Number of pages: 12
Publication date: 2006

Publication information
ISBN (Print): 978-87-92158-55-0
Original language: English
Source: orbit
Source-ID: 271029
Research output: Research - peer-review › Report – Annual report year: 2006

Ringtest for identifikation og resistensbestemmelse af mastitispagogener - 2006

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Aarestrup, F. M., Krogh, K.
Pages: 20-23
Publication date: 2006
Peer-reviewed: No

Publication information
Journal: Dansk Veterinær Tidsskrift
Volume: 89
Issue number: 18
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 236450
Research output: Research › Journal article – Annual report year: 2006

Salmonella lamphun: first isolation of a new Salmonella serovar in Thailand
Staphylococci and streptococci

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Schwarz, S., Aarestrup, F. M. (ed.)
Pages: 187-206
Publication date: 2006

Host publication information
Title of host publication: Antimicrobial resistance in bacteria of animal origin
Place of publication: Washington DC, USA
Publisher: ASM Press
Research output: Research - peer-review › Book chapter – Annual report year: 2006

Ten years of integrated monitoring of antimicrobial resistance in Denmark – what have we learnt about foodborne zoonoses?

General information
State: Published
Organisations: Communications and Management Secretariat, National Food Institute, Division of Microbiology and Risk Assessment, Department of Microbiology
Publication date: 2006
Peer-reviewed: No
Event: Poster session presented at 5th International Conference on Emerging Infectious Diseases, Atlanta, GA, United States.
Source: orbit
Research output: Research › Poster – Annual report year: 2006

Ten years of integrated monitoring of antimicrobial resistance in Denmark – what have we learnt about food borne Zoonoses?

General information
State: Published
Organisations: Communications and Management Secretariat, National Food Institute, Division of Microbiology and Risk Assessment
Publication date: 2006
Peer-reviewed: No
Event: Abstract from 5th International Conference on Emerging Infectious Diseases, Atlanta, GA, United States.
Source: orbit
Research output: Research › Conference abstract for conference – Annual report year: 2006

Tetracycline consumption and occurrence of tetracycline resistance in Salmonella Typhimurium from Danish pigs

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Number of pages: 284
Training risk assessment in non-human antimicrobials usage (TRAINAU) in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Publication date: 2006
Peer-reviewed: No
Event: Poster session presented at 11th International Society for Veterinary Epidemiology and Economics, Cairns, Australia.
Source: orbit
Source-ID: 239857
Research output: Research › Poster – Annual report year: 2006

Use of fluoroquinolones in food-producing animals in the European Union: development of resistance and impact on human and animal health: Discussion paper from the Scientific Advisory Group on Antimicrobials (SAGAM)

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M. (ed.)
Publication date: 2006

Worldwide Networking on Proficiency Testing of Salmonella - Five Years of WHO Global Salm-Surv

General information
State: Published
beta-Lactamases among extended-spectrum beta-lactamase (ESBL)-resistant Salmonella from poultry, poultry products and human patients in The Netherlands

Objectives: The purpose of this work was to study the genetic determinants responsible for extended-spectrum beta-lactamase (ESBL) resistance of Salmonella isolated from Dutch poultry, poultry meat and hospitalized humans. Methods: Thirty-four ESBL-resistant Salmonella isolates from The Netherlands were tested towards 21 antimicrobial agents. PCR and sequencing were used to determine the underlying genetic determinants responsible for the ESBL phenotypes. The transferability of the ESBL phenotypes was tested by conjugation to a susceptible Salmonella enterica serovar Dublin and plasmid purification, restriction fragment length polymorphism (RFLP) and pulsed-field gel electrophoresis (PFGE) were employed to further characterize a subset of the isolates. Results: A great genetic diversity was seen among the isolates. The bla(TEM-52) gene was most predominant and was found among Salmonella enterica serovars Blockley, Thomson, London, Enteritidis phage type 14b, Paratyphi B, Virchow and Typhimurium phage types 11 and 507. We also found the bla(TEM-20) gene in S. Paratyphi B var. Java and the bla(TEM-63) gene in S. Isangi. Furthermore, we detected the bla(CTX-M-28) gene in S. Isangi and the bla(CTX-M-3) gene in S. Typhimurium phage type 507. The bla(CTX-M-2) gene was identified in S. Virchow, which also contained a copy of the bla(SHV-2) gene and a copy of the bla(TEM-1) gene. The bla(SHV-12) gene was found alone in S. Concord and together with the bla(TEM-52) gene in S. Typhimurium. Finally, the bla(ACC-1) gene was cloned from a S. Bareilly isolate and was found to be present on indistinguishable plasmids in all S. Bareilly isolates examined as well as in a S. Braenderup isolate and a S. Infantis isolate. Conclusions: Our data underscore the diversity of ESBL genes in Salmonella enterica isolated from animals, food products and human patients.
Campylobacter concisus: an evaluation of certain phenotypic and genotypic characteristics

The clinical relevance of Campylobacter concisus in gastrointestinal disease has not been determined definitively. This study investigated the phenotypic and genotypic characteristics of 39 C. concisus isolates from Danish patients with diarrhoea, three isolates from healthy individuals and the type strain. A cytolethal distending toxin (CDT)-like effect on Vero cells was observed in 35 (90%) isolates from patients with diarrhoea, in all three isolates from healthy individuals and in the type strain. Analysis of SDS-PAGE protein profiles and PCR amplification of 23S rDNA assigned the isolates into two distinct, but discordant groups. Automated ribotyping (RiboPrinting) identified 34 distinct patterns among the 43 isolates, but cluster analysis did not separate isolates from patients with diarrhoea from isolates from healthy patients. Random amplified polymorphic DNA (RAPD) analysis with three primers identified 37 unique profiles, but requires further evaluation. The isolates obtained from healthy carriers were distinguished by cluster analysis from the isolates obtained from patients with diarrhoea. All the isolates were susceptible to 11 antimicrobial agents tested. Overall, there was considerable variability between the C. concisus isolates, but there were no clear phenotypic or genotypic differences between isolates from patients with diarrhoea and isolates from healthy carriers. Further evidence is needed to support the possible role of C. concisus as a human enteric pathogen.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Engberg, J., Bang, D. D., Aabenhus, R., Aarestrup, F. M., Fussing, V., Gerner-Smidt, P.
Pages: 288-295
Publication date: 2005
Peer-reviewed: Yes

Publication information
Journal: CLINICAL MICROBIOLOGY AND INFECTION
Volume: 11
Issue number: 4
ISSN (Print): 1198-743X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.57 SJR 2.569 SNIP 1.854
Web of Science (2017): Impact factor 5.394
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.99 SJR 2.424 SNIP 1.757
Web of Science (2016): Impact factor 5.292
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 5.11 SJR 2.637 SNIP 1.996
Web of Science (2015): Impact factor 4.575
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 5.49 SJR 2.73 SNIP 2.22
Web of Science (2014): Impact factor 5.768
Diversity and stability of Plasmids from glycopeptide-resistant Enterococcus faecium (GRE) isolated from pigs in Denmark

In this paper, we examine the plasmid variation between a subset of unrelated GRE isolated from pigs in Denmark between 1995 and 2001 (five from each of the years). The isolates were tested with PFGE, plasmid RFLP, and subsequently Southern blotting with an IS1216V probe. Of the 35 isolates, 31 belonged to the same PFGE type (type I), and the last four belonged to a completely different PFGE type (type II). All 35 isolates contained the same type of large plasmid (approximate size of 150-200 kb), which could be divided into eight different variant types (V0 to V7). Most variance among the plasmid was seen at the end of the 7-year period, coinciding with the ban in 1998 of the macrolide tylosin as growth promoter for pig production. The stability of the plasmid in its original host was compared with stability of the same plasmid in BM4105RF, when both strains were maintained in liquid cultures without the presence of antibiotics for 1,100 generations. Here, the plasmid proved far more stable in its original host environment than in the new host.

General information
Diversity and stability of plasmids from glycopeptide resistant Enterococcus faecium isolated from pigs in Denmark

In this paper, we examine the plasmid variation between a subset of unrelated GRE isolated from pigs in Denmark between 1995 and 2001 (five from each of the years). The isolates were tested with PFGE, plasmid RFLP, and subsequently Southern blotting with an IS1216V probe. Of the 35 isolates, 31 belonged to the same PFGE type (type I), and the last four belonged to a completely different PFGE type (type II). All 35 isolates contained the same type of large plasmid (approximate size of 150-200 kb), which could be divided into eight different variant types (V0 to V7). Most variance among the plasmid was seen at the end of the 7-year period, coinciding with the ban in 1998 of the macrolide tylosin as growth promoter for pig production. The stability of the plasmid in its original host was compared with stability of the same plasmid in BM4105RF, when both strains were maintained in liquid cultures without the presence of antibiotics for 1,100 generations. Here, the plasmid proved far more stable in its original host environment than in the new host.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hasman, H., Villadsen, A. G., Aarestrup, F. M.
Pages: 178-184
Publication date: 2005
Peer-reviewed: Yes

Publication information
Journal: MICROBIAL DRUG RESISTANCE
Volume: 11
Issue number: 2
ISSN (Print): 1076-6294
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
Web of Science (2017): Impact factor 2.344
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
Web of Science (2016): Impact factor 2.306
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
Web of Science (2015): Impact factor 2.529
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
Diversity of the tetracycline resistance genes tet(M) and identification of Tn5397-like transposons in enterococci isolated from humans, pigs and poultry in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Agersø, Y., Petersen, A. G., Aarestrup, F. M.
Pages: 832-839
Publication date: 2005
Occurrence of integrons and resistance genes among sulphonamide-resistant Shigella spp. from Brazil

Objectives: To determine the occurrence of class 1 and 2 integrons and antimicrobial resistance genes among sulphonamide-resistant Shigella strains isolated in Brazil during 1999-2003. Methods: Sixty-two Shigella (Shigella flexneri, n = 47 and Shigella sonnei, n = 15) were tested against 21 antimicrobial agents. The presence of integrons classes 1 and 2 and antimicrobial resistance genes was investigated by PCR using specific primers. Results: A total of eight antimicrobial resistance profiles were identified, with the profile of resistance to sulfamethoxazole, trimethoprim, spectinomycin, streptomycin and tetracycline being the most common among S. sonnei, and additionally to ampicillin and chloramphenicol among S. flexneri. Class 1 integrons were found in only two strains, whereas class 2 integrons were found in 56 (90.3%) of the strains. All class 2-positive strains had a similar fragment of 2214 bp harbouring a gene cassette array conferring resistance to trimethoprim, streptomycin and spectinomycin/streptomycin. The genes coding for resistance to chloramphenicol (catA1), tetracycline [tet(A) and tet(B)] and ampicillin (bla(OXA) and bla(TEM)), were detected in resistant strains. Conclusions: The detection of class 1 and 2 integrons and additional antimicrobial resistance genes allowed us to identify the most frequent antimicrobial resistance patterns of Shigella spp. isolated in Brazil.
Regulation of the erm(C) gene in staphylococci from reservoir with different usage of macrolides
Relationship between copper, glycopeptide, and macrolide resistance among Enterococcus faecium strains isolated from pigs in Denmark between 1997 and 2003

A significant relationship between copper resistance (tcrB), glycopeptide resistance (Tn1546), and macrolide resistance [erm(B)] in Enterococcus faecium isolated from pigs was found. The tcrB gene was located closely upstream of the Tn1546 element. However, the continued use of copper sulfate has not been able to maintain high levels of macrolide and glycopeptide resistance.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hasman, H., Aarestrup, F. M.
Pages: 454-456
Publication date: 2005
Peer-reviewed: Yes

Publication information
Journal: Antimicrobial Agents and Chemotherapy
Volume: 49
Issue number: 1
ISSN (Print): 0066-4804
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.15 SJR 2.291 SNIP 1.263
Web of Science (2017): Impact factor 4.255
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.45 SJR 2.361 SNIP 1.428
Web of Science (2014): Impact factor 4.476
Resistant Salmonella virchow in quail products

General information

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Hasman, H., Jensen, L. B.
Pages: 1984-1985
Publication date: 2005
Ringtest for identifikation og resistensbestemmelse af mastitispatogener

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Aarestrup, F. M., Krogh, K.
Pages: 22-23
Publication date: 2005
Peer-reviewed: No

Publication information
Journal: Dansk Veterinær Tidsskrift
Volume: 88
Issue number: 18
ISSN (Print): 0106-6854

Ringtest for identifikation og resistensbestemmelse af mastitispatogener: Evalueringsrapport – den første ringtest

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hendriksen, R. S., Aarestrup, F. M., Krogh, K.
Veterinary drug usage and antimicrobial resistance in bacteria of animal origin

In the production of food animals, large amounts of antimicrobial agents are used for therapy and prophylaxis of bacterial infections and in feed to promote growth. There are large variations in the amounts of antimicrobial agents used to produce the same amount of meat among the different European countries, which leaves room for considerable reductions in some countries. The emergence of resistant bacteria and resistance genes due to the use of antimicrobial agents are well documented. In Denmark it has been possible to reduce the usage of antimicrobial agents for food animals significantly and in general decreases in resistance have followed. Guidelines for prudent use of antimicrobial agents may help to slow down the selection for resistance and should be based on knowledge regarding the normal susceptibility patterns of the causative agents and take into account the potential problems for human health. Current knowledge regarding the occurrence of antimicrobial resistance in food animals, the quantitative impact of the use of different antimicrobial agents on selection of resistance and the most appropriate treatment regimes to limit the development of resistance is incomplete. Programmes monitoring the occurrence and development of resistance and consumption of antimicrobial agents are strongly desirable, as is research into the most appropriate ways to use antimicrobial agents in veterinary medicine.
Voluntary withdrawal of imported quail products from the Danish market following the found of quinolone and cephalosporin resistant Salmonella enterica serovar Virchow

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Hasman, H., Jensen, L. B.
Pages: 1984-5
Publication date: 2005
Peer-reviewed: Yes

Publication information
Journal: Emerging Infectious Diseases
Volume: 11
ISSN (Print): 1080-6040
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 4.78 SJR 3.278 SNIP 1.916
Web of Science (2017): Impact factor 7.422
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.92 SJR 3.428 SNIP 2.198
Web of Science (2016): Impact factor 8.222
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.23 SJR 3.101 SNIP 2.012
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.59 SJR 3.509 SNIP 2.406
Web of Science (2014): Impact factor 6.751
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.68 SJR 3.254 SNIP 2.266
Web of Science (2013): Impact factor 7.327
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.25 SJR 2.858 SNIP 2.131
Web of Science (2012): Impact factor 5.993
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 4.46 SJR 2.785 SNIP 2.19
Web of Science (2011): Impact factor 6.169
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.021 SNIP 2.319
Web of Science (2010): Impact factor 6.859
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.168 SNIP 2.701
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.231 SNIP 2.277
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.709 SNIP 2.341
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.879 SNIP 2.345
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.816 SNIP 2.297
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.683 SNIP 2.562
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.267 SNIP 2.373
Web of Science (2003): Indexed yes
Antimicrobial susceptibility of Haemophilus parasuis and Histophilus somni from pigs and cattle in Denmark

A total of 52 Haemophilus parasuis and 80 Histophilus somni isolates were tested for antimicrobial susceptibility by MIC-determinations. None of the isolates were resistant to ampicillin, ceftiofur, ciprofloxacin, erythromycin, florphenicol, penicillin, spectinomycin, tetracycline, tiamulin, or tilmicosin. Two H. parasuis isolates were resistant to trimethoprim + sulfamethoxazole. Six H. parasuis isolates had reduced susceptibility (0.06-0.5 μg/ml) to ciprofloxacin and 10 reduced susceptibility to TMP + sulfamethoxazole (1-2 μg/ml). This study showed that Danish isolates of H. parasuis and H. somni in general are fully susceptible to antimicrobial agents currently used for treatment of infections with these pathogens. (C) 2004 Elsevier B.V. All rights reserved.
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**Antibiotic resistance in bacteria of animal origin: ARBAO-II: Collection of routine susceptibility data**

**General Information**
- **State:** Published
- **Organisations:** Division of Microbiology and Risk Assessment, National Food Institute
- **Contributors:** Aarestrup, F. M., Hendriksen, R. S., Wong, D. M. A. L. F.
- **Publication date:** 2004

**Publication information**
- **Original language:** English
- **Source:** orbit
Antibiotic resistance in bacteria of animal origin: ARBAO-II: External Quality Assurance System (EQAS)

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Wong, D. L. F., Hendriksen, R. S., Mevius, D., Aarestrup, F. M.
Publication date: 2004

Publication information
Original language: English
Source: orbit
Source-ID: 236575
Research output: Report – Annual report year: 2004

Antibiotic resistance in bacteria of animal origin: II

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Hendriksen, R. S., Wong, D. M. A. L. F.
Pages: 14-16
Publication date: 2004
Peer-reviewed: Unknown

Publication information
Journal: Knudepunktet
Volume: 3
Original language: English
Source: orbit
Source-ID: 236573
Research output: Communication – Journal article – Annual report year: 2004

Bestemmelse af forskellige bakteriearters følsomhed overfor kobbersulfat, zinkklorid og forskellige desinfektionsmidler

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Hasman, H.
Pages: 34-36
Publication date: 2004
Peer-reviewed: No

Publication information
Journal: Dansk Veterinær Tidsskrift
Volume: 87
Issue number: 24
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
Characterization of Streptococcus suis serotype 7 isolates from diseased pigs in Denmark

Isolates of Streptococcus suis serotype 7 from diseased pigs in Denmark were characterized by ribotyping, pulsed field gel electrophoresis (PFGE), MIC-determinations and detection of resistance genes. Forty-one different ribotype profiles were found among the 103 isolates and could be divided into two main clusters. No obvious relationship between ribotypes and the clinical origin of the isolates could be observed. Fifty-four isolates, including all 24 isolates belonging to the main ribotype profile were examined by PFGE and 50 different profiles were found. A high frequency of resistance to erythromycin (41%), tetracycline (24%) and streptomycin (28%) was observed. Furthermore, almost all isolates (101) were resistant to sulphamethoxazol. Most isolates were susceptible to ceftiofur, chloramphenicol, florfenicol, penicillin, ciprofloxacin, trimethoprim and trimethoprim + sulphonamides. The tet(M) gene was found among 11 (44%) and the tet(O) gene in six (24%) of 25 tetracycline resistant isolates. The tet(L) and tet(S) genes were not detected in any isolates. The erm(B) gene was detected in 39 (93%) of 42 erythromycin resistant isolates.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Tian, Y., Aarestrup, F. M., Lu, C.
Pages: 55-62
Publication date: 2004
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
Volume: 103
Issue number: 1-2
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Characterizations of Streptococcus suis serotype 7 isolates from diseased pigs in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Tian, Y., Aarestrup, F. M., Lu, C. P.
Pages: 55-62
Publication date: 2004
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
A standardized agar dilution susceptibility testing method was developed for Campylobacter that consisted of testing on Mueller-Hinton medium supplemented with 5% defibrinated sheep blood in an atmosphere of 10% CO₂, 5% O₂, and 85% N₂. Campylobacter jejuni ATCC 33560 was identified as a quality-control (QC) strain. Minimal inhibitory concentration (MIC) QC ranges were determined for two incubation time/temperature combinations: 36°C for 48 hr and 42°C for 24 hr. Quality-control ranges were determined for ciprofloxacin, doxycycline, erythromycin, gentamicin, and meropenem. For all antimicrobial agents tested at both temperatures, 95-100% of the QC MIC results fell within recommended QC ranges. Twenty-one Campylobacter clinical isolates, encompassing five species of Campylobacter (C. jejuni, C. coli, C. jejuni, subsp. doylei, C. fetus, and C. lari) were tested in conjunction with the C. jejuni QC strain. While C. jejuni and C. coli could be reliably tested under both test conditions, growth of C. jejuni subsp. doylei, C. fetus, and C. lari isolates was inconsistent when incubated at 42°C. Therefore, it is recommended that these species only be tested at 36°C.
Effects of termination of AGP use on antimicrobial resistance in food animals

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Effects of termination of antibiotic growth promoters use on presence of resistance genes in bacterial isolates from food animals

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Microbiology
Contributors: Jensen, L. B., Hammerum, A. M., Hasman, H., Aarestrup, F. M.
Publication date: 2004

Epidemiology of Salmonella Weltevreden in Southeast Asia and the Western Pacific: A WHO Global Salm-Surv Regional Research Project

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Patrick, M. E., Hendriksen, R. S., Lertworapreecha, M., Aarestrup, F. M., Chalermchaikit, T., Wegener, H. C., Wong, D. L. F.
Publication date: 2004
Peer-reviewed: No
Event: Poster session presented at The 3rd International Conference on Emerging Infectious Diseases, Atlanta, Georgia, USA.
Source: orbit
Source-ID: 236558
Research output: Research › Poster – Annual report year: 2004

Found of putative virulent genes of Streptococcus suis serotype 2 strains

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Tian, Y., Aarestrup, F. M., Lu, C. P.
Pages: 613-616
Publication date: 2004
Peer-reviewed: No

Publication information
Journal: Acta Microbiologica Sinica
Volume: 44
Original language: Chinese
Source: orbit
Source-ID: 236445
Research output: Research › Journal article – Annual report year: 2004

International spread of bla(CMY-2)-mediated cephalosporin resistance in a multiresistant Salmonella enterica serovar Heidelberg isolate stemming from the importation of a boar by Denmark from Canada
Kortlægning og strategi for forsknings- og udviklingsaktiviteter vedrørende kvæg i Danmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2004

Publication information
Original language: Danish
Source: orbit
Source-ID: 236339
Research output: Research › Report – Annual report year: 2004

MIC-bestemmelser af Haemophilus parasuis og Histophilus somni fra grise og kvæg i Danmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Seyfarth, A. M., Angen, Ø.
Pages: 36-37
Publication date: 2004
Peer-reviewed: No

Publication information
Journal: Dansk Veterinær Tidsskrift
Volume: 87
Issue number: 21
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
Monitoring of antimicrobial resistance among food animals: Principles and limitations

Large amounts of antimicrobial agents are in the production of food animals used for therapy and prophylactics of bacterial infections and in feed to promote growth. The use of antimicrobial agents causes problems in the therapy of infections through the selection for resistance among bacteria pathogenic for animals or humans. Current knowledge regarding the occurrence of antimicrobial resistance in food animals, the quantitative impact of the use of different antimicrobial agents on selection for resistance and the most appropriate treatment regimes to limit the development of resistance is incomplete. Programmes monitoring the occurrence and development of resistance are essential to determine the most important areas for intervention and to monitor the effects of interventions. When designing a monitoring programme it is important to decide on the purpose of the programme. Thus, there are major differences between programmes designed to detect changes in a national population, individual herds or groups of animals. In addition, programmes have to be designed differently according to whether the aim is to determine changes in resistance for all antimicrobial agents or only the antimicrobial agents considered most important in relation to treatment of humans. In 1995 a continuous surveillance for antimicrobial resistance among bacteria isolated from food animals was established in Denmark. Three categories of bacteria, indicator bacteria, zoonotic bacteria and animal pathogens are continuously isolated from broilers, cattle and pigs and tested for susceptibility to antimicrobial agents used for therapy and growth promotion by disc diffusion or minimal inhibitory concentration determinations. This programme will only detect changes on a national level. However, isolating the bacteria and testing for several antimicrobial agents will enable us to determine the effect of linkage of resistance. Since 1995 major differences in the consumption pattern of different antimicrobial agents have occurred in Denmark. The Danish monitoring programme has enabled us to determine the effect of these changes on the occurrence of resistance. The Danish monitoring is, however, not suited to determine changes on a herd level or to detect emergence of new types of resistance only occurring at a low level.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Pages: 380-388
Publication date: 2004
Peer-reviewed: Yes

Publication information
Journal: Journal of Veterinary Medicine Series B-Infectious Diseases and Veterinary Public Health
Volume: 51
Issue number: 8-9
ISSN (Print): 0931-1793
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes
Original language: English
DOIs:
10.1111/j.1439-0450.2004.00775.x
Source: orbit
Monitoring of antimicrobial resistance in food production animals in Europe. How to build a coherent system

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Mevius, D., Wong, D. M. A. L. F., Aarestrup, F. M.
Publication date: 2004

Penicillinresistens hos bovine Staphylococcus aureus

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Vintov, J., Aarestrup, F. M., Olsen, J. E.
Pages: 21-25
Publication date: 2004
Peer-reviewed: No

Prevalence of beta-lactamases among ampicillin-resistant Escherichia coli and Salmonella isolated from food animals in Denmark

The genetic background for beta-lactamase-mediated resistance to beta-lactam antibiotics was examined by PCR and sequencing in 160 ampicillin-resistant isolates (109 Escherichia coli and 51 Salmonella) obtained from healthy and diseased food animals in Denmark. Sequencing revealed three different variants of bla(TEM-1), of which bla(TEM-1b) was the most frequently detected (80 E. coli and 47 Salmonella), followed by bla(TEM-1a) (eight E. coli, one Salmonella) and bla(TEM-1c) (seven E. coli). A few isolates were found to express OXA, TEM-30, or PSE beta-lactamases. Mutations in the ampC promoter leading to increased production of the AmpC beta-lactamase were demonstrated in 11 cefoxitin-
resistant or intermediate E. coli isolates. Nine of these isolates did not contain any bla(TEM) genes, whereas the
remaining two did. No genes encoding SHV or extended-spectrum beta-lactamases were detected. Two new variants of
bla(TEM) were detected, which have been designated bla(TEM-127) and bla(TEM-128.) In TEM-127, amino acid 158 is
substituted from His to Asn, whereas a substitution from Asp to Glu is seen at amino acid 157 in TEM-128. According to
MIC determinations, these novel enzymes do not possess activity against extended-spectrum beta-lactams.

**General information**

State: Published
Organisations: Department of Systems Biology, Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Olesen, I., Hasman, H., Aarestrup, F. M.
Pages: 334-340
Publication date: 2004
Peer-reviewed: Yes

**Publication information**

Journal: Microbial Drug Resistance-mechanisms Epidemiology and Disease
Volume: 10
Issue number: 4
ISSN (Print): 1076-6294
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
Web of Science (2017): Impact factor 2.344
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
Web of Science (2016): Impact factor 2.306
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
Web of Science (2015): Impact factor 2.529
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
Web of Science (2014): Impact factor 2.49
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.87 SJR 1.265 SNIP 1.118
Web of Science (2013): Impact factor 2.524
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.45 SJR 0.963 SNIP 0.9
Web of Science (2012): Impact factor 2.364
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.76 SJR 1.163 SNIP 1.14
Web of Science (2011): Impact factor 2.153
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.054 SNIP 0.8
Web of Science (2010): Impact factor 1.936
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.915 SNIP 0.838
BFI (2008): BFI-level 1
Principles for monitoring of antimicrobial resistance among food animals

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2004

Host publication information
Title of host publication: International Society for Animal Hygiene
Source: orbit
Source-ID: 236562
Research output: Research › Article in proceedings – Annual report year: 2004

Quinolone resistant campylobacter infections in Denmark: risk factors and clinical consequences

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Engberg, J., Neimann, J., Nielsen, E. M., Aarestrup, F. M., Fussing, V.
Pages: 1056-1063
Publication date: 2004
Peer-reviewed: Yes

Publication information
Journal: EMERGING INFECTIOUS DISEASES
Volume: 10
Issue number: 6
ISSN (Print): 1080-6040
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 4.78 SJR 3.278 SNIP 1.916
Web of Science (2017): Impact factor 7.422
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.92 SJR 3.428 SNIP 2.198
Web of Science (2016): Impact factor 8.222
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.23 SJR 3.101 SNIP 2.012
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.59 SJR 3.509 SNIP 2.406
Web of Science (2014): Impact factor 6.751
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.68 SJR 3.254 SNIP 2.266
Web of Science (2013): Impact factor 7.327
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.25 SJR 2.858 SNIP 2.131
Web of Science (2012): Impact factor 5.993
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 4.46 SJR 2.785 SNIP 2.19
Web of Science (2011): Impact factor 6.169
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.021 SNIP 2.319
Web of Science (2010): Impact factor 6.859
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.168 SNIP 2.701
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.231 SNIP 2.277
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.709 SNIP 2.341
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.879 SNIP 2.345
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.816 SNIP 2.297
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.683 SNIP 2.562
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.267 SNIP 2.373
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 3.094 SNIP 2.545
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.346 SNIP 2.904
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.522 SNIP 2.856
Scopus rating (1999): SJR 1.71 SNIP 2.61
**Results from the WHO GSS EQAS 2004: The External Quality Assurance Systems of the WHO Global Salmonella Surveillance and Laboratory Support Project**

**General information**
State: Published
Organisations: National Food Institute, Division of Food Microbiology, Division of Epidemiology and Microbial Genomics
Contributors: Seyfarth, A. M., Wong, D. L. F., Hendriksen, R. S., Aarestrup, F. M.
Number of pages: 13
Publication date: 2004

**Publication information**
Publisher: National Food Institute
ISBN (Print): 978-87-92158-42-0
Original language: English
Research output: Research › Report – Annual report year: 2004

**Salmonella serotyper fra mennesker, miljøet og dyr i Thailand fra 1993 til 2002**

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Hendriksen, R. S., Wong, D. M. A. L. F.
Pages: 26-30
Publication date: 2004
Peer-reviewed: No

**Publication information**
Journal: Dansk Veterinær Tidsskrift
Volume: 87
Issue number: 7
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 236438
Research output: Research › Journal article – Annual report year: 2004

**Salmonella serovars from humans and other sources in Thailand, 1993-2002**
We serotyped 44,087 Salmonella isolates from humans and 26,148 from other sources from 1993 through 2002. The most common serovar causing human salmonellosis in Thailand was Salmonella enterica Weltevreden. Serovars causing human infections in Thailand differ from those in other countries and seem to be related to Salmonella serovars in different
food products and reservoirs.

**General information**

**State:** Published

**Organisations:** Division of Microbiology and Risk Assessment, National Food Institute

**Contributors:** Bangtrakulnonth, A., Pornreongwong, S., Pulsrikarn, C., Sawanpanyalert, P., Hendriksen, R. S., Wong, D. L. F., Aarestrup, F. M.

**Pages:** 131-136

**Publication date:** 2004

**Peer-reviewed:** Yes

**Publication information**

**Journal:** Emerging Infectious Diseases

**Volume:** 10

**Issue number:** 1

**ISSN (Print):** 1080-6040

**Ratings:**

- BFI (2018): BFI-level 2
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 2
- Scopus rating (2017): CiteScore 4.78 SJR 3.278 SNIP 1.916
- Web of Science (2017): Impact factor 7.422
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 2
- Scopus rating (2016): CiteScore 4.92 SJR 3.428 SNIP 2.198
- Web of Science (2016): Impact factor 8.222
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 2
- Scopus rating (2015): CiteScore 4.23 SJR 3.101 SNIP 2.012
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 2
- Scopus rating (2014): CiteScore 4.59 SJR 3.509 SNIP 2.406
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 2
- Scopus rating (2013): CiteScore 4.68 SJR 3.254 SNIP 2.266
- Web of Science (2013): Impact factor 7.327
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 2
- Scopus rating (2012): CiteScore 4.25 SJR 2.858 SNIP 2.131
- Web of Science (2012): Impact factor 5.993
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 2
- Scopus rating (2011): CiteScore 4.46 SJR 2.785 SNIP 2.19
- ISI indexed (2011): ISI indexed yes
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 2
- Scopus rating (2010): SJR 3.021 SNIP 2.319
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 2
- Scopus rating (2009): SJR 3.168 SNIP 2.701
Susceptibility of different bacterial species isolated from food animals to copper sulphate, zinc chloride and antimicrobial substances used for disinfection

A total of 569 different bacterial isolates (156 Salmonella, 202 E. coli, 43 S. aureus, 38 S. hyicus, 52 E. faecalis, 78 E. faecium) were tested for susceptibility to copper sulphate, benzalkonium chloride, hydrogen peroxide and chlorhexidine using MIC determinations. A total of 442 isolates were also tested for susceptibility to formaldehyde and 177 isolates for susceptibility to zinc chloride. Enterococcal isolates formed a bimodal distribution of MICs to copper sulphate, whereas the other bacterial species formed one large population. Otherwise the isolates formed one large population of susceptibilities to the different antimicrobial agents. Large variations were observed in the susceptibility of the different bacterial species to the different compounds. Staphylococci were in general very susceptible to all antimicrobial compounds tested. The Salmonella isolates were in general less susceptible to copper sulphate, benzalkonium chloride and chlorhexidine followed by E. coli and the Gram-positive species. The opposite was the case for zinc chloride. All isolates were very susceptible to H2O2 with MICs ranging from 0.002 to 0.016%, and to formaldehyde with MICs at 0.003 and 0.006%. This study showed that Danish bacterial isolates from livestock so far have not or have only to a limited degree developed resistance to antimicrobial compounds commonly used for disinfection. Acquired copper resistance was only found in enterococci. There were large differences in the intrinsic susceptibility of the different bacterial species to these compounds, and Salmonella especially seems intrinsically less susceptible than the other bacterial species, which might have human health implications. (C) 2004 Elsevier B.V. All rights reserved.
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
Web of Science (2010): Impact factor 3.256
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.309 SNIP 1.466
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.164 SNIP 1.29
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.048 SNIP 1.315
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.03 SNIP 1.396
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.089 SNIP 1.259
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.873 SNIP 1.248
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.905 SNIP 1.181
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.905 SNIP 1.13
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.828 SNIP 1.051
Web of Science (2001): Indexed yes
Antimicrobial susceptibility and occurrence of resistance genes among Salmonella enterica serovar Weltevreden from different countries

Objectives: This study was conducted to investigate the occurrence of antimicrobial resistance among Salmonella Weltevreden isolates from different sources in South-East Asia (Indonesia, Laos, Malaysia, Taiwan, Thailand, Vietnam), Australia, Denmark, New Zealand and the USA. Methods: A total of 503 isolates were examined for susceptibility to antimicrobial agents, and resistant isolates were examined for the presence of selected resistance genes by PCR. Results: Only 48 (9.5%) of the isolates were resistant to one or more of the antimicrobial agents tested. A low frequency of resistance was found towards ampicillin (1.8%), chloramphenicol (1.6%), florphenicol (0.4%), nalidixic acid (1.6%), neomycin (0.6%), streptomycin (4.4%), sulfamethoxazole (4.2%), tetracycline (4.0%) and trimethoprim (1.4%), whereas all isolates were susceptible to co-amoxiclav, cefotiofur, ciprofloxacin, colistin and gentamicin. All nine ampicillin-resistant isolates contained a sequence similar to the bla(TEM-1b) gene, one of the eight chloramphenicol-resistant isolates a sequence similar to the catA1 gene, all three neomycin-resistant isolates a sequence similar to the aphA-2 gene, 16 (73%) of the 22 streptomycin-resistant isolates a sequence similar to the aadA gene, the remaining six (27%) a sequence similar to the strA gene, and all 21 sulfamethoxazole-resistant isolates a sequence similar to the sul2 gene. Thirteen (65%) of the 20 tetracycline-resistant isolates contained the tet(A) gene, four (20%) the tet(B) gene, and one (5%) the tet...
Aspects of the epidemiology and ecology of enterococci in animals, humans and the environment: – a European study

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 133-145
Publication date: 2003
Peer-reviewed: Yes

Publication information
Journal: International Journal of Food Microbiology
Volume: 88
ISSN (Print): 0168-1605
Ratings:
  BFI (2018): BFI-level 2
  Web of Science (2018): Indexed yes
  BFI (2017): BFI-level 2
  Scopus rating (2017): CiteScore 3.76 SJR 1.366 SNIP 1.436
  Web of Science (2017): Impact factor 3.451
  Web of Science (2017): Indexed yes
  BFI (2016): BFI-level 2
  Scopus rating (2016): CiteScore 3.97 SJR 1.481 SNIP 1.553
  Web of Science (2016): Indexed yes
  BFI (2015): BFI-level 2
  Scopus rating (2015): CiteScore 4.02 SJR 1.614 SNIP 1.683
  Web of Science (2015): Indexed yes
  BFI (2014): BFI-level 2
  Scopus rating (2014): CiteScore 3.62 SJR 1.493 SNIP 1.695
  Web of Science (2014): Impact factor 3.082
  Web of Science (2014): Indexed yes
  BFI (2013): BFI-level 2
  Scopus rating (2013): CiteScore 3.8 SJR 1.612 SNIP 1.841
  Web of Science (2013): Impact factor 3.155
  ISI indexed (2013): ISI indexed yes
  Web of Science (2013): Indexed yes
  BFI (2012): BFI-level 2
  Scopus rating (2012): CiteScore 3.7 SJR 1.603 SNIP 1.705
  Web of Science (2012): Impact factor 3.425
  ISI indexed (2012): ISI indexed yes
  Web of Science (2012): Indexed yes
  BFI (2011): BFI-level 2
  Scopus rating (2011): CiteScore 3.63 SJR 1.607 SNIP 1.713
  Web of Science (2011): Impact factor 3.327
  ISI indexed (2011): ISI indexed yes
  Web of Science (2011): Indexed yes
  BFI (2010): BFI-level 2
  Scopus rating (2010): SJR 1.61 SNIP 1.666
Association between phage types and antimicrobial resistance among bovine isolates of Staphylococcus aureus in 10 countries

This study was conducted to investigate the diversity of phage types and associations between penicillin resistance and phage types among 815 Staphylococcus aureus isolates from bovine mastitis in nine European countries and USA. All isolates were examined for susceptibility to antimicrobial agents and characterised by phage typing. Penicillin resistance was found among strains from all countries with an average occurrence of 32.4% (2-71.4%). A total of 76% of isolates were identifiable by phage typing and 144 different phage types were observed. The most predominant types were phage type 29 (11% of the 815 isolates), phage type 52 (5%), and phage type 80 (5%). Phage type 95 and 29/52/52A/80 were both distributed within seven countries. In the countries with the highest occurrence of penicillin resistance a reduced diversity of phage types and phage groups was observed. Phage group In was significantly associated with penicillin resistance in contrast to phage group I (P = 0.0023) and phage complex-80 (P = 0.0066). This study confirms that a large number of phage types of S. aureus cause bovine mastitis, but that some types predominate. In addition, these findings could indicate that the use of penicillin in the bovine environment has selected for specific types of S. aureus in countries with a high frequency of resistance. (C) 2003 Elsevier B.V. All rights reserved.
Association between phage types and antimicrobial resistance among bovine Staphylococcus aureus from 10 countries

This study was conducted to investigate the diversity of phage types and associations between penicillin resistance and phage types among 815 Staphylococcus aureus isolates from bovine mastitis in nine European countries and USA. All isolates were examined for susceptibility to antimicrobial agents and characterised by phage typing. Penicillin resistance was found among strains from all countries with an average occurrence of 32.4% (2-71.4%). A total of 76% of isolates were identifiable by phage typing and 144 different phage types were observed. The most predominant types were phage type 29 (11% of the 815 isolates), phage type 52 (5%), and phage type 80 (5%). Phage type 95 and 29/52/52A/80 were both distributed within seven countries. In the countries with the highest occurrence of penicillin resistance a reduced diversity of phage types and phage groups was observed. Phage group In was significantly associated with penicillin resistance in contrast to phage group I (P = 0.0023) and phage complex-80 (P = 0.0066). This study confirms that a large number of phage types of S. aureus cause bovine mastitis, but that some types predominate. In addition, these findings could indicate that the use of penicillin in the bovine environment has selected for specific types of S. aureus in countries with a high frequency of resistance.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Vintov, J., Aarestrup, F. M., Zinn, C. E., Olsen, J. E.
Pages: 133-147
Publication date: 2003
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
Volume: 95
Issue number: 1-2
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Bakteriel resistens overfor kobber anvendt i foderet til dyr

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hasman, H., Aarestrup, F. M.
Pages: 6-8
Publication date: 2003
Cephalosporin-resistent Salmonella fundet i Danmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Pages: 38-41
Publication date: 2003
Peer-reviewed: No

Evaluation of the surveillance programme of streptococcus agalactiae in Danish dairy herds

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Andersen, H. J., Pedersen, I. H., Aarestrup, F. M., Chriél, M.
Pages: 1233-1239
Publication date: 2003
Peer-reviewed: Yes
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.84 SJR 1.35 SNIP 1.491
Web of Science (2017): Impact factor 2.749
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.66 SJR 1.331 SNIP 1.484
Web of Science (2016): Impact factor 2.474
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.63 SJR 1.479 SNIP 1.488
Web of Science (2015): Impact factor 2.408
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.78 SJR 1.434 SNIP 1.504
Web of Science (2014): Impact factor 2.573
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 2.82 SJR 1.411 SNIP 1.589
Web of Science (2013): Impact factor 2.55
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 2.79 SJR 1.443 SNIP 1.717
Web of Science (2012): Impact factor 2.566
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 2.59 SJR 1.413 SNIP 1.582
Web of Science (2011): Impact factor 2.564
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.354 SNIP 1.518
Web of Science (2010): Impact factor 2.497
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.329 SNIP 1.724
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.219 SNIP 1.51
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.987 SNIP 1.874
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.178 SNIP 1.65
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.988 SNIP 1.631
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.033 SNIP 1.581
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.134 SNIP 1.64
Web of Science (2003): Indexed yes
Evaluation of the surveillance program of Streptococcus agalactiae in Danish dairy herds

The aim of this study was to evaluate the Danish surveillance program of Streptococcus agalactiae in dairy herds with respect to 1) fluctuation over time of the presence of S. agalactiae in bulk tank milk, 2) sensitivity and specificity of the bacteriological method used, and 3) contamination of bulk tank milk samples with milk from other herds. From June to September 1996, bulk tank milk was sampled from 100 Danish dairy herds seven times, with intervals of 2 wk. The samples were examined for the presence of S. agalactiae by four different methods: 1) by the method approved for the program, 2) after ultrasonic treatment of the milk before examination, 3) after freezing down the milk before examination, and 4) after selective preparation of the milk. Selected strains of S. agalactiae were examined by restriction fragment length polymorphism of the gene encoding rRNA to discriminate between the isolates. Streptococcus agalactiae was found in eight of 96 herds in which S. agalactiae had never previously been found during the surveillance program. Streptococcus agalactiae was not found in all seven sampling rounds in any of the eight herds. Comparing the approved method with supplemental findings by the other methods, the estimated sensitivity was (95% confidence limits): 0.786 (0.628; 0.892) and the estimated specificity (95% confidence limits): 0.995 (0.985; 0.999). Using all four methods on the same sample could increase the sensitivity, but by comparing the methods individually, there was no significant difference between any of them (P > 0.10). In milk samples from three herds, the ribotype of S. agalactiae was the same as in milk from herds sampled just before; therefore, it could not be ruled out that cross-contamination could occur. Taking into account that S. agalactiae in bulk tank milk reflects the presence of S. agalactiae in at least one udder quarter, this investigation gives further reason to assume that S. agalactiae can be seen sporadically in several herds. A surveillance program based on annual bulk tank milk sample examinations will only detect a limited number of S. agalactiae infected herds. If the overall aim is to identify herds where the infection is established, annual bulk tank milk sample examinations combined with the information of number of colonies of S. agalactiae in the sample will be sufficient.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Andersen, H. J., Pedersen, L. H., Aarestrup, F. M., Chriél, M.
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Publication date: 2003
Peer-reviewed: Yes

Publication information
Journal: JOURNAL OF DAIRY SCIENCE
Volume: 86
Issue number: 4
ISSN (Print): 0022-0302
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.84 SJR 1.35 SNIP 1.491
Web of Science (2017): Impact factor 2.749
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.66 SJR 1.331 SNIP 1.484
Web of Science (2016): Impact factor 2.474
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.63 SJR 1.479 SNIP 1.488
Web of Science (2015): Impact factor 2.408
Første cephalosporin resistente Salmonella i Danmark

General information
Harmonization of antimicrobial susceptibility testing among veterinary diagnostic laboratories in the five Nordic countries

A total of 100 bacterial strains (25 Escherichia coli, 25 Salmonella enterica, 25 Staphylococcus aureus, and 25 Enterococcus strains) and four reference strains were tested for susceptibility toward 8-12 antimicrobial agents in 12 veterinary diagnostic laboratories in the five Nordic countries using routine methodology. In addition, the 25 Enterococcus strains were identified to species level. A total of 22,598 (97.2%) out of 23,259 test results were in accordance when the data were categorized as susceptible or resistant. When the reported results were categorized according to the National Committee of Clinical Laboratory Standards breakpoints, the percentage of concordant results increased to 98.4% and the performance between laboratories varied between 94.2 and 99.4% concordant results. For E. coli, S., aureus, and Salmonella, all laboratories except one had more than 97% concordant results, whereas for Enterococcus spp., two laboratories had less than 90 % concordant results. Susceptibility testing of Salmonella to fluoroquinolones gave rise to almost 0.5% nonconcordant results and susceptibility testing of S. aureus to vancomycin resulted in that 1.8% of the strains were incorrectly reported as vancomycin resistant. Ten laboratories identified the Enterococcus spp. to species level. All five Enterococcus faecium and 10 Enterococcus faecalis selected from the strain collection at the Danish Veterinary Institute were correctly identified by all laboratories, whereas some problems were observed identifying other enterococcal species. This study showed a good performance and agreement in antimicrobial susceptibility testing at the 12 participating laboratories and that surveillance data covering susceptibility test results of E. coli, S. aureus, and Salmonella from animals in the Nordic countries are comparable. But it also showed that some aspects can be improved. In addition, the study showed that the different laboratories are capable of identifying E. faecalis and E. faecium.
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
Web of Science (2017): Impact factor 2.344
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
Web of Science (2016): Impact factor 2.306
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
Web of Science (2015): Impact factor 2.529
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
Web of Science (2014): Impact factor 2.49
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.87 SJR 1.265 SNIP 1.118
Web of Science (2013): Impact factor 2.524
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.45 SJR 0.963 SNIP 0.9
Web of Science (2012): Impact factor 2.364
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.76 SJR 1.163 SNIP 1.14
Web of Science (2011): Impact factor 2.153
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.054 SNIP 0.8
Web of Science (2010): Impact factor 1.936
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.915 SNIP 0.838
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.038 SNIP 0.73
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.042 SNIP 0.764
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.319 SNIP 0.908
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.364 SNIP 0.983
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.998 SNIP 0.968
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.303 SNIP 1.029
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.42 SNIP 0.918
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.791 SNIP 1.006
Is it time to change fluoroquinolone breakpoints for Salmonella spp.?

**General information**

State: Published  
Organisations: Division of Microbiology and Risk Assessment, National Food Institute  
Contributors: Aarestrup, F. M., Wiuff, C., Mølbak, K., Threlfall, E.  
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Publication date: 2003  
Peer-reviewed: Yes

**Publication information**

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Volume: 47  
Issue number: 2  
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Ratings:  
BFI (2018): BFI-level 1  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 1  
Scopus rating (2017): CiteScore 4.15 SJR 2.291 SNIP 1.263  
Web of Science (2017): Impact factor 4.255  
Web of Science (2017): Indexed yes  
BFI (2016): BFI-level 1  
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328  
Web of Science (2016): Impact factor 4.302  
Web of Science (2016): Indexed yes  
BFI (2015): BFI-level 1  
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361  
Web of Science (2015): Indexed yes  
BFI (2014): BFI-level 1  
Scopus rating (2014): CiteScore 4.45 SJR 2.361 SNIP 1.428  
Web of Science (2014): Impact factor 4.476  
Web of Science (2014): Indexed yes  
BFI (2013): BFI-level 1  
Scopus rating (2013): CiteScore 4.67 SJR 2.423 SNIP 1.411  
Web of Science (2013): Impact factor 4.451  
ISI indexed (2013): ISI indexed yes  
Web of Science (2013): Indexed yes  
BFI (2012): BFI-level 1  
Scopus rating (2012): CiteScore 4.88 SJR 2.363 SNIP 1.5  
Web of Science (2012): Impact factor 4.565  
ISI indexed (2012): ISI indexed yes  
Web of Science (2012): Indexed yes  
BFI (2011): BFI-level 1  
Scopus rating (2011): CiteScore 5.02 SJR 2.523 SNIP 1.574
Is it time to change the break-points for fluoroquinolones for Salmonella

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Wiuff, C., Mølbak, K., Threlfall, E. J.
Pages: 827-829
Publication date: 2003
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Publication information
Journal: Antimicrobial Agents and Chemotherapy
Volume: 47
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Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.15 SJR 2.291 SNIP 1.263
Web of Science (2017): Impact factor 4.255
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.45 SJR 2.361 SNIP 1.428
Web of Science (2014): Impact factor 4.476
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.67 SJR 2.423 SNIP 1.411
Web of Science (2013): Impact factor 4.451
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.88 SJR 2.363 SNIP 1.5
Web of Science (2012): Impact factor 4.565
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 5.02 SJR 2.523 SNIP 1.574
Web of Science (2011): Impact factor 4.841
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.458 SNIP 1.54
Web of Science (2010): Impact factor 4.672
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.424 SNIP 1.65
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.45 SNIP 1.448
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.167 SNIP 1.49
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.339 SNIP 1.401
Scopus rating (2005): SJR 2.321 SNIP 1.52
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.929 SNIP 1.614
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.208 SNIP 1.644
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 2.173 SNIP 1.553
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.334 SNIP 1.542
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.899 SNIP 1.617
Web of Science (2000): Indexed yes
Ny multi-resistent salmonellabakterie fundet i importeret gris

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2003

Publication information
Media of output: Fødevareministeriets hjemmeside
Year: 2003
Original language: Danish
Source: orbit
Source-ID: 236540
Research output: Research › Net publication - Internet publication – Annual report year: 2003

Organic dairy farmers’ decision making in the first 2 years after conversion in relation to mastitis treatments

In organic dairy farming, a goal about improved animal welfare and avoidance of the use of chemicals has introduced restrictions in the use of antimicrobials for treatment of infectious diseases. Mastitis is the major cause of antimicrobial treatments in Danish dairy farming. In order to improve and minimise the use of antimicrobials and the risk of antimicrobial resistance in organic farming, a study based on qualitative research interviews with newly converted organic farmers was carried out. Twenty farmers, 18-26 months after conversion, were interviewed focusing on mastitis treatment patterns and the farmers’ own perception of possible changes in strategies, choices and daily routines linked to mastitis handling. Antimicrobial treatment was the dominant treatment method in these herds, and regarded as the treatment method with best and most well known prognosis concerning a prognosis of cure. Severe symptoms of mastitis and affected general condition of the cow would cause antimicrobial treatment in all herds. Almost all other mastitis treatment choices were based on herd level considerations. Changes due to conversion to organic farming were experienced on the level of land and crop production, and only to a very little extent directly linked to the herd and management choices related to disease prevention and treatment. Veterinary involvement in choices and professional discussions seemed very sparse, and a major challenge for the future development of organic dairy farming must be outlined, in relation to development of explicit treatment strategies based on well-evaluated data analyses, founded on the results from the individual herd. (C) 2002 Published by Elsevier Science B.V.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Vaarst, M., Thamsborg, S. M., Bennedsgaard, T. W., Houe, H., Enevoldsen, C., Aarestrup, F. M., Snoo, A. D.
Pages: 109-120
Publication date: 2003
Peer-reviewed: Yes

Publication information
Journal: Livestock Production Science
Volume: 80
Issue number: 1-2
ISSN (Print): 0301-6226
Ratings:
BFI (2008): BFI-level 1
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Original language: English
Source: orbit
Source-ID: 236590
Research output: Research › peer-review › Journal article – Annual report year: 2003
Phage types and antimicrobial resistance among Danish bovine Staphylococcus aureus isolates since the 1950s
A total of 292 bovine Staphylococcus aureus isolates obtained from the 1950s (86 isolates), 1992 (107 isolates), and 2000 (99 isolates) were examined for antimicrobial susceptibility and phage typing. The same types of S. aureus (80, 52, 3A, 3A/3C, 42E, 77) were found among the isolates from all three time periods, representing 43.3% of the typeable isolates. This indicates that the Danish S. aureus population related to bovine mastitis has remained relatively unchanged over the last 50 years. The occurrence of antimicrobial resistance has remained low in Denmark in comparison to other countries in Europe. (C) 2003 Elsevier B.V. All rights reserved.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Vintov, J., Aarestrup, F. M., Zinn, C. E., Olsen, J. E.
Pages: 63-72
Publication date: 2003
Peer-reviewed: Yes

Publication information
Journal: VETERINARY MICROBIOLOGY
Volume: 97
Issue number: 1-2
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
Results from EQAS 2002: The External Quality Assurance System 2002 of the WHO Global Salmonella Surveillance and Laboratory Support Project (Global Salm-Surv)

An international external quality assurance program on serotyping and antimicrobial susceptibility testing of eight Salmonella enterica strains was performed to enhance the capacity of national and regional reference laboratories in WHO Global Salm-Surv (WHO GSS). In 2002 a total of 117 laboratories from 67 countries participated. For serotyping, almost 90 % of the results were correct. For susceptibility testing, 91 % of the results were in agreement with the expected results, and 86 % of the performed tests with the reference strain E. coli ATCC 25922 were inside the quality control range specified by NCCLS guidelines. Comparing the results of EQAS 2002 to the results from 2000 and 2001 showed a clear improvement in the laboratories capacity to accurately serotype and susceptibility test Salmonella. We attribute this improvement to the training provided by WHO GSS, the EQAS and the high quality Salmonella typing antisera, provided to most participants as a part of the WHO GSS.

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Division of Food Microbiology
Number of pages: 8
Publication date: 2003

Publication information
Publisher: Danmarks Tekniske Universitetet, Fødevareinstituttet
ISBN (Print): 978-87-92158-40-6
Original language: English
Research output: Research - peer-review › Report – Annual report year: 2003
Susceptibility of Escherichia coli and Enterococcus faecium isolated from pigs and broiler chickens to tetracycline degradation products and distribution of tetracycline resistance determinants in E-coli from food animals

One hundred Escherichia coli isolates from diseased and healthy pigs, cattle and broiler chickens were screened for the presence of tetracycline resistance genes tet(A), (13), (C), (D) or (E). The tet(A) gene was the most abundant (71% of the 100 isolates) followed by tet(B) (25%). The predominance of tet(A) and tet(B) applied to all three animal species, and there was no difference between the distribution of tet(A) and tet(B) genes among non-pathogenic and pathogenic E. coli in any of the animal species. The susceptibility of 20 of these isolates together with 10 tetracycline sensitive E. coli and 18 tetracycline resistant and 10 sensitive Enterococcus faecium to tetracyclines and tetracycline degradation products was determined. The resistant isolates showed reduced resistance to anhydrotetracycline, 4-epi-anhydrotetracycline, anhydrochlortetracycline and 4-epi-anhydrochlortetracycline. In general both the tetracycline resistant and susceptible E. faecium were more susceptible to the compounds tested than E. coli. (C) 2003 Elsevier B.V.. All rights reserved.
The effects of oral and intramuscular administration and dose escalation of enrofloxacin on the selection of quinolone resistance among Salmonella and coliforms in pigs

The effect of route of administration and dose of enrofloxacin (Baytril(R)) on the development of fluoroquinolone resistance in Salmonella and Escherichia coli in the intestinal tract of pigs was investigated. Healthy pigs at the age of 8-10 weeks were infected with a mixture of susceptible wild-type (MICciprofloxacin = 0.03 mg/ml) and a mutant Salmonella typhimurium with reduced susceptibility to fluoroquinolones (MICciprofloxacin 0.5 mg/ml) (in the ratio 99: 1) and treated with 2.5 mg/kg bwt enrofloxacin by either intramuscular (i.m.) or oral (p.o.) administration at time points either 4 or 24 h after the infection. The treatment via the intramuscular route of administration (24 h after the infection) was carried out with...
elevated doses of 7.5 and 15 mg/kg bwt as well. Emergence of resistance during a 3-day treatment period and persistence up to 13 days after treatment, was monitored by counting the resistant and total number of coliforms and Salmonella in faeces of the pigs. High frequencies of fluoroquinolone resistance developed rapidly among the coliform flora independent of route of administration, dose or time of initiation of the treatment. Selection for resistance among the artificially introduced Salmonella was reduced by using the intramuscular route and by escalating the dose 3 or 6 times the recommended dose of 2.5 mg/kg bwt, which also resulted in shortening of the period, in which the pigs were shedding Salmonella. The resistance among the coliform flora persisted for at least 2 weeks. The Salmonella infection was cleared in all cases during the 2 weeks independent of frequency of resistance. The study showed that resistance is very easily selected by treatment with enrofloxacin at the recommended dose 2.5 mg/kg bwt, but also that the intensity of selection can be reduced by using intramuscular dosing (instead of oral dosing) and by escalating that i.m. dose. The results obtained with Salmonella also showed that even very small changes in the active drug concentrations might completely change the intensity of selection. (C) 2003 Elsevier Science Ltd. All rights reserved.

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Wiuff, C., Lykkesfeldt, J., Svendsen, O., Aarestrup, F. M.
Pages: 185-193
Publication date: 2003
Peer-reviewed: Yes

**Publication information**
Journal: RESEARCH IN VETERINARY SCIENCE
Volume: 75
Issue number: 3
ISSN (Print): 0034-5288
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 1.82 SJR 0.593 SNIP 0.941
Web of Science (2017): Impact factor 1.616
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.46 SJR 0.646 SNIP 0.779
Web of Science (2016): Impact factor 1.298
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 1.57 SJR 0.774 SNIP 0.933
Web of Science (2015): Impact factor 1.504
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 1.58 SJR 0.687 SNIP 0.887
Web of Science (2014): Impact factor 1.409
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 1.62 SJR 0.691 SNIP 0.945
Web of Science (2013): Impact factor 1.511
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 1.63 SJR 0.633 SNIP 1.067
Web of Science (2012): Impact factor 1.774
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 1.65 SJR 0.726 SNIP 1.054
Web of Science (2011): Impact factor 1.649
ISI indexed (2011): ISI indexed yes
Udvikling i antibiotikaresistens og forekomst af resistensgener blandt Staphylococcus hyicus fra sodeksem hos grise i Danmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, L. B.
Pages: 6-8
Publication date: 2003
Peer-reviewed: No

Publication information
Journal: Dansk Veterinær Tidsskrift
Volume: 86
Issue number: 6
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
Antimicrobial resistance among enterococci from pigs in three European countries

Enterococci from pigs in Denmark, Spain, and Sweden were examined for susceptibility to antimicrobial agents and copper and the presence of selected resistance genes. The greatest levels of resistance were found among isolates from Spain and Denmark compared to those from Sweden, which corresponds to the amounts of antimicrobial agents used in food animal production in those countries. Similar genes were found to encode resistance in the different countries, but the tet(L) and let(S) genes were more frequently found among isolates from Spain. A recently identified transferable copper resistance gene was found in all copper-resistant isolates from the different countries.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Hasman, H., Jensen, L. B., Moreno, M., Herrero, I., Dominguez, L., Finn, M., Franklin, A.
Pages: 4127-4129
Publication date: 2002
Peer-reviewed: Yes

Publication information
Journal: Applied and Environmental Microbiology
Volume: 68
Issue number: 8
ISSN (Print): 0099-2240
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 3.99
Web of Science (2017): Impact factor 3.633
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.08
Web of Science (2016): Impact factor 3.807
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.14 SJR 1.891 SNIP 1.308
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.02 SJR 1.857 SNIP 1.384
Web of Science (2014): Impact factor 3.668
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.25 SJR 1.899 SNIP 1.414
Web of Science (2013): Impact factor 3.952
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.29 SJR 1.975 SNIP 1.429
Web of Science (2012): Impact factor 3.678
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Distribution of enrofloxacin in intestinal tissue and contents of healthy pigs after oral and intramuscular administrations

The concentration of enrofloxacin in plasma, intestinal tissue, lymph nodes and intestinal contents was investigated in healthy pigs after oral (p.o.) and intramuscular (i.m.) administration of a single dose of 2.5 mg/kg bw. Tissue and content samples were collected from jejunum, ileum, caecum and colon from pigs killed at 2, 3 and 6 h after dosing. Intramuscular administration resulted in significantly higher concentrations in plasma, intestinal tissue and lymph nodes at 2 h but not at 3 or 6 h compared with p.o. administration. The absorption and distribution phase was longer after oral administration, and maximum concentrations in tissue and plasma were determined later than after i.m. administration. No difference between route of administration was observed in the intestinal content. Enrofloxacin concentrations in faeces during a 5-day dosing regimen with i.m. and p.o. administration were determined by both HPLC and bio-assay. Higher concentrations were found after i.m. administration during the first day, but the difference was not significant after 2 days. The biologically active concentrations determined by bio-assay constituted 48-75% of the total concentrations determined by HPLC. On the basis of these results it was concluded that in order to ensure an immediate high concentration of enrofloxacin, and thereby avoid an initial selection for resistant mutants, the intramuscular route seems to be preferable to the oral route.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Wiuff, C., Lykkefeldt, J., Aarestrup, F. M., Svendsen, O.
Pages: 335-342
Publication date: 2002
Peer-reviewed: Yes
Publication information
Journal: Journal of Veterinary Pharmacology and Therapeutics
Volume: 25
Issue number: 5
ISSN (Print): 0140-7783
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 1.55 SJR 0.7 SNIP 0.966
Web of Science (2017): Impact factor 1.441
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.24 SJR 0.716 SNIP 0.992
Web of Science (2016): Impact factor 1.202
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 1.14 SJR 0.651 SNIP 0.85
Web of Science (2015): Impact factor 1.279
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 1.31 SJR 0.823 SNIP 0.845
Web of Science (2014): Impact factor 1.189
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 1.27 SJR 0.693 SNIP 0.869
Web of Science (2013): Impact factor 1.323
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 0.96 SJR 0.535 SNIP 0.795
Web of Science (2012): Impact factor 1.349
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 0.91 SJR 0.583 SNIP 0.809
Web of Science (2011): Impact factor 1.181
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.556 SNIP 0.657
Web of Science (2010): Impact factor 1.675
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.648 SNIP 1.141
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.631 SNIP 0.842
Scopus rating (2007): SJR 0.805 SNIP 1.068
Scopus rating (2006): SJR 0.675 SNIP 1.114
Scopus rating (2005): SJR 0.584 SNIP 0.921
Scopus rating (2004): SJR 0.411 SNIP 0.762
Scopus rating (2003): SJR 0.465 SNIP 0.788
Scopus rating (2002): SJR 0.327 SNIP 0.807
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.423 SNIP 0.93
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.714 SNIP 1.099
Scopus rating (1999): SJR 0.624 SNIP 1.128
Original language: English
Source: orbit
Source-ID: 236535

General information
State: Published
Organisations: Communications and Management Secretariat, National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Wegener, H. C., Petersen, A., Evans, M. C., Hendriksen, R. S., Wong, D. M. A. L. F., Aarestrup, F. M.
Pages: 10-15
Publication date: 2002
Peer-reviewed: No

Publication information
Journal: Alimenta
Volume: 2
ISSN (Print): 0002-5402
Ratings:
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 236429
Research output: Research - peer-review › Journal article – Annual report year: 2002

External Quality Assurance System (EQAS) demonstrate continued need for improving Salmonella serotyping and susceptibility testing

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Publication date: 2002
Peer-reviewed: No
Event: Poster session presented at The International Conference on Emerging Infectious Diseases, Atlanta, USA.
Source: orbit
Source-ID: 246770
Research output: Research › Poster – Annual report year: 2002

External Quality Assurance System (EQAS) of the WHO Global Salmonella Surveillance and Laboratory Support Project (Global Salm-Surv) Results from 2001
An international collaborative study on serotyping and antimicrobial susceptibility testing of eight Salmonella enterica strains was performed to enhance the capacity of national and regional reference laboratories in WHO Global Salm-Surv to conduct Salmonella serotyping and antimicrobial susceptibility testing. A total of 103 laboratories in 60 countries participated. For serotyping, 78% of the results were correct. For susceptibility testing, 91% of the results were in agreement with the expected results. However, 17% of the performed tests with the E. coli ATCC 25922 reference strain were out of the quality control range specified by NCCLS guidelines.

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Geographical variation in the presence of genes encoding superantigenic exotoxins and beta-hemolysin among Staphylococcus aureus isolated from bovine mastitis in Europe and USA

The object was to examine the geographical variation in the presence of superantigenic exotoxins and beta-hemolysin among epidemiologically independent Staphylococcus aureus isolates from bovine mastitis. A total of 462 S. aureus isolates from nine European countries and USA were examined for the presence of genes encoding staphylococcal enterotoxins A-E, and H, toxic shock toxin-1 (TSST-1), and beta-hemolysin, and 128 of these were examined for exfoliative toxins A and B. The detection was done by PCR. Phenotypic methods were used to confirm the PCR-results. None of the 128 isolates carried the genes for exfoliative toxin A or B. The total proportion of isolates in which superantigenic exotoxins were detected varied from 2% (one isolate) of the Danish isolates to 65% (32 isolates) of the Norwegian isolates. This marked and highly significant geographical variation was also present for the individual exotoxins. The genes encoding enterotoxin C, TSST-1, and enterotoxin D were the most common superantigens. The present and earlier studies demonstrate that the superantigenic exotoxins that were investigated in this study, do not play a role in the pathogenesis of bovine S. aureus mastitis. In contrast to the geographical variation among superantigenic exotoxins, 97% of the isolates were PCR-positive for and/or produced beta-hemolysin on 5% calf blood agar. Except for three isolates, the Norwegian isolates were PCR-negative, but positive on 5% calf blood agar. Sequence variation in the primer regions in the beta-hemolysin encoding gene of the Norwegian isolates is suggested, and should be investigated further. The consistent presence of beta-hemolysin suggests that this factor, or a co-existing gene correlated to beta-hemolysin, may be an active virulence factor in the pathogenesis of bovine S. aureus mastitis. (C) 2002 Elsevier Science B.V. All rights reserved.
Incidence of high-level evernimicin resistance in Enterococcus faecium among food animals and humans

Six high-level evernimicin-resistant Enterococcus faecium isolates were identified among 304 avliaricin-resistant E. faecium isolates from animals and 404 stool samples from humans with diarrhea. All four animal isolates, and one of the human isolates, were able to transfer resistance to a susceptible E. faecium strain. The resulting transconjugants all tested positive for the presence of emtA, a gene encoding a methyltransferase previously linked with high-level evernimicin resistance. The four transconjugants derived from animal isolates all carried the same plasmid, while a differently sized plasmid was found in the isolate from humans. This study demonstrated a low incidence of high-level evernimicin resistance mediated by the emtA gene in different E. faecium isolates of animal and human origin.
Quantification of bioavailable chlortetracycline in pig feces using a bacterial whole-cell biosensor

Bacterial whole-cell biosensors were used to measure the concentration of chlortetracycline (CTC) in the feces of pigs. In this study, the Escherichia coli biosensor used has a detection limit of 0.03 mg/kg CTC in pig feces. The tetracycline concentration was correlated with the appearance and maintenance of fecal coliform bacteria resistant to tetracycline. Initially, large quantities of water-extractable CTC were excreted from the pigs and measurable amounts were detected even at 30 days after treatment cessation. This led to a sharp rise in the number of tetracycline resistant coliform bacteria in the feces, to within the same order of magnitude as the total coliform count. The high level of tetracycline resistance was maintained in spite of the declining concentration of tetracycline. (C) 2002 Elsevier Science B.V. All rights reserved.
Spread of Staphylococcus aureus resistant to penicillin and tetracycline within and between dairy herds

One hundred and seven bovine isolates of penicillin and tetracycline resistant Staphylococcus aureus, recovered from 25 different dairy herds in various parts of Norway, were characterized using antimicrobial susceptibility testing, multilocus enzyme electrophoresis, ribotyping, plasmid analysis and serotyping of capsular polysaccharide. Forty-one isolates from one particular herd, 37 isolates from 5 herds that used a common pasture and milking parlour in summer and 21 isolates from 12 herds in 8 different counties belonged to the same strain. The remaining 8 isolates, which originated from herds in 5 different counties, were assigned to 6 different strains. Seven out of these 8 isolates had the same plasmid restriction profile. In conclusion, penicillin and tetracycline resistant S. aureus occurring in dairy herds in Norway mainly seems to represent one particular strain that has achieved widespread distribution or belong to one of several different strains carrying identical plasmids.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Waage, S., Bjorland, J., Caugant, D. A., Oppegaard, H., Tollersrud, T., Mørk, T., Aarestrup, F. M.
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BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.29 SJR 1.349 SNIP 1.052
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Scopus rating (2014): CiteScore 2.19 SJR 1.305 SNIP 1.016
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Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.69 SJR 1.437 SNIP 1.17
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ISI indexed (2012): ISI indexed yes
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BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.71 SJR 1.326 SNIP 1.214
Web of Science (2011): Impact factor 2.843
Streptogramin resistance among Enterococcus faecium isolated from production animals in Denmark in 1997

The genetic background for streptogramin resistance was examined in Enterococcus faecium isolated from pigs (n = 55) and broilers (n = 207) in 1997 in Denmark. Fifty-one percent and 67%, respectively, of the isolates were resistant to streptogramins. Among streptogramin-resistant E. faecium (SREF), the genetic background for streptogramin A resistance could be determined in 96% of the isolates from broilers, compared with 14% among SREF from pigs. For broiler isolates 89% of SREF contained the vat(E) gene and 10% the vat(D) gene. Three of these isolates contained both resistance genes. Among SREF from pigs two isolates contained the vat(E) gene and two others the vat(D) gene. The genetic background for streptogramin B was most often identified as the erm(B) gene encoding macrolide, lincosamide, and streptogramin B (MLSβ) resistance. Among SREF, 84% and 86% of isolates from broilers and pigs, respectively, contained the erm(B). In SREF from broilers, the erm(B) gene was physically linked to the vat(E) gene in 62% of the vat(E)-positive isolates and 79% of the isolates containing vat(D), erm(A) was detected in two SREF of broiler origin. Both isolates also contained the erm(B) gene. No SREF contained the vgb(A) gene encoding streptogramin B resistance. On the basis of genetic characterization, streptogramin-resistant isolates from broiler were divided into subgroups, according to the presence of the streptogramin A genes, to determine possible co-resistance to antimicrobials, especially glycopeptides. Twenty-five percent of the SREF from broilers were glycopeptide resistant (MIC > 16 μg/ml). None of the isolates containing the streptogramin A gene vat(D) was resistant to glycopeptide, whereas isolates containing the vat(E) gene had a lower prevalence to glycopeptide resistance than the streptogramin-sensitive isolates.

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Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Microbiology, Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Contributors: Jensen, L. B., Hammerum, A. M., Bager, F., Aarestrup, F. M.
tcrB, a gene conferring transferable copper resistance in Enterococcus faecium: occurrence, transferability, and linkage to macrolide and glycopeptide resistance

A newly discovered gene, designated tcrB, which is located on a conjugative plasmid conferring acquired copper resistance in Enterococcus faecium, was identified in an isolate from a pig. The tcrB gene encodes a putative protein belonging to the CPx-type ATPase family with homology (46%) to the CopB protein from Enterococcus hirae. The tcrB gene was found in E. faecium isolated from pigs (75%), broilers (34%), calves (16%), and humans (10%) but not in isolates from sheep. Resistant isolates, containing the tcrB gene, grew on brain heart infusion agar plates containing up to 28 mM CuSO4 compared to only 4 mM for the susceptible isolates. Copper resistance, and therefore the presence of the tcrB gene, was strongly correlated to macrolide and glycopeptide resistance in isolates from pigs, and the tcrB gene was shown to be located on the same conjugative plasmid as the genes responsible for resistance to these two antimicrobial agents. The frequent occurrence of this new copper resistance gene in isolates from pigs, where copper sulfate is being used in large amounts as feed additive, suggests that the use of copper has selected for resistance.

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Contributors: Hasman, H., Aarestrup, F. M.
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BFI (2016): BFI-level 1
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Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
Web of Science (2015): Indexed yes
Trends in antimicrobial susceptibility and presence of resistance genes in Staphylococcus hyicus isolated from exudative epidermitis in pigs
Trends in antimicrobial susceptibility in relation to antimicrobial usage and presence of resistance genes in Staphylococcus hyicus isolated from exudative epidermitis in pigs

From 1996 to 2001 a total of 467 Staphylococcus hyicus isolates from exudative epidermitis (EE) in pigs in Denmark were examined for susceptibility to 13 different antimicrobial agents. The presence of selected genes encoding macrolide (erm(A), erm(B) and erm(C)), penicillin (blaZ), streptogramin (vat, vga, vga(B), vat(B), vat(D) and vat(E)), streptomycin (aadE) and tetracycline resistance (tet(K), tet(L), tet(M) and tet(O)) were determined in selected isolates. The occurrence of erythromycin resistance increased from 33% in 1996 to a maximum of 62% in 1997 and decreased to 26% in 2001. Resistance to sulphametazole increased from 17% in 1996 to 30% in 1998 but has since decreased to 4% in 2001. Resistance to trimethoprim increased to 51% in 1997 and decreased to 21% in 2001. Resistance to tetracycline (21-31%) remained relatively constant during 1996-2000, but increased to 47% in 2001. Resistance to penicillin (54-75%) and streptomycin (33-53%) and tetracycline (21-47%) remained relatively constant over the time investigated. All 48 penicillin resistant isolates examined contained the blaZ gene and 40 (85%) of the streptomycin resistant isolates the aadE gene. It was not possible to detect any streptogramin resistance gene in four streptogramin resistant isolates. Of the 55 erythromycin resistant isolates examined, five contained erm(A), 13 erm(B), 35 erm
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
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Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
Web of Science (2010): Impact factor 3.256
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.309 SNIP 1.466
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.164 SNIP 1.29
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.048 SNIP 1.315
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.03 SNIP 1.396
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.089 SNIP 1.259
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.873 SNIP 1.248
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.905 SNIP 1.181
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.905 SNIP 1.13
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.828 SNIP 1.051
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.699 SNIP 1.066
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.714 SNIP 1.089
WHO global salm-surv external quality assurance system (EQAS): an important step toward improving the quality of Salmonella serotyping and antimicrobial susceptibility testing worldwide

Initiated in 2000, WHO Global Salm-Surv is a global network of epidemiologists and microbiologists involved in Salmonella surveillance. WHO Global Salm-Surv seeks to enhance the capacity of national and regional reference laboratories to conduct Salmonella serotyping and antimicrobial susceptibility testing through international training courses and an External Quality Assurance System (EQAS). In 2000, 44 WHO Global Salm-Surv member laboratories from 35 countries determined the serotype and antimicrobial susceptibility pattern for eight "blinded" Salmonella isolates. For serotyping, 73% of the results were correct. For susceptibility testing, 92% of the results were in agreement with the expected results. However, only 78% of the performed tests with the E. coli ATCC 25922 reference strain were within the quality control range specified by National Committee for Clinical Laboratory Standards (NCCLS) guidelines. These EQAS results demonstrate the need for further training to improve the performance of some of the laboratories. WHO Global Salm-Surv activities, including international training courses and EQAS, represent an important step toward improving the quality of Salmonella serotyping and antimicrobial susceptibility testing worldwide, and improving the current reliability and comparability of Salmonella surveillance data obtained from different countries.
Comparative ribotyping of Staphylococcus intermedius isolated from members of the Canoidea gives possible evidence for host-specificity and co-evolution of bacteria and hosts

A total of 41 Staphylococcus intermedius isolates were isolated from skin of healthy members of six phylogenetic groups within the Canoidea (the dog family, skunk subfamily, weasel subfamily, racoon family, red panda and bear family) of different geographical origin and compared by EcoRI ribotyping and cluster analysis. The S. intermedius isolates from the different families and subfamilies clustered together in separate groups, almost completely following the phylogenetic relationship of the animal hosts. These ribotype data indicate host-specificity of different types of S. intermedius and suggest co-evolution between the animal hosts within the Canoidea and S. intermedius.

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Contributors: Aarestrup, F. M.
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Antimicrobial growth promoter ban and resistance to macrolides and vancomycin in enterococci from pigs

Ninety-six enterococcus isolates from fecal samples of pigs receiving tylosin as an antimicrobial growth promoter and 59 isolates obtained in the same farms 5 to 6 months after the ban of antimicrobial growth promoters in Switzerland were tested for susceptibility to nine antimicrobial agents. A clear decrease in resistance to macrolides, lincosamides, and tetracycline was visible after the ban. Vancomycin-resistant Enterococcus faecium belonged to the same clonal lineage as vancomycin-resistant isolates previously isolated from Danish pigs.

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Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Boerlin, P., Wissing, A., Aarestrup, F. M., Frey, J., Nicolet, J.
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Scopus rating (2016): CiteScore 3.57 SJR 2.196 SNIP 1.4
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BFI (2015): BFI-level 1
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Web of Science (2015): Indexed yes
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Scopus rating (2014): CiteScore 3.84 SJR 2.231 SNIP 1.528
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BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.18 SJR 2.438 SNIP 1.63
Web of Science (2013): Impact factor 4.232
Antimicrobial resistance among Pseudomonas spp. and the Bacillus cereus group isolated from Danish agricultural soil

From four Danish pig farms, bacteria of Pseudomonas spp. and the Bacillus cereus group were isolated from soil and susceptibility towards selected antimicrobials was tested. From each farm, soil samples representing soil just before and after spread of animal waste and undisturbed agricultural soil, when possible, were collected. Soil from a well-characterized Danish farm soil (Hojbakkegaard) was collected for comparison. The Psudomonas spp. and B. cereus were chosen as representative for Gram-negative and Gram-positive indigenous soil bacteria to test the effect of spread of animal waste on selection of resistance among soil bacteria. No variations in resistance levels were observed between farms; but when the four differently treated soils were compared, resistance was seen for carbadox, chloramphenicol, nalidixan (nalidixic acid), nitrofurantoin, streptomycin and tetracycline for Pseudomonas spp., and for bacitracin, erythromycin, penicillin and streptomycin for the B. cereus group. Variations in resistance levels were observed when soil before and after spread of animal waste was compared, indicating an effect from spread of animal waste.
Antimicrobial resistance of thermophilic Campylobacter

Campylobacter has become the leading cause of zoonotic enteric infections in developed and developing countries worldwide. Antimicrobial resistance has emerged among Campylobacter mainly as a consequence of the use of antimicrobial agents in food animal production. Resistance to drugs of choice for the treatment of infections, macrolides and fluoroquinolones has emerged as a clinical problem and interventions to reduce this are recommended. Resistance to fluoroquinolones and macrolides is mediated by chromosomal mutations. Resistance to other relevant antimicrobial agents, mediated by acquired resistance genes, has not become widespread so far. However, resistance genes originating from both Gram-positive and Gram-negative bacterial species have been found, showing the potential for acquired resistance to emerge in Campylobacter.
Bakteriel resistens overfor desinfektionsmidler

General information
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Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Effect of abolishment of the use of antimicrobial agents for growth promotion on occurrence of antimicrobial resistance in fecal enterococci from food animals in Denmark

From 1995 to 2000, a total of 673 Enterococcus faecium and 1,088 Enterococcus faecalis isolates from pigs together with 856 E. faecium isolates from broilers were isolated and tested for susceptibility to four classes of antimicrobial agents used for growth promotion as part of the Danish program of monitoring for antimicrobial resistance. The four antimicrobials were avilamycin, erythromycin, vancomycin, and virginiamycin. Major changes in the use of antimicrobial agents for growth promotion have occurred during the last 6 years in Denmark. The government banned the use of avoparcin in 1995 and of virginiamycin in 1998. Furthermore, the producers have voluntarily stopped all use beginning in 1999. The avoparcin ban in 1995 was followed by a decrease in the occurrence of glycopeptide-resistant E. faecium (GRE) in broilers, from 72.7% in 1995 to 5.8% in 2000. The occurrence of glycopeptide resistance among isolates from pigs remained constant at around 20% from 1995 to 1997. It was shown that, in GRE from pigs, the genes encoding macrolide and glycopeptide resistance were genetically linked and that, following the decrease in the use of tylosin during 1998 and 1999, the occurrence of GRE in pigs decreased to 6.0% in 2000. From 1995 to 1997 the occurrence of erythromycin resistance among E. faecium and E. faecalis isolates from pigs was almost 90%. Use of tylosin decreased considerably during 1998 and 1999, and this decrease was followed by decreases in the occurrence of resistance to 46.7 and 28.1% among E. faecium and E. faecalis isolates from pigs, respectively. Erythromycin resistance among E. faecium isolates from broilers reached a maximum of 76.3% in 1997 but decreased to 12.7% in 2000 concomitantly with more limited use of virginiamycin. Use of virginiamycin increased from 1995 to 1997 and was followed by an increased occurrence of virginiamycin resistance among E. faecium isolates in broilers, from 27.3% in 1995 to 66.2% in 1997. In January 1998 the use of virginiamycin was banned in Denmark, and the occurrence of virginiamycin resistance decreased to 33.9% in 2000. Use of avilamycin increased from 1995 to 1996 and was followed by an increase in avilamycin resistance among E. faecium isolates from broilers, from 63.6% in 1995 to 77.4% in 1996. Since 1996 avilamycin usage has decreased, followed by a decrease in resistance to 4.8% in 2000. Our observations show that it is possible to reduce the occurrence of antimicrobial resistance in a national population of food animals when the selective pressure is removed. Cases in which resistance to vancomycin was linked to resistance to erythromycin were exceptions. In such cases resistance did not decrease until the use of both avoparcin and tylosin was limited.
Effekterne af ophørt anvendelse af antimikrobielle vækstfremmere på forekomst af resistens blandt produktionsdyr i Danmark

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Contributors: Aarestrup, F. M., Seyfarth, A. M., Emborg, H., Pedersen, K., Hendriksen, R. S., Bager, F.
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EmtA, a rRNA methyltransferase conferring high-level evernimicin resistance

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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.7 SJR 2.631 SNIP 0.987
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BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.95 SJR 2.956 SNIP 1.094
Web of Science (2015): Impact factor 3.761
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Scopus rating (2014): CiteScore 4.25 SJR 3.184 SNIP 1.218
Web of Science (2014): Impact factor 4.419
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BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.9 SJR 3.652 SNIP 1.301
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Web of Science (2013): Indexed yes
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ISI indexed (2012): ISI indexed yes
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BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 4.72 SJR 3.475 SNIP 1.285
Web of Science (2011): Impact factor 5.01
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 3.678 SNIP 1.203
Web of Science (2010): Impact factor 4.819
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.981 SNIP 1.333
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Forekomst, selektion og spredning af resistens overfor antimikrobielle stoffer. Sammendrag af doktorafhandling

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BFI (2012): BFI-level 1
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ISI indexed (2011): ISI indexed no
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BFI (2009): BFI-level 1
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Identification of a Tn1546-like (type 2) element in vancomycin-resistant Enterococcus faecium isolated from hospitalized patients in Japan

General information
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Contributors: Kariyama, R., Kumon, H., Hammerum, A. M., Aarestrup, F. M., Jensen, L. B.
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
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Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
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Scopus rating (2014): CiteScore 4.45 SJR 2.361 SNIP 1.428
Web of Science (2014): Impact factor 4.476
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.67 SJR 2.423 SNIP 1.411
Web of Science (2013): Impact factor 4.451
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.88 SJR 2.363 SNIP 1.5
Web of Science (2012): Impact factor 4.565
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 5.02 SJR 2.523 SNIP 1.574
Web of Science (2011): Impact factor 4.841
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.458 SNIP 1.54
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Macrolide resistance in Campylobacter coli of animal origin in Denmark

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Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Jensen, L. B., Aarestrup, F. M.
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Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
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Non-human reservoirs of enterococci

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Butaye, P., Witte, W., Gilmore, M. (ed.)
Pages: 55-99
Publication date: 2001

Host publication information
Title of host publication: The enterococci: Pathogenesis, Molecular Biology and Antibiotic Resistance
Place of publication: Washington DC, USA
Publisher: ASM Press
Edition: 1st
Source: orbit
Source-ID: 236035
Research output: Research - peer-review → Book chapter – Annual report year: 2001

Quinolone and macrolide resistance in Campylobacter jejuni and C-coli: Resistance mechanisms and trends in human isolates

The incidence of human Campylobacter jejuni and C. coli infections has increased markedly in many parts of the world in the last decade as has the number of quinolone-resistant and, to a lesser extent, macrolide-resistant Campylobacter strains causing infections. We review macrolide and quinolone resistance in Campylobacter and track resistance trends in human clinical isolates in relation to use of these agents in food animals. Susceptibility data suggest that erythromycin and other macrolides should remain the drugs of choice in most regions, with systematic surveillance and central measures maintained, but fluoroquinolones may now be of limited use in the empiric treatment of Campylobacter infections in many regions.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 24-34
Publication date: 2001
Peer-reviewed: Yes

Publication information
Journal: Emerging Infectious Diseases
Volume: 7
Issue number: 1
ISSN (Print): 1080-6040
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 4.78 SJR 3.278 SNIP 1.916
Web of Science (2017): Impact factor 7.422
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.92 SJR 3.426 SNIP 2.198
Web of Science (2016): Impact factor 8.222
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.23 SJR 3.101 SNIP 2.012
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.59 SJR 3.509 SNIP 2.406
Web of Science (2014): Impact factor 6.751
Spontaneous nisin-resistant Listeria monocytogenes mutants with increased expression of a putative penicillin-binding protein and their sensitivity to various antibiotics

A concern regarding the use of bacteriocins, as for example the lantibiotic nisin, for biopreservation of certain food products is the possibility of resistance development and potential cross-resistance to antibiotics in the target organism. The genetic basis for nisin resistance development is as yet unknown. We analyzed changes in gene expression following nisin resistance development in Listeria monocytogenes 412 by restriction fragment differential display. The mutant had increased expression of a protein with strong homology to the glycosyltransferase domain of high-molecular-weight penicillin-binding proteins (PBPs), a histidine protein kinase, a protein of unknown function, and ClpB (putative functions from homology). The three former proteins had increased expression in a total of six out of 10 independent mutants originating from five different wildtype strains, indicating a prevalent nisin resistance mechanism under the employed
isolation conditions. Increased expression of the putative PBP may affect the cell wall composition and thereby alter the sensitivity to cell wall-targeting compounds. The mutants had an isolate-specific increase in sensitivity to different beta-lactams and a slight decrease in sensitivity to another lantibiotic, mersacidin. A model incorporating these observations is proposed based on current knowledge of nisin's mode of action.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Gravesen, A., Sorensen, K., Aarestrup, F. M., Knochel, S.
Pages: 127-135
Publication date: 2001
Peer-reviewed: Yes

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Journal: Microbial Drug Resistance
Volume: 7
Issue number: 2
ISSN (Print): 1076-6294
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
Web of Science (2017): Impact factor 2.344
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
Web of Science (2016): Impact factor 2.306
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
Web of Science (2015): Impact factor 2.529
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
Web of Science (2014): Impact factor 2.49
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.87 SJR 1.265 SNIP 1.118
Web of Science (2013): Impact factor 2.524
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.45 SJR 0.963 SNIP 0.9
Web of Science (2012): Impact factor 2.364
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.76 SJR 1.163 SNIP 1.14
Web of Science (2011): Impact factor 2.153
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.054 SNIP 0.8
Web of Science (2010): Impact factor 1.936
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.915 SNIP 0.838
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.038 SNIP 0.73
Veterinary drug use in farm animal production and the antibiotic resistance problem

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 153-170
Publication date: 2001

Host publication information
Title of host publication: Food Safety Assurance and Veterinary Public Health: Food Safety Assurance in the Pre-Harvest Phase
Volume: 1
Place of publication: The Netherlands
Publisher: Wageningen Academic Publishers
Source: orbit
Source-ID: 236039
Research output: Research - peer-review › Book chapter – Annual report year: 2001

WHO Global Salm-Surv external quality assurance programme (EQAS): An important step towards improving the quality of Salmonella serotyping and antimicrobial susceptibility testing

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Publication date: 2001
Peer-reviewed: No
Event: Poster session presented at Proc. ASM Conference, Orlando, USA
Source: orbit
Source-ID: 245489
Research output: Research › Poster – Annual report year: 2001
Antibiotic use in food-animal production in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Contributors: Aarestrup, F. M., Seyfarth, A. M., Emborg, H., Bager, F., Pedersen, K., Jorsal, S. E.
Pages: 1-3
Publication date: 2000
Peer-reviewed: No

Publication information
Journal: APUA newsletter
Volume: 18
Original language: English
Source: orbit
Source-ID: 236421
Research output: Research › Journal article – Annual report year: 2000

Antimicrobial susceptibility and presence of resistance genes in staphylococci from poultry
The species distribution, susceptibility to 19 antimicrobial agents and presence of selected genes encoding resistance to macrolides, streptogramins and tetracyclines were examined among 118 staphylococcal isolates from infections of poultry in Denmark. Isolates were identified using a combination of conventional biochemical testing and 16S rDNA sequencing. The most common species were Staphylococcus aureus (83), Staphylococcus hyicus (11), Staphylococcus xylosus (9) and Staphylococcus cohnii (6). The isolates were susceptible to most antimicrobials tested. A high frequency of S. aureus (30%) was resistant to ciprofloxacin. Only six (7%) S. aureus isolates and one Staphylococcus saprophyticus were penicillin resistant. Resistance to sulphamethoxazole was observed among 16 (19%) of S. aureus isolates and two coagulase negative staphylococci (CNS). Twenty (24%) of the S. aureus isolates were resistant to erythromycin and 19 of these isolates contained the ermA gene, whereas the remaining isolate contained the ermC gene. Eleven (48%) of the novobiocin resistant CNS were resistant to erythromycin and all these isolates contained the ermA gene. Two isolates identified as S. xylosus, were found to be resistant to streptogramins and both contained the vatB- and the vgaB-genes. Thirty-nine (47%) of the S. aureus isolates, three of nine S. hyicus and eight of the 23 novobiocin resistant CNS were tetracycline resistant and all contained the tct(K) gene. A single S. aureus isolate also contained the tet(M) gene. The present study showed a frequent occurrence of resistance to fluoroquinolones, tetracycline and macrolides among staphylococci isolated from broilers in Denmark, whereas the occurrence of resistance to other antimicrobial agents remains low. Similar genes, encoding resistance to erythromycin, tetracycline and streptogramins to those previously observed, were detected.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, National Veterinary Institute, Division of Poultry, Fish and Fur Animals
Pages: 353-364
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
Volume: 74
Issue number: 4
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
Web of Science (2010): Impact factor 3.256
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.309 SNIP 1.466
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.164 SNIP 1.29
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.048 SNIP 1.315
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.03 SNIP 1.396
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.089 SNIP 1.259
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.873 SNIP 1.248
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.905 SNIP 1.181
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.905 SNIP 1.13
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.828 SNIP 1.051
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.699 SNIP 1.066
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.714 SNIP 1.089

Original language: English
Keywords: genetics, chicken, Staphylococcus spp., macrolide, tetracycline, Streptogramin, antimicrobial agents
DOIs: 10.1016/S0378-1135(00)00197-8
Antimicrobial susceptibility of *Staphylococcus aureus* isolated from bovine mastitis in Europe and the United States

Minimum inhibitory concentrations were determined for 811 strains of *Staphylococcus aureus* isolated from cases of bovine mastitis in 11 countries. The countries and number of isolates included Denmark (105), England (92), Finland (95), Germany (103), Iceland (22), Ireland (42), Norway (101), Sweden (123), Switzerland (69), United States (53), and Zimbabwe (6). The antimicrobial agents tested were penicillin, ampicillin, oxacillin, cephalothin, ceftiofur, amoxicillin + clavulanate, penicillin + novobiocin, enrofloxacin, premafloxacin, erythromycin, clindamycin, lincomycin, pirlimycin, neomycin, lincomycin + neomycin, and sulfamethazine. The MIC90 for these antimicrobial agents for all strains were 0.5, 1.0, 1.0, 0.5, 1.0, less than or equal to 0.06, 0.125, 0.125, less than or equal to 0.0078, 0.5, 1.0, 16.0, 1.0, 2.0, 0.5, and 4.0 μg/ml, respectively. Overall, only small variations between countries were seen in the MIC90 for the majority of compounds tested. Of the strains tested, 35.6% were positive for beta-lactamase production on initial testing, with an additional 21.3% positive after induction by penicillin. In conclusion, the overall level of resistance was generally low for all antimicrobial agents tested regardless of country. Given the differences in antimicrobial use in various countries, the widespread adoption of mastitis control programs to prevent infections limits the exposure of *S. aureus* infected animals to antimicrobial drugs.

**General information**

*State:* Published

*Organisations:* Division of Microbiology and Risk Assessment, National Food Institute

*Contributors:* De Oliveira, A. P., Watts, J. L., Salmon, S. A., Aarestrup, F. M.

*Pages:* 855-862

*Publication date:* 2000

*Peer-reviewed:* Yes

**Publication information**

*Journal:* Journal of Dairy Science

*Volume:* 83

*Issue number:* 4

*ISSN (Print):* 0022-0302

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- BFI (2018): BFI-level 2
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 2
- Scopus rating (2017): CiteScore 2.84 SJR 1.35 SNIP 1.491
- Web of Science (2017): Impact factor 2.749
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 2
- Scopus rating (2016): CiteScore 2.66 SJR 1.331 SNIP 1.484
- Web of Science (2016): Impact factor 2.474
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 2
- Scopus rating (2015): CiteScore 2.63 SJR 1.479 SNIP 1.488
- Web of Science (2015): Impact factor 2.408
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 2
- Scopus rating (2014): CiteScore 2.78 SJR 1.434 SNIP 1.504
- Web of Science (2014): Impact factor 2.573
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 2
- Scopus rating (2013): CiteScore 2.82 SJR 1.411 SNIP 1.589
- Web of Science (2013): Impact factor 2.55
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 2
- Scopus rating (2012): CiteScore 2.79 SJR 1.443 SNIP 1.717
- Web of Science (2012): Impact factor 2.566
Association between the use of avilamycin for growth promotion and the occurrence of resistance among Enterococcus faecium from broilers: Epidemiological study and changes over time

This study describes the changes in the occurrence of resistance to avilamycin among Enterococcus faecium from broilers in Denmark and the epidemiological association between usage of avilamycin for growth promotion and the occurrence of avilamycin-resistant E. faecium on broiler farms. The consumption of avilamycin for growth promotion increased from 10 kg in 1990 to 2,740 kg 1996 and decreased in the following years to only 7 kg in 1998, Most of this has been used for broilers. As part of the nationwide monitoring program for antimicrobial resistance, a total of 473 E, faecium isolates from broilers and 290 isolates from pigs have been tested for their susceptibility to avilamycin from 1995 to 1998, A very limited number of isolates from pigs were resistant to avilamycin, whereas the occurrence of resistance among isolates from broilers increased from 63.6% at the end of 1995 to a maximum of 80.7% during the last half of 1996, Since then, the occurrence of resistance has decreased to 23.3% in the last half of 1998, The epidemiological association between consumption of avilamycin and occurrence of resistant E. faecium fecal droppings were examined on 10 poultry farms that had not used avilamycin for growth promotion during 1996 or 1997 and eight farms that had used avilamycin during 1997, We tested a total of E, faecium isolates from the exposed farms and 104 from the nonexposed farms for their susceptibility to avilamycin, Resistant isolates were found on all eight exposed farms, and on seven of 10 nonexposed farms, Sixty-four isolates (72%) from the exposed farms were resistant, compared with 24 (23%) of the isolates from nonexposed farms. The adjusted chi-square p value equaled 0.01065, and showed a significant association between use of avilamycin and occurrence of resistance. The national monitoring program showed a decrease in the occurrence of resistance following a decreased use of avilamycin in Denmark, and the epidemiological study showed a statistically significant association between the use of avilamycin for growth promotion and the occurrence of avilamycin-resistant E. faecium on broiler farms.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Contributors: Aarestrup, F. M., Bager, F., Andersen, J. S.
Pages: 71-75
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Microbial Drug Resistance
Volume: 6
Issue number: 1
ISSN (Print): 1076-6294
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
Web of Science (2017): Impact factor 2.344
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
Web of Science (2016): Impact factor 2.306
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
Web of Science (2015): Impact factor 2.529
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
Web of Science (2014): Impact factor 2.49
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.87 SJR 1.265 SNIP 1.118
Web of Science (2013): Impact factor 2.524
Associations between the use of antimicrobial agents for growth promotion and the occurrence of resistance among Enterococcus faecium from broilers and pigs in Denmark, Finland, and Norway

This study compares the susceptibility of Enterococcus faecium isolated from pigs and poultry in Denmark, Finland, and Norway to antimicrobial agents used for growth promotion. E. faecium was isolated from 211 broilers and 55 pigs in Denmark in 1997, from Norwegian 55 poultry farms (turkey and broiler farms) and 4 swine farms between 1995 and 1997, and Finnish poultry (52) and swine (43) in 1996 and examined for susceptibility to avilamycin, avoparcin, bacitracin, flavomycin, monensin, salinomycin, spiramycin, tylosin, and virginiamycin. Only a limited number of isolates were categorized as resistant to monensin or salinomycin. In general, an association between the usage of antimicrobials in the respective countries and the occurrence of associated resistance was observed. Resistance to avilamycin was frequently observed among isolates from broilers in Denmark, where avilamycin has been used, whereas all isolates from Finland and Norway, where these drugs have not been used, were susceptible. The same phenomenon could be observed for avoparcin, bacitracin, tylosin, and virginiamycin; resistance was frequently observed among isolates from where these antimicrobials have been widely used, but rarely among isolates from where the use has been limited. Also for avoparcin and bacitracin, an association between usage and occurrence of resistance was observed. All isolates categorized as avoparcin resistant contained the vanX gene; isolates from broilers had the T variant in position 8,234 and...
isolates from pigs the G variant. Three (1%) of the 222 isolates resistant to tylosin contained the ermA gene and 196 (88%) ermB. Sixteen (11%) of the 146 virginiamycin-resistant isolates from broilers and two (7%) of the 27 virginiamycin-resistant isolates from pigs in Denmark contained the satA gene, whereas satA was not observed among any of the virginiamycin-resistant isolates from Finland. A total of 72% of the virginiamycin-resistant E. faecium from broilers in Denmark and all nine virginiamycin-resistant E. faecium from Finland contained satG. This gene was also observed among two (7%) of the virginiamycin-resistant isolates from pigs in Denmark. This study indicates that the use of antimicrobial agents for growth promotion in Denmark, Finland, and Norway have selected for resistance to most of these drugs among E. faecium in food animals.
Scopus rating (2009): SJR 0.915 SNIP 0.838
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.038 SNIP 0.73
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.042 SNIP 0.764
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.319 SNIP 0.908
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.998 SNIP 0.968
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.364 SNIP 0.983
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.303 SNIP 1.029
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.42 SNIP 0.918
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.791 SNIP 1.006
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.902 SNIP 1.36
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.563 SNIP 1.031
Original language: English
Source: orbit
Source-ID: 230803
Research output: Research - peer-review › Journal article – Annual report year: 2000

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Pages: 26-27
Publication date: 2000
Peer-reviewed: No

Publication information
Journal: Bovilogisk - om kvægbrug
Volume: 12
Original language: Danish
Source: orbit
Source-ID: 236424
Research output: Research › Journal article – Annual report year: 2000

Characterisation of streptomycin resistance determinants in Danish isolates of Salmonella typhimurium
Fifty six Danish streptomycin (Sm) resistant isolates of Salmonella enterica serotype Typhimurium from pigs (n=34), calves (n=3) and humans (n=19) were characterised with respect to co-resistances (14 drugs), transferability of Sm-resistance by conjugation, genetic determinants encoding Sm-resistance and diversity with respect to localisation of genes in the genome and DNA-sequences. Forty-six strains carried resistance(s) other than Sm-resistance. Nineteen different co-resistance patterns were observed and tetracycline was the most commonly observed resistance in these patterns. In 22 of the strains, Sm-resistance was transferred by conjugation. Eleven strains contained the gene aadA only, six strains contained aadA+strA+strB, and 35 strains contained strA+strB. Partial sequences of aadA were obtained from four strains. Three strains showed identical sequences to a published aadA sequence from the transposon Tn7, and in one strain the sequence showed one synonymous substitution compared to this sequence. Partial sequences were obtained of strA and strB in seven strains, The sequence of strB was identical to the published sequence of the plasmid RSF1010 in all strains. All seven sequences of sri-A were identical and differed from the sequence of strA in RSF1010 by two non-synonymous substitutions. (C) 2000 Elsevier Science B.V. All rights reserved.

General information
Characterization of aminoglycoside resistance genes and class 1 integrons in porcine and bovine gentamicin-resistant Escherichia coli

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Technical University of Denmark
Contributors: Sandvang, D., Aarestrup, F. M.
Pages: 19-27
Publication date: 2000
Peer-reviewed: Yes
Characterization of glycopeptide-resistant Enterococcus faecium (GRE) from broilers and pigs in Denmark: Genetic evidence that persistence of GRE in pig herds is associated with coselection by resistance to macrolides

Glycopeptide-resistant enterococci (GRE) from broilers and pigs were characterized to investigate the background for the persistence of GRE in pig herds. All porcine isolates belonged to closely related pulsed-field gel electrophoretic (PFGE) types, with the ermB and vanA genes located on the same transferable genetic element. Broiler isolates belonged to different PFGE types. The persistence of GRE in Danish pig herds after the ban of glycopeptides may be explained by the genetic link between ermB and vanA and coselection by use of macrolides for treatment and growth promotion.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Characterization of Salmonella enterica Serovar Typhimurium DT104 Isolated from Denmark and Comparison with Isolates from Europe and the United States

A total of 136 isolates of Salmonella enterica serovar Typhimurium DT104 from Denmark (n = 93), Germany (n = 10), Italy (n = 4), Spain (n = 5), and the United Kingdom (n = 9) were characterized by antimicrobial resistance analysis, plasmid profiling, pulsed-field gel electrophoresis (PFGE) with the restriction enzymes XbaI and BlnI, and analysis for the presence of integrons and antibiotic resistance genes. The isolates from Denmark were from nine pig herds, while the isolates from other countries were both of animal and of human origin. All but 10 isolates were resistant to ampicillin, chloramphenicol, spectinomycin, streptomycin, sulfonamides, and tetracycline. Five isolates from the United Kingdom and Spain were sensitive to all antibiotics examined, whereas four isolates from the United Kingdom and the United States were also resistant to one or more of the antibiotics, namely, gentamicin, neomycin, and trimethoprim. All but two strains had the same PFGE profiles when the XbaI restriction enzyme was used, while seven different profiles were observed when the BlnI restriction enzyme was used. Different dominating BlnI types were observed among European isolates compared with those from the United States. All the isolates harbored common 95-kb plasmids either alone or in combination with smaller plasmids, and a total of 11 different plasmid profiles were observed. Furthermore, all but one of the multidrug-resistant isolates contained two integrons, ant(3')-Ia and pse-l. Sensitive isolates contained no integrons, and isolates that were resistant to spectinomycin, streptomycin, and sulfonamides had only one integron containing ant(3').-Ia. When restriction enzyme BlnI was used, the 14 isolates from one of the nine herds in Denmark showed unique profiles, whereas isolates from the remaining herds were homogeneous. Among isolates from seven of nine herds, the same plasmid profile (95 kb) was observed, but isolates from two herds had different profiles. Thus, either PFGE (with BlnI) or plasmid profiling could distinguish isolates from three of nine pig herds in Denmark. The epidemiological markers (antimicrobial susceptibility testing, plasmid profiling, and PFGE) applied demonstrated high in vivo stability in the Danish herds. This may indicate that some different strains of multidrug-resistant S. enterica serovar Typhimurium DT104 have been introduced into Danish food animal herds. The presence of isolates from six different countries with similar profiles by PFGE with XbaI and highly homogeneous profiles by PFGE with BlnI indicate that multidrug-resistant S. enterica serovar Typhimurium DT104 has probably been spread clonally in these countries. However, some minor variation could be observed by using plasmid profiling and profiling by PFGE with BlnI. Thus, a more sensitive technique for subtyping of strains of DT104 and a broader investigation may help in elucidating the epidemiological spread of DT104 in different parts of the world.
Characterization of vancomycin-resistant and vancomycin-susceptible Enterococcus faecium isolates from humans, chickens and pigs by RiboPrinting and pulsed-field gel electrophoresis

Forty-eight vancomycin-resistant and 35 vancomycin-sensitive Danish Enterococcus faecium isolates obtained from pigs, chickens and humans, as well as the human vanA reference isolate BM4147, were characterized by EcoRI RiboPrinting and Smal pulsed-field gel electrophoresis. RiboPrinting of the 84 isolates yielded 40 types whereas PFGE-typing yielded 57 types discriminated by differences in more than three bands. By molecular typing, both clonal spread of E. faecium as well as horizontal transmission of Tn1546 between animals and humans was supported. Furthermore, it was found that the population of E. faecium spreads freely between the animal and human reservoir.

General information

State: Published
Organisations: Department of Microbiology, Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Hammerum, A. M., Fussing, V., Aarestrup, F. M., Wegener, H. C.
Pages: 677-680
Publication date: 2000
Peer-reviewed: Yes

Publication information

Journal: JOURNAL OF ANTIMICROBIAL CHEMOTHERAPY
Volume: 45
Issue number: 5
ISSN (Print): 0305-7453
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.34 SJR 2.419 SNIP 1.568
Web of Science (2017): Impact factor 5.217
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Impact factor 5.071
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.06 SJR 2.259 SNIP 1.516
Web of Science (2015): Impact factor 4.919
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.61 SJR 2.298 SNIP 1.765
Web of Science (2014): Impact factor 5.313
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.7 SJR 2.479 SNIP 1.824
Comparison of antimicrobial resistance phenotypes and resistance genes in Enterococcus faecalis and Enterococcus faecium from humans in the community, broilers and pigs in Denmark

Enterococcus faecalis and E. faecium isolated from humans in the community (98 and 65 isolates), broilers (126 and 122), and pigs (102 and 88) during 1998 were tested for susceptibility to 12 different antimicrobial agents and for the presence of selected genes encoding resistance using PCR. Furthermore, the presence of vancomycin resistant enterococci was examined in 38 human stool samples using selective enrichment. Widespread resistance to chloramphenicol, macrolides, kanamycin, streptomycin, and tetracycline was found among isolates from all three sources. All E. faecium isolates from humans and pigs were susceptible to avilamycin, whereas 35% of isolates from broilers were resistant. All E. faecium isolates from humans were susceptible to vancomycin, whereas 10% and 17% of isolates from broilers and pigs, respectively, were resistant. A vancomycin resistant E. faecium isolate was found in one of the 38 human fecal samples examined using selective enrichment. All vancomycin resistant isolates contained the vanA gene, all chloramphenicol resistant isolates the catIP501 gene, and all five gentamicin resistant isolates the aac6-aph2 gene. Sixty-one (85%) of 72 erythromycin resistant E. faecalis examined and 57 (90%) of 63 erythromycin resistant E. faecium isolates examined
contained ermB. Forty (91%) of the kanamycin resistant E. faecalis and 18 (72%) of the kanamycin resistant E. faecium isolates contained aphA3. The tet(M) gene was found in 95% of the tetracycline resistant E. faecalis and E. faecium isolates of human and animal origin, examined. tet(K) was not observed, whereas tet(L) was detected in 17% of tetracycline resistant E. faecalis isolates and in 16% of the E. faecium isolates. tet(O) was not detected in any of the isolates from pigs, but was observed in 38% of E. faecalis isolates from broilers, in two E. faecalis isolates from humans and in three E. faecium isolates from broilers. tet(S) was not detected among isolates from animals, but was observed in 31% of E. faecalis and one E. faecium isolate from humans. This study showed a frequent occurrence of antimicrobial resistance and the presence of selected resistance genes in E. faecalis and E. faecium isolated from humans, broilers and pigs. Differences in the occurrence of resistance and tetracycline resistance genes were observed among isolates from the different sources. However, similar resistance patterns and resistance genes were detected frequently indicating that transmission of resistant enterococci or resistance genes takes place between humans, broilers, and pigs.

**General information**

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Technical University of Denmark
Contributors: Aarestrup, F. M., Agersø, Y., Gerner-Smidt, P., Madsen, M., Jensen, L. B.
Pages: 127-137
Publication date: 2000
Peer-reviewed: Yes

**Publication information**
Journal: Diagnostic Microbiology and Infectious Disease
Volume: 37
Issue number: 2
ISSN (Print): 0732-8893
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.4 SJR 1.157 SNIP 0.899
Web of Science (2017): Impact factor 2.341
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.62 SJR 1.237 SNIP 1.041
Web of Science (2016): Impact factor 2.401
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.57 SJR 1.187 SNIP 1.029
Web of Science (2015): Impact factor 2.45
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.55 SJR 1.203 SNIP 0.989
Web of Science (2014): Impact factor 2.457
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.67 SJR 1.281 SNIP 1.076
Web of Science (2013): Impact factor 2.568
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.54 SJR 1.144 SNIP 1.056
Web of Science (2012): Impact factor 2.26
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.6 SJR 1.229 SNIP 1.067
Web of Science (2011): Impact factor 2.528
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.259 SNIP 1.107
Web of Science (2010): Impact factor 2.426
BFI (2009): BFI-level 1
Dealing with antimicrobial resistance - the Danish experience

Following the discovery in 1994 and 1995 that use of the glycopeptide antimicrobial avoparcin for growth promotion was associated with the occurrence of vancomycin resistant Enterococcus faecium in food animals and in food, the Danish Minister of Food, Agriculture and Fisheries banned the use of avoparcin in May 1995. The ban was later extended by the European Commission to include all EU member states. In May 1999, the EU Scientific Steering Committee recommended that use for growth promotion of antimicrobials, which are or may be used in human or veterinary medicine should be phased out as soon as possible and ultimately abolished. During the first half of the 1990s the consumption of tetracyclines, mainly in pig production, increased markedly. This was countered by severely reducing through legal means the financial enticement for veterinarians to prescribe medicines and by restricting the availability of tetracycline as non-registered speciality products. The focus on consumption of antimicrobials and on resistance prompted a number of initiatives by Danish authorities to limit the increase in antimicrobial resistance. One such initiative was the implementation of an integrated programme (DANMAP), which monitors resistance among bacteria from food animals, food and humans. A programme to monitor all use of prescription medicine in food animals at the herd level is presently being implemented. Another initiative was the elaboration of a series of practical recommendations to veterinarians on the prudent use of antimicrobials in order to reduce the development of resistance without compromising therapeutic efficacy. Our experience with avoparcin shows that a restrictive policy on the use of antimicrobials can curb the development of resistance. However, the occurrence and persistence of specific resistance phenotypes is the end-result of complex interactions of, among others, antimicrobial co-selection, clonal spread of resistant strains and Various herd management factors.

General information
State: Published
Organisations: Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Bager, F., Aarestrup, F. M., Wegener, H. C.
Pages: 223-228
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Canadian Journal of Animal Science
Volume: 80
Issue number: 2
ISSN (Print): 0008-3984
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 0.99 SJR 0.403 SNIP 0.708
Web of Science (2017): Impact factor 0.657
Diagnosis and Antimicrobial Susceptibility of Campylobacter species

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 45-66
Publication date: 2000
DNA-baserede metoder til påvisning, identifikation og karakterisering af bakterier på SVS

General information
State: Published
Organisations: Bacteriology & Pathology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Microbial Ecology, Management
Pages: 12-23
Publication date: 2000
Peer-reviewed: No

Publication information
Journal: Dansk Veterinærtidsskrift
Volume: 83
Issue number: 3
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 236420
Research output: Research Journal article – Annual report year: 2000

Effect of Intervention on the occurrence of antimicrobial resistance

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Seyfarth, A. M.
Pages: 99-103
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Acta Veterinaria Scandinavica (Print Edition)
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Impact factor 1.472
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.98 SJR 0.644 SNIP 1.641
Web of Science (2015): Impact factor 1.23
Emergence of resistance to fluoroquinolones among bacteria causing infections in food animals in Denmark from 1993 to 1998

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, N. E., Jorsal, S. E., Nielsen, T. K.
Epidemiology and ecology of enterococci, with special reference to antibiotic resistant strains, in animals, humans and the environment - Example of an ongoing project within the European research programme

The objectives of the present study are to generate knowledge of the ecology and epidemiology of enterococci in the food chain by studying the following: (1) the population structure (in measures of abundance, number of vancomycin resistant strains, antibiotic resistance patterns, diversity, and stability) among enterococcal populations in different geographical regions and in different links of the food chain (2) possible transmission of strains through the food chain and between hospital environments and the food chain (3) the association between vancomycin resistance and individual strains of enterococci and (4) the diversity of the drug resistance genes in enterococci. So far, 1578 samples have been collected from different countries within the EU (Sweden, Denmark, UK and Spain), and from different habitats (pig farms, carcasses in slaughter houses, soil, manure, water, sewage, and humans). Total and vancomycin resistant enterococcal populations in each sample have been enumerated and more than 12 000 isolates have been characterised by phenotyping. Representative isolates are further species identified and characterised by genotyping and MIC determination and from antibiotic resistant isolates the resistance genes are characterised. (C) 2000 Elsevier Science B.V. and International Society of Chemotherapy. All rights reserved.
External Quality Assurance System (EQAS) of the WHO Global Salmonella Surveillance and Laboratory Support Project (Global Salm-Surv)

To assure the quality of methods for serotyping and antimicrobial susceptibility testing among laboratories in WHO Global Salm-Surv, an international collaborative study on serotyping and antimicrobial susceptibility testing of eight Salmonella enterica strains was performed. A total of 44 laboratories in 35 countries participated. For serotyping, 76% of the results were correct. For susceptibility testing, 92% of the results for the eight Salmonella strains were in agreement with the expected results. However, 28% of the performed tests with the E. coli ATCC 25922 reference strain were out of the quality control range specified by NCCLS guidelines.

General information
State: Published
Fluoroquinolone resistance in Salmonella: A web discussion

General information
State: Published
Organisations: Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Carnevale, R., Mølbak, K., Bager, F., Aarestrup, F. M.
Pages: 128-130
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Clinical Infectious Diseases
Volume: 31
Issue number: 1
ISSN (Print): 1058-4838
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 5.42 SJR 5.051 SNIP 2.795
Web of Science (2017): Impact factor 9.117
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.88 SJR 4.614 SNIP 2.56
Web of Science (2016): Impact factor 8.216
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 5.47 SJR 4.827 SNIP 3.001
Web of Science (2015): Impact factor 8.736
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 6.11 SJR 5.258 SNIP 3.415
Web of Science (2014): Impact factor 8.886
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 6.37 SJR 4.751 SNIP 3.298
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 6.25 SJR 4.573 SNIP 3.193
Web of Science (2012): Impact factor 9.374
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 6.09 SJR 4.292 SNIP 3.233
ISI indexed (2011): ISI indexed yes
Genetic comparison of Tn1546-like elements in vancomycin-resistant enterococci isolated from hospitalized patients in Japan and from human and animals in Europe

State: Published
Organisations: Department of Microbiology, Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Kariyama, R., Hammerum, A. M., Aarestrup, F. M., Jensen, L. B.
Publication date: 2000
Peer-reviewed: No
Event: Poster session presented at The 1st International ASM conference on Enterococci, Banff, Canada.
Source: orbit
Source-ID: 236025
Research output: Research › peer-review › Editorial – Annual report year: 2000

Linkage of vat(E) and erm(B) in streptogramin-resistant Enterococcus faecium isolates from Europe

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Microbiology
Contributors: Jensen, L. B., Hammerum, A. M., Aarestrup, F. M.
Pages: 2231-2232
Publication date: 2000
Peer-reviewed: Yes

Publication Information
Journal: ANTIMICROBIAL AGENTS AND CHEMOTHERAPY
Volume: 44
Issue number: 8
ISSN (Print): 0066-4804
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Linkage of vatE and ermB in streptogramin resistant Enterococcus faecium isolates from Europe

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Microbiology
Contributors: Jensen, L. B., Hammerum, A. M., Aarestrup, F. M.
Pages: 2231-2232
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Antimicrobial Agents and Chemotherapy
Volume: 44
Issue number: 8
ISSN (Print): 0066-4804
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.15 SJR 2.291 SNIP 1.263
Web of Science (2017): Impact factor 4.255
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.45 SJR 2.361 SNIP 1.428
Web of Science (2014): Impact factor 4.476
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.67 SJR 2.423 SNIP 1.411
Web of Science (2013): Impact factor 4.451
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.88 SJR 2.363 SNIP 1.5
Web of Science (2012): Impact factor 4.565
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 5.02 SJR 2.523 SNIP 1.574
Web of Science (2011): Impact factor 4.841
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.458 SNIP 1.54
Web of Science (2010): Impact factor 4.672
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.424 SNIP 1.65
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.45 SNIP 1.448
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.167 SNIP 1.49
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.339 SNIP 1.401
Scopus rating (2005): SJR 2.321 SNIP 1.52
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.929 SNIP 1.614
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.208 SNIP 1.644
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 2.173 SNIP 1.553
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.334 SNIP 1.542
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.899 SNIP 1.617
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.884 SNIP 1.596
Original language: English
Source: orbit
Source-ID: 245955
Research output: Research - peer-review › Journal article – Annual report year: 2000

Medicin, sundhed og antibiotikaresistens

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2000
Peer-reviewed: No

Publication information
Journal: Kongeå-projektet - et nyhedsbrev fra Mejeriforeningen
Volume: 5
Original language: Danish
Source: orbit
Source-ID: 236423
Research output: Research › Journal article – Annual report year: 2000

Occurence, selection and spread of resistance to antimicrobial agents used for growth promotion in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Pages: 1-48
Publication date: 2000
Occurrence, selection and spread of resistance to antimicrobial agents used for growth promotion for food animals in Denmark

General information
State: Published
Organisations: Danish Veterinary Laboratory
Contributors: Aarestrup, F. M.
Publication date: 2000

Publication information
Original language: English
Source: orbit
Source-ID: 236327
Research output: Research › Doctoral thesis – Annual report year: 2000

Ødemsyge i danske svinebesætninger

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Jorsal, S. E., Johansen, M., Ahrens, P., Aarestrup, F. M., Bækbo, P.
Pages: 6-11
Publication date: 2000
Peer-reviewed: No

Publication information
Journal: Dansk Veterinær Tidsskrift
Volume: 83
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 236419
Research output: Research › Journal article – Annual report year: 2000

Pharmacodynamics of amoxicillin and danofloxacin against Salmonella Typhimurium in an in vitro pharmacodynamic model

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Lindecrona, R. H., Friis, C., Aarestrup, F. M.
Pages: 261-264
Presence of variations in ribosomal protein L16 corresponding to susceptibility to oligosaccharides (avilamycin and everninomycin) among enterococci

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, L. B.
Publication date: 2000
Peer-reviewed: No
Event: Poster session presented at The 1st International ASM conference on Enterococci, Banff, Canada.
Source: orbit
Source-ID: 246152
Research output: Research › Poster – Annual report year: 2000

Presence of variations in ribosomal protein L16 corresponding to susceptibility of enterococci to oligosaccharides (avilamycin and evernimicin)

Fragments (414 bp) of the gene encoding ribosomal protein L16 from Enterococcus faecium and Enterococcus faecalis that were resistant and susceptible to the oligosaccharide antibiotics avilamycin and evernimicin (SCH 27899) were sequenced and compared. The susceptible E. faecalis and E.faecium isolates had sequences that were similar to those of the type strains. All resistant E.faecalis isolates contained the same base pair variation [CGT (Arg-56) --> CAT (His-56)]. The same variation and two additional variations [ATC (Ile-52) --> ACC (Thr-52) and ATC (Ile-52) --> AGC (Ser-52)] were found in the resistant E.faecium isolates. This study indicated that resistance to the oligosaccharides in enterococci is associated with variations in the ribosomal protein L16.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, L. B.
Pages: 3425-3427
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: ANTIMICROBIAL AGENTS AND CHEMOTHERAPY
Volume: 44
Issue number: 12
ISSN (Print): 0066-4804
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.15 SJR 2.291 SNIP 1.263
Web of Science (2017): Impact factor 4.255
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
Quinolone Resistance among Salmonella enterica from Cattle, Broilers and Swine in Denmark

This study was conducted to determine the susceptibility to nalidixic acid and fluoroquinolones of Salmonella Dublin, S. Enteritidis, and S. Typhimurium isolates from cattle, broilers, and pigs over time in Denmark and to characterise the gyrA,
gyrB, and parC genes in quinolone-resistant isolates. A total of 584 S. Typhimurium and 573 S. Dublin isolates from cattle during 1984 through 1999, and 241 S. Enteritidis and 131 S. Typhimurium from broilers and 452 S. Typhimurium from pigs isolated during 1997-1999 were tested. All isolates from cattle from the period 1984 through 1992 were susceptible to quinolones. A single (1.1%) S. Typhimurium isolate from 1995 and three (5.9%) from 1998 were resistant to nalidixic acid. Six (9.0%) S. Dublin isolates from 1996, four (4.2%) from 1997, and one (1.7%) from 1998 were resistant to nalidixic acid. Resistance was not observed among isolates from cattle in 1999. All broiler isolates from 1997 except for one were susceptible to nalidixic acid, whereas seven (6.2%) S. Enteritidis and two (6.3%) of the S. Typhimurium isolates from 1998 and 9 S. Enteritidis (26.5%) from 1999 were resistant. Among isolates from pigs, four isolates from 1997, three from 1998, and one from 1999 were resistant to nalidixic acid. All the nalidixic acid-resistant isolates had reduced susceptibility to fluoroquinolones. Sequence analysis of the gyrA gene in 37 nalidixic-resistant isolates identified two different base substitutions at codon serine-83 and two at aspartate-87. The base substitutions in serine-83 were TCC (Ser)-->TAC (Tyr), and TCC (Ser)-->TTC (Phe). The base substitutions in aspartic-87 were GAC (Asp)--->AAC (Asn), and GAC (Asp)--->GGC (Gly). Sequence analysis of the gyrB and parC genes revealed no mutations in 27 selected isolates. This study showed that quinolone-resistant isolates have emerged in recent years among food-producing animals, especially among S. Enteritidis from broilers in Denmark, and that the resistance mainly is associated with mutations in gyrA.
Stop for udvikling af antibiotikum

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2000
Peer-reviewed: No

Publication information
Journal: Fødevareministeriets eksterne ugebrev
Original language: Danish
Source: orbit
Source-ID: 236374
Research output: Research - peer-review › Journal article – Annual report year: 2000

The consequences of discontinued use of antimicrobial growth promoters (AGP's) for food producing animals in Denmark

General information
State: Published
Organisations: Communications and Management Secretariat, National Food Institute, Division of Microbiology and Risk Assessment, Department of Microbiology, Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Publication date: 2000
Peer-reviewed: No
The dynamics of Staphylococcus aureus intramammary infection in nine Danish dairy herds

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 89-102
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
Volume: 67
Issue number: 1-2
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
The pharmacodynamic effect of amoxicillin and danofloxacin against Salmonella typhimurium in an in-vitro pharmacodynamic model

The pharmacodynamic effect of amoxicillin and danofloxacin against two strains of Salmonella typhimurium was examined in an in-vitro pharmacodynamic model. For amoxicillin, peak concentrations of 1, 2 and 4 mg ml(-1) and half-lives (t(1/2)) of 3 and 15 hours were evaluated. For danofloxacin peak concentrations of 0.25, 0.50 and 1.50 mg ml(-1) and half-lives of 7 and 15 hours were examined. For amoxicillin both the peak concentration and the half-life influenced the pharmacodynamic effect (P <0.001). Maximal pharmacodynamic effect was observed when the antibiotic concentration was greater than minimum inhibitory concentration for 79 per cent or more of the dosing interval. The hires of the isolates increased when the amoxicillin concentrations were close to the nac during the first hours of exposure. For danofloxacin the pharmacodynamic effect was dependent on the peak concentration only (P <0.001). Increases in MIC were found in two cases with the less susceptible strain, where peak concentration/MIC ratios were equal to or less than 4.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Technical University of Denmark
Contributors: Lindecrona, R., Friis, C., Aarestrup, F. M.
Pages: 261-264
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Research in Veterinary Science
Volume: 68
Issue number: 3
ISSN (Print): 0034-5288
Ratings:
BFI (2018): BFI-level 2
The use of antimicrobial agents and the occurrence of antimicrobial resistance among food animals in Taiwan

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 2000

Association between the consumption of antimicrobial agents in animal husbandry and the occurrence of resistant bacteria among food animals
Antimicrobial agents are used in food animals for therapy and prophylaxis of bacterial infections and in feed to promote growth. The use of antimicrobial agents for food animals may cause problems in the therapy of infections by selecting for resistance among bacteria pathogenic for animals or humans. The emergence of resistant bacteria and resistance genes following the use of antimicrobial agents is relatively well documented and it seems evident that all antimicrobial agents will select for resistance. However, current knowledge regarding the occurrence of antimicrobial resistance in food animals, the quantitative impact of the use of different antimicrobial agents on selection for resistance and the most appropriate treatment regimens to limit the development of resistance is incomplete. Surveillance programmes monitoring the occurrence and development of resistance and consumption of antimicrobial agents are urgently needed, as is research into the most appropriate ways to use antimicrobial agents in veterinary medicine to limit the emergence and spread of antimicrobial resistance. (C) 1999 Elsevier Science B.V. and International Society of Chemotherapy. All rights reserved.
Associations of Streptococcus suis serotype 2 ribotype profiles with clinical disease and antimicrobial resistance

A total of 122 Streptococcus suis serotype 2 strains were characterized thoroughly by comparing clinical and pathological observations, ribotype profiles, and antimicrobial resistance. Twenty-one different ribotype profiles were found and compared by cluster analysis, resulting in the identification of three ribotype clusters. A total of 58% of all strains investigated were of two ribotypes belonging to different ribotype clusters. A remarkable relationship existed between the observed ribotype profiles and the clinical-pathological observations because strains of one of the two dominant ribotypes were almost exclusively isolated from pigs with meningitis, while strains of the other dominant ribotype were never associated with meningitis. This second ribotype was isolated only from pigs with pneumonia, endocarditis, pericarditis, or septicemia. Cluster analysis revealed that strains belonging to the same ribotype cluster as one of the dominant ribotypes came from pigs that showed clinical signs similar to those of pigs infected with strains with the respective dominant ribotype profiles. Furthermore, strains belonging to different ribotype clusters had totally different patterns of resistance to antibiotics because strains isolated from pigs with meningitis were resistant to sulfamethoxazole and strains isolated...
from pigs with pneumonia, endocarditis, pericarditis, or septicemia were resistant to tetracycline.
An outbreak of multidrug-resistant, quinolone-resistant Salmonella enterica serotype typhimurium DT104

Background Food-borne salmonella infections have become a major problem in industrialized countries. The strain of Salmonella enterica serotype typhimurium known as definitive phage type 104 (DT104) is usually resistant to five drugs: ampicillin, chloramphenicol, streptomycin, sulfonamides, and tetracycline. An increasing proportion of DT104 isolates also have reduced susceptibility to fluoroquinolones. Methods The Danish salmonella surveillance program determines the phage types of all typhimurium strains from the food chain, and in the case of suspected outbreaks, five-drug-resistant strains are characterized by molecular methods. All patients infected with five-drug-resistant typhimurium are interviewed to obtain clinical and epidemiologic data. In 1998, an outbreak of salmonella occurred, in which the strain of typhimurium DT104 was new to Denmark. We investigated this outbreak and report our findings here. Results Until 1997, DT104 infections made up less than 1 percent of all human salmonella infections. The strain isolated from patients in the first community outbreak of DT104 in Denmark, in 1998, was resistant to nalidixic acid and had reduced susceptibility to fluoroquinolones. The outbreak included 25 culture-confirmed cases. Eleven patients were hospitalized, and two died. The molecular epidemiology and data from patients indicated that the primary source was a Danish swine herd. Furthermore, the investigation suggested reduced clinical effectiveness of treatment with fluoroquinolones. Conclusions Our investigation of an outbreak of DT104 documented the spread of quinolone-resistant bacteria from food animals to humans; this spread was associated with infections that were difficult to treat. Because of the increase in quinolone resistance in salmonella, the use of fluoroquinolones in food animals should be restricted. (N Engl J Med 1999;341:1420-5.) (C)1999, Massachusetts Medical Society.
Ratings:
BFI (2018): BFI-level 3
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 14.75 SJR 19.476 SNIP 13.405
Web of Science (2017): Impact factor 79.258
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 12.82 SJR 18.009 SNIP 14.79
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 12.5 SJR 16.591 SNIP 15.538
Web of Science (2015): Impact factor 59.558
BFI (2014): BFI-level 2
Web of Science (2014): Impact factor 55.873
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 12.21 SJR 14.796 SNIP 15.59
Web of Science (2013): Impact factor 54.42
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 12.09 SJR 13.984 SNIP 15.598
Web of Science (2012): Impact factor 51.658
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 11.7 SJR 13.674 SNIP 15.349
Web of Science (2011): Impact factor 53.298
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 13.149 SNIP 13.903
Web of Science (2010): Impact factor 53.486
BFI (2009): BFI-level 2
BFI (2008): BFI-level 2
Scopus rating (2007): SJR 10.481 SNIP 11.858
Scopus rating (2004): SJR 11.349 SNIP 13.973
Scopus rating (2002): SJR 8.613 SNIP 11.412
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 8.571 SNIP 10.681
Scopus rating (2000): SJR 7.41 SNIP 10.513
Scopus rating (1999): SJR 7.361 SNIP 10.968
Original language: English
Source: orbit
Source-ID: 230915
Research output: Research - peer-review › Journal article – Annual report year: 1999
Characterization of *Staphylococcus simulans* strains isolated from cases of bovine mastitis

This study was conducted to characterize *Staphylococcus simulans* isolated from cases of bovine mastitis. A total of 134 isolates of *S. simulans* selected from 80 quarters from 61 cows or heifers in 37 different herds were characterized by EcoRI ribotyping. From 22 quarters two to seven consecutive isolates taken at weekly intervals were selected. Furthermore, three isolates from clinical infections in humans and two reference strains were included. A total of 16 different ribotypes were found, however, two types predominated. In most herds more than one type was found. From the 22 different quarters, where 76 paired or multiple isolates were at disposal, the same ribotype was constantly found in the same quarter. This study showed that *S. simulans* causing bovine mastitis could be divided into relatively large number of different types, but that two types predominated. More than one type could be found in the same herd and within different quarters of the same cow, but ribotyping confirmed that *S. simulans* could be the cause of persistent and stable infections.

General information

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Larsen, H. D., Jensen, N. E.
Pages: 165-170
Publication date: 1999
Peer-reviewed: Yes

Publication information

Journal: VETERINARY MICROBIOLOGY
Volume: 66
Issue number: 2
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
Comparison of two agar dilution methods and three agar diffusion methods including the Etest for antibiotic susceptibility testing of thermophilic Campylobacter species

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Engberg, J., Andersen, S., Skov, R., Aarestrup, F. M., Gerner-Smidt, P.
Pages: 580-584
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: Clinical Microbiology and Infection
Volume: 5
ISSN (Print): 1198-743X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.57 SJR 2.569 SNIP 1.854
Web of Science (2017): Impact factor 5.394
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.99 SJR 2.424 SNIP 1.757
Web of Science (2016): Impact factor 5.292
Web of Science (2016): Indexed yes

BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 5.11 SJR 2.637 SNIP 1.996
Web of Science (2015): Impact factor 4.575
Web of Science (2015): Indexed yes

BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 5.49 SJR 2.73 SNIP 2.22
Web of Science (2014): Impact factor 5.768
Web of Science (2014): Indexed yes

BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.92 SJR 2.306 SNIP 1.852
Web of Science (2013): Impact factor 5.197
ISI indexed (2013): ISI indexed yes

Scopus rating (2012): CiteScore 3.93 SJR 1.868 SNIP 1.483
Web of Science (2012): Impact factor 4.578
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes

BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.63 SJR 1.814 SNIP 1.489
Web of Science (2011): Impact factor 4.54
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes

BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.809 SNIP 1.307
Web of Science (2010): Impact factor 4.784

BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.815 SNIP 1.666
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.664 SNIP 1.269
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.436 SNIP 1.376
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.131 SNIP 1.219
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.099 SNIP 1.15
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.826 SNIP 0.974
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.722 SNIP 0.942
Scopus rating (2002): SJR 0.484 SNIP 0.457
Scopus rating (2001): SJR 0.411 SNIP 0.347
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.392 SNIP 0.665
Scopus rating (1999): SJR 0.486 SNIP 0.562

Original language: English
Source: orbit
Source-ID: 236356
Research output: Research - peer-review : Journal article – Annual report year: 1999
Design of a system for monitoring antimicrobial resistance in pathogenic, zoonotic and indicator bacteria from food animals

**General information**
State: Published
Organisations: Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Bager, F., Aarestrup, F. M., Jensen, N. E., Madsen, M., Meyling, A., Wegener, H. C.
Pages: 77-86
Publication date: 1999
Peer-reviewed: Yes

**Publication information**
Journal: Acta Veterinaria Scandinavica (Print Edition)
Volume: 92
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Impact factor 1.472
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.98 SJR 0.644 SNIP 1.641
Web of Science (2015): Impact factor 1.23
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.54 SJR 0.753 SNIP 1.21
Web of Science (2014): Impact factor 1.377
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.41 SJR 0.539 SNIP 1.11
Web of Science (2013): Impact factor 1.382
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.26 SJR 0.591 SNIP 0.789
Web of Science (2012): Impact factor 1.345
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 1.42 SJR 0.664 SNIP 0.997
Web of Science (2011): Impact factor 1.367
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.551 SNIP 1.005
Web of Science (2010): Impact factor 1.196
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.409 SNIP 0.716
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Experimental infection of pregnant cows with Bacillus licheniformis bacteria

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Agerholm, J. S., Jensen, N. E., Dantzer, V., Jensen, H. E., Aarestrup, F. M.
Pages: 191-201
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: VETERINARY PATHOLOGY
Volume: 36
Issue number: 3
ISSN (Print): 0300-9858
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.16 SJR 1.078 SNIP 1.356
Web of Science (2017): Impact factor 1.795
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.68 SJR 0.938 SNIP 1.148
Web of Science (2016): Impact factor 1.996
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.05 SJR 1.09 SNIP 1.308
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.74 SJR 0.916 SNIP 1.155
Web of Science (2014): Impact factor 1.869
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2 SJR 1.12 SNIP 1.288
Web of Science (2013): Impact factor 2.038
Frequency and distribution of - and -haemolysin in Staphylococcus aureus of bovine and human origin: A comparison between pheno- and genotype

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Larsen, H. D., Eriksen, N. H. R.
Pages: 425-430
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: APMIS
Volume: 107
ISSN (Print): 0903-4641
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.95
Frequency of alpha- and beta-haemolysin in Staphylococcus aureus of bovine and human origin - A comparison between pheno- and genotype and variation in phenotypic expression

The phenotypic expression of haemolysins and the presence of genes encoding alpha and beta-haemolysin were determined in 105 S. aureus isolates from bovine mastitis, 100 isolates from the nostrils of healthy humans, and 60 isolates from septicaemia in humans. Furthermore, the possible change in expression of haemolysins after subcultivation in human and bovine blood and milk was studied in selected isolates. Alpha-haemolysin was expressed phenotypically in 39 (37%) of the bovine isolates, in 59 (59%) of the human carrier isolates, and in 40 (67%) of the isolates from septicaemia. Beta-haemolysin was expressed in 76 (72%) bovine, 11 (11%) carrier, and 8 (13%) septicaemia isolates. Significantly more bovine than human isolates expressed beta-haemolysin and significantly fewer expressed alpha-haemolysin. Genotypically, the gene encoding alpha-haemolysin was detected in all isolates. A significant difference
in the prevalence of the gene encoding P-haemolysin between the bovine (96%), human carrier (56%) and isolates from septicaemia (57%) was found. Of the bovine isolates, 75% of those carrying the gene encoding beta-haemolysin expressed beta-haemolysin phenotypically, whereas only 20% of the carrier isolates and 24% of the septicaemia isolates did so. No change in expression of haemolysins could be observed after subcultivation of bovine isolates in human blood and milk. After 5 to 10 subcultures in bovine blood and 1 to 4 in bovine milk, 9 of 10 human isolates originally phenotypically beta-haemolysin negative initiated the expression of beta-haemolysin. This study showed that a larger proportion of S. aureus of bovine origin carry the beta-haemolysin gene compared to isolates from humans. Furthermore, a larger number of the isolates of bovine origin carrying the beta-haemolysin gene express this gene phenotypically compared to isolates of human origin.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Larsen, H., Eriksen, N., Elsberg, C., Jensen, N.
Pages: 425-430
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: Apmis
Volume: 107
Issue number: 4
ISSN (Print): 0903-4641
Ratings:
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): CiteScore 1.95
- Web of Science (2017): Impact factor 2.026
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 1.87
- Web of Science (2016): Impact factor 1.795
- BFI (2015): BFI-level 1
- Scopus rating (2015): CiteScore 1.92
- Web of Science (2015): Impact factor 1.933
- BFI (2014): BFI-level 1
- Scopus rating (2014): CiteScore 1.95
- Web of Science (2014): Impact factor 2.042
- BFI (2013): BFI-level 1
- Scopus rating (2013): CiteScore 2.07
- Web of Science (2013): Impact factor 1.922
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): CiteScore 2.06
- Web of Science (2012): Impact factor 2.068
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): CiteScore 1.97
- Web of Science (2011): Impact factor 1.991
- ISI indexed (2011): ISI indexed yes
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 1
- Web of Science (2010): Impact factor 1.944
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 1
From the stable to the table: an outbreak of multiresistant, quinolone-resistant Salmonella Typhimurium DT104 in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 1420-1425
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: The New England Journal of Medicine
Volume: 341
ISSN (Print): 0028-4793
Ratings:
BFI (2018): BFI-level 3
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 14.75 SJR 19.476 SNIP 13.405
Web of Science (2017): Impact factor 79.258
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 12.82 SJR 18.009 SNIP 14.79
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 12.5 SJR 16.591 SNIP 15.538
Web of Science (2015): Impact factor 59.558
BFI (2014): BFI-level 2
Web of Science (2014): Impact factor 55.873
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 12.21 SJR 14.796 SNIP 15.59
Web of Science (2013): Impact factor 54.42
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 12.09 SJR 13.984 SNIP 15.598
Glycopeptide resistance in Enterococcus faecium from broilers and pigs following discontinued use of avoparcin

The use of the glycopeptide growth promoter avoparcin was discontinued in Denmark in 1995 following concerns that vancomycin-resistant Enterococcus faecium occurring as a result of its use could be transferred to humans via food. The present study is an analysis of results obtained by the continuous surveillance of an antimicrobial resistance in Denmark (DANMAP) with the aim of determining the effect of the ban on the occurrence of glycopeptide resistance among E. faecium isolated from broilers and pigs. Among isolates from broilers, the proportion that were resistant to glycopeptides has shown a statistically highly significant decline between the end of 1995 and the first half of 1998, whereas in pigs the ban appears to have had no such effect. One possible explanation is that the broiler industry generally uses all in-all out production compared with continuous production in pig herds. Alternatively, the results indicate that the different outcomes may result from different co-selection patterns in pigs and broilers. In pigs, the antimicrobials most commonly used favored co-selection of glycopeptide-resistant strains of E. faecium while in broilers the antimicrobials most widely used selected for glycopeptide-susceptible strains. The results show that intervention to reduce antimicrobial resistance may not always be effective and preventing resistance problems therefore becomes essential.

General information
State: Published
Organisations: Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Bager, F., Aarestrup, F. M., Madsen, M., Wegener, H. C.
Pages: 53-56
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: Microbial Drug Resistance
Volume: 5
Issue number: 1
ISSN (Print): 1076-6294
Ratings:
BFI (2018): BFI-level 1
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<td>2000</td>
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Glycopeptide resistance in Enterococcus faecium in broilers and pigs following discontinued use of avoparcin

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Bager, F., Aarestrup, F. M., Madsen, M., Wegener, H. C.
Pages: 53-56
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: MICROBIAL DRUG RESISTANCE
Volume: 5
Issue number: 1
ISSN (Print): 1076-6294
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
Web of Science (2017): Impact factor 2.344
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
Web of Science (2016): Impact factor 2.306
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
Web of Science (2015): Impact factor 2.529
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
Web of Science (2014): Impact factor 2.49
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.87 SJR 1.265 SNIP 1.118
Web of Science (2013): Impact factor 2.524
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.45 SJR 0.963 SNIP 0.9
Web of Science (2012): Impact factor 2.364
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.76 SJR 1.163 SNIP 1.14
Web of Science (2011): Impact factor 2.153
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.054 SNIP 0.8
Web of Science (2010): Impact factor 1.936
Occurrence of the blaZ gene in penicillin resistant Staphylococcus aureus isolated from bovine mastitis in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Vesterholm-Nielsen, M., Larsen, M. Ø., Olsen, J. E., Aarestrup, F. M.
Pages: 279-286
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: Acta Veterinaria Scandinavica
Volume: 40
Issue number: 3
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Impact factor 1.472
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.98 SJR 0.644 SNIP 1.641
Penicillinresistens blandt Staphylococcus aureus isoleret fra mastitis hos kvæg i Danmark og andre lande

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, N. E.
Presence of erm gene classes in Gram-positive bacteria of animal and human origin in Denmark

A classification of the different erm gene classes based on published sequences was performed, and specific primers to detect some of these classes designed. The presence of ermA (Tn554), ermB (class IV) and ermC (class VI) was determined by PCR in a total of 113 enterococcal, 77 streptococcal and 68 staphylococcal erythromycin resistant isolates of animal and human origin. At least one of these genes was detected in 88% of the isolates. Four isolates contained more than one erm gene. ermB dominated among the enterococci (88%) and streptococci (90%) and ermC among staphylococci (75%) with ermA (Tn554) present in some isolates (16%). Variations in the presence of the different genes when comparing staphylococcal isolates of human and animal origin were observed.

General information

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Jensen, L. B., Frimodt-Moller, N., Aarestrup, F. M.
Pages: 151-158
Publication date: 1999
Peer-reviewed: Yes
Web of Science (2016): Impact factor 12.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.08 SJR 1.156 SNIP 0.756
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.17 SJR 1.136 SNIP 0.767
Web of Science (2014): Impact factor 13.244
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.25 SJR 1.053 SNIP 0.719
Web of Science (2013): Impact factor 13.806
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.25 SJR 1.073 SNIP 0.804
Web of Science (2012): Impact factor 13.231
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.26 SJR 1.105 SNIP 0.764
Web of Science (2011): Impact factor 10.96
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.081 SNIP 0.754
Web of Science (2010): Impact factor 11.796
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.13 SNIP 0.834
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.084 SNIP 0.834
Scopus rating (2007): SJR 1.103 SNIP 0.864
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.105 SNIP 0.86
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1 SNIP 0.8
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.005 SNIP 0.725
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.018 SNIP 0.866
Scopus rating (2002): SJR 0.902 SNIP 0.791
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.944 SNIP 0.752
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.936 SNIP 0.739
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.979 SNIP 0.748
Original language: English
Keywords: erm gene classification, erythromycin resistance, animal
DOIs: 10.1016/S0378-1097(98)00539-4
Prevalence of the erm genes in gram positive bacterial spp. of animal and human origin

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Jensen, L. B., Møller, N. F., Aarestrup, F. M.
Pages: 151-158
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: FEMS Microbiology Letters
Volume: 170
ISSN (Print): 0378-1097
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.8 SJR 0.79 SNIP 0.58
Web of Science (2017): Impact factor 11.392
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.76 SJR 0.842 SNIP 0.615
Web of Science (2016): Impact factor 12.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.08 SJR 1.156 SNIP 0.756
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.17 SJR 1.136 SNIP 0.767
Web of Science (2014): Impact factor 13.244
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.25 SJR 1.053 SNIP 0.719
Web of Science (2013): Impact factor 13.806
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.25 SJR 1.073 SNIP 0.804
Web of Science (2012): Impact factor 13.231
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.26 SJR 1.105 SNIP 0.764
Web of Science (2011): Impact factor 10.96
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.081 SNIP 0.754
Web of Science (2010): Impact factor 11.796
Web of Science (2010): Indexed yes
Survival of Salmonella in nutrient stressed environments (saline and pig farm manure supernatant)

**General information**
State: Published
Organisations: Microbial Ecology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Baloda, S., Boye, M., Aarestrup, F. M., Jensen, L. B.
Publication date: 1999
Peer-reviewed: No
Event: Abstract from ASM 98th General Meeting, Atlanta, GA, United States.
Source: orbit
Source-ID: 236322
Research output: Research - peer-review › Journal article – Annual report year: 1999

Susceptibility testing of Actinobacillus pleuropneumoniae in Denmark. Evaluation of three different media for MIC-determinations and tablet diffusion tests

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, N. E.
Pages: 299-305
Publication date: 1999
Peer-reviewed: No

**Publication information**
Journal: VETERINARY MICROBIOLOGY
Volume: 64
Issue number: 4
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
Web of Science (2010): Impact factor 3.256
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.309 SNIP 1.466
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.164 SNIP 1.29
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.048 SNIP 1.315
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.03 SNIP 1.396
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.089 SNIP 1.259
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.873 SNIP 1.248
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.905 SNIP 1.181
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.905 SNIP 1.13
Web of Science (2002): Indexed yes
The effect of tylosin containing feed on subclinical infection with Salmonella enterica serovar Typhimurium in experimentally infected pigs

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Baggesen, D. L., Wingstrand, A., Carstensen, B., Nielsen, B., Aarestrup, F. M.
Pages: 1201-1206
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: American Journal of Veterinary Research
Volume: 60
ISSN (Print): 0002-9645
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 1.17 SJR 0.567 SNIP 0.773
Web of Science (2017): Impact factor 0.833
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.08 SJR 0.641 SNIP 0.769
Web of Science (2016): Impact factor 1.004
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 1.3 SJR 0.829 SNIP 0.884
Web of Science (2015): Impact factor 1.124
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 1.6 SJR 1.01 SNIP 1.059
Web of Science (2014): Impact factor 1.335
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 1.4 SJR 0.936 SNIP 0.876
Web of Science (2013): Impact factor 1.214
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 1.48 SJR 0.829 SNIP 1.03
Web of Science (2012): Impact factor 1.348
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 1.48 SJR 0.922 SNIP 1.03
Web of Science (2011): Impact factor 1.269
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
The effects of antibiotic usage in food animals on the development of antimicrobial resistance of importance for humans in Campylobacter and Escherichia coli

Modern food animal production depends on use of large amounts of antibiotics for disease control. This provides favourable conditions for the spread and persistence of antimicrobial-resistant zoonotic bacteria such as Campylobacter and E. coli O157. The occurrence of antimicrobial resistance to antimicrobials used in human therapy is increasing in human pathogenic Campylobacter and E. coli from animals. There is an urgent need to implement strategies for prudent use of antibiotics in food animal production to prevent further increases in the occurrence of antimicrobial resistance in food-borne human pathogenic bacteria such as Campylobacter and E. coli. (C) Elsevier, Paris.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Wegener, H. C.
Pages: 639-644
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: Microbes and Infection
Volume: 1
Issue number: 8
ISSN (Print): 1286-4579
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.41 SJR 1.205 SNIP 0.653
Web of Science (2017): Impact factor 2.924
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.92 SJR 1.102 SNIP 0.632
The need for a veterinary antibiotic policy

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Communications and Management Secretariat
Pages: 50-53
Publication date: 1999
Peer-reviewed: Yes

Publication information
Transfer of antibiotic resistant bacteria from animals to man

Antibiotic resistance develops in zoonotic bacteria in response to antibiotics used in food animals. A close association exists between the amounts of antibiotics used and the levels of resistance observed. The classes of antibiotics routinely used for treatment of human infections are also used for animals either for therapy or for growth promotion. Antibiotic resistance in zoonotic bacteria constitute a public health hazard, primarily through the increased risk of treatment failures. This paper describes the zoonotic bacteria, salmonella, campylobacter, yersinia and enterohaemorrhagic E. coli (EHEC). Infections with these agents do not generally require antibiotic therapy, but in some cases antibiotics are essential to obtain a successful cure. The levels and types of resistance observed in zoonotic bacteria in some countries, especially the increasing levels of fluoroquinolone resistance in salmonella and campylobacter, gives cause for concern. The principles of controlling resistance development involve infection control at herd level and prudent use of antibiotics.

General information

State: Published
Organisations: Communications and Management Secretariat, National Food Institute, Division of Microbiology and Risk Assessment, Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Contributors: Wegener, H. C., Aarestrup, F. M., Gerner-Smidt, P., Bager, F.
Pages: 51-57
Publication date: 1999
Peer-reviewed: Yes

Publication information

Journal: Acta Veterinaria Scandinavica
Volume: S92
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Impact factor 1.472
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.98 SJR 0.644 SNIP 1.641
Web of Science (2015): Impact factor 1.23
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.54 SJR 0.753 SNIP 1.21
Web of Science (2014): Impact factor 1.377
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.41 SJR 0.539 SNIP 1.11
Web of Science (2013): Impact factor 1.382
Supplementing animal feed with antimicrobial agents to enhance growth has been common practice for more than 30 years and is estimated to constitute more than half the total antimicrobial use worldwide. The potential public health consequences of this use have been debated; however, until recently, clear evidence of a health risk was not available. Cumulating evidence now indicates that the use of the glycopeptide avoparcin as a growth promoter has created in food animals a major reservoir of Enterococcus faecium, which contains the high level glycopeptide resistance determinant vanA, located on the Tn1546 transposon. Furthermore, glycopeptide-resistant strains, as well as resistance determinants, can be transmitted from animals to humans. Two antimicrobial classes expected to provide the future therapeutic options for treatment of infections with vancomycin-resistant enterococci have analogues among the growth promoters, and a huge animal reservoir of resistant E. faecium has already been created, posing a new public health problem.
Characterisation of integrons and antibiotic resistance genes in Danish multiresistant Salmonella enterica Typhimurium DT104

The presence and genetic content of integrons was investigated in eight Salmonella enterica Typhimurium DT104 isolates from different pig herds in Denmark. Two different integrons were identified using PCR and sequencing. Each of the integrons carried a single resistance cassette in addition to the sul1 and qacE Delta 1 genes characteristic of integrons. The first integron encoded the ant (3')-Ia gene that specified resistance to spectinomycin and streptomycin. The second contained the pse-1 beta-lactamase gene. All the multiresistant strains contained both integrons. The presence of these two integrons did not account for the total phenotypic resistance of all the isolates and does not exclude the presence of other mobile DNA elements.
Antimicrobial susceptibility of Mycoplasma hyorhinis in a liquid medium compared to a disc assay

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Friis, N. F., Szancer, J.
Pages: 145-147
Publication date: 1998
Peer-reviewed: Yes

Publication information
Journal: Acta Veterinaria Scandinavica (Print Edition)
Volume: 39
Issue number: 1
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Scopus rating (2018): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
Web of Science (2017): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Impact factor 1.472
Web of Science (2016): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.41 SJR 0.539 SNIP 1.11
Web of Science (2015): Impact factor 1.382
Web of Science (2015): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.98 SJR 0.644 SNIP 1.641
Web of Science (2014): Impact factor 1.23
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.54 SJR 0.753 SNIP 1.21
Web of Science (2014): Impact factor 1.377
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.41 SJR 0.539 SNIP 1.11
Web of Science (2013): Impact factor 1.382
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.26 SJR 0.591 SNIP 0.789
Web of Science (2012): Impact factor 1.345
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 1.42 SJR 0.664 SNIP 0.997
Web of Science (2011): Impact factor 1.367
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Antimicrobial susceptibility testing of Mycoplasma hyosynoviae isolated from pigs during 1968 to 1971 and during 1995 and 1996

This study was conducted to compare the Minimal Inhibitory Concentrations (MICs) for enrofloxacin, lincomycin, tetracycline, tiamulin and tylosin, of Mycoplasma hyosynoviae, isolated from pigs at notably different intervals (1968-71 and 1995-96). Each group comprised 21 low passage isolates and a Danish reference strain (M60) and the type strain (S16). MICs were determined in liquid medium with both initial and final readings. Enrofloxacin, lincomycin, tetracycline and tiamulin were active against all isolates, and tiamulin showed the highest activity. For tylosin all the isolates from 1968-71 were highly susceptible, whereas the isolates from 1995-96 could be divided into a highly susceptible (nine isolates) and relatively resistant (12 isolates) group. This difference between old and new strains was statistically significant (p=0.0000415). The remaining agents, enrofloxacin, lincomycin, tiamulin and tetracycline, showed an unaltered good activity against M. hyosynoviae. The resistance to tylosin seems now to occur so often that this antibiotic cannot be recommended for therapeutic use any more. The most probable explanation for the emergence of resistance is the intensive use of tylosin during many years for therapy and growth promotion.
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
Web of Science (2010): Impact factor 3.256
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.309 SNIP 1.466
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.164 SNIP 1.29
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.048 SNIP 1.315
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.03 SNIP 1.396
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.089 SNIP 1.259
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.873 SNIP 1.248
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.905 SNIP 1.181
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.905 SNIP 1.13
Web of Science (2002): Indexed yes
Association between decreased susceptibility to a new antibiotic for treatment of human diseases, everninomicin (SCH 27899), and resistance to an antibiotic used for growth promotion in animals, avilamycin

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Pages: 137-141
Publication date: 1998
Peer-reviewed: Yes

Publication information
Journal: MICROBIAL DRUG RESISTANCE
Volume: 4
Issue number: 2
ISSN (Print): 1076-6294
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
Web of Science (2017): Impact factor 2.344
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
Web of Science (2016): Impact factor 2.306
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
Web of Science (2015): Impact factor 2.529
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
Characterisation of integrons and antibiotic resistance genes in Danish multiresistant Salmonella enterica Typhimurium DT104 (vol 157, pg 177, 1997)

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Technical University of Denmark
Contributors: Sandvang, D., Aarestrup, F. M., Jensen, L. B.
Pages: 271-271
Publication date: 1998
Characterisation of recently emerged multiple antibiotic-resistant Salmonella enterica serovar typhimurium DT104 and other multiresistant phage types from Danish pig herds

A total of 670 isolates of Salmonella enterica were isolated from Danish pig herds, phage typed and tested for susceptibility to amoxycillin + clavulanate, ampicillin, colistin, enrofloxacin, gentamicin, neomycin, spectinomycin, streptomycin, tetracyclines, and trimethoprim + sulphadiazine. S enterica serovar typhimurium (S typhimurium) isolates resistant to ampicillin, streptomycin and tetracycline and three isolates of S typhimurium DT104, two from 1994 and one from 1995, were further tested for resistance against chloramphenicol and sulphonamide and analysed by pulsed-field gel electrophoresis (PFGE) using the restriction enzyme Xba I. Overall, 66 per cent of the 670 isolates were sensitive to all the antimicrobial agents tested. Eleven isolates of S typhimurium were resistant to ampicillin, streptomycin and tetracycline and also resistant to other antibiotics in different resistance patterns. Seven different multiresistant clones were identified, The most common clones were four isolates of DT104 and three isolates of DT193. TWO Of the three S typhimurium DT104 from 1994 and 1995 were sensitive to all the antimicrobials tested whereas the remaining isolate from 1994 was resistant to spectinomycin, streptomycin and sulphonamides. All three isolates showed PFGE profiles identical to the four multiresistant DT104 isolates. Compared with most other countries antimicrobial resistance among S enterica isolated from Danish pig herds is uncommon, However, several different multiresistant clones were found.
Characterization of recently emerged multiple resistant Salmonella typhimurium DT104 and other multiresistant phage types among danish pig herds
Detection of the satA gene and transferability of virginiamycin resistance in Enterococcus faecium from food-animals

General information
State: Published
Organisations: Department of Microbiology, Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Hammerum, A. M., Jensen, L. B., Aarestrup, F. M.
Pages: 145-151
Publication date: 1998
Peer-reviewed: Yes

Publication information
Journal: FEMS MICROBIOLOGY LETTERS
Volume: 168
Issue number: 1
ISSN (Print): 0378-1097
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.8 SJR 0.79 SNIP 0.58
Web of Science (2017): Impact factor 11.392
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.76 SJR 0.842 SNIP 0.615
Web of Science (2016): Impact factor 12.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.08 SJR 1.156 SNIP 0.756
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.17 SJR 1.136 SNIP 0.767
Web of Science (2014): Impact factor 13.244
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.25 SJR 1.053 SNIP 0.719
Effect of tylosin used as a growth promoter on the occurrence of macrolide resistant enterococci and staphylococci in pigs

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Carstensen, B.
Pages: 307-312
Publication date: 1998
Peer-reviewed: Yes

Publication information
Effekten af vækstfremmeren tylosin på bakteriel resistensudvikling og salmonellaudskillelse

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 1998

Publication information
Original language: Danish
Source: orbit
Source-ID: 236329
Research output: Research › Report – Annual report year: 1998

Effekten af vækstfremmeren virginiamycin på bakteriel resistensudvikling

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 1998

Publication information
Original language: Danish
Source: orbit
Source-ID: 236331
Research output: Research › Report – Annual report year: 1998

Environmental microbiology research at the Danish Veterinary Laboratory

General information
State: Published
Organisations: Microbial Ecology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 1998
Peer-reviewed: No
Event: Abstract from Effects of Microbial Biotechnology on Soil Ecosystems, Roskilde, Denmark.
Source: orbit
Source-ID: 240908
Research output: Research › Conference abstract for conference – Annual report year: 1998

Forbruget af antibiotika halveret siden 1994

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Fremtidens fødevareproduktion

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Pages: 2-3
Publication date: 1998
Peer-reviewed: No

Publication information
Journal: Plus Proces
Volume: 3
Original language: Danish
Source: orbit
Source-ID: 236406
Research output: Research › Journal article – Annual report year: 1998

MIC-værdier for 8 antibiotika for klonalt beslægtede Escherichia coli O139 isoleret fra ødemsyge i Danmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, N. E.
Pages: 7-8
Publication date: 1998
Peer-reviewed: No

Publication information
Journal: Dansk Veterinær Tidsskrift
Volume: 81
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Minimum inhibitory concentrations for selected antimicrobial agents against organisms isolated from the mammary glands of dairy heifers in New Zealand and Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Salmon, S. A., Watts, J. L., Aarestrup, F. M., Pankey, J. W., Yancey, R. J.
Pages: 570-578
Publication date: 1998
Peer-reviewed: Yes

Publication information
Journal: JOURNAL OF DAIRY SCIENCE
Volume: 81
Issue number: 2
ISSN (Print): 0022-0302
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.84 SJR 1.35 SNIP 1.491
Web of Science (2017): Impact factor 2.749
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.66 SJR 1.331 SNIP 1.484
Web of Science (2016): Impact factor 2.474
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.63 SJR 1.479 SNIP 1.488
Web of Science (2015): Impact factor 2.408
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.78 SJR 1.434 SNIP 1.504
Web of Science (2014): Impact factor 2.573
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 2.82 SJR 1.411 SNIP 1.589
Web of Science (2013): Impact factor 2.55
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 2.79 SJR 1.443 SNIP 1.717
Web of Science (2012): Impact factor 2.566
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 2.59 SJR 1.413 SNIP 1.582
Web of Science (2011): Impact factor 2.564
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.354 SNIP 1.518
Molecular analysis of Tn1546 in Enterococcus faecium isolated from animals and humans

The internal areas and the position of integration of the glycopeptide resistance element Tn1546 were characterized by using PCR fragment length polymorphism, sequencing, and DNA hybridization techniques with 38 high-level vancomycin-resistant Enterococcus faecium isolates of human and animal origins from Europe and the United States. Only minor variations in the coding regions within Tn1546 were found, suggesting high genetic stability. The isolates originated from broilers (n = 5), a chicken (n = 1), a duck (n = 1), a turkey (n = 1), pigs (n = 8), a pony (n = 1), and humans (n = 23). A total of 13 different types were defined based on a single-nucleotide difference in the vanX gene, the presence of insertion sequences, and hybridization patterns. For some types more than one isolate were found. For type 1, 10 isolates of both human and animal origins were found. All were indistinguishable from the reference strain, BM4147. For type 2, 11 isolates of human and animal origins were found. Six human isolates from England were all of type 3. Two human isolates from the United States, indistinguishable from each other, were type 9. These results showed that vancomycin-resistant E. faecium of animal and human origins can contain indistinguishable genetic elements coding for vancomycin resistance, indicating either horizontal gene transfer between E. faecium organisms of human and animal origins or the existence of a common reservoir for glycopeptide resistance.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, National Veterinary Institute, Department of Microbiology
Pages: 437-442
Publication date: 1998
Peer-reviewed: Yes

Publication information
Journal: Journal of Clinical Microbiology
Volume: 36
Issue number: 2
ISSN (Print): 0095-1137
Ratings:
Occurrence of the satA and vgb genes in streptogramin resistant Enterococcus faecium isolates of animal and human origin from the Netherlands

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Microbiology
Contributors: Jensen, L. B., Hammerum, A. M., Aarestrup, F. M., Stobberingh, E. E., van der Bogaard, A. E.
Pages: 3330-3331
Publication date: 1998
Peer-reviewed: Yes

Publication information
Journal: Antimicrobial Agents and Chemotherapy
Volume: 42
ISSN (Print): 0066-4804
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.15 SJR 2.291 SNIP 1.263
Web of Science (2017): Impact factor 4.255
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.45 SJR 2.361 SNIP 1.428
Web of Science (2014): Impact factor 4.476
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.67 SJR 2.423 SNIP 1.411
Web of Science (2013): Impact factor 4.451
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.88 SJR 2.363 SNIP 1.5
Web of Science (2012): Impact factor 4.565
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Occurrence of satA and vgb genes in streptogramin-resistant Enterococcus faecium isolates of animal and human origins in the Netherlands

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Microbiology
Contributors: Jensen, L. B., Hammerum, A. M., Aarestrup, F. M., Bogaard, A. E. V. D., Stobberingh, E. E.
Pages: 3330-3331
Publication date: 1998
Peer-reviewed: Yes

Publication information
Journal: ANTIMICROBIAL AGENTS AND CHEMOTHERAPY
Volume: 42
Issue number: 12
ISSN (Print): 0066-4804
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 4.15 SJR 2.291 SNIP 1.263
Web of Science (2017): Impact factor 4.255
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.45 SJR 2.361 SNIP 1.428
Web of Science (2014): Impact factor 4.476
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.67 SJR 2.423 SNIP 1.411
Web of Science (2013): Impact factor 4.451
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.88 SJR 2.363 SNIP 1.5
Web of Science (2012): Impact factor 4.565
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 5.02 SJR 2.523 SNIP 1.574
Web of Science (2011): Impact factor 4.841
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.458 SNIP 1.54
Web of Science (2010): Impact factor 4.672
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.424 SNIP 1.65
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.45 SNIP 1.448
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.167 SNIP 1.49
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.339 SNIP 1.401
Scopus rating (2005): SJR 2.321 SNIP 1.52
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.929 SNIP 1.614
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.208 SNIP 1.644
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 2.173 SNIP 1.553
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.334 SNIP 1.542
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.899 SNIP 1.617
Øget forekomst af resistens mod fluoroquinoloner blandt dyrepatogene bakterier i Danmark i lyset af et stigende forbrug

**General information**

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, N. E., Jorsal, S. E., Nielsen, T. K.
Pages: 794-796
Publication date: 1998
Peer-reviewed: No

**Publication information**

Journal: Dansk Veterinær Tidsskrift
Volume: 81
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 236411
Research output: Research - peer-review > Journal article – Annual report year: 1998

Resistance to antimicrobial agents used for animal therapy in pathogenic, zoonotic and indicator bacteria isolated from different food animals in Denmark: A baseline study for the Danish Integrated Antimicrobial Resistance Monitoring Programme (DANMAP)

This study describes the establishment and first results of a continuous surveillance system of antimicrobial resistance among bacteria isolated from pigs, cattle and broilers in Denmark. The three categories of bacteria tested were: 1) indicator bacteria (Escherichia coli, Enterococcus faecalis, Enterococcus faecium), 2) zoonotic bacteria (Campylobacter coli/jejuni, Salmonella enterica, Yersinia enterocolitica), and 3) animal pathogens (E. coli, Staphylococcus aureus, coagulase-negative staphylococci (CNS), Staphylococcus hyicus, Actinobacillus pleuropneumoniae). A total of 3304 bacterial isolates collected from October 1995 through December 1996 were tested for susceptibility to all major classes of antimicrobial agents used for therapy in Denmark. Bacterial species intrinsically resistant to an antimicrobial were not tested towards that antimicrobial. Acquired resistance to all antimicrobials was found. The occurrence of resistance varied by animal origin and bacterial species. In general, resistance was observed more frequently among isolates from pigs than from cattle and broilers. The association between the occurrence of resistance and the consumption of the antimicrobial is discussed, as is the occurrence of resistance in other countries. The results of this study show the present level of resistance to antimicrobial agents among a number of bacterial species isolated from food animals in Denmark. Thus, the baseline for comparison with future prospective studies has been established, enabling the determination of trends over time.

**General information**
Resistens mod antibiotiske vækstfremmere og nært beslægtede antibiotika

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Jensen, L. B., Aarestrup, F. M.
Pages: 8-9
Publication date: 1998
Peer-reviewed: No

Publication information
Journal: Dansk Kemi
Volume: 79
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Web of Science (2007): Indexed yes
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 236416
Research output: Research › Journal article – Annual report year: 1998

Serological characterization and antimicrobial susceptibility of Streptococcus suis isolates from diagnostic samples in Denmark during 1995 and 1996.

At the Danish Veterinary Laboratory Streptococcus suis infections in pigs were diagnosed in 114 cases in 1995 and in 151 cases in 1996. Isolates were serotyped using specific antisera against type 1 through 28 and a total of 67 cases from 1995 and 113 cases in 1996 were tested for resistance to 11 antimicrobial agents. The majority of cases were lung diseases (57%), followed by septicaemia (16%), meningitis (15%) and endocarditis (8%). Almost 96% of the isolates could be typed using the 28 antisera. The most common serotype was serotype 2 (29%), followed by serotype 7 (17%), and serotypes 3, 4 and 8 (9-10%). The remaining serotypes were observed in frequencies of less than 5%. Serotype 7 was more commonly isolated from septicaemia than the other serotypes. Serotype 2 was more commonly isolated from pies older than 1 weeks compared to the other serotypes. Most isolates were susceptible to amoxycillin + clavulanate, ampicillin, ceftiofur, enrofloxacin, penicillin, spectinomycin, tiamulin and trimethoprim + sulphadiazine. A high frequency (> 30%) of resistance to tetracydine was observed. Among isolates of serotype 2, 9.7% were resistant to lincomycin and 12.9% to spiramycin. Among other serotypes 56.5% were resistant to lincomycin and spiramycin. The differences in susceptibility between isolates of serotype 2 and the other serotypes were statistically significant. Compared to a previous Danish study the distribution of serotypes of S. suis causing infections among pigs in Denmark has changed during the last 15 years.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Aarestrup, F. M., Jorsal, S. E. L., Jensen, N. E.
Pages: 59-66
Publication date: 1998
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
Volume: 60
Issue number: 1
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
Web of Science (2010): Impact factor 3.256
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.309 SNIP 1.466
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.164 SNIP 1.29
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.048 SNIP 1.315
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.03 SNIP 1.396
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.089 SNIP 1.259
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.873 SNIP 1.248
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.905 SNIP 1.181
Stigende problemer med resistens mod antibiotika

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Pages: 26-27
Publication date: 1998
Peer-reviewed: No

Publication information
Journal: Landsbladet Kvaeg
Volume: 3
Original language: Danish
Source: orbit
Source-ID: 236405
Research output: Research - peer-review › Journal article – Annual report year: 1998

Surveillance of antimicrobial resistance in bacteria isolated from food animals to antimicrobial growth promoters and related therapeutic agents in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Bager, F., Madsen, M., Jensen, N. E., Meyling, A., Wegener, H. C.
Pages: 606-622
Publication date: 1998
Peer-reviewed: Yes

Publication information
Journal: APMIS
Volume: 106
Issue number: 6
ISSN (Print): 0903-4641
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.95
Web of Science (2017): Impact factor 2.026
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.87
Web of Science (2016): Impact factor 1.795
BFI (2015): BFI-level 1
Survival and prevalence of Salmonella typhimurium in pig farms, agricultural soil and laboratory microcosms

General information
State: Published
Organisations: Microbial Ecology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 1998
Peer-reviewed: No
Event: Abstract from 8th International Symposium on Microbial Ecology, Halifax, Canada.
Source: orbit
Source-ID: 236102
Research output: Research - peer-review › Journal article – Annual report year: 1998

The association between the use of antimicrobial growth promoters and development of resistance in pathogenic bacteria towards growth promoting and therapeutic antimicrobials
General information
State: Published
Organisations: Communications and Management Secretariat, National Food Institute, Division of Microbiology and Risk Assessment, Department of Microbiology, Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Contributors: Wegener, H. C., Aarestrup, F. M., Jensen, L. B., Hammerum, A. M., Bager, F.
Pages: 7-14
Publication date: 1998
Peer-reviewed: No

Publication information
Journal: Journal of Animal and Feed Sciences
Volume: 7
Issue number: Suppl. 1
ISSN (Print): 1230-1388
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 0.92 SJR 0.405 SNIP 0.599
Web of Science (2017): Impact factor 0.9
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.9 SJR 0.394 SNIP 0.822
Web of Science (2016): Impact factor 1.024
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.78 SJR 0.4 SNIP 0.779
Web of Science (2015): Impact factor 0.511
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 0.63 SJR 0.391 SNIP 0.667
Web of Science (2014): Impact factor 0.543
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 0.6 SJR 0.307 SNIP 0.469
Web of Science (2013): Impact factor 0.591
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 0.8 SJR 0.377 SNIP 0.63
Web of Science (2012): Impact factor 0.757
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 0.87 SJR 0.387 SNIP 0.669
Web of Science (2011): Impact factor 0.636
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.291 SNIP 0.555
Web of Science (2010): Impact factor 0.659
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.307 SNIP 0.517
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.196 SNIP 0.271
Scopus rating (2007): SJR 0.282 SNIP 0.337
Scopus rating (2006): SJR 0.29 SNIP 0.26
Scopus rating (2005): SJR 0.203 SNIP 0.338
Scopus rating (2004): SJR 0.22 SNIP 0.421
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.263 SNIP 0.429
The effect of virginiamycin on bacterial antimicrobial resistance development

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, L. B.
Publication date: 1998

Publication information
Original language: English
Source: orbit
Source-ID: 236410
Research output: Research › Journal article – Annual report year: 1998

Trends in the resistance to antimicrobial agents of Streptococcus suis isolates from Denmark and Sweden

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Rasmussen, S. R., Artursson, K., Jensen, N. E.
Pages: 71-80
Publication date: 1998
Peer-reviewed: Yes

Publication information
Journal: VETERINARY MICROBIOLOGY
Volume: 63
Issue number: 1
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
Web of Science (2010): Impact factor 3.256
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.309 SNIP 1.466
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.164 SNIP 1.29
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.048 SNIP 1.315
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.03 SNIP 1.396
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.089 SNIP 1.259
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.873 SNIP 1.248
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.905 SNIP 1.181
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.905 SNIP 1.13
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.828 SNIP 1.051
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.699 SNIP 1.066
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.714 SNIP 1.089
Original language: English
Source: orbit
Source-ID: 236110
Research output: Research - peer-review › Journal article – Annual report year: 1998

Vækstfremmere

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Pages: 307-314
Publication date: 1998
Peer-reviewed: No
Antibiotikaresistens - Er det gammel vin på nye flasker?

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Nielsen, B., Olsen, J. E., Aarestrup, F. M.
Pages: 3-10
Publication date: 1997
Peer-reviewed: No

Publication information
Journal: Veterinær Information
Volume: 1
ISSN (Print): 0906-253X
Original language: Danish
Source-ID: 236400
Research output: Research › Journal article – Annual report year: 1997

Antimicrobial susceptibility patterns of thermophilic Campylobacter spp. from humans, pigs, cattle, and broilers in Denmark

The MICs of 16 antimicrobial agents were determined for 202 Campylobacter jejuni isolates, 123 Campylobacter coli isolates, and 6 Campylobacter lari isolates from humans and food animals in Denmark. The C. jejuni isolates originated from humans (75), broilers (95), cattle (29), and pigs (3); the C. coli isolates originated from humans (7), broilers (17); and pigs (99); and the C. lari isolates originated from broilers (5) and cattle (1). All isolates were susceptible to apramycin, neomycin, and gentamicin. Only a few C. jejuni isolates were resistant to one or more antimicrobial agents. Resistance to tetracycline was more common among C. jejuni isolates from humans (11%) than among C. jejuni isolates from animals (0 to 2%). More resistance to streptomycin was found among C. jejuni isolates from cattle (10%) than among those from humans (4%) or broilers (1%). A greater proportion of C. coli than of C. jejuni isolates were resistant to the other antimicrobial agents tested. Isolates were in most cases either coresistant to tylosin, spiramycin, and erythromycin or susceptible to all three antibiotics. More macrolide-resistant isolates were observed among C. coli isolates from swine (79%) than among C. coli isolates from broilers (18%) and humans (14%). Twenty-four percent of C. coli isolates from pigs were resistant to enrofloxacin, whereas 29% of C, coli isolates from humans and none from broilers were resistant. More resistance to streptomycin was observed among C. coli isolates from swine (48%) than among C. coli isolates from broilers (6%) or humans (0%). The six C. lari isolates were susceptible to all antimicrobial agents except ampicillin and nalidixic acid. This study showed that antimicrobial resistance was found only at relatively low frequencies among C. jejuni and C. lari isolates. Among C. coli isolates, especially from swine, there was a high level of resistance to macrolides and streptomycin. Furthermore, this study showed differences in the resistance to antimicrobial agents among Campylobacter
isolates of different origins.

**General information**

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Contributors: Aarestrup, F. M., Nielsen, E. M., Madsen, M., Engberg, J.
Pages: 2244-2250
Publication date: 1997
Peer-reviewed: Yes

**Publication information**

Journal: Antimicrobial Agents and Chemotherapy
Volume: 41
Issue number: 10
ISSN (Print): 0066-4804

Ratings:

BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.15 SJR 2.291 SNIP 1.263
Web of Science (2017): Impact factor 4.255
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.45 SJR 2.361 SNIP 1.428
Web of Science (2014): Impact factor 4.476
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.67 SJR 2.423 SNIP 1.411
Web of Science (2013): Impact factor 4.451
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.88 SJR 2.363 SNIP 1.5
Web of Science (2012): Impact factor 4.565
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 5.02 SJR 2.523 SNIP 1.574
Web of Science (2011): Impact factor 4.841
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.458 SNIP 1.54
Web of Science (2010): Impact factor 4.672
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.424 SNIP 1.65
Association between production of fibrinolysin and virulence of Staphylococcus hyicus in relation to exudative epidermitis in pigs

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Wegener, H. C.
Pages: 295-297
Publication date: 1997
Peer-reviewed: Yes

Publication information
Journal: Acta Veterinaria Scandinavica (Print Edition)
Volume: 38
Issue number: 3
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Impact factor 1.472
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.98 SJR 0.644 SNIP 1.641
Web of Science (2015): Impact factor 1.23
BFI (2014): BFI-level 1
A study of phage- and ribotype patterns of Staphylococcus aureus isolated from bovine mastitis in the Nordic countries

This study was conducted to investigate the geographical distribution of phage and ribotypes of Staphylococcus aureus causing bovine mastitis in the 5 Nordic countries. A total of 403 isolates of S. aureus was isolated from 403 different dairy herds. One hundred five strains were isolated in Denmark, 81 in Finland, 17 in Iceland, 96 in Norway and 104 in Sweden. The isolates were phage typed and characterized for their EcoRI restriction fragment length polymorphisms of the genes encoding ribosomal RNA (ribotyping). A total of 351 (87%) of the 403 isolates could be typed by phages assigning them to 25 different phage types. Two to 3 different phage types predominated within each country. One type (29/52) accounted for 36% of all the isolates and was found in 4 of the countries. A total of 87 different ribotypes was found among the isolates investigated. As for phage typing 2 to 3 different types predominated within countries. However, except for one
type (ribotype 1), which was commonly found in Denmark, Sweden and Finland, different ribotypes predominated within each country. The combination of phage and ribotyping assigned the isolates to 178 different types. Ninety-six percent of the isolates of ribotype 1 belonged to phage type 29/52. This combined type accounted for 17% of all the 403 isolates. These findings show that a large number of different types of S. aureus can be isolated from cases of bovine mastitis. However, few types predominate within different countries. These predominating types seem to be specific in each country, however, a single type was common for both Denmark, Sweden and Finland. This could suggest differences in the virulence or in modes of transmission of predominating and rare types of S. aureus associated with bovine mastitis.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Wegener, H. C., Jensen, N., Jonsson, O., Myllys, V., Thorberg, B., Waage, S., Rosdahl, V.
Pages: 243-252
Publication date: 1997
Peer-reviewed: Yes

Publication information
Journal: Acta Veterinaria Scandinavica
Volume: 38
Issue number: 3
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Impact factor 1.472
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.98 SJR 0.644 SNIP 1.641
Web of Science (2015): Impact factor 1.23
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.54 SJR 0.753 SNIP 1.21
Web of Science (2014): Impact factor 1.377
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.41 SJR 0.539 SNIP 1.11
Web of Science (2013): Impact factor 1.382
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.26 SJR 0.591 SNIP 0.789
Web of Science (2012): Impact factor 1.345
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 1.42 SJR 0.664 SNIP 0.997
Web of Science (2011): Impact factor 1.367
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.551 SNIP 1.005
Web of Science (2010): Impact factor 1.196
Web of Science (2010): Indexed yes
Avoparcin used as a growth promoter is associated with the occurrence of vancomycin-resistant Enterococcus faecium on Danish poultry and pig farms

We determined the association between the use of the glycopeptide antibiotic avoparcin as a growth promoter and the occurrence of Enterococcus faecium (VREF) with high-level resistance to vancomycin (MIC greater than or equal to 64 μg ml(-1)) on poultry and pig farms. The investigations were conducted as retrospective cohort studies, where groups of farms exposed or not exposed to avoparcin between September 1994 and April 1995 were compared. In poultry, the association between the use of avoparcin and the occurrence of VREF was confounded by the use of broad-spectrum antibiotics, and the adjusted relative risk was 2.9 (1.4-5.9). In pigs, the association had a similar magnitude with a non-adjusted relative risk of 3.3 (0.9-12.3). The similar findings in the two studies provide evidence in favour of a causal association between the use of avoparcin and the occurrence of VREF on farms, and suggest that food animals constitute a potential reservoir of infection for VREF in humans.

General information
State: Published
Organisations: Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Technical University of Denmark
Contributors: Bager, F., Madsen, M., Christensen, J., Aarestrup, F. M.
Pages: 95-112
Publication date: 1997
Peer-reviewed: Yes

Publication information
Journal: Preventive Veterinary Medicine
Volume: 31
Issue number: 1-2
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.26 SJR 1.144 SNIP 1.31
Web of Science (2017): Impact factor 1.924
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Impact factor 1.987
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.1 SJR 1.282 SNIP 1.177
Web of Science (2015): Impact factor 2.182
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.37 SJR 1.27 SNIP 1.407
Web of Science (2014): Impact factor 2.167
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 2.49 SJR 1.264 SNIP 1.529
Web of Science (2013): Impact factor 2.506
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 2.45 SJR 1.265 SNIP 1.436
Web of Science (2012): Impact factor 2.389
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 2.24 SJR 1.194 SNIP 1.295
Web of Science (2011): Impact factor 2.046
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.156 SNIP 1.284
Web of Science (2010): Impact factor 2.07
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.032 SNIP 1.338
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.056 SNIP 1.258
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.009 SNIP 1.353
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.06 SNIP 1.277
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.931 SNIP 1.414
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.812 SNIP 1.146
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.846 SNIP 1.323
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.857 SNIP 1.427
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.045 SNIP 1.48
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.623 SNIP 1.261
Web of Science (2000): Indexed yes
Characterisation of integrons and antibiotic resistance genes in Danish multiresistant Salmonella enterica Typhimurium DT104

The presence and genetic content of integrons was investigated in eight Salmonella enterica Typhimurium DT104 isolates from different pig herds in Denmark. Two different integrons were identified using PCR and sequencing. Each of the integrons carried a single resistance cassette in addition to the sul1 and qacE Delta 1 genes characteristic of integrons. The first integron encoded the ant (3')-Ia gene that specified resistance to spectinomycin and streptomycin. The second contained the pse-I beta-lactamase gene. All the multiresistant strains contained both integrons. The presence of these two integrons did not account for the total phenotypic resistance of all the isolates and does not exclude the presence of other mobile DNA elements.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Sandvang, D., Aarestrup, F. M., Jensen, L. B.
Pages: 177-181
Publication date: 1997
Peer-reviewed: Yes

Publication information
Journal: FEMS MICROBIOLOGY LETTERS
Volume: 157
Issue number: 1
ISSN (Print): 0378-1097
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.8 SJR 0.79 SNIP 0.58
Web of Science (2017): Impact factor 11.392
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.76 SJR 0.842 SNIP 0.615
Web of Science (2016): Impact factor 12.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.08 SJR 1.156 SNIP 0.756
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.17 SJR 1.136 SNIP 0.767
Web of Science (2014): Impact factor 13.244
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.25 SJR 1.053 SNIP 0.719
Web of Science (2013): Impact factor 13.806
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.25 SJR 1.073 SNIP 0.804
Web of Science (2012): Impact factor 13.231
Characterization of integrons and antibiotic resistance genes in Danish multiresistant Salmonella enterica Typhimurium DT104

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Sandvang, D., Aarestrup, F. M., Jensen, L. B.
Pages: 177-181
Publication date: 1997
Peer-reviewed: Yes

Publication information
Journal: FEMS Microbiology Letters
Volume: 157
ISSN (Print): 0378-1097
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.8 SJR 0.79 SNIP 0.58
Web of Science (2017): Impact factor 11.392
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.76 SJR 0.842 SNIP 0.615
Web of Science (2016): Impact factor 12.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.08 SJR 1.156 SNIP 0.756
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.17 SJR 1.136 SNIP 0.767
Web of Science (2014): Impact factor 13.244
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.25 SJR 1.053 SNIP 0.719
Web of Science (2013): Impact factor 13.806
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.25 SJR 1.073 SNIP 0.804
Web of Science (2012): Impact factor 13.231
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.26 SJR 1.105 SNIP 0.764
Web of Science (2011): Impact factor 10.96
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.081 SNIP 0.754
Web of Science (2010): Impact factor 11.796
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.13 SNIP 0.834
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.084 SNIP 0.834
Scopus rating (2007): SJR 1.103 SNIP 0.864
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.105 SNIP 0.86
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1 SNIP 0.8
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.005 SNIP 0.725
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.018 SNIP 0.866
Scopus rating (2002): SJR 0.902 SNIP 0.791
Web of Science (2002): Indexed yes
Clonal spread of tetracycline resistant Salmonella Typhimurium in Danish dairy herds

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, N. E., Baggesen, D. L.
Pages: 313-314
Publication date: 1997
Peer-reviewed: Yes

Publication information
Journal: VETERINARY RECORD
Volume: 140
Issue number: 12
ISSN (Print): 0042-4900
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 0.39 SJR 0.464 SNIP 0.858
Web of Science (2017): Impact factor 2.05
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.3 SJR 0.482 SNIP 0.745
Web of Science (2016): Impact factor 1.737
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.39 SJR 0.521 SNIP 0.796
Web of Science (2015): Impact factor 1.741
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 0.41 SJR 0.489 SNIP 0.844
Web of Science (2014): Impact factor 1.493
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 0.5 SJR 0.506 SNIP 0.821
Web of Science (2013): Impact factor 1.633
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 0.52 SJR 0.505 SNIP 0.878
Web of Science (2012): Impact factor 1.803
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 0.62 SJR 0.569 SNIP 0.903
Web of Science (2011): Impact factor 1.248
ISI indexed (2011): ISI indexed yes
Fremkomst af resistens mod fluoroquinoloner blandt dyrepatogene bakterier i Danmark efter introduktion af enrofloxacin til veterinær anvendelse

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, N. E., Jorsal, S. E., Nielsen, T. K.
Pages: 95-98
Publication date: 1997
Peer-reviewed: No

Publication information
Journal: Dansk Veterinær Tidsskrift
Volume: 80
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
Isolation of vancomycin resistant Enterococcus faecium from food

In a survey of vancomycin resistant Enterococcus faecium (VREF) in Danish meat products, VREF could be detected in 16% of 160 samples of broilers collected at slaughterhouses and in 15% of 26 samples of pork collected from the retail trade. VREF were isolated by enrichment for 24 h in nutrient broth supplemented with vancomycin (50 μg/ml) prior to plating on Slanetz and Bartley agar. Using direct plating on Slanetz and Bartley agar, VREF could be isolated from only 1.7% of 540 samples of broilers from slaughterhouses and 2.2% of 90 samples of broilers from retail outlets. VREF was not detected in 124 samples of pork and 128 samples of beef from retail outlets by the direct plating method. An additional enrichment step in nutrient broth supplemented with vancomycin enhanced the detection rate of VREF by approximately three times compared to the direct plating method when investigating the same 160 samples of broilers by the two methods. The implications and public health aspects of VREF in food is discussed.

General information

State: Published
Organisations: Communications and Management Secretariat, National Food Institute, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Division of Microbiology and Risk Assessment
Contributors: Wegener, H. C., Madsen, M., Nielsen, N., Aarestrup, F. M.
Pages: 57-66
Publication date: 1997
Peer-reviewed: Yes

Publication information

Journal: International Journal of Food Microbiology
Volume: 35
Issue number: 1
ISSN (Print): 0168-1605
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 3.76 SJR 1.366 SNIP 1.436
Web of Science (2017): Impact factor 3.451
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.97 SJR 1.481 SNIP 1.553
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.02 SJR 1.614 SNIP 1.683
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.62 SJR 1.493 SNIP 1.695
Web of Science (2014): Impact factor 3.082
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Klonal spredning af tetracyklinresistente Salmonella Typhimurium isolater i danske kvægbesætninger

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, N. E., Baggesen, D. L.
Molecular characterization of Escherichia coli strains isolated from pigs with edema disease

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jorsal, S. E., Ahrens, P., Jensen, N. E., Meyling, A.
Pages: 20-24
Publication date: 1997
Peer-reviewed: Yes

Publication information
Journal: JOURNAL OF CLINICAL MICROBIOLOGY
Volume: 35
Issue number: 1
ISSN (Print): 0095-1137
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.55 SJR 2.256 SNIP 1.443
Web of Science (2017): Impact factor 4.054
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.196 SNIP 1.4
Web of Science (2016): Impact factor 3.712
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.56 SJR 2.206 SNIP 1.431
Prevalence and duration of intramammary infection in Danish heifers during the peripartum period
Resistensmæssige problemer ved anvendelse af vækstfremmere

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Pages: 8-10
Publication date: 1997
Peer-reviewed: No

Publication information
Journal: DS-nyt
Volume: 9
Original language: Danish
Source: orbit
Source-ID: 236402
Research output: Research › Journal article – Annual report year: 1997

Streptococcus suis hos svin

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Rasmussen, S., Jorsal, S. E. L., Jensen, N. E., Aarestrup, F. M., Andresen, L. O.
Pages: 56
Publication date: 1997
Peer-reviewed: No

Publication information
Journal: Årsberetning 1997
ISSN (Print): 0902-0276
Ratings:
Web of Science (2000): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 243980
Research output: Research › Journal article – Annual report year: 1997
Scopus rating (2006): SJR 0.384
Scopus rating (2005): SJR 0.78
Scopus rating (2004): SJR 0.457
Scopus rating (2003): SJR 0.309
Scopus rating (2002): SJR 0.231
Original language: English
Source: orbit
Source-ID: 236401
Research output: Research › Journal article – Annual report year: 1997

Surveillance of antimicrobial resistance - requirements for monitoring programmes

General information
State: Published
Organisations: Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Communications and Management Secretariat, National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Bager, F., Wegener, H. C., Jensen, N. E., Aarestrup, F. M.
Publication date: 1997
Peer-reviewed: No
Event: Abstract from Epidemiol Sante Anim (ISVEE).
Source: orbit
Source-ID: 246780
Research output: Research › Conference abstract for conference – Annual report year: 1997

Distribution and antibiotic resistance patterns of common mastitis pathogens (Gram-positive cocci) in selected dairy herds of three dairy farming sectors in Zimbabwe

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Makaya, P. V., Aarestrup, F. M., Olsen, J. E.
Pages: 65-75
Publication date: 1996
Peer-reviewed: No

Publication information
Journal: Zimbabwe Veterinary Journal
Volume: 27
ISSN (Print): 1016-1511
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: English
Source: orbit
Source-ID: 236397
Research output: Research › Journal article – Annual report year: 1996

Epidemiological aspects of group B streptococci of bovine and human origin
Restoration of group B streptococci of bovine and human origin
Restriction fragment length polymorphism of the gene encoding rRNA (ribotyping) was used in combination with conventional epidemiological markers to study phenotypic variations among Streptococcus agalactiae of bovine origin and the possible epidemiological interrelationship between the bovine and human reservoirs of Streptococcus agalactiae. The bovine material constituted 53 strains (9 antigen combinations) isolated from 11 herds. Herds with a uniform as well as heterogenic antigenic pattern were included. Furthermore, strains isolated in the course of time from the same persistently infected quarters were examined. The human material constituted 16 strains, 4 each of 4 serotypes, isolated from healthy carriers. Finally, nine serotype- and the group reference strains were examined. All strains were serotyped by double diffusion in agarose gel, biotyped (lactose +/-), and ribotyped using two restriction enzymes, HindIII and Hhal. All isolates could be typed by ribotyping and seven ribotypes were identified among the reference strains. The restriction enzymes used alone or in combination gave typing results that allowed discrimination between and within serotype. Combined use of serotype, HindIII and Hhal ribotypes produced 11 types among the 16 human strains. Ribotype analysis discriminated between herds infected with the same serotype. Strains of varying antigenic patterns from the same herd had the same ribotype. Phenotypic variations in serotype observed in persistent intramammary infection were not related to genetic changes as monitored by ribotype. Two ribotypes were represented among both bovine and human strains. The
discriminating capability of lactose fermentation was of limited value.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Jensen, N. E., Aarestrup, F. M.
Pages: 417-422
Publication date: 1996
Peer-reviewed: Yes

Publication information
Journal: Epidemiology and Infection
Volume: 117
Issue number: 3
ISSN (Print): 0950-2688
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.88 SJR 1.128 SNIP 0.807
Web of Science (2017): Impact factor 2.044
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.98 SJR 1.18 SNIP 0.866
Web of Science (2016): Impact factor 2.075
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.29 SJR 1.349 SNIP 1.052
Web of Science (2015): Impact factor 2.515
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.19 SJR 1.305 SNIP 1.016
Web of Science (2014): Impact factor 2.535
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.57 SJR 1.337 SNIP 1.113
Web of Science (2013): Impact factor 2.491
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.69 SJR 1.437 SNIP 1.17
Web of Science (2012): Impact factor 2.867
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.71 SJR 1.326 SNIP 1.214
Web of Science (2011): Impact factor 2.843
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.066 SNIP 1.042
Web of Science (2010): Impact factor 2.257
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.065 SNIP 1.197
Web of Science (2009): Indexed yes
Glycopeptide susceptibility among Danish Enterococcus faecium and Enterococcus faecalis isolates of animal and human origin and PCR identification of genes within the vanA cluster

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, National Veterinary Institute, Division of Poultry, Fish and Fur Animals
Pages: 1938-1940
Publication date: 1996
Peer-reviewed: Yes

Publication information
Journal: ANTIMICROBIAL AGENTS AND CHEMOTHERAPY
Volume: 40
Issue number: 8
ISSN (Print): 0066-4804
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.15 SJR 2.291 SNIP 1.263
Web of Science (2017): Impact factor 4.255
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Listeria monocytogenes in bovine mastitis. Possible implication for human health

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Jensen, N. E., Aarestrup, F. M., Jensen, J., Wegener, H. C.
Ødemsyge

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Jorsal, S. E. L., Andresen, L. O., Frydendal, K., Ahrens, P., Aarestrup, F. M.
Pages: 53-55
Publication date: 1996
Peer-reviewed: No

Publication information
Journal: Årsberetning 1996
ISSN (Print): 0902-0276
Ratings:
Original language: Danish
Source: orbit
Source-ID: 236037
Research output: Research - peer-review › Journal article – Annual report year: 1996

Oedema disease caused by O-rough Escherichia coli

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Aarestrup, F. M., Jorsal, S. E. L., Ahrens, P., Wiuff, C., Scheutz, F.
Pages: 373-373
Publication date: 1996
Peer-reviewed: Yes

Publication information
Journal: VETERINARY RECORD
Volume: 139
Issue number: 15
ISSN (Print): 0042-4900
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
A comparative study of Staphylococcus aureus strains isolated from bovine subclinical mastitis during 1952-1956 and 1992

Fiftytwo strains of S. aureus isolated from cases of bovine subclinical mastitis in 52 different dairy herds in Denmark, in the periods 1952 to 1956 and 1992, were compared with regard to their phage- and EcoRI ribotypes. Furthermore, susceptibility to penicillin and production of fibrinolysin were used as additional phenotypic markers. Fortynine strains (94%) could be separated into 12 phage types. Ribotyping assigned the 52 strains to 21 different types. Both methods showed that 57% of the 1950's strains and between 38-45% of the 1992 strains belonged to 3 dominating types. The remaining strains were placed by ribotyping in 8 types occurring among the 1952-1956 strains and 10 types occurring among the 1992 strains. In 87% of the strains the results of the 2 typing methods were in accordance. However, 7 strains gave different results by the 2 methods including 2 strains with major differences. Penicillin resistance only occurred in a single genotype from the 1950's compared to 6 different genotypes among the 1992 strains.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Wegener, H. C., Rosdahl, V.
Pages: 237-243
Publication date: 1995
Peer-reviewed: Yes
Analysis of associations between major histocompatibility complex (BoLA) class I haplotypes and subclinical mastitis of dairy cows

The associations between BoLA class I haplotypes and subclinical mastitis were investigated using information on 333 cows from three different breeds and crossbreeds from 14 dairy herds in Denmark. Somatic cell count and bacteriological status were used as markers for subclinical mastitis. Associations between BoLA class I haplotypes and IMI status were also determined. The association between BoLA class I haplotypes and subclinical mastitis was weak. The A10(W50), A11, A12(A30), A16, A19(A6), A21, A26, and A31(A30) alleles were associated with different markers of subclinical mastitis. Susceptibility or resistance to the two bacteria categories was associated with different alleles. This study indicated that BoLA antigens may be involved in resistance to mastitis and that resistance may be specific for a particular pathogen.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, N. E., Østergård, H.
Pages: 1684-1692
Publication date: 1995
Peer-reviewed: Yes

Publication information
A study of phage- and ribotype patterns of Staphylococcus aureus isolated from bovine mastitis in the nordic countries

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Jensen, N. E., Wegener, H. C., Johnson, O., Myllys, V., Thorberg, B., Waage, S., Rosdahl, V. T.
Publication date: 1995
Peer-reviewed: No
Event: Poster session presented at The 3rd International Mastitis Seminar, Tel Aviv, Israel.
Source: orbit
Source-ID: 246795
Research output: Research › Poster – Annual report year: 1995

Characterization of Staphylococcus aureus from bovine mastitis

General information
State: Published
Organisations: University of Copenhagen
Contributors: Aarestrup, F. M.
Publication date: 1995

Publication information
Original language: English
Source: orbit
Source-ID: 236326
Research output: Research › Ph.D. thesis – Annual report year: 1995

Evaluation of phenotypic and genotypic methods for epidemiological typing of Staphylococcus aureus isolates from bovine mastitis in Denmark

The value of five different typing methods (antibiogram typing, biotyping, phage typing, plasmid profiling and restriction fragment length polymorphism of the gene encoding 16S and 23S ribosomal RNA (ribotyping)), in discriminating 105 Staphylococcus aureus strains from bovine milk samples obtained from 105 different Danish dairy herds was investigated. A total of 85 strains (81%) proved susceptible to all of the 11 antibiotics tested, and the remaining 20 strains could be divided into 5 different antibiogram patterns. The predominant resistance pattern, penicillin resistance, was observed in 15 (75%) of the 20 antibiotic resistant strains. Biotyping assigned the strains to 14 different types, with the most common type accounting for 25.7% of the strains. Ninety eight (93.3%) strains could be typed by phages, assigning them to 19 different phage types. The predominant phage type accounted for 31.4% of the strains. Eight different plasmid profiles was observed among 24 (23%) strains harbouring plasmids. Ribotyping yielded 30 different types, with the most common accounting for 29.5% of the strains. The single most discriminatory typing method was ribotyping (0.863) followed by biotyping (0.842) and phage typing (0.795). Plasmid profiling (0.395) and antibiogram typing (0.327) had low discriminatory indices. Correspondence among ribotypes and the presence or absence of plasmids were observed, as was some degree of correspondence between ribotype, phage type and biotype. In general the correspondence between phage type and ribotype were stronger than between biotype and ribotype and between biotype and phage type. All combinations of two or more methods led to an improved index of discrimination compared to the individual methods.
indicating, that some subdivision of types had taken place. The combination of phage, bio- or ribotyping or all three methods in combination are considered to be an efficient combination of typing methods for epidemiological investigation of S. aureus mastitis.

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Wegener, H. C., Rosdahl, V. T.
Pages: 139-150
Publication date: 1995
Peer-reviewed: Yes

**Publication information**
Journal: VETERINARY MICROBIOLOGY
Volume: 45
Issue number: 2-3
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Impact factor 2.524
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
Web of Science (2010): Impact factor 3.256
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.309 SNIP 1.466
Hver tredje kirtel hos kvierne er inficeret

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Pages: 8-9
Publication date: 1995
Peer-reviewed: No

Publication information
Journal: Landsbladet Kvæg
Volume: 1
Original language: Danish
Source: orbit
Source-ID: 236394
Research output: Research > Journal article – Annual report year: 1995

Kviemastitis, bakteriologisk baggrund

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, N. E.
Pages: 324-326
Publication date: 1995
Peer-reviewed: No

Publication information
Journal: Dansk Veterinær Tidsskrift
Volume: 78
ISSN (Print): 0106-6854
Ratings:
LACK OF STAPHYLOCOCCAL-ENTEROTOXIN PRODUCTION AMONG STRAINS OF STAPHYLOCOCCUS-AUREUS FROM BOVINE MASTITIS IN DENMARK

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Andersen, J. K., Jensen, N. E.
Pages: 273-275
Publication date: 1995
Peer-reviewed: Yes

Publication information
Journal: ACTA VETERINARIA SCANDINAVICA
Volume: 36
Issue number: 2
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Impact factor 1.472
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.98 SJR 0.644 SNIP 1.641
Web of Science (2015): Impact factor 1.23
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.54 SJR 0.753 SNIP 1.21
Web of Science (2014): Impact factor 1.377
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.41 SJR 0.539 SNIP 1.11
Web of Science (2013): Impact factor 1.382
ISI indexed (2013): ISI indexed no
Listeria monocytogenes in bovine mastitis

General information
State: Published
Organisations: Communications and Management Secretariat, National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Jensen, J., Jensen, N. E., Wegener, H. C., Aarestrup, F. M.
Publication date: 1995
Peer-reviewed: No
Event: Poster session presented at The 3rd International Mastitis Seminar, Tel Aviv, Israel.
Source: orbit
Source-ID: 236028
Research output: Research - peer-review › Journal article – Annual report year: 1995

Source: orbit
Source-ID: 246796
Research output: Research › Poster – Annual report year: 1995
Occurrence of glycopeptide resistance among Enterococcus faecium isolates from conventional and ecological poultry farms

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Pages: 255-257
Publication date: 1995
Peer-reviewed: Yes

Publication information
Journal: MICROBIAL DRUG RESISTANCE
Volume: 1
Issue number: 3
ISSN (Print): 1076-6294
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 0.957 SNIP 0.919
Web of Science (2017): Impact factor 2.344
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.37 SJR 1.015 SNIP 0.88
Web of Science (2016): Impact factor 2.306
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.25 SJR 1.04 SNIP 0.887
Web of Science (2015): Impact factor 2.529
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.48 SJR 0.959 SNIP 1.01
Web of Science (2014): Impact factor 2.49
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.87 SJR 1.265 SNIP 1.118
Web of Science (2013): Impact factor 2.524
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.45 SJR 0.963 SNIP 0.9
Web of Science (2012): Impact factor 2.364
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.76 SJR 1.163 SNIP 1.14
Web of Science (2011): Impact factor 2.153
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.054 SNIP 0.8
Web of Science (2010): Impact factor 1.936
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.915 SNIP 0.838
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.038 SNIP 0.73
Web of Science (2008): Indexed yes
Prevalence of coagulase gene polymorphism in Staphylococcus aureus isolates causing bovine mastitis

This study was conducted to investigate polymorphism of the coagulase gene of Staphylococcus aureus causing bovine mastitis. One hundred eighty-seven strains of S. aureus were isolated from bovine mastitic milk samples obtained from 187 different Danish dairy farms. The isolates were characterised for restriction fragment length polymorphism (RFLP) of the coagulase gene. A variable region of the coagulase gene was amplified using the polymerase chain reaction (PCR) followed by AluI restriction enzyme digestion. A total of 15 different RFLP patterns were observed. The predominant pattern was found in 35% of the isolates. The ease of analysing coagulase gene polymorphisms among a large number of strains, and the multiple distinct polymorphic patterns generated, supports the use of this technique in epidemiological investigations of bovine mastitis. The predominating variants may have predelection for causing intramammary infections.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Dangler, C. A., Sordillo, L. M.
Pages: 124-128
Publication date: 1995
Peer-reviewed: Yes
Stafylokokdiagnostik, en oversigt

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Jensen, N. E.
Pages: 379-386
Publication date: 1995
Peer-reviewed: No

Publication information
Journal: Dansk Veterinær Tidsskrift
Staphylococcal and other bacterial species associated with intramammary infections in Danish dairy herds

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Wegener, H. C., Rosdahl, V. T., Jensen, N. E.
Pages: 475-487
Publication date: 1995
Peer-reviewed: Yes

Publication information
Journal: ACTA VETERINARIA SCANDINAVICA
Volume: 36
Issue number: 4
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Impact factor 1.472
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.98 SJR 0.644 SNIP 1.641
Web of Science (2015): Impact factor 1.23
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.54 SJR 0.753 SNIP 1.21
Web of Science (2014): Impact factor 1.377
BFI (2013): BFI-level 1
The effect of avoparcin as a feed additive on the occurrence of vancomycin resistant Enterococcus faecium in pig and poultry production

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Administration and Service, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Bager, F., Madsen, M., Christensen, J., Ahrens, P., Westh, H., Poulsen, R. L., Wegener, H. C.
Number of pages: 428
Publication date: 1995
Peer-reviewed: No
The effect of avoparcin used as a feed additive on the occurrence of vancomycin resistant Enterococcus faecium in pig and poultry production

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M.
Publication date: 1995

Ability of Staphylococcus aureus coagulase genotypes to resist neutrophil bactericidal activity and phagocytosis

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Aarestrup, F. M., Scott, N. L., Sordillo, L. M.
Pages: 5679-5682
Publication date: 1994
Peer-reviewed: Yes

Publication information
Journal: INFECTION AND IMMUNITY
Volume: 62
Issue number: 12
ISSN (Print): 0019-9567
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.43 SJR 1.954 SNIP 0.953
Web of Science (2017): Impact factor 3.256
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.34 SJR 2.04 SNIP 0.915
Web of Science (2016): Impact factor 3.593
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.72 SJR 2.361 SNIP 1.053
Web of Science (2015): Impact factor 3.603
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.74 SJR 2.344 SNIP 1.08
Web of Science (2014): Impact factor 3.731
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.25 SJR 2.433 SNIP 1.168
Web of Science (2013): Impact factor 4.156
ISI indexed (2013): ISI indexed yes
A comparative analysis of historical and contemporary strains of Staphylococcus aureus from bovine subclinical mastitis by phage- and ribotyping

**General information**

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Wegener, H. C., Rosdahl, V. T.
Publication date: 1993
Peer-reviewed: No

Source: orbit
Source-ID: 236020
Research output: Research - peer-review › Journal article – Annual report year: 1994

Bakteriel paronychia (klovoldsbetændelse) hos kat forårsaget af Staphylococcus fells
Comparison of biotyping, phage typing, plasmid profiling and ribotyping for discrimination of strains of Staphylococcus aureus from bovine mastitis

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Wegener, H. C., Rosdahl, V. T.
Publication date: 1993
Peer-reviewed: No
Event: Abstract from The 74th Annual Meeting of the Conference of Research Workers in Animal Diseases, Chicago, Illinois, USA.
Source: orbit
Source-ID: 246809
Research output: Research › Conference abstract for conference – Annual report year: 1993

Eksfoliativ dermatitis hos kat forårsaget af Staphylococcus saprophyticus

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Contributors: Aarestrup, F. M., Nielsen, R., Wegener, H. C.
Pages: 924-925
Publication date: 1993
Peer-reviewed: No
Evaluation of the uncorrected erythrocyte sedimentation rate and the serum/plasma urea concentration in the diagnosis of the cystic endometrial hyperplasia/pyometra complex in the female dog

**General information**
- State: Published
- Organisations: Division of Microbiology and Risk Assessment, National Food Institute
- Contributors: Jensen, A. L., Bantz, M., Poulsen, J. S. D., Aarestrup, F. M.
- Pages: 20-26
- Publication date: 1993
- Peer-reviewed: No

**Publication information**
- Journal: European Journal of Companion Animal Practice
- Volume: 4
- Original language: English
- Source: orbit
- Source-ID: 236391

Exfoliativ dermatitis hos kat forårsaget af Staphylococcus saprophyticus

**General information**
- State: Published
- Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
- Contributors: Aarestrup, F. M., Nielsen, R., Wegener, H. C.
- Pages: 924-925
- Publication date: 1993
- Peer-reviewed: No

**Publication information**
- Journal: Dansk Veterinærtidsskrift
- Volume: 76
- ISSN (Print): 1600-2032
- Ratings:
  - BFI (2008): BFI-level 1
The morphology of synovial grooves (Fossae synoviales) in joints of cattle of different age groups

The joint cartilage of the head of the radius, the metacarpal bone, the tibial cochlea, the proximal trochlea of the talus and the metatarsal bone of 26 cattle in the age groups fetuses, 0 days, 2-5 weeks, 2-5 months, 7-13 months, 2-3.5 years, and 5-7 years were examined macroscopically and histologically. Synovial grooves developed on all joint surfaces examined, but at different times. At some locations the development of the grooves began prenatally. During the groove development the same features were in principle observed on all joint surfaces: Degeneration and progressive thinning of the joint cartilage, invasion of connective tissue into the cartilage, cessation of the endochondral ossification, and depression of the groove area into the subchondral bone. The findings indicated that the synovial grooves should be considered as being part of the normal morphology of the joints. In 4 animals aged from 3 weeks to 13 months dyschondroplastic (osteochondrotic) lesions were observed in the joint cartilage both inside and outside the groove areas on one or more joint surfaces.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Wegener, K. M., Heje, N. I., Aarestrup, F. M., Ravn, B. T., Østerby, J.
Pages: 359-370
Publication date: 1993
Peer-reviewed: Yes

Publication information
Journal: Journal of the American Veterinary Medical Association
Volume: 40
Issue number: 5
ISSN (Print): 0003-1488
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 0.6 SJR 0.714 SNIP 1.025
Web of Science (2017): Impact factor 1.508
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 0.55 SJR 0.764 SNIP 0.929
Web of Science (2016): Impact factor 1.497
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 0.62 SJR 0.726 SNIP 0.946
Web of Science (2015): Impact factor 1.501
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 0.68 SJR 0.773 SNIP 1.012
Web of Science (2014): Impact factor 1.557
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 0.78 SJR 0.812 SNIP 1.204
Web of Science (2013): Impact factor 1.672
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 0.75 SJR 0.749 SNIP 1.073
Web of Science (2012): Impact factor 1.715
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 0.9 SJR 0.989 SNIP 1.279
Web of Science (2011): Impact factor 1.791
Cystik endometrie hyperplasi/pyometra-komplekset hos hund

**General information**

State: Published  
Organisations: Division of Microbiology and Risk Assessment, National Food Institute  
Contributors: Jensen, A. L., Bantz, M., Poulsen, J. S. D., Aarestrup, F. M.  
Pages: 683-689  
Publication date: 1992  
Peer-reviewed: No

**Publication information**

Journal: Dansk Veterinær Tidsskrift  
Volume: 75  
ISSN (Print): 0106-6854  
Ratings:  
BFI (2018): BFI-level 1  
BFI (2017): BFI-level 1  
Web of Science (2017): Indexed yes  
BFI (2016): BFI-level 1  
BFI (2015): BFI-level 1  
BFI (2014): BFI-level 1  
BFI (2013): BFI-level 1  
ISI indexed (2013): ISI indexed no  
BFI (2012): BFI-level 1  
ISI indexed (2012): ISI indexed no  
BFI (2011): BFI-level 1  
ISI indexed (2011): ISI indexed no  
BFI (2010): BFI-level 1  
BFI (2009): BFI-level 1  
BFI (2008): BFI-level 1  
Original language: Danish  
Source: orbit  
Source-ID: 236316  
Research output: Research - peer-review › Journal article – Annual report year: 1993
Projects:

**Human microbiome interaction**
Jespersen, M. L., PhD Student, National Food Institute
Rasmussen, S., Main Supervisor
Aarestrup, F. M., Supervisor, National Food Institute
Nielsen, H. B., Supervisor
Fonde
01/09/2018 → 31/08/2021
Award relations: Human microbiome interaction
Project: PhD

**Infectious Diseases and Whole Genome Sequencing**
Rebelo, A. R. B., PhD Student, National Food Institute
Aarestrup, F. M., Main Supervisor, National Food Institute
Bortolaia, V., Supervisor, National Food Institute
Samfinansieret - Andet
01/06/2018 → 31/05/2021
Award relations: Infectious Diseases and Whole Genome Sequencing
Project: PhD

**Surveillance of Network Effects in Antimicrobial Resistance Genes**
Röder, T., PhD Student, National Food Institute
Aarestrup, F. M., Main Supervisor, National Food Institute
Petersen, T. N., Supervisor, National Food Institute
Samfinansieret - Andet
01/01/2018 → 31/12/2020
Award relations: Surveillance of Network Effects in Antimicrobial Resistance Genes
Project: PhD

**Evergreen methods for phylogeny**
Szarvas, J., PhD Student, National Food Institute
Lund, O., Main Supervisor
Aarestrup, F. M., Supervisor, National Food Institute
Samfinansieret - Andet
01/08/2017 → 31/07/2020
Award relations: Evergreen methods for phylogeny
Project: PhD

**Typing and pheno typing based on direct sequencing of samples**
Clausen, P. T. L. C., PhD Student, National Food Institute
Lund, O., Main Supervisor
Aarestrup, F. M., Supervisor, National Food Institute
Samfinansieret - Andet
01/07/2017 → 30/06/2020
Award relations: Typing and pheno typing based on direct sequencing of samples
Project: PhD

**Global sewage surveillance project**
The project will serve as proof-of-concept for applying metagenomic approaches, which could initiate a global surveillance of human infectious diseases including antimicrobial resistance from sewage collected in major cities around the world to detect, control, prevent and predict human infectious diseases. Along with The National Food Institute, DTU (WHO Collaborating Centre and European Union Reference Laboratory for Antimicrobial Resistance in Foodborne Pathogens), several other partners from COMPARE are involved in this joint study with WHO, including Erasmus MC, The Netherlands, and National Institute for Public Health and the Environment, RIVM (WHO Collaborating Centre for Risk Assessment of Pathogens in Water and Food).
Hendriksen, R. S., Project Participant, National Food Institute, Research Group for Genomic Epidemiology
Aarestrup, F. M., Project Manager, National Food Institute, Research Group for Genomic Epidemiology
01/01/2016 → …
GMI: Global Microbial Identifier
GMI envisions a global system of DNA genome databases for microbial and infectious disease identification and diagnostics. Such a system will benefit those tackling individual problems at the frontline, clinicians, veterinarians, etc., as well as policy-makers, regulators, and industry. By enabling access to this global resource, a professional response on health threats will be within reach of all countries with basic laboratory infrastructure.

Hendriksen, R. S., Project Participant, National Food Institute, Research Group for Genomic Epidemiology
Aarestrup, F. M., Project Manager, National Food Institute, Research Group for Genomic Epidemiology
01/09/2011 → ...
Project: Research

Generic open science data platform for surveillance, exposure assessment and risk analysis
Backhaus, L. L. V., PhD Student, National Food Institute
Aarestrup, F. M., Main Supervisor, National Food Institute
Lund, O., Supervisor
Pamp, S. J., Supervisor, National Food Institute
Vigre, H., Supervisor, National Food Institute
Institut stipendie (DTU)
01/12/2016 → 10/02/2020
Award relations: Generic open science data platform for surveillance, exposure assessment and risk analysis
Project: PhD

Evaluering og optimering af overvågningsprogrammer for antibiotika resistens og antibiotikaforbrug
Struve, T., PhD Student, National Food Institute
Hald, T., Main Supervisor, National Food Institute
Aarestrup, F. M., Supervisor, National Food Institute
Emborg, H., Supervisor, National Food Institute
Jensen, L. B., Examiner, National Food Institute
Bækbo, P., Examiner
Greiner, M., Examiner
Institut stipendie (DTU) Samf.
01/10/2008 → 25/04/2012
Award relations: Evaluering og optimering af overvågningsprogrammer for antibiotika resistens og antibiotikaforbrug
Project: PhD

Karakterisering af antibiotika resistens i grampositive bakterier i relation til brug af antibiotiske vækstfremmere
Hammerum, A. M., PhD Student
Molin, S., Main Supervisor
Aarestrup, F. M., Supervisor
Jensen, L. B., Supervisor
Givskov, M. C., Examiner, Department of Systems Biology
Krogfelt, K. A., Examiner
Woodford, N., Examiner
Sektorministerium, Stip-SU
01/10/1997 → 14/09/2001
Award relations: Karakterisering af antibiotika resistens i grampositive bakterier i relation til brug af antibiotiske vækstfremmere
Project: PhD

Metagenomic Approaches for Determining the Structure and Function of Complex Microbiomes
Kirstahler, P., PhD Student, National Food Institute
Aarestrup, F. M., Main Supervisor, National Food Institute
Lund, O., Supervisor
Pamp, S. J., Supervisor, National Food Institute
Samfinansieret - Andet
01/01/2016 → 06/05/2019
Award relations: Metagenomic Approaches for Determining the Structure and Function of Complex Microbiomes
Project: PhD
Detection of Pathogens and Antimicrobial Resistance in Microbiomes
Poulsen, C. S., PhD Student, National Food Institute
Aarestrup, F. M., Main Supervisor, National Food Institute
Kaas, R. S., Supervisor, National Food Institute
Pamp, S. J., Supervisor, National Food Institute
Samfinansieret - Andet
01/10/2015 → 31/03/2019
Award relations: Detection of Pathogens and Antimicrobial Resistance in Microbiomes
Project: PhD

Interactions Between the Microbiome and Host Immune System
Masche, A. C., PhD Student, National Food Institute
Pamp, S. J., Main Supervisor, National Food Institute
Aarestrup, F. M., Supervisor, National Food Institute
Lund, O., Supervisor
Müller, K. G., Supervisor
Samfinansieret - Andet
01/10/2015 → 31/12/2018
Award relations: Interactions Between the Microbiome and Host Immune System
Project: PhD

Next-generation sequencing and meta-genomics for detection, identification, characterisation and molecular epidemiology of microorganisms in drinking water used for irrigation
Hellmér, M., PhD Student, National Food Institute
Schultz, A. C., Main Supervisor, National Food Institute
Aarestrup, F. M., Supervisor, National Food Institute
Löfström, C., Supervisor, National Food Institute
Hendriksen, R. S., Examiner, National Food Institute
Dalsgaard, A., Examiner
Simonsson, M., Examiner
Forskningsrådsfinansiering
15/12/2014 → 15/08/2018
Award relations: Next-generation sequencing and meta-genomics for detection, identification, characterisation and molecular epidemiology of microorganisms in drinking water used for irrigation
Project: PhD

Diagnostic use of Microbial Whole Genome Sequencing (WGS)
Tetzschner, A. M. M., PhD Student, Department of Bio and Health Informatics
Lund, O., Main Supervisor, Department of Bio and Health Informatics
Aarestrup, F. M., Supervisor
Pamp, S. J., Supervisor, Department of Bio and Health Informatics
Samfinansieret - Andet
15/12/2014 → 05/07/2019
Award relations: Diagnostic use of Microbial Whole Genome Sequencing (WGS)
Project: PhD

Genome sequencing of important animal pathogenic bacteria
Ronco, T., PhD Student, National Veterinary Institute
Pedersen, K., Main Supervisor, National Veterinary Institute
Aarestrup, F. M., Supervisor
Schou, K. K., Examiner, National Veterinary Institute
Damborg, P. P., Examiner
Van Immerseel, F., Examiner
Institut stipendie (DTU)
15/12/2014 → 18/04/2018
Award relations: Genome sequencing of important animal pathogenic bacteria
Project: PhD

Optimal client-server methods for Next Generation Sequencing Analysis
Bellod Cisneros, J. L., PhD Student, Department of Bio and Health Informatics
Lund, O., Main Supervisor, Department of Bio and Health Informatics
Aarestrup, F. M., Supervisor
Anden EU-finansiering
15/12/2014 → 13/12/2018
Award relations: Optimal client-server methods for Next Generation Sequencing Analysis
Project: PhD

Rapid computational identification and elucidation of infectious disease outbreak
Thomsen, M. C. F., PhD Student, Department of Bio and Health Informatics
Lund, O., Main Supervisor, Department of Bio and Health Informatics
Aarestrup, F. M., Supervisor
Petersen, B., Examiner, Department of Bio and Health Informatics
Dallman, T., Examiner
Hansen, D. S., Examiner
Forskningsrådsfinansiering
15/04/2014 → 10/09/2018
Award relations: Rapid computational identification and elucidation of infectious disease outbreak
Project: PhD

Antibiotic Resistance Transferability from Lactic Acid Bacteria in the Food Chain
Feld, L., PhD Student
Hammer, K., Main Supervisor
Wilcks, A., Supervisor
Aarestrup, F. M., Examiner
Andrup, L., Examiner
Midtvedt, T., Examiner
Ansat eksternt
01/04/2004 → 02/06/2008
Award relations: Antibiotic Resistance Transferability from Lactic Acid Bacteria in the Food Chain
Project: PhD

Whole Genome Epidemiological Typing Of Escherichia Coli
Kaas, R. S., PhD Student, National Food Institute
Aarestrup, F. M., Main Supervisor, National Food Institute
Lund, O., Supervisor
Ussery, D., Supervisor
Hendriksen, R. S., Examiner, National Food Institute
Krogh, A. S., Examiner
Underwood, A., Examiner
Institut stipendie (DTU) Samf.
01/11/2010 → 26/01/2015
Award relations: Whole Genome Epidemiological Typing Of Escherichia Coli
Project: PhD

Characterization of ESBL and MRSA from production animals and food products in Denmark
Christiansen, M. T., PhD Student, National Food Institute
Aarestrup, F. M., Main Supervisor, National Food Institute
Agersø, Y., Supervisor, National Food Institute
Hasman, H., Supervisor, National Food Institute
Cavaco, L., Examiner, National Food Institute
Lindsay, J. A., Examiner
Westh, H., Examiner
Institut stipendie (DTU) Samf.
01/06/2010 → 04/06/2014
Award relations: Characterization of ESBL and MRSA from production animals and food products in Denmark
Project: PhD

Global Occurrence and Spread of Antimicrobial Resistant Salmonella and other Bacteria of Animal Origin
Hendriksen, R. S., PhD Student, National Food Institute
Aarestrup, F. M., Main Supervisor, National Food Institute
Wegener, H. C., Supervisor, National Food Institute
Christensen, B. B., Examiner, National Food Institute
**Bacterial response to stress by biocides**

Seier-Petersen, M. A., PhD Student, National Food Institute  
Aarestrup, F. M., Main Supervisor, National Food Institute  
Agersø, Y., Supervisor, National Food Institute  
Ussery, D., Supervisor  
Aabo, S., Examiner, National Food Institute  
Guardabassi, L., Examiner  
Webber, M., Examiner  
Forskningsrådsfinansiering  
01/12/2009 → 18/09/2013  
Award relations: Bacterial response to stress by biocides  
Project: PhD

**Microbiological and molecular characterization of succesful salmonella**

Müller, A. K., PhD Student, National Food Institute  
Agersø, Y., Main Supervisor, National Food Institute  
Aabo, S., Supervisor, National Food Institute  
Aarestrup, F. M., Supervisor, National Food Institute  
Pedersen, K., Examiner, National Food Institute  
McDermott, P. F., Examiner  
Olsen, J. E., Examiner  
Offentlig finansiering  
01/12/2008 → 23/05/2012  
Award relations: Microbiological and molecular characterization of succesful salmonella  
Project: PhD

**Whole Genome Epidemiological Typing of Salmonella**

Leekitcharoenphon, P., PhD Student, National Food Institute  
Aarestrup, F. M., Main Supervisor, National Food Institute  
Lund, O., Supervisor  
Hasman, H., Examiner, National Food Institute  
Allard, M. W., Examiner  
Torpdahl, M., Examiner  
Institut stipendie (DTU) Samf.  
01/01/2011 → 30/09/2014  
Award relations: Whole Genome Epidemiological Typing of Salmonella  
Project: PhD

**Bioinformatics approaches to identify antimicrobial, virulence and other important genes in bacteria**

Zankari, E., PhD Student, National Food Institute  
Aarestrup, F. M., Main Supervisor, National Food Institute  
Lund, O., Supervisor  
Petersen, T. N., Examiner, National Food Institute  
Schultsz, C., Examiner  
Seemann, T., Examiner  
Institut stipendie (DTU) Samf.  
01/10/2011 → 17/11/2016  
Award relations: Bioinformatics approaches to identify antimicrobial, virulence and other important genes in bacteria  
Project: PhD

**Use of next-generation sequencing and meta-genomics for detection, identification, characterization and molecular epidemiology of primarily foodborne virus**

Hjelmsø, M. H., PhD Student, National Food Institute  
Aarestrup, F. M., Main Supervisor, National Food Institute  
Lund, O., Supervisor
Genomic antimicrobial resistance, prediction of functionality, resistance gene mobility and zoonotic relevance
Munk, P., PhD Student, National Food Institute
Aarestrup, F. M., Main Supervisor, National Food Institute
Agersø, Y., Supervisor, National Food Institute
Vigre, H., Supervisor, National Food Institute
Bahl, M. I., Examiner, National Food Institute
Hansen, L. H., Examiner
van Schaik, W., Examiner
Samfinansieret - Andet
15/12/2013 → 16/05/2018
Award relations: Genomic antimicrobial resistance, prediction of functionality, resistance gene mobility and zoonotic relevance
Project: PhD

Adaptability and promiscuity among pathogenic and commensal microorganisms
Roer, L., PhD Student, National Food Institute
Aarestrup, F. M., Main Supervisor, National Food Institute
Hasman, H., Supervisor, National Food Institute
Jensen, L. B., Examiner, National Food Institute
Hansen, L. H., Examiner
Wain, J., Examiner
Institut stipendie (DTU) Samf.
01/07/2012 → 21/04/2016
Award relations: Adaptability and promiscuity among pathogenic and commensal microorganisms
Project: PhD

Application of whole genome sequencing for diagnostics, surveillance and outbreak detection of foodborne pathogens
Joensen, K. G., PhD Student, National Food Institute
Aarestrup, F. M., Main Supervisor, National Food Institute
Hasman, H., Supervisor, National Food Institute
Baggesen, D. L., Examiner, National Food Institute
Dallman, T., Examiner
Persson, S., Examiner
Institut stipendie (DTU) Samf.
15/12/2011 → 28/10/2015
Award relations: Application of whole genome sequencing for diagnostics, surveillance and outbreak detection of foodborne pathogens
Project: PhD

Plasmid diversity and epidemiology in Enterobacteriae from human and non-human reservoirs
Bielak, E. M., PhD Student, National Food Institute
Hasman, H., Main Supervisor, National Food Institute
Aarestrup, F. M., Supervisor, National Food Institute
Jensen, L. B., Examiner, National Food Institute
Guardabassi, L., Examiner
Guerra Román, B., Examiner
Institut stipendie (DTU) Samf.
01/12/2008 → 27/06/2012
Award relations: Plasmid diversity and epidemiology in Enterobacteriae from human and non-human reservoirs
Project: PhD
ADAP: Adaptability and promiscuity among pathogenic and commensal microorganisms
Vi vil i dette projekt undersøge, hvorfor nogle bakterier hyppigere udvikler antibiotikaresistens end andre. Sygdomsfremkaldende bakterier og andre bakterier udveksler gener gennem en proces, der kaldes horizontal genoverførsel. Undersøgelserne vil specielt fokusere på at kortlægge de egenskaber, som beviker, at nogle bakterier er mindre modtagelige for genoverførsler end andre. Ved anvendelse af den nyeste teknologi, såsom 2. generations DNA-sekventering og flowcytometri vil vi undersøge den grundlæggende mekanisme bag den evolutionære proces på en måde, der ikke hidtil har været mulig. Vi vil søge forklaringen på, hvorfor specielt sygdomsfremkaldende bakterier er bedre i stand til at modtage gener end andre, hvilket øger disse bakteriers evne til at tilpasse og udvikle sig. En sådan viden vil kunne bruges til at udvikle strategier til at stoppe udviklingen af antibiotikaresistens hos sygdomsfremkaldende bakterier, samt gøre det muligt at forudsiges potentielt for at der udvikles resistens i ellers følsomme bakterier. Projektet vil således medvirke til at finde metoder til at undgå en hurtig global spredning af sygdomme forårsaget af bakterier, som er resistente over for moderne medicin.

Aarestrup, F. M., Project Manager, National Food Institute, Research Group for Genomic Epidemiology
Hasman, H., Project Participant, National Food Institute, Research Group for Genomic Epidemiology
Roer, L., Project Participant, National Food Institute, Research Group for Genomic Epidemiology
Carlsson, S., Other, National Food Institute, Research Group for Genomic Epidemiology

External Project ID: Det Frie Forskningsråd
Det Frie Forskningsråd: DKK4,890,449.00
01/01/2012 → 31/12/2015
Keywords: ADAP, Adaptability, promiscuity, commensal, microorganisms
Collaborators: University of Copenhagen
Award relations: ADAP: Adaptability and promiscuity among pathogenic and commensal microorganisms
Project: Research

REINSURE: Revolutionizing Infectious disease surveillance
A pilot study for “real-time” surveillance of very large human populations and risk based urban water management based on complete DNA-sequencing of sewage samples. Novel or re-emerging infectious agents are often not detected before they have emerged and spread locally and globally. Rapid detection and identification is essential in both crisis detection and prevention. Especially the challenge of monitoring the large healthy human populations is a so far completely unsolved challenge. An increasing part of the world’s population is connected to a sewage system. This have prompted attempt to perform surveillance for a few selected health risks, but has also proven tremendous complicated and technologically demanding because of the need to look for so many different agents. Recent developments in sequencing technologies have now made it technologically feasible to sequence sufficient amounts in a short time and thereby make this available for completely novel applications. This may completely change the paradigm of microbiological surveillance and control and for the first time in history make it possibly to monitor healthy populations and not only the sentinel or sick populations. Treatment of waste water has greatly reduced the burden of infectious disease and reduced discharges to the environment. However, discharges from waste water treatment plants and sewer overflows still pose a significant health risk, but the estimation hereof are hampered by insufficient knowledge of pathogen concentrations, making the urban water management inefficient. Todays new sequence technologies offer an unprecedented source of information related to waste water related health risks.

Aarestrup, F. M., Project Manager, National Food Institute, Research Group for Genomic Epidemiology
Bergmark, L., Project Participant, National Food Institute, Research Group for Genomic Epidemiology
Carlsson, S., Other, National Food Institute, Research Group for Genomic Epidemiology

External Project ID: Villum Fonden
Villum Fonden: DKK4,980,551.00
30/05/2013 → 29/05/2017
Collaborators: DHI
Project: Research

Biocide: Biocide Resistance; An emerging threat to public health
Biocides are chemical substances capable of killing or inhibiting bacteria and their use have become an integrated part of the industrialized world. The potential negative effects of biocides on development of virulence and antimicrobial resistance in bacteria is to a large extent unknown. The purpose of this project is to determine the response of bacteria to selected biocides. The work will include studies of bacterial gene transcription, as well as determination of mutation-rates and horizontal gene-transfer when exposed to different biocides.

Aarestrup, F. M., Project Manager, National Food Institute, Research Group for Genomic Epidemiology
Carlsson, S., Other, National Food Institute, Research Group for Genomic Epidemiology

External Project ID: Innovationsfonden
InnovationsFonden: DKK4,993,406.00
01/01/2009 → 01/05/2015
Keywords: Biocides, Resistance, Biocides resistance
Collaborators: University of Copenhagen, DHI, Hvidovre Hospital
Award relations: Biocide: Biocide Resistance; An emerging threat to public health
Project: Research
The advancement of genome technologies holds great promise for improving the quality and speed of public health laboratory investigations, and for decreasing their cost. The latest genome DNA sequencers are now suitable for routine use in public health laboratories and may replace conventional culture-based and molecular bacterial methods for laboratory diagnosis. Especially in low income areas this might create new options, and enable laboratories in developing countries to “leapfrog”, avoiding the development of very costly and often insufficient laboratory systems similar to those that are implemented in OECD countries where separate specialist testing capacities exist for each of the many microbiological families. The problem is the need of very specialized knowledge, computation and tools to analyze the data generated in a standardized and comparable way and provide plain language reports to the primary care users. Such tools are developed or under development in a web-accessible format at DTU. In the project the latest sequencing technology is made available in a diagnostic laboratory in Tanzania and combined with analytic facilities at one of the world’s largest bioinformatic centers at DTU. Two PhD-students from Tanzania are being educated in sequencing technology and use this on routine diagnostic samples. To ensure dissemination to other countries in the region and provide capacity Building, Kilimanjaro Clinical Research Institute (KCRI) at the Kilimanjaro Christian Medical Centre is used as a focal point for WHO GFN training courses.

The main objective of the project is to find out the links between infections and autoimmune diseases. INTRICATE examines the connection between specific bacterial infections and the autoimmune disease “Systemic Vasculitis”. DTU Food contributes to the part of the project where it is investigated whether genetic variation in the bacterial Type 1 fimbrial adhesin FimH influences bacterial uptake and pathogenesis. We are specifically working on making mutations in FimH to assemble, process and handle the large amount of data in a standardized way that will make the information useful, especially for diagnostic and surveillance. The aim of this center is to provide the scientific foundation for future internet-based solutions where a central database will enable simplification of total genome sequence information and comparison to all other sequenced including spatial-temporal analysis. We will develop algorithms for rapid analyses of whole genome DNA-sequences, tools for analyses and extraction of information from the sequence data and internet/web-interfaces for using the tools in the global scientific and medical community. The activity is being expanded to also include other microorganisms, such as vira and parasites as well as metagenomic samples.

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Escherichiacoli: Comparative Pathogenomics and Transcriptomics of Escherichia coli

Klemm, P., Project Manager, National Food Institute
Hancock, V., Project Participant, National Food Institute
Aarestrup, F. M., Contact Person, National Food Institute, Division of Epidemiology and Microbial Genomics
Lundbeckfonden: DKK2,000,000.00
01/01/2008 → 31/12/2012
Award relations: Comparative Pathogenomics and Transcriptomics of Escherichia coli
Project: Research

GFN: World Health Organization Collaborating Center Global Foodborne Infection Network
The Global Foodborne Infections Network (formerly Global Salm-Surv (GSS)) is a global network of laboratories and individuals involved in surveillance, isolation, identification and antimicrobial resistance testing of various foodborne pathogens. It is part of endeavours of WHO to strengthen the capacities of its Member States in the surveillance and control of major foodborne diseases and to contribute to the global effort of containment of antimicrobial resistance in foodborne pathogens. The objective of the network is to strengthen and enhance the capacities of national and regional laboratories in the surveillance of major foodborne pathogens, e.g. the work with antimicrobial resistance in Salmonella and Campylobacter from humans, food and animals. The National Food Institute, Technical University of Denmark conducts: External Quality Assurance System (EQAS) on serotyping and susceptibility testing of Salmonella and Shigella as well as identification and MIC determination of Campylobacter and an unknown foodborne pathogen Training courses in isolation, identification, serotyping, PFGE and susceptibility testing of major foodborne pathogens. Individual training Reference testing of problem strains Participation in various research projects with member countries.

Hendriksen, R. S., Contact Person, National Food Institute, Division of Epidemiology and Microbial Genomics
Aarestrup, F. M., Project Manager, National Food Institute, Division of Epidemiology and Microbial Genomics
Karlsmose Pedersen, S., Contact Person, National Food Institute, Division of Epidemiology and Microbial Genomics
01/01/2000 → …
Collaborators: Centers for Disease Control and Prevention, Public Health Agency of Canada, Utrecht University, World Health Organization, Czech National Institute of Public Health, United States Food and Drug Administration, Institut Pasteur du Maroc, OzFoodNet, European Centre for Disease Prevention and Control
Project: Research

Biogeography of Pathogens: Unveiling their Diversity, Distribution, and Function in Space and Time
Biogeography of Pathogens: Unveiling their Diversity, Distribution, and Function in Space and Time
Pamp, S. J., Project Applicant, National Food Institute, Division of Epidemiology and Microbial Genomics
Aarestrup, F. M., Project Participant, National Food Institute, Division of Epidemiology and Microbial Genomics
Carlsbergfondet
01/04/2014 → 31/03/2015
Keywords: Microbial Biogeography, Microbial Ecology, Metagenomics, Staphylococcus aureus
Award relations: Biogeography of Pathogens: Unveiling their Diversity, Distribution, and Function in Space and Time
Project: Research
**Evaluation and optimisation of surveillance programmes for antimicrobial resistance and drug use**

The overall objective of the project is to provide a quantitative risk assessment of the relationship between consumption of antimicrobials in food animals and the occurrence of antimicrobial resistant bacteria in animals and foods including their potential adverse health effects in humans. The assessment is expected to provide the scientific basis for future recommendations, partly in order to optimize the existing surveillance for antibiotic resistance (DANMAP), and partly in order to develop guidelines regarding antimicrobial consumption and management of specific risk factors in the primary production. The project focuses on the development of resistance to antimicrobial (cephalosporins, macrolides and quinolones), which is critically important for human therapy, for example, persons having a foodborne infection with Salmonella or Campylobacter. The project is a pilot study of transfer of resistance determinants through the food-production chain.

Hald, T., Project Manager, National Food Institute, Division of Microbiology and Risk Assessment
Struve, T., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Aarestrup, F. M., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Emborg, H., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Vigre, H., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment

01/10/2008 → 31/10/2011

Project: Research

**Global surveillance of Salmonella in animals, food and humans: Identification of major sources and analysis of global trends**

The objectives are to provide an overview of Salmonella serovars in different countries and regions, evaluate trends over the years and analyze the worldwide epidemiology of the various serovars. The overall aim is to estimate the attribution of the global burden of human salmonellosis on the various animal-food sources, by: 1) Reviewing the Salmonella serovar distribution in animal reservoirs to obtain the expected distribution and prevalence of Salmonella serovars in different countries, by animal host. 2) Developing a Global Atlas of Food Consumption from several food consumption databases worldwide, which will provide data on the estimated consumption of animal-originated food items in different countries/regions. 3) Use the Global Livestock Production and Health Atlas (GLiPHA) to provide data on global distribution of animal hosts and other possible animal-originated sources of Salmonella contamination. The project is done in close collaboration with WHO, and supports the WHO initiative to estimate the global burden of foodborne disease (FERG).

Hald, T., Project Manager, National Food Institute, Division of Microbiology and Risk Assessment
de Knegt, L., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Aarestrup, F. M., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Pires, S. M., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Lo Wong, D., Project Participant, World Health Organization Guinea

01/04/2009 → 02/03/2012

Collaborators: World Health Organization, World Health Organization Guinea

Project: Research

**Center for genomic epidemiology**

Within five years the costs for a total bacterial genome sequencing will be less than 5 000 DKK and the equipment needed will cost less than 500 000 DKK. Thus, in 5 to 10 years most clinical and industrial microbiological laboratories will have a sequencer in use on a daily basis. As prices decline to less than 1000 DKK whole genome sequencing will also find worldwide application in human and veterinary practices, in the biotech industry, as well as many other places where bacteria are handled. In Denmark alone this equals more than 100,000 isolates annually in 15-20 laboratories and globally up to half a billion isolates per year. Thus, in the future, the limiting factor will not be the cost of the sequencing, but how to assemble, process and handle the large amount of data in a standardized way that will make the information useful for diagnosis, outbreak investigation, source tracking and surveillance. The biotechnology industry and environmental microbiology will have a similar need. The proposed center will provide the bioinformatic and scientific foundation for future
web-based solutions where a central database will provide simplified whole genome sequence information and enable rapid whole genome comparisons to all other sequences including spatial-temporal analysis. Thus, we will develop algorithms for rapid whole genome sequence analyses, tools for extraction of biologically and epidemiologically relevant information from the sequence data, and web-based interfaces to enable use of the system by the global scientific, public health and medical communities. The activity can be expanded to also include other microorganisms, such as viruses and parasites. To build up such a service and have it accepted by the medical and scientific community it must be a well-organized and stably funded project; therefore, we are applying for 6 years of funding in order to develop a strategic research centre. Following this period, we expect that these functions will be imbedded in the basic activities of the project partners.

Aarestrup, F. M., Project Manager, National Food Institute, Division of Microbiology and Risk Assessment
Det Strategiske Forskningsråd: DKK36,000,000.00
01/04/2010 → 30/09/2016
Award relations: Center for genomic epidemiology
Project: Research

**Training risk-assessment in non-human antibiotic usage, TRAINAU**

TRAINAU is a multidisciplinary early-stage training programme on identification, characterisation, and assessment of public health risks associated with non-human use of antimicrobials. The development of human resources capable to carry out this task requires multidisciplinary training. Accordingly, TRAINAU is bringing together early-stage researchers with different backgrounds and providing them the scientific and technological competences necessary to perform research and obtain substantial progress in this field. Descriptive and analytical epidemiological studies will investigate the association between different antimicrobial usage patterns and occurrence of antimicrobial resistance in animals. Experimental research will include laboratory experiments to validate results from field studies and to provide quantitative data to be used by the risk assessment. The multidisciplinary approach of TRAINAU is expected to generate new information needed for assessment of risks to public health associated with non-human use of antimicrobials.

Dalsgaard, A., Project Participant, University of Copenhagen, Faculty of Life Sciences,
Guardabassi, L., Project Participant, University of Copenhagen, Faculty of Life Sciences,
Ersbøll, A. K., Project Participant, University of Copenhagen, Faculty of Life Sciences,
Houe, H., Project Participant, University of Copenhagen, Faculty of Life Sciences,
Olsen, J. E., Project Participant, University of Copenhagen, Faculty of Life Sciences,
Halling-Sørensen, B., Project Participant, University of Copenhagen, Faculty of Life Sciences,
Frimodt-Møller, N., Project Participant, Statens Serum Institut
Hammerum, A. M., Project Participant, Statens Serum Institut
Wegener, H. C., Project Manager, National Food Institute
Emborg, H., Project Participant, National Food Institute
Aarestrup, F. M., Project Participant, National Food Institute
Jensen, L. B., Project Participant, National Food Institute
01/10/2005 → 30/09/2008
Collaborators: Statens Serum Institut, University of Copenhagen, University of Copenhagen, Faculty of Life Sciences,
Project: Research

**MRSA and ESBL in the Danish pig production**

Antimicrobial resistance is one of our greatest public health problems. Especially the emergence of Methicillin resistant Staphylococcus aureus (MRSA) and extended-spectrum beta-lactamase (ESBL) producing bacteria are considered some of the main problems. Several studies have shown that food animals can be a reservoir for these bacteria. The occurrence, spread and factors of importance herefore in Denmark are not known, which makes it difficult to determine intervention strategies. This project will determine the occurrence and spread of ESBL and MRSA in the Danish pig production and examine the most important risk factors.

Aarestrup, F. M., Project Manager, National Food Institute
01/01/2010 → 30/06/2013
Collaborators: Statens Serum Institut, University of Copenhagen, Danish Agriculture and Food Council
Project: Research

**Evolution and adaptation of antimicrobial resistance in bacterial populations**

It is generally believed that evolution of resistance occurs as a series of random single point mutations. However, we believe that emergence of new characters occurs as multiple mutations probably in sub-populations as a consequence of fluctuating stresses caused by lethal substances, such as antibiotics, and that these populations are so limited in size that the selection process is greatly affected by chance (stochastic). We will combine expertise in bacteriology, molecular biology, microbial epidemiology, mathematical modelling and phylogeny to study the evolution and adaptation of antimicrobial resistance in bacterial populations. Focus will be on resistance in staphylococci and Pseudomonas because of the major clinical problems with resistance in these bacteria. The results are expected to be useful in predicting appearance of new antimicrobial resistance problems, guide intervention strategies for the future, lead to new treatment strategies and possible also lead to industrial development of new biotechnologies based on evolutionary concepts.

Ingmer, H., Project Participant, University of Copenhagen, Faculty of Life Sciences,
Evaluation and optimisation of surveillance programmes for antimicrobial resistance and drug use
The overall objective of the project is to provide a quantitative risk assessment of the relationship between consumption of antimicrobials in food animals and the occurrence of antimicrobial resistant bacteria in animals and foods including their potential adverse health effects in humans. The assessment is expected to provide the scientific basis for future recommendations, partly in order to optimize the existing surveillance for antibiotic resistance (DANMAP), and partly in order to develop guidelines regarding antimicrobial consumption and management of specific risk factors in the primary production. The project focuses on the development of resistance to antimicrobial (cephalosporins, macrolides and quinolones), which is critically important for human therapy, for example, persons having a foodborne infection with Salmonella or Campylobacter. The project is a pilot study of transfer of resistance determinants through the food-production chain.

Struve, T., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Hald, T., Project Manager, National Food Institute, Division of Microbiology and Risk Assessment
Emborg, H., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment

01/10/2008 → 30/11/2011
Project: Research

Activities:

Antimicrobial resistance: epidemiology and control options: The 4th International meeting on antimicrobial agents in veterinary medicine
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: Prague, Republic of Czech

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Diversity of tetracycline resistance genes and mobile elements in enterococci and staphylococci from human and animals
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: Copenhagen, Denmark

Related external organisation
Multi drug resistant Salmonella Concord in adoptee from Ethiopia A collaborative international investigation
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment
Description
Place: Copenhagen, Denmark

Using free-cost spatial technology as a tool for assessment of antimicrobial consumption data and spatial distribution of pig herds
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment
Description
Place: Copenhagen, Denmark

The Danish Risk Management Strategy for Antimicrobial Usage and Antimicrobial Resistance in Food Producing Animals
Period: 22 Oct 2007
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

WHO activities for containment of antimicrobial resistance arising from non-human use of antimicrobials
Period: 22 Oct 2007
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

4th International Workshop on Antimicrobial Resistance
22/10/2007 → …
Seoul, Korea, Democratic People’s Republic of
**RUFF - Seminar om Fremtidens Fiskeforskning**
Period: 4 Sep 2007
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

**Related event**

**RUFF - Seminar om Fremtidens Fiskeforskning**
Landbrugsraadet, Danmark
Activity: Talks and presentations › Conference presentations

**Experiences with project management and in particular management of large-scale projects**
Frank Møller Aarestrup (Lecturer)
Division of Microbiology and Risk Assessment
National Food Institute

**Related external organisation**

**Dalum Landbrugsskole**
Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Anvendelse af antibiotika og forekomst af antibiotikaresistens hos dyr - behov og muligheder for kontrol**
Period: 9 May 2007
Frank Møller Aarestrup (Lecturer)
Division of Microbiology and Risk Assessment
National Food Institute

**Related external organisation**

**Det Biovidenskabelige Fakultet, Danmark**
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Principles for monitoring of antimicrobial resistance**
Period: 8 Mar 2007
Frank Møller Aarestrup (Lecturer)
Division of Microbiology and Risk Assessment
National Food Institute

**Related external organisation**

**Det Biovidenskabelige Fakultet, Denmark**
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**In vivo study on selection of ESBL-producing Escherichia coli in the intestinal tract of pigs treated with extended-spectrum cephalosporins**
Period: 1 Jan 2007 → …
Frank Møller Aarestrup (Speaker)
National Food Institute
**Description**
Place: 2nd Symposium on Antimicrobial resistance in animals and the environment. Tours, France

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**Anvendelse af antibiotika og forekomst af antibiotikaresistens hos dyr - behov og muligheder for kontrol**
Period: 22 Nov 2006
Frank Møller Aarestrup (Speaker)
Division of Microbiology and Risk Assessment
National Food Institute

**Description**
Anvendelse af antibiotika og forekomst af antibiotikaresistens hos dyr - behov og muligheder for kontrol

**Related event**
Debatatføn arrangeret af Lægekredsforeningen for Sjælland, Dyr lægeforeningen for Lolland-Falster, samt Præstø Amts Dyr lægeforening
Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

**11th International Society for Veterinary Epidemiology and Economics**
Frank Møller Aarestrup (Participant)
Division of Microbiology and Risk Assessment
National Food Institute

**Description**
Antimicrobial consumption and occurrence of resistance in Salmonella Typhimurium from Danish pigs

**Place**: Cairns, Australia
Degree of recognition: International

**Related event**
11th International Society for Veterinary Epidemiology and Economics
Cairns, Australia
Activity: Attending an event › Participating in or organising a conference

**Tetracycline consumption and occurrence of tetracycline resistance in Salmonella Typhimurium from Danish pigs**
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

**Description**
Place: The 11th Symposium of the International Society for Veterinary Epidemiology and Economics, Cairns, Australia

**Related external organisation**
Activity: Talks and presentations › Conference presentations
What impact does the European ban of antibiotics in animal feed have on antibiotic resistance of animal bacteria?: The 16th European Congress of Clinical Microbiology and Infectious Diseases
Period: 1 Apr 2006 → 4 Apr 2006
Frank Møller Aarestrup (Keynote speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Related external organisation
Nice, France
Activity: Talks and presentations › Conference presentations

Spread of Multiple Resistant Salmonella Schwarzengrund from Thailand to Denmark and USA through International trade with food products
Period: 19 Mar 2006 → 22 Mar 2006
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: The International Conference on Emerging Infectious Diseases, Atlanta, USA

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Spread of Multiple Resistant Salmonella Schwarzengrund from Thailand to Denmark and USA through International Trade with Food Products: The 5th International Conference on Emerging Infectious Diseases
Period: 19 Mar 2006 → 21 Mar 2006
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Related event
5th International Conference on Emerging Infectious Diseases
19/03/2006 → 22/03/2006
Atlanta, GA, United States
Activity: Talks and presentations › Conference presentations

Ten years of integrated monitoring of antimicrobial resistance in Denmark - what have we learnt about food borne Zoonoses?
Period: 19 Mar 2006 → 22 Mar 2006
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: The International Conference on Emerging Infectious Diseases, Atlanta, USA

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations
Antimicrobial resistance - Research in a globalised world
Period: 24 Feb 2006
Frank Møller Aarestrup (Lecturer)
Division of Microbiology and Risk Assessment
National Food Institute

Related external organisation
Royal Veterinary College University of London
United Kingdom
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Overview to the work in the antibiotic resistance group at DFVF and risk assessment of food
Period: 21 Feb 2006
Frank Møller Aarestrup (Lecturer)
Division of Microbiology and Risk Assessment
National Food Institute

Related external organisation
Chr. Hansen A/S
Bæge Allé 10-12, 2970, Hørsholm, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Overview and introduction. Antimicrobial growth promotors. Future aspects
Period: 26 Jan 2006
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Related event
Overview and introduction. Antimicrobial growth promotors. Future aspects
26/01/2006 → 26/01/2006
Danmarks Fødevareforskning, Denmark
Activity: Talks and presentations › Conference presentations

Udvikling og spredning af antibiotikaresistens - nationalt og internationalt
Period: 20 Jan 2006
Frank Møller Aarestrup (Speaker)
National Food Institute
Ten years of integrated monitoring of antimicrobial resistance in Denmark – what have we learnt about foodborne zoonoses?
Period: 1 Jan 2006 → …
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: The 2006 International Conference on Emerging Infectious Diseases, Atlanta

Mastitis diagnostik for dyrlæger
Period: 22 Nov 2005
Frank Møller Aarestrup (Guest lecturer)
Division of Microbiology and Risk Assessment
National Food Institute

Mastitis diagnostik for dyrlæger
Period: 16 Nov 2005
Frank Møller Aarestrup (Guest lecturer)
Division of Microbiology and Risk Assessment
National Food Institute

Mastitis diagnostik for dyrlæger
Period: 9 Nov 2005
Frank Møller Aarestrup (Guest lecturer)
Division of Microbiology and Risk Assessment
National Food Institute

Rebild bakker, Danmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities
Mastitis diagnostik for dyrlæger  
Period: 9 Nov 2005  
Frank Møller Aarestrup (Guest lecturer)  
Division of Microbiology and Risk Assessment  
National Food Institute

Related external organisation
Rebild bakker, Danmark  
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Risikovurdering i relation til forskellige antibiotikagrupper og forbrug  
Period: 4 Nov 2005  
Frank Møller Aarestrup (Guest lecturer)  
Division of Microbiology and Risk Assessment  
National Food Institute

Related external organisation
Dansk Veterinær Hyologisk Selskab, Kolding, Danmark  
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Monitoring of antimicrobial resistance  
Period: 28 Aug 2005 → 31 Aug 2005  
Frank Møller Aarestrup (Keynote speaker)  
National Food Institute  
Division of Microbiology and Risk Assessment

Related event
2nd International ASM-FEMS Conference on Enterococci  
28/08/2005 → 31/08/2005  
Helsingør, Denmark  
Activity: Talks and presentations › Conference presentations

Survivel of enterococci and fate of resistance genes from enterococci of animal origin in agricultural farmland soil  
Period: 28 Aug 2005 → 31 Aug 2005  
Frank Møller Aarestrup (Speaker)  
National Food Institute  
Division of Microbiology and Risk Assessment

Description  
Place: The 2nd International ASM-FEMS conference on enterococci, Marienlyst, Helsingør, Denmark

Related external organisation
Unknown external organisation  
Activity: Talks and presentations › Conference presentations

Antimicrobial resistance in staphylococci  
Period: 25 May 2005  
Frank Møller Aarestrup (Guest lecturer)  
Division of Microbiology and Risk Assessment
National Food Institute

**Related event**

**Antimicrobial resistance in staphylococci**

25/05/2005 → 25/05/2005  
Den Kongelige Veterinær- og Landbohøjskole, Denmark  
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Antibiotikaresistens**

Period: 1 Jan 2005 → …  
Frank Møller Aarestrup (Lecturer)

Division of Microbiology and Risk Assessment  
National Food Institute

**Related external organisation**

**Dyrlægeforeningens årsmøde, Nyborg Strand, Danmark**

Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Efteruddannelsesdag for kliniske mikrobiologer**

Period: 11 Nov 2004  
Frank Møller Aarestrup (Speaker)

National Food Institute

**Description**

Place: Statens Seruminstitut, Danmark

**Related external organisation**

**Unknown external organisation**

Activity: Talks and presentations › Conference presentations

**Antimicrobial resistance in food**

Period: 8 Jun 2004  
Frank Møller Aarestrup (Keynote speaker)

Division of Microbiology and Risk Assessment  
National Food Institute  
Degree of recognition: International

**Related event**

**5th World Congress on Foodborne Infections and Intoxications**

07/06/2004 → 11/06/2004  
Berlin, Germany  
Activity: Talks and presentations › Conference presentations

**Antimicrobial resistance in staphylococci**

Period: 4 Jun 2004  
Frank Møller Aarestrup (Guest lecturer)

Division of Microbiology and Risk Assessment  
National Food Institute

**Related event**

**Antimicrobial resistance in staphylococci**
Kursus i klinisk mikrobiologi
Period: 2 Jun 2004
Frank Møller Aarestrup (Lecturer)
Division of Microbiology and Risk Assessment
National Food Institute

Related external organisation
Skejby Sygehus
Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Antibiotikaresistens
Period: 19 May 2004
Frank Møller Aarestrup (Lecturer)
Division of Microbiology and Risk Assessment
National Food Institute

Related external organisation
Lægemiddelstyrelsen
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Documentation of health status in dairy herds with focus on udder health and antibiotic resistance
Period: 15 May 2004
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Related event
Documentation of health status in dairy herds with focus on udder health and antibiotic resistance
15/05/2004 → 15/05/2004
Activity: Talks and presentations › Conference presentations

Antibiotikaresistens
Period: 26 Apr 2004
Frank Møller Aarestrup (Lecturer)
Division of Microbiology and Risk Assessment
National Food Institute

Related external organisation
Farum, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Courses on Zoonoses
Period: 23 Jan 2004
Frank Møller Aarestrup (Course lecturer)
Division of Microbiology and Risk Assessment
Antibiotikaresistens
Period: 1 Jan 2004 → …
Frank Møller Aarestrup (Speaker)

National Food Institute
Division of Microbiology and Risk Assessment

Related event
Dansk Veterinær Hyologisk Selskabs Efterårsmede
01/01/2004 → 01/01/2004
Kolding, Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

The WHO Global Salmonella surveillance programme
Period: 1 Jan 2002 → …
Frank Møller Aarestrup (Speaker)

National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: Proc. Int Symp on Salmonella and Salmonellosis. Ploufragan, France

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

 Longer duration of illness among Campylobacter patients treated with fluoroquinolones
Period: 1 Jan 2001 → …
Frank Møller Aarestrup (Speaker)

National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: Int. Conf. on Campylobacter, Helicobacter and Related Organisms. Freiburg

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Programmes in Denmark aimed at limiting the occurrence of antimicrobial resistance in bacteria from food animals
Period: 1 Jan 2001 → …
Frank Møller Aarestrup (Speaker)

National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: EU invitational conference on the microbial threat, Visby, Sweden

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations
The consequences of discontinued use of antimicrobial growth promoters (AGP's) for food producing animals in Denmark
Period: 1 Jan 2000 → …
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Surveillance of antimicrobial resistance among bacteria from food animals in Denmark, 1995-1998
Period: 1 Jan 1999
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Examples of in vitro quinolone resistance prevalence - Trends in foodborne salmonella and campylobacter in Denmark
Period: 1 Jan 1998 → …
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

The association between the use of avoparcin in food animals in Europe and the occurrence of nosocomial infections with VRE in USA
Period: 1 Jan 1998 → …
Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment
Surveillance of antimicrobial resistance - requirements for monitoring programmes

Period: 1 Jan 1997 → …

Frank Møller Aarestrup (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: Epidemiol Sante Anim (ISVEE)

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Press clippings:

Veterinaerforlig III
Frank Møller Aarestrup
14/12/2017
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

Veterinaerforlig III
14/12/2017
Ingeniøren, Denmark, Web
Hanne Kokkergård
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press/Media: Press / Media

Indberetning af MRSA data til EFSA
Frank Møller Aarestrup
06/03/2017
National Food Institute, Research Group for Genomic Epidemiology

Media coverage (1)

Indberetning af MRSA data til EFSA
06/03/2017
Information (National), Denmark, Print
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press/Media: Press / Media

WHO's prioritieringsliste for R&D
Frank Møller Aarestrup
28/02/2017
National Food Institute, Research Group for Genomic Epidemiology

Media coverage (1)

WHO's prioritieringsliste for R&D
28/02/2017
Videnskab.dk (National), Denmark, Web
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press/Media: Press / Media
MRSA ekspertgruppe
Frank Møller Aarestrup
28/02/2017
National Food Institute, Research Group for Genomic Epidemiology

Media coverage (1)

MRSA ekspertgruppe
28/02/2017
BT (National), Denmark, Print
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press/Media: Press / Media

MRSA
Frank Møller Aarestrup
24/02/2017
National Food Institute, Research Group for Genomic Epidemiology

Media coverage (1)

MRSA
24/02/2017
Forskerforum (National), Denmark, Web
Mads Ølgaard
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press/Media: Press / Media

Antibiotika vægtning
Frank Møller Aarestrup
17/02/2017
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

Antibiotika vægtning
17/02/2017
Landbrugsmedierne, Web
Mette Boas
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press/Media: Press / Media

Zinkforbrug i svin
Frank Møller Aarestrup
05/02/2017
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

Zinkforbrug i svin
05/02/2017
Ingeniøren, Web
Magnus Bredsdorf
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press/Media: Press / Media

DTU Fødevareinstituttets rådgivning af Fødevarestyrelsen om MRSA
Frank Møller Aarestrup
17/11/2016
DTU Fødevareinstituttets rådgivning af Fødevarestyrelsen om MRSA
17/11/2016
Magisterbladet, Print
Thomas Kølln
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press / Media

Debatindlæg om MRSA og andre former for resistens
Frank Møller Aarestrup
09/10/2016
National Food Institute, Research Group for Genomic Epidemiology

MRSA bekæmpelse
Frank Møller Aarestrup
19/09/2016

Ifm MRSA-dokumentar
Frank Møller Aarestrup
14/09/2016

Er der blevet lagt pres på mig?
National Food Institute, Research Group for Genomic Epidemiology

Ifm MRSA-dokumentar
14/09/2016
Politiken, Web
Maj Bak Madsen
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press / Media
MRSA
Frank Møller Aarestrup
14/09/2016

Subject
MRSA
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

MRSA
14/09/2016
Politiken, Print
Maj Bak Madsen
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press/Media: Press / Media

FN's topmøde om resistens; hvad er situationen globalt og mine forhåbninger.
Frank Møller Aarestrup
14/09/2016

Subject
FN's topmøde om resistens; hvad er situationen globalt og mine forhåbninger.
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

FN's topmøde om resistens; hvad er situationen globalt og mine forhåbninger.
14/09/2016
Jyllandsposten, Print
Klaus Dohn
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press/Media: Press / Media

Hvad synes jeg om at DTU-foods anbefalinger om MRSA ikke er blevet fulgt
Frank Møller Aarestrup
14/09/2016

Subject
Hvad synes jeg om at DTU-foods anbefalinger om MRSA ikke er blevet fulgt
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

Hvad synes jeg om at DTU-foods anbefalinger om MRSA ikke er blevet fulgt
14/09/2016
TV2, Television
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press/Media: Press / Media

MRSA og DRs dokumentar
Frank Møller Aarestrup
13/09/2016

Subject
MRSA og DRs dokumentar
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

MRSA og DRs dokumentar
13/09/2016
Resistens, MRSA, mv
Frank Møller Aarestrup
08/02/2016
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

Resistens, MRSA, mv
08/02/2016
DR, Web
George Larsen, Poul-Erik Heilbutt
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology

Subject
Resistens, MRSA, mv
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

MRSA
Frank Møller Aarestrup
10/11/2015

Subject
MRSA
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

DANMAP
Frank Møller Aarestrup
06/10/2015

Subject
DANMAP
National Food Institute, Research Group for Genomic Epidemiology
MRSA
16/09/2014
Radio 24/7, Radio
Mette Larsen
Frank Møller Aarestrup
National Food Institute, Division of Epidemiology and Microbial Genomics
Press/Media: Press / Media

MRSA, samråd, Dan Jørgensen
Frank Møller Aarestrup
16/09/2014

Subject
MRSA, samråd, dan Jørgensen
National Food Institute, Division of Epidemiology and Microbial Genomics

Media contribution (1)

MRSA, samråd, Dan Jørgensen
16/09/2014
Ingeniøren, Web
Helle Erhardsen
Frank Møller Aarestrup
National Food Institute, Division of Epidemiology and Microbial Genomics
Press/Media: Press / Media

MRSA
Frank Møller Aarestrup
27/06/2014
National Food Institute, Division of Epidemiology and Microbial Genomics

Media contribution (1)

MRSA
27/06/2014
Ingeniøren, Print
Helle Erhardsen
Frank Møller Aarestrup
National Food Institute, Division of Epidemiology and Microbial Genomics
Press/Media: Press / Media

MRSA
Frank Møller Aarestrup
02/06/2014
National Food Institute, Division of Epidemiology and Microbial Genomics

Media contribution (1)

MRSA
02/06/2014
Politiken, Print
Lars Igum Rasmussen
Frank Møller Aarestrup
National Food Institute, Division of Epidemiology and Microbial Genomics
Press/Media: Press / Media

MRSA
Frank Møller Aarestrup
02/06/2014
National Food Institute, Division of Epidemiology and Microbial Genomics

Media contribution (1)

MRSA
MRSA
Frank Møller Aarestrup
30/10/2010
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

MRSA
30/10/2010
Television
Frank Møller Aarestrup
National Food Institute, Division of Microbiology and Risk Assessment
Press/Media: Press / Media

MRSA og DANMAP
Frank Møller Aarestrup
21/10/2010
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

MRSA og DANMAP
21/10/2010
Print
Frank Møller Aarestrup
National Food Institute, Division of Microbiology and Risk Assessment
Press/Media: Press / Media

Resistens og MRSA
Frank Møller Aarestrup
01/01/2010
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Resistens og MRSA
01/01/2010
Print
Frank Møller Aarestrup
National Food Institute, Division of Microbiology and Risk Assessment
Press/Media: Press / Media

Antibiotikaresistens og forbrug
Frank Møller Aarestrup
01/01/2010
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Antibiotikaresistens og forbrug
01/01/2010
Television
Frank Møller Aarestrup
National Food Institute, Division of Microbiology and Risk Assessment
Press/Media: Press / Media

Resistens og MRSA
Frank Møller Aarestrup
01/01/2010
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)
Interview til Der Spiegel
Frank Møller Aarestrup
01/01/2004
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Interview til Der Spiegel
01/01/2004
Television
Frank Møller Aarestrup
National Food Institute, Division of Microbiology and Risk Assessment
Press/Media: Press / Media

Interview i Søndagsmagasinet
Frank Møller Aarestrup
01/01/2004
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Interview i Søndagsmagasinet
01/01/2004
Television
Frank Møller Aarestrup
National Food Institute, Division of Microbiology and Risk Assessment
Press/Media: Press / Media