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 $1.38 \times 10^{-11}$ SNPs/site/year or $1.4 \times 10^{-6}$ 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.
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.
Analysis of 28 Arcobacter genomes belonging to different species

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Universitat Rovira i Virgili
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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
Authors: Mardal, M. (Ekstern), Aarestrup, F. M. (Intern), Rasmussen, B. S. (Ekstern), Mollerup, C. B. (Ekstern), Dalsgaard, P. W. (Ekstern), Linnet, K. (Ekstern)
Pages: 1-6
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Main Research Area: Technical/natural sciences

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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.

General information
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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Authors: Henri, C. (Ekstern), Leekitcharoenphon, P. (Intern), Carleton, H. A. (Ekstern), Radomski, N. (Ekstern), Kaas, R. S. (Intern), Mariet, J. (Ekstern), Felten, A. (Ekstern), Aarestrup, F. M. (Intern), Smidt, P. G. (Ekstern), Roussel, S. (Ekstern), Guillier, L. (Ekstern), Mistou, M. (Ekstern), Hendriksen, R. S. (Intern)
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Antimicrobial peptide CAP18 and its effect on Yersinia ruckeri infections in rainbow trout Oncorhynchus mykiss (Walbaum): comparing administration by injection and oral routes

The antimicrobial peptide CAP18 has been demonstrated to have a strong in vitro bactericidal effect on Yersinia ruckeri, but its activity in vivo has not been described. In this work, we investigated whether CAP18 protects rainbow trout Oncorhynchus mykiss (Walbaum) against enteric red mouth disease caused by this pathogen either following i.p. injection or by oral administration (in feed). It was found that injection of CAP18 into juvenile rainbow trout before exposure to Y. ruckeri was associated with lowered mortality compared to non-medicated fish although it was less effective than the conventional antibiotic oxolinic acid. Oral administration of CAP18 to trout did not prevent infection. The proteolytic effect of secretions on the peptide CAP18 in the fish gastrointestinal tract is suggested to account for the inferior effect of oral administration.

General information
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Organisations: National Food Institute, Research Group for Gut Microbiology and Immunology, Research Group for Genomic Epidemiology, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen, Aalborg University, BioMar A/S
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Scopus rating (2016): CiteScore 2.12
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Scopus rating (2015): CiteScore 1.71
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Scopus rating (2014): CiteScore 1.99
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Application of Probabilistic Modeling to Quantify the Reduction Levels of Hepatocellular Carcinoma Risk Attributable to Chronic Aflatoxins Exposure

Epidemiological studies show a definite connection between areas of high aflatoxin content and a high occurrence of human hepatocellular carcinoma (HCC). Hepatitis B virus in individuals further increases the risk of HCC. The two risk factors are prevalent in rural Kenya and continuously predispose the rural populations to HCC. A quantitative cancer risk assessment therefore quantified the levels at which potential pre- and postharvest interventions reduce the HCC risk attributable to consumption of contaminated maize and groundnuts. The assessment applied a probabilistic model to derive probability distributions of HCC cases and percentage reductions levels of the risk from secondary data. Contaminated maize and groundnuts contributed to 1,847 +/- 514 and 158 +/- 52 HCC cases per annum, respectively. The total contribution of both foods to the risk was additive as it resulted in 2,000 +/- 518 cases per annum. Consumption and contamination levels contributed significantly to the risk whereby lower age groups were most affected. Nonetheless, pre- and postharvest interventions might reduce the risk by 23.0-83.4% and 4.8-95.1%, respectively. Therefore, chronic exposure to aflatoxins increases the HCC risk in rural Kenya, but a significant reduction of the risk can be achieved by applying specific pre- and postharvest interventions.

General information
State: Published
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Applied Genomics of Foodborne Pathogens
This book provides a timely and thorough snapshot into the emerging and fast evolving area of applied genomics of foodborne pathogens. Driven by the drastic advance of whole genome shot gun sequencing (WGS) technologies, genomics applications are becoming increasingly valuable and even essential in studying, surveying and controlling foodborne microbial pathogens. The vast opportunities brought by this trend are often at odds with the lack of bioinformatics know-how among food safety and public health professionals, since such expertise is not part of a typical food microbiology curriculum and skill set. Further complicating the challenge is the large and ever evolving body of bioinformatics tools that can obfuscate newcomers to this area. Although reviews, tutorials and books are not in short supply in the fields of bioinformatics and genomics, until now there has not been a comprehensive and customized source of information designed for and accessible to microbiologists interested in applying cutting-edge genomics in food safety and public health research. This book fills this void with a well-selected collection of topics, case studies, and bioinformatics tools contributed by experts at the forefront of foodborne pathogen genomics research.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology
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Applying LCA in decision making - the need and the future perspective

General information
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Authors: Dong, Y. (Intern), Miraglia, S. (Intern), Manzo, S. (Intern), Georgiadis, S. (Intern), Sørup, H. J. D. (Intern), Boriani, E. (Intern), Hald, T. (Intern), Thøns, S. (Intern), Hauschild, M. Z. (Intern)
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Attribution of global foodborne disease to specific foods: Findings from a World Health Organization structured expert elicitation
Background Recently the World Health Organization, Foodborne Disease Burden Epidemiology Reference Group (FERG) estimated that 31 foodborne diseases (FBDs) resulted in over 600 million illnesses and 420,000 deaths worldwide in 2010. Knowing the relative role importance of different foods as exposure routes for key hazards is critical to preventing illness. This study reports the findings of a structured expert elicitation providing globally comparable food source attribution estimates for 11 major FBDs in each of 14 world subregions. Methods and findings We used Cooke’s Classical Model to elicit and aggregate judgments of 73 international experts. Judgments were elicited from each expert individually and aggregated using both equal and performance weights. Performance weighted results are reported as they increased the informativeness of estimates, while retaining accuracy. We report measures of central tendency and uncertainty bounds on food source attribution estimate. For some pathogens we see relatively consistent food source attribution estimates across subregions of the world; for others there is substantial regional variation. For example, for non-typhoidal
salmonellosis, pork was of minor importance compared to eggs and poultry meat in the American and African subregions, whereas in the European and Western Pacific subregions the importance of these three food sources were quite similar. Our regional results broadly agree with estimates from earlier European and North American food source attribution research. As in prior food source attribution research, we find relatively wide uncertainty bounds around our median estimates. Conclusions We present the first worldwide estimates of the proportion of specific foodborne diseases attributable to specific food exposure routes. While we find substantial uncertainty around central tendency estimates, we believe these estimates provide the best currently available basis on which to link FBDs and specific foods in many parts of the world, providing guidance for policy actions to control FBDs.
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.
Carbapenemase VCC-1-Producing Vibrio cholerae in Coastal Waters of Germany
During antimicrobial drug resistance testing for Vibrio spp. from coastal waters of Germany, we identified 4 nontoxigenic, carbapenem-resistant V. cholerae isolates. We used whole-genome sequencing to identify the carbapenemase gene bla(VCC-1). In addition, a molecular survey showed that more bla(VCC-1)-harboring isolates are present in coastal waters of Germany.
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.

General information
State: Published
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CHROMagar COL-APSE: a selective bacterial culture medium for the isolation and differentiation of colistin-resistant Gram-negative pathogens

Purpose. A selective chromogenic culture medium for the laboratory isolation and differentiation of colistin resistant Acinetobacter, Pseudomonas, Stenotrophomonas and Enterobacteriaceae spp. (CHROMagar COL-APSE) was developed, evaluated and compared to an existing selective bacterial culture medium (SuperPolymyxin).

Methodology. The medium was challenged with 84 isolates, including polymyxin B (POL B)-susceptible and -resistant type strains and colistin (COL)-resistant organisms recovered from human and animal samples. Susceptibility to COL and POL B was determined by agar dilution and broth microtitre dilution. The lower limit for the detection of COL-resistant organisms was also calculated for both CHROMagar COL-APSE and SuperPolymyxin media. The ability to isolate and correctly differentiate COL-resistant organisms within mixed cultures was also assessed and compared using both media.

Results. Using CHROMagar COL-APSE, Gram-negative pathogens (n=71) with intrinsic (n=8) or acquired COL (n=63) resistance were recovered with 100% specificity down to the lower limit of detection of 101 colony-forming units (c.f.u.). The growth on SuperPolymyxin was similar, but notably weaker for COL-resistant non-fermentative bacteria (Acinetobacter, Pseudomonas and Stenotrophomonas). CHROMagar COL-APSE was also more sensitive in supporting the growth of Enterobacteriaceae with COL resistance associated with the carriage of mcr-1.

Conclusion. CHROMagar COL-APSE is a sensitive and specific medium for the growth of COL-resistant bacterial pathogens. Due to the low limit of detection (101 c.f.u.), it may be useful as a primary isolation medium in the surveillance and recovery of COL-resistant bacteria from complex human, veterinary and environmental samples, especially those with plasmid-mediated MCR-1 or novel mechanisms of polymyxin resistance.

General information
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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Queen Mary University of London, Federation University Australia, Université Lyon
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Scopus rating (2014): SJR 1.038 SNIP 1.062 CiteScore 2.26
Web of Science (2014): Indexed yes
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Scopus rating (2011): SJR 1.118 SNIP 1.117 CiteScore 2.47
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Combating antibiotic resistance - A Policy Roadmap to Reduce Use of Medically Important Antibiotics in Livestock

Medical and public health organizations around the world agree that more prudent use of antibiotics in human medicine and in livestock production is paramount to slow the spread of antibiotic resistance. Of particular concern is the widespread use of antibiotics important to human medicine in food animals. In the U.S., such use accounts for 70% of all sales of medically important antibiotics. It is against this backdrop that 12 antibiotic resistance experts from the fields of infectious disease medicine, veterinary medicine, microbiology, epidemiology and public health joined to craft a policy roadmap to help move the U.S. forward in addressing the contribution of livestock antibiotic use to the growing global threat of antibiotic resistance.

The policy roadmap consists of 11 core policy recommendations that are aimed at a broad set of stakeholders: federal, state and local policymakers, food companies, institutional food purchasers (i.e. hospitals, schools and universities), and medical groups. The recommendations are split into three key areas: 1) decreasing livestock use of medically important antibiotics; 2) monitoring livestock antibiotic use, and 3) enhancing surveillance and data integration to inform antibiotic resistance policy.

**General information**

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**Organisations:** National Food Institute, Research Group for Genomic Epidemiology, George Washington University, Washington University St. Louis, Texas Technical University, Kent State University, Johns Hopkins Bloomberg School of Public Health, Utrecht University, Statens Serum Institut

**Authors:** Price, L. B. (Ekstern), Newland, J. (Ekstern), Bole, A. (Ekstern), Bortolaia, V. (Intern), Larsen, J. (Ekstern), Loneragan, G. H. (Ekstern), Roach, S. (Ekstern), Smith, T. C. (Ekstern), So, A. D. (Ekstern), Tollefson, L. (Ekstern), Wagenaar, J. (Ekstern), Zaoutis, T. (Ekstern)

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Authors: Schlundt, J. (Intern), Aarestrup, F. M. (Intern)
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Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.878 SNIP 1.208 CiteScore 4.15
Web of Science (2015): Indexed yes
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Scopus rating (2014): SJR 1.861 SNIP 1.16 CiteScore 3.76
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.751 SNIP 0.951 CiteScore 3.56
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Scopus rating (2012): SJR 1.415 SNIP 0.725 CiteScore 2.78
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Scopus rating (2011): SJR 0.626 SNIP 0.187
Web of Science (2011): Indexed yes
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Computational algorithm for lifetime exposure to antimicrobials in pigs using register data – the LEA algorithm
Accurate and detailed data on antimicrobial exposure in pig production are essential when studying the association between antimicrobial exposure and antimicrobial resistance. Due to difficulties in obtaining primary data on antimicrobial exposure in a large number of farms, there is a need for a robust and valid method to estimate the exposure using register data. An approach that estimates the antimicrobial exposure in every rearing period during the lifetime of a pig using register data was developed into a computational algorithm. In this approach data from national registers on antimicrobial
purchases, movements of pigs and farm demographics registered at farm level are used. The algorithm traces batches of pigs retrospectively from slaughter to the farm(s) that housed the pigs during their finisher, weaner, and piglet period. Subsequently, the algorithm estimates the antimicrobial exposure as the number of Animal Defined Daily Doses for treatment of one kg pig in each of the rearing periods. Thus, the antimicrobial purchase data at farm level are translated into antimicrobial exposure estimates at batch level. A batch of pigs is defined here as pigs sent to slaughter at the same day from the same farm. In this study we present, validate, and optimise a computational algorithm that calculate the lifetime exposure of antimicrobials for slaughter pigs. The algorithm was evaluated by comparing the computed estimates to data on antimicrobial usage from farm records in 15 farm units. We found a good positive correlation between the two estimates. The algorithm was run for Danish slaughter pigs sent to slaughter in January to March 2015 from farms with more than 200 finishers to estimate the proportion of farms that it was applicable for. In the final process, the algorithm was successfully run for batches of pigs originating from 3,026 farms with finisher units (77% of the initial population). This number can be increased if more accurate register data can be obtained. The algorithm provides a systematic and repeatable approach to estimating the antimicrobial exposure throughout the rearing period, independent of rearing site for finisher batches, as a lifetime exposure measurement.
Cross-border outbreak of listeriosis caused by cold-smoked salmon, revealed by integrated surveillance and whole genome sequencing (WGS), Denmark and France, 2015 to 2017

In August 2017, an outbreak of six listeriosis cases in Denmark was traced to cold-smoked salmon, using epidemiological investigations and whole-genome sequencing (WGS) analyses. Exchange of genome sequences allowed identification in France of a food isolate from a salmon-derived product and a human isolate from 2016 within the same cgMLST cluster as the Danish isolates (L2-SL8-ST8-CT771). The salmon product came from a third European Union country. WGS can rapidly link human cases and food isolates across Europe.

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Scopus rating (2016): CiteScore 3.05
Cross-sectional survey on the use and impact of the Danish national antibiotic use guidelines for companion animal practice

Background: The Danish antibiotic use guidelines for companion animal practice were published by the Danish Veterinary Association in 2012. Since then, national surveillance data indicate a 10% reduction in the total use of antibiotics for companion animals, particularly a marked reduction in the use of third generation cephalosporins. The aim of the study was to assess if and how the guidelines have impacted diagnostic and antibiotic prescription habits of the users, and to identify user perceived barriers to implementation. Results: An online questionnaire was sent to all 882 members of the Danish Small Animal Veterinary Association in October 2015. The survey was completed by 151 veterinarians. Respondents most frequently consulted the recommendations on skin and urinary tract infections (UTI), and users generally reported a high degree of adherence to the recommendations. Sixty-five per cent indicated that the guidelines had influenced their habits in one or more of the areas being investigated, i.e. perioperative use of antibiotics, use of first line antibiotics for the treatment of pyoderma or UTI, and/or use of microbiological diagnostics. Perioperative use of antibiotics for clean surgeries was uncommon, irrespective of whether respondents had consulted the relevant recommendations or not. On the contrary, significant differences in the prescribing habits between guideline users and non-users were observed for pyoderma and UTI, suggesting an impact of the guidelines towards more prudent antimicrobial use. The diagnostic habits were examined in a subgroup of 63 guideline users. Of those, 19 and 39% reported frequent use of culture and susceptibility (C&S) testing prior to treating pyoderma and UTI respectively, whereas 68-84% reported C&S testing in the event of poor response to treatment or recurrence of infections. The main barriers for implementation of therapeutic recommendations were confidence in old prescribing practices and unavailability of recommended drugs. The main barriers for C&S testing were good experience with empiric treatment, and the owners’ financial situation. Conclusions: The findings suggest a positive influence of the national antibiotic guidelines on prescription patterns among companion animal practitioners in Denmark. Sustained campaign activity is encouraged and should include promotion of bacteriological testing.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen
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DANMAP 2016 - Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark

General information
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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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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Corporación Colombiana de Investigación Agropecuaria (CORPOICA), Pan American Health Organization
Authors: Cavaco, L. (Intern), Bernal, J. F. (Ekstern), Zankari, E. (Intern), Léon, M. (Ekstern), Hendriksen, R. S. (Intern), Perez-Gutierrez, E. (Ekstern), Aarestrup, F. M. (Intern), Donado-Godoy, P. (Ekstern)
Pages: 678-683
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Publication information
Journal: Journal of Antimicrobial Chemotherapy
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.
Acinetobacter johnsonii C6 originates from creosote-polluted groundwater and performs ecological and evolutionary interactions with Pseudomonas putida in biofilms. The draft genome of A. johnsonii C6 is 3.7 Mbp and was shaped by mobile genetic elements. It reveals genes facilitating the biodegradation of aromatic hydrocarbons and resistance to antimicrobials and metals.
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.
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.
Aeromonas salmonicida subsp. salmonicida, Furunculosis, Rainbow trout, Whole genome sequencing, SNP analysis, BEAST, Virulence factors
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.
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 concentrations 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, NucliSENS® miniMAG®, or PowerViral® Environmental RNA/DNA Isolation Kit) 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.
First detection of linezolid resistance due to the optrA gene in enterococci isolated from food products in Denmark

General information
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Organisations: National Food Institute, Division of Risk Assessment and Nutrition, Research Group for Genomic Epidemiology, Danish Veterinary and Food Administration
Authors: Cavaco, L. (Intern), Korsgaard, H. B. (Intern), Kaas, R. S. (Intern), Seyfarth, A. M. (Ekstern), Leekitcharoenphon, P. (Intern), Hendriksen, R. S. (Intern)
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Framework to Define Structure and Boundaries of Complex Health Intervention Systems: The ALERT Project

Health intervention systems are complex and subject to multiple variables in different phases of implementation. This constitutes a concrete challenge for the application of translational science in real life. Complex systems as health-oriented interventions call for interdisciplinary approaches with carefully defined system boundaries. Exploring individual components of such systems from different viewpoints gives a wide overview and helps to understand the elements and the relationships that drive actions and consequences within the system. In this study, we present an application and assessment of a framework with focus on systems and system boundaries of interdisciplinary projects. As an example on how to apply our framework, we analyzed ALERT [an integrated sensors and biosensors’ system (BEST) aimed at monitoring the quality, health, and traceability of the chain of the bovine milk], a multidisciplinary and interdisciplinary project based on the application of measurable biomarkers at strategic points of the milk chain for improved food security (including safety), human, and ecosystem health (1). In fact, the European food safety framework calls for science-based support to the primary producers’ mandate for legal, scientific, and ethical responsibility in food supply. Because of its multidisciplinary and interdisciplinary approach involving human, animal, and ecosystem health, ALERT can be considered as a One Health project. Within the ALERT context, we identified the need to take into account the main actors, interactions, and relationships of stakeholders to depict a simplified skeleton of the system. The framework can provide elements to highlight how and where to improve the project development when project evaluations are required.

General information

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Transport DTU, Department of Management Engineering, Quantitative Sustainability Assessment, Istituto Superiore di Sanita, University of Zurich
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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.

General information

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Technical University of Denmark, Erasmus University Medical Centre, Nanyang Technological University
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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 pfcr1, pfmdr1, pfhfr, pfhdps, 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.

General information
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Organisations: Department of Biotechnology and Biomedicine, DTU Multi Assay Core, National Food Institute, Research Group for Genomic Epidemiology, Department of Bio and Health Informatics, University of Copenhagen, University of Southern Denmark, Karolinska Institutet, Statens Seruminstitute
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Scopus rating (2016): CiteScore 4.63 SJR 1.625 SNIP 1.401
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.057 SNIP 1.684 CiteScore 5.3
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.103 SNIP 1.544 CiteScore 4.75
Web of Science (2014): Indexed yes
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Scopus rating (2013): SJR 1.886 SNIP 1.51 CiteScore 4.06
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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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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Department of Bio and Health Informatics, Genomic Epidemiology, Technical University of Denmark
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Scopus rating (2016): CiteScore 2.55 SJR 1.473 SNIP 1.143
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.524 SNIP 1.251 CiteScore 2.4
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.295 SNIP 1.113 CiteScore 2.3
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.577 SNIP 1.177 CiteScore 2.7
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.539 SNIP 1.252 CiteScore 2.82
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.563 SNIP 1.145 CiteScore 2.78
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.491 SNIP 1.265
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.258 SNIP 1.282
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.212 SNIP 1.153
Identification of a novel transposon-associated phosphoethanolamine transferase gene, mcr-5, conferring colistin resistance in d-tartrate fermenting Salmonella enterica subsp. enterica serovar Paratyphi B

Plasmid-mediated mobilized colistin resistance is currently known to be caused by phosphoethanolamine transferases termed MCR-1, MCR-2, MCR-3 and MCR-4. However, this study focuses on the dissection of a novel resistance mechanism in mcr-1-, mcr-2- and mcr-3- negative d-tartrate fermenting Salmonella enterica subsp. enterica serovar Paratyphi B (Salmonella Paratyphi B d Ta+) isolates with colistin MIC values >2 mg/L. A selected isolate from the strain collection of the German National Reference Laboratory for Salmonella was investigated by WGS and bioinformatical analysis to identify novel phosphoethanolamine transferase genes involved in colistin resistance. Subsequently PCR screening, S1-PFGE and DNA-DNA hybridization were performed to analyse the prevalence and location of the identified mcr-5 gene. Cloning and transformation experiments in Escherichia coli DH5α and Salmonella Paratyphi B d Ta+ control strains were carried out and the activity of MCR-5 was determined in vitro by MIC testing. In this study, we identified a novel phosphoethanolamine transferase in 14 mcr-1-, mcr-2- and mcr-3-negative d-tartrate fermenting Salmonella Paratyphi B d Ta+ isolates with colistin MIC values >2 mg/L that were received during 2011-13. The respective gene, further termed as mcr-5 (1644 bp), is part of a 7337 bp transposon of the Tn 3 family and usually located on related multi-copy ColE-type plasmids. Interestingly, in one isolate an additional subclone with a chromosomal location of the mcr-5 transposon was observed. Our findings suggest that the transfer of colistin-resistance-mediating phosphoethanolamine transferase genes from bacterial chromosomes to mobile genetic elements has occurred in multiple independent events raising concern regarding their variety, prevalence and impact on public health.
Improving institutional memory on challenges and methods for estimation of pig herd antimicrobial exposure based on data from the Danish Veterinary Medicines Statistics Program (VetStat)

With the increasing occurrence of antimicrobial resistance, more attention has been directed towards surveillance of both human and veterinary antimicrobial use. Since the early 2000s, several research papers on Danish pig antimicrobial usage have been published, based on data from the Danish Veterinary Medicines Statistics Program (VetStat). VetStat was established in 2000, as a national database containing detailed information on purchases of veterinary medicine. This paper presents a critical set of challenges originating from static system features, which researchers must address when estimating antimicrobial exposure in Danish pig herds. Most challenges presented are followed by at least one robust solution. A set of challenges requiring awareness from the researcher, but for which no immediate solution was available, were also presented. The selection of challenges and solutions was based on a consensus by a cross-institutional group of researchers working in projects using VetStat data. No quantitative data quality evaluations were performed, as the
frequency of errors and inconsistencies in a dataset will vary, depending on the period covered in the data. Instead, this paper focuses on clarifying how VetStat data may be translated to an estimation of the antimicrobial exposure at herd level, by suggesting uniform methods of extracting and editing data, in order to obtain reliable and comparable estimates on pig antimicrobial consumption for research purposes.

**General information**

State: Published

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

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**In silico assessment of virulence factors in strains of Streptococcus oralis and Streptococcus mitis isolated from patients with Infective Endocarditis**

Streptococcus oralis and Streptococcus mitis belong to the Mitis group, which are mostly commensals in the human oral cavity. Even though S. oralis and S. mitis are oral commensals, they can be opportunistic pathogens causing infective endocarditis. A recent taxonomic re-evaluation of the Mitis group has embedded the species Streptococcus tigurinus and Streptococcus dentisani into the species S. oralis as subspecies. In this study, the distribution of virulence factors that contribute to bacterial immune evasion, colonization and adhesion was assessed in clinical strains of S. oralis (subsp. oralis, subsp. tigurinus and subsp. dentisani) and S. mitis. Forty clinical S. oralis (subsp. oralis, subsp. dentisani and subsp. tigurinus) and S. mitis genomes were annotated with the pipeline PanFunPro and aligned against the VFDB database for assessment of virulence factors. Results/Key findings. Three homologues of pavA, psaA and Imb, encoding adhesion proteins, were present in all strains. Seven homologues of nanA, nanB, ply, lytA, lytB, lytC and iga, of importance regarding survival in blood and modulation of the human immune system, were variously present in the genomes. Few S. oralis subspecies specific differences were observed. iga homologues were identified in S. oralis subsp. oralis, whereas lytA homologues were identified in S. oralis subsp. oralis and subsp. tigurinus. Differences in the presence of virulence factors among the three S. oralis subspecies were observed. The virulence gene profiles of the 40 S. mitis and S. oralis (subsp. oralis, subsp. dentisani and subsp. tigurinus) contribute with important new knowledge regarding these species and new subspecies.

**General information**

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Organisations: Department of Bio and Health Informatics, Metagenomics, National Food Institute, Research Group for Genomic Epidemiology, Roskilde University, Slagelse Hospital, University of Copenhagen, Copenhagen University Hospital, Vejle Hospital

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Investigation of Outbreaks of Salmonella enterica Serovar Typhimurium and Its Monophasic Variants Using Whole-Genome Sequencing, Denmark

Whole-genome sequencing is rapidly replacing current molecular typing methods for surveillance purposes. Our study evaluates core-genome single-nucleotide polymorphism analysis for outbreak detection and linking of sources of Salmonella enterica serovar Typhimurium and its monophasic variants during a 7-month surveillance period in Denmark. We reanalyzed and defined 8 previously characterized outbreaks from the phylogenetic relatedness of the isolates, epidemiologic data, and food traceback investigations. All outbreaks were identified, and we were able to exclude unrelated and include additional related human cases. We were furthermore able to link possible food and veterinary sources to the outbreaks. Isolates clustered according to sequence types (STs) 19, 34, and 36. Our study shows that core-genome single-nucleotide polymorphism analysis is suitable for surveillance and outbreak investigation for Salmonella Typhimurium (ST19 and ST36), but whole genome-wide analysis may be required for the tight genetic clone of monophasic variants (ST34).
Meta-analysis of proportion estimates of extended-spectrum-beta-lactamase-producing Enterobacteriaceae in East Africa hospitals

General information
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Organisations: Department of Bio and Health Informatics, Genomic Epidemiology, National Food Institute, Research Group for Genomic Epidemiology, KCRI Kilimanjaro Clinical Research Institute, Copenhagen University Hospital
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Scopus rating (2011): SJR 1.563 SNIP 1.145 CiteScore 2.78
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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.

General information
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Organisations: Department of Bio and Health Informatics, Metagenomics, National Food Institute, Research Group for Genomic Epidemiology, Genomic Epidemiology, Department of Systems Biology, Center for Biological Sequence Analysis
Authors: Petersen, T. N. (Intern), Lukjancenko, O. (Intern), Thomsen, M. C. F. (Intern), Sperotto, M. M. (Intern), Lund, O. (Intern), Aarestrup, F. M. (Intern), Sicheritz-Pontén, T. (Intern)
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**Microbial Performance of Food Safety Control and Assurance Activities in a Fresh Produce Processing Sector Measured Using a Microbial Assessment Scheme and Statistical Modeling**

Current approaches such as inspections, audits, and end product testing cannot detect the distribution and dynamics of microbial contamination. Despite the implementation of current food safety management systems, foodborne outbreaks linked to fresh produce continue to be reported. A microbial assessment scheme and statistical modeling were used to systematically assess the microbial performance of core control and assurance activities in five Kenyan fresh produce processing and export companies. Generalized linear mixed models and correlated random-effects joint models for multivariate clustered data followed by empirical Bayes estimates enabled the analysis of the probability of contamination across critical sampling locations (CSLs) and factories as a random effect. Salmonella spp. and Listeria monocytogenes were not detected in the final products. However, none of the processors attained the maximum safety level for environmental samples. Escherichia coli was detected in five of the six CSLs, including the final product. Among the processing-environment samples, the hand or glove swabs of personnel revealed a higher level of predicted contamination with E. coli, and 80% of the factories were E. coli positive at this CSL. End products showed higher predicted probabilities of having the lowest level of food safety compared with raw materials. The final products were E. coli positive despite the raw materials being E. coli negative for 60% of the processors. There was a higher probability of contamination with coliforms in water at the inlet than in the final rinse water. Four (80%) of the five assessed processors...
had poor to unacceptable counts of Enterobacteriaceae on processing surfaces. Personnel-, equipment-, and product-related hygiene measures to improve the performance of preventive and intervention measures are recommended.

**General information**
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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Authors: Njage, P. M. K. (Intern), Sawe, C. T. (Ekstern), Onyango, C. M. (Ekstern), Habib, I. (Ekstern), Njagi, E. N. (Ekstern), Aerts, M. (Ekstern), Molenberghs, G. (Ekstern)
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Scopus rating (2015): SJR 0.96 SNIP 1.031 CiteScore 2.03
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BFI (2014): BFI-Level 1
Scopus rating (2014): SJR 0.91 SNIP 0.957 CiteScore 1.94
Web of Science (2014): Indexed yes
BFI (2013): BFI-Level 1
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ISI indexed (2013): ISI indexed yes
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Scopus rating (2010): SJR 1.006 SNIP 0.946
Web of Science (2010): Indexed yes
BFI (2009): BFI-Level 1
Scopus rating (2009): SJR 1.104 SNIP 1.118
Web of Science (2009): Indexed yes
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Scopus rating (2008): SJR 1.123 SNIP 1.026
Web of Science (2008): Indexed yes
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Web of Science (2007): Indexed yes
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Web of Science (2006): Indexed yes
Modelling Dietary Exposure to Chemical Components in Heat-Processed Meats
Several chemical compounds that potentially increase the risk of developing cancer in humans are formed during heat processing of meat. Estimating the overall health impact of these compounds in the population requires accurate estimation of the exposure to the chemicals, as well as the probability that different levels of exposure result in disease. The overall goal of this study was to evaluate the impact of variability of exposure patterns and uncertainty of exposure data in burden of disease estimates. We focus on the first phase of burden of disease modelling, i.e. the estimation of exposure to selected compounds in the Danish population, based on concentration and consumption data. One of the challenges that arises in the probabilistic modelling of exposure is the presence of “artificial” zero counts in concentration data due to the detection level of the applied tests. Zero-inflated models, e.g. the Poisson-Lognormal approach, are promising tools to address this obstacle. The exposure estimates can then be applied to dose-response models to quantify the cancer risk.

Molecular Methods for Detection of Antimicrobial Resistance
The increase in bacteria harboring antimicrobial resistance (AMR) is a global problem because there is a paucity of antibiotics available to treat multidrug-resistant bacterial infections in humans and animals. Detection of AMR present in bacteria that may pose a threat to veterinary and public health is routinely performed using standardized phenotypic methods. Molecular methods are often used in addition to phenotypic methods but are set to replace them in many laboratories due to the greater speed and accuracy they provide in detecting the underlying genetic mechanism(s) for AMR. In this article we describe some of the common molecular methods currently used for detection of AMR genes. These include PCR, DNA microarray, whole-genome sequencing and metagenomics, and matrix-assisted laser desorption ionization-time of flight mass spectrometry. The strengths and weaknesses of these methods are discussed, especially in the context of implementing them for routine surveillance activities on a global scale for mitigating the risk posed by AMR.
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.

General information
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Organisations: Department of Bio and Health Informatics, Genomic Epidemiology, National Food Institute, Research Group for Genomic Epidemiology, KCRI Kilimanjaro Clinical Research Institute, University of Copenhagen, Kilimanjaro Christian Medical College
Phenotypic and genotypic comparison of salmonellae from diarrhoeic and healthy humans and cattle, Nigeria

The sources and modes of transmission of non-typhoidal Salmonella particularly zoonotic transmission are poorly understood in Africa. This study compared phenotypic and genotypic characteristics of Salmonellae isolated from cattle and humans. Faecal samples of diarrhoeic patients (n = 234), and a healthy population (n = 160), beef cattle at slaughter (n = 250), farms (n = 72) and market (n = 100) were cultured for salmonellae and serotyping and antimicrobial susceptibility were determined. Whole-genome sequence typing (WGST) of selected isolates and bioinformatic analysis were used to identify the multilocus sequence type (MLST), plasmid replicons, antimicrobial resistance genes and genetic relatedness by single nucleotide polymorphism (SNP) analysis. The Salmonella isolates, diarrhoeic patients (n = 17), healthy population (n = 13), cattle (abattoir, n = 67; farms, n = 10; market n = 5), revealed 49 serovars; some serovars were common to humans and cattle. Rare serovars were prevalent: Colindale (cattle and humans); Rubislaw and Bredeney (humans); and Dublin, Give, Eastbourne, Hadar, Marseille, Sundsvall, Bergen, Ekotedo, Cano and Ealing (cattle). The sequence types (ST) include ST 584, ST 198, ST 562 and ST 512 for S. Colindale, S. Kentucky S. Rubislaw and S. Urbana, respectively. Clonal cluster shared by cattle and human WGST isolates was not found. Antimicrobial resistance rates were generally low and towards only chloramphenicol, ampicillin, gentamicin, ciprofloxacin, tetracycline and streptomycin, range 2.7% (chloramphenicol) to 8.9% (streptomycin). Multiply resistant isolates included serovars Kentucky, 4,5,12:i:- and Typhimurium. The study presents a baseline description of the prevalence, serotypes, antimicrobial resistance phenotypes and genetic relatedness of Salmonella isolated from healthy and diarrhoeic humans, and cattle at harvest, on farm and at market. Cattle are a reservoir of diverse salmonellae with shared serovars with humans, but WGST does not support zoonotic transmission. Further study with larger samples is recommended to determine whether epidemiological link exists between cattle and humans.

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Scopus rating (2014): SJR 1.026 SNIP 0.951 CiteScore 1.97
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Scopus rating (2013): SJR 0.905 SNIP 1.039 CiteScore 2.24
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.049 SNIP 1.226 CiteScore 2.35
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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.

General information

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Organisations: Department of Systems Biology, Center for Biological Sequence Analysis, National Food Institute, Research Group for Genomic Epidemiology, Department of Bio and Health Informatics, Genomic Epidemiology, Statens Serum Institute
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Prevalence and risk factors of CTX-M Enterobacteriaceae in hospitalised patients at a tertiary hospital in Kilimanjaro, Tanzania

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Organisations: Department of Bio and Health Informatics, Genomic Epidemiology, National Food Institute, Research Group for Genomic Epidemiology, KCRI Kilimanjaro Clinical Research Institute, University of Copenhagen, Kilimanjaro Christian Medical College
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BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.563 SNIP 1.145 CiteScore 2.78
ISI indexed (2011): ISI indexed yes
Probabilistic quantitative microbial risk assessment model of farmer exposure to Cryptosporidium spp. in irrigation water within Kumasi Metropolis-Ghana

Cryptosporidium is a protozoan parasite which can be transmitted via food and water. Some studies have shown irrigation water to be routes of transmission for Cryptosporidium into the food chain, however, little information is known about Cryptosporidium levels in wastewater used for irrigation in the Kumasi Metropolis of Ghana. Kumasi and for that matter Ghana is not immune to the widespread practice of wastewater irrigation for farm produce in developing countries which has attracted attention of both, policy makers and academia. However, most previous studies of microbial risk assessment focus on the possible health effects and risk estimation for consumers of wastewater irrigated produce, whereas farmers who actually come into direct contact with the wastewater have received little attention. This study estimated the possible risk/diseases from farmer exposure to Cryptosporidium, a zoonotic pathogen causing gastroenteritis. The results indicate high positive levels of Cryptosporidium in the irrigation water, however, the levels of Cryptosporidium decreases during the rainfall seasons, risk assessment results show that, farmers face a higher risk of being infected by Cryptosporidium due to frequent exposure to wastewater. An adoption of a possible on-farm wastewater treatment option was found to reduce the risk of infection of the farmers. The results of this study highlight the need for a proactive policy to integrate a multi-barrier approach to reduce direct contact of farmers with wastewater for irrigation, to minimise risk of infection.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Office for Innovation & Sector Services, South Dakota State University, Kwame Nkrumah University of Science and Technology, University of Ghana
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Probabilistic quantitative microbial risk assessment model of norovirus from wastewater irrigated vegetables in Ghana using genome copies and fecal indicator ratio conversion for estimating exposure dose

The need to replace the commonly applied fecal indicator conversions ratio (an assumption of $10^{-5}$ virus to fecal indicator organism) in Quantitative Microbial Risk Assessment (QMRA) with models based on quantitative data on the virus of interest has gained prominence due to the different physical and environmental factors that might influence the reliability of using indicator organisms in microbial risk assessment. The challenges facing analytical studies on virus enumeration (genome copies or particles) have contributed to the already existing lack of data in QMRA modelling. This study attempts to fit a QMRA model to genome copies of norovirus data. The model estimates the risk of norovirus infection from the intake of vegetables irrigated with wastewater from different sources. The results were compared to the results of a corresponding model using the fecal indicator conversion ratio to estimate the norovirus count. In all scenarios of using different water sources, the application of the fecal indicator conversion ratio underestimated the norovirus disease burden, measured by the Disability Adjusted Life Years (DALYs), when compared to results using the genome copies norovirus data. In some cases the difference was > 2 orders of magnitude. All scenarios using genome copies met the $10^{-4}$ DALY per person per year for consumption of vegetables irrigated with wastewater, although these results are considered to be highly conservative risk estimates. The fecal indicator conversion ratio model of stream-water and drain-water sources of wastewater achieved the $10^{-6}$ DALY per person per year threshold, which tends to indicate an underestimation of health risk when compared to using genome copies for estimating the dose.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Kwame Nkrumah University of Science and Technology, South Dakota State University, University of Copenhagen
Authors: Owusu-Ansah, E. D. J. (Ekstern), Sampson, A. (Ekstern), Amponsah, S. K. (Ekstern), Abaidoo, R. C. (Ekstern), Dalsgaard, A. (Ekstern), Hald, T. (Intern)
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Web of Science (2016): Indexed yes
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Scopus rating (2015): SJR 1.674 SNIP 1.642 CiteScore 4.33
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.635 SNIP 1.847 CiteScore 4.2
Web of Science (2014): Indexed yes
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ISI indexed (2013): ISI indexed yes
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Scopus rating (2012): SJR 1.773 SNIP 1.811 CiteScore 3.7
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.798 SNIP 1.681 CiteScore 3.61
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.644 SNIP 1.513
Quantitative assessment of human exposure to extended spectrum and AmpC β-lactamases bearing E. coli in lettuce attributable to irrigation water and subsequent horizontal gene transfer

The contribution of the fresh produce production environment to human exposure with bacteria bearing extended spectrum β-lactamases and AmpC β-lactamases (ESBL/AmpC) has not been reported. High prevalence of ESBLs/AmpC bearing E. coli as well as a high gene transfer efficiency of lettuce and irrigation water E. coli isolates was previously reported. This stochastic modeling was aimed at quantitatively assessing human exposure to ESBL/AmpC bearing E. coli through lettuce attributable to irrigation water and subsequent horizontal gene transfer. Modular process risk approach was used for the quantitative exposure assessment and models were constructed in Ms. Excel spreadsheet with farm to consumption chain accounted for by primary production, processing, retail and consumer storage. Probability distributions were utilised to take into account the variability of the exposure estimates. Exposure resulting from ESBL/AmpC positive E. coli and gene transfer was taken into account. Monte Carlo simulation was carried out using @Risk software followed by sensitivity and scenario analysis to assess most effective single or combinations of mitigation strategies for the ESBL/AmpC positive E. coli events from farm to fork. Three percent of South African lettuce consumers are exposed to lettuce contaminated with about 10(6.4)±10(6.7) (95% CI: 10(5.1)-10(7)) cfu of ESBL/AmpC positive E. coli per serving. The contribution of originally positive isolates and conjugative genetic transfer was 10(6)±10(6.7) (95% CI: 10(5)-10(7)) and 10(5.2)±10(5.6) (95% CI: 10(3.9)-10(5.8)) cfu per serving respectively. Proportion of ESBL/AmpC positive E. coli (Spearman's correlation coefficient (p)=0.85), conjugative gene transfer (p=0.05-0.14), washing in chlorine water (p=0.18), further rinsing (p=0.15), and prevalence of E. coli in irrigation water (p=0.16) had highest influence on consumer exposure. The most effective single methods in reducing consumer exposure were reduction in irrigation water microbial quality variation (87.4% reduction), storage period (49.9-87.4% reduction) and growth rate reduction by 75% (90% reduction). Reduction in growth rate together with storage time (92.1-99.4%) and reduction in storage time combined with E. coli concentration in irrigation water (95-96% reduction) were most effective combinations of mitigation measures. The high variation in exposure reflected the high irrigation water quality variation. The exposure levels may impose higher consumer risk than acceptable for irrigation water risk. E. coli contamination and growth related measures, as well as measures to reduce contamination with antimicrobial resistant E. coli from lettuce production environment are recommended. This exposure model could form a basis for the development of similar models assessing the impact of contaminated irrigation water and gene transfer in other microbial hazards, antimicrobial resistance types and fresh produce types.

General information
"Recycled paper for food packaging: burden of disease methodology to link sustainability and safety"

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Research Group for Analytical Food Chemistry, Research Group for Risk-Benefit, Research Group for Molecular and Reproductive Toxicology
Authors: Boriani, E. (Intern), Pieke, E. N. (Intern), Hald, T. (Intern), Pires, S. M. (Intern), Boberg, J. (Intern), Jakobsen, L. S. (Intern)
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Electronic versions:
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Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2017

Scale of production and implementation of food safety programs influence the performance of current food safety management systems: Case of dairy processors
An FSMS-Diagnostic Instrument was used to evaluate fifteen Kenyan dairy processors based on indicators and descriptive grids for context riskiness, FSMS activities, and microbial food safety (FS) output with respect to scale of production. Contextual riskiness was diagnosed as low, moderate or high. FSMS activities were diagnosed as absent, basic, average or advanced. FS output was diagnosed as not performed, poor, moderate or good. Four clusters with significantly different (p

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, University of Nairobi
Authors: Njage, P. M. K. (Intern), Opiyo, B. (Ekstern), Wangoh, J. (Ekstern), Wambui, J. (Ekstern)
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Web of Science (2018): Indexed yes
Spatial patterns of antimicrobial resistance genes in a cross-sectional sample of pig farms with indoor non-organic production of finishers
Antimicrobial resistance (AMR) in pig populations is a public health concern. There is a lack of information of spatial distributions of AMR genes in pig populations at large scales. The objective of the study was to describe the spatial pattern of AMR genes in faecal samples from pig farms and to test if the AMR genes were spatially randomly distributed with respect to the geographic distribution of the pig farm population at risk. Faecal samples from 687 Danish pig farms were collected in February and March 2015. DNA was extracted and the levels of seven AMR genes (ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W)) were quantified on a high-throughput real-time PCR array. Spatial differences for the levels of the AMR genes measured as relative quantities were evaluated by spatial cluster analysis and creating of risk maps using kriging analysis and kernel density estimation. Significant spatial clusters were identified for ermB, ermF, sulII and tet(W). The broad spatial trends in AMR resistance evident in the risk maps were in agreement with the results of the cluster analysis. However, they also showed that there were only small scale spatial differences in the gene levels. We conclude that the geographical location of a pig farm is not a major determinant of the presence or high levels of AMR genes assessed in this study.

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Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
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Web of Science (2014): Indexed yes
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ISI indexed (2013): ISI indexed yes
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BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.42 SNIP 1.175 CiteScore 2.69
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.327 SNIP 1.223 CiteScore 2.71
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.034 SNIP 1.045
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.053 SNIP 1.192
TEACH FOOD – Developing a teacher’s community of practice

The National Food Institute (DTU FOOD) at DTU teaches and educates engineers for the food sector, the public authorities and the research communities. To meet these objectives faculty needs to be at the forefront of food science as well as in teaching and continuously develop the approach to how to teach. Learning environments with suitable student challenges requires devoted and involved faculty members, who continuously develop their competences in teaching. At DTU FOOD the faculty consists of scientist in a broad range of disciplines and cultures. TEACH FOOD was established to promote and enhance the development of community of practice, i.e. a Professional Learning Community (PLC) focusing on optimizing the learning outcome of the students. To achieve this, a 1½ residential seminar for all teachers was arranged. In the first seminar 76% of the teachers and the head of institute participated. Five core activities were identified and a series of half years seminars were started focusing on challenges in every day teaching experiences. The participation of DTU FOOD faculty members in the internal DTU conferences about teaching and learning has increased from 3 to 11 since the start of TEACH FOOD. These activities illustrate the extended willingness to discuss teaching and learning as well as share experiences from teaching at DTU FOOD exemplifying the growing PLC.

General information
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Organisations: National Food Institute, Research Group for Analytical Food Chemistry, Research Group for Genomic Epidemiology, Office for Study Programmes and Student Affairs, Research Group for Microbial Food Safety
Authors: Duedahl-Olesen, L. (Intern), Vigre, H. (Intern), Andersson, P. H. (Intern), Jensen, L. B. (Intern)
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The 20th EURL-AR Proficiency Test - Enterococci, Staphylococci and E. coli 2016

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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Authors: Bortolaia, V. (Intern), Karlsmose Pedersen, S. (Intern), Roer, L. (Intern), Cavaco, L. (Intern), Hendriksen, R. S. (Intern), Aarestrup, F. M. (Intern)
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The 21st EURL-AR Proficiency Test Salmonella, Campylobacter and genotypic characterisation 2016

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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Authors: Karlsmose Pedersen, S. (Intern), Cavaco, L. (Intern), Hendriksen, R. S. (Intern), Bortolaia, V. (Intern)
Number of pages: 16
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The 2nd EURL-AR Proficiency Test on selective isolation of E. coli with presumptive ESBL or AmpC phenotypes from meat or caecal samples - 2016

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology
Authors: Cavaco, L. (Intern), Karlsmose Pedersen, S. (Intern), Hendriksen, R. S. (Intern), Bortolaia, V. (Intern)
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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 faeces 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 and tetracycline use, a significant effect was observed on the occurrence of genes coding for the AM resistance 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
Authors: Dalhoff Andersen, V. (Intern), de Knegt, L. (Intern), Munk, P. (Intern), Jensen, M. S. (Intern), Agersø, Y. (Intern), Aarestrup, F. M. (Intern), Vigre, H. (Intern)
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BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.288 SNIP 1.026 CiteScore 2.19
Web of Science (2014): Indexed yes
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Web of Science (2012): Indexed yes
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
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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Organisations: Department of Systems Biology, Department of Bio and Health Informatics, Center for Biological Sequence Analysis, Genomic Epidemiology, National Food Institute, Research Group for Genomic Epidemiology, Immunoinformatics and Machine Learning, Metagenomics, Statens Seruminstitute, Osaka University
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Place of publication: Switzerland
Publisher: Springer
Chapter: 5
The invasome of Salmonella Dublin as revealed by whole genome sequencing

Salmonella enterica serovar Dublin is a zoonotic infection that can be transmitted from cattle to humans through consumption of contaminated milk and milk products. Outbreaks of human infections by S. Dublin have been reported in several countries including high-income countries. A high proportion of S. Dublin cases in humans are associated with invasive disease and systemic illness. The genetic basis of virulence in S. Dublin is not well characterized. Whole genome sequencing was applied to a set of clinical invasive and non-invasive S. Dublin isolates from different countries in order to characterize the putative genetic determinants involved in the virulence and invasiveness of S. Dublin in humans. We identified several virulence factors that form the bacterial invasome and may contribute to increasing bacterial virulence and pathogenicity including mainly Gifsy-2 prophage, two different type 6 secretion systems (T6SSs) harbored by Salmonella pathogenicity islands; SPI-6 and SPI-19 respectively and virulence genes; ggt and PagN. Although Vi antigen and the virulence plasmid have been reported previously to contribute to the virulence of S. Dublin we did not detect them in all invasive isolates indicating that they are not the main virulence determinants in S. Dublin. Several virulence factors within the genome of S. Dublin might contribute to the ability of S. Dublin to invade humans' blood but there were no genomic markers that differentiate invasive from non-invasive isolates suggesting that host immune response play a crucial role in the clinical outcome of S. Dublin infection.
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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Transmission of extended-spectrum cephalosporin (ESC) resistance through the broiler production system in Denmark

General information
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Organisations: National Food Institute, Research Group for Microbial Food Safety, Research Group for Genomic Epidemiology, Danish Veterinary and Food Administration
Authors: Jensen, L. B. (Intern), Birk, T. (Intern), Hendriksen, R. S. (Intern), Ortvéd Bjergager, G. (Ekstern), Lundsby, K. (Ekstern), Aabo, S. (Intern)
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Use of multiple-locus variable-number of tandem repeats analysis (MLVA) to investigate genetic diversity of Salmonella enterica subspecies enterica serovar Typhimurium isolates from human, food, and veterinary sources

Salmonella enterica subspecies enterica serovar Typhimurium is the most common zoonotic pathogen in Bulgaria. To allow efficient outbreak investigations and surveillance in the food chain, accurate and discriminatory methods for typing are needed. This study evaluated the use of multiple-locus variable-number of tandem repeats analysis (MLVA) and compared results with antimicrobial resistance (AMR) determinations for 100 S. Typhimurium strains isolated in Bulgaria during 2008-2012 (50 veterinary/food and 50 human isolates). Results showed that isolates were divided into 80 and 34 groups using MLVA and AMR, respectively. Simpson's index of diversity was determined to 0.994 ± 0.003 and 0.945 ± 0.012. The most frequently encountered MLVA profiles were 3-11-9-NA-211 (n = 5); 3-12-9-NA-211 (n = 3); 3-12-11-21-311 (n = 3); 3-17-10-NA-311 (n = 3); 2-20-9-7-212 (n = 3); and 2-23-NA-NA-111 (n = 3). No clustering of isolates related to susceptibility/resistance to antimicrobials, source of isolation, or year of isolation was observed. Some MLVA types were found in both human and veterinary/food isolates, indicating a possible route of transmission. A majority (83%) of the isolates were found to be resistant against at least one antimicrobial and 44% against ≥4 antimicrobials. Further studies are needed to verify MLVA usefulness over a longer period of time and with more isolates, including outbreak strains.

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Organisations: National Veterinary Institute, Bacteriology & Parasitology, Research Group for Analytical and Predictive Microbiology, Research Group for Genomic Epidemiology, National Food Institute, National Diagnostic and Research Veterinary Medical Institute, National Center of Infectious and Parasitic Diseases Bulgaria, Bulgarian Academy of Sciences
Authors: Mateva, G. (Ekstern), Pedersen, K. (Intern), Sørensen, G. (Intern), Asseva, G. (Ekstern), Daskalov, H. (Ekstern), Petrov, P. (Ekstern), Kantardjiev, T. (Ekstern), Alexandar, I. (Ekstern), Löfström, C. (Intern)
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Main Research Area: Technical/natural sciences

Use of multiple-locus variable-number of tandem repeats analysis (MLVA) to investigate genetic diversity of Salmonella enterica subspecies enterica serovar Typhimurium isolates from human, food, and veterinary sources

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General information
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Organisations: National Veterinary Institute, Bacteriology & Parasitology, Research Group for Analytical and Predictive Microbiology, Research Group for Genomic Epidemiology, National Food Institute, National Diagnostic and Research Veterinary Medical Institute, National Center of Infectious and Parasitic Diseases Bulgaria, Bulgarian Academy of Sciences
Authors: Mateva, G. (Ekstern), Pedersen, K. (Intern), Sørensen, G. (Intern), Asseva, G. (Ekstern), Daskalov, H. (Ekstern), Petrov, P. (Ekstern), Kantardjiev, T. (Ekstern), Alexandar, I. (Ekstern), Löfström, C. (Intern)
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Scopus rating (2014): SJR 1.183 SNIP 1.06 CiteScore 2.19
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.

Whole-genome sequence of the first sequence type 27 Brucella ceti strain isolated from European waters

Brucella spp. that cause marine brucellosis are becoming more important, as the disease appears to be more widespread than originally thought. Here, we report a whole and annotated genome sequence of Brucella ceti CRO350, a sequence type 27 strain isolated from a bottlenose dolphin carcass found in the Croatian part of the northern Adriatic Sea.
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.
Adaptation and mitigation options to manage aflatoxin contamination in food with a climate change perspective
Understanding the impact of climate change remains vital for food safety and public health. Of particular importance is the influence of climatic conditions on the growth of Aspergillus flavus and production of their toxins. Nevertheless, little is known about the actual impact of climate change on the issue. Setting up of relevant measures to manage the impact has therefore become a daunting task especially in developing nations. Therefore, this study aimed at providing adaptation and mitigation options to manage this risk with a special focus on Kenya where cases of aflatoxicosis have been recurrent.
We used a systematic literature review of review and research articles, with limited searching but systematic screening to
explore available qualitative and quantitative data. Projections from the data, showed that on average, a 58.9% increase of aflatoxin contamination in the Central and Western parts and a decrease of 44.6% in the Eastern and Southern parts is expected but with several possible scenarios. This makes the impact of climate change on aflatoxin contamination in Kenya complex. To protect the public and environment from the negative impact, a regulatory framework that allows for an integrated management of aflatoxins in a changing climate was proposed. The management practices in the framework are divided into agronomic, post-harvest and institutional levels. Given the multiple points of application, coordination amongst stakeholders along the chain is fundamental. We therefore proposed a complimentary framework that allows the food safety issues to be addressed in an integrated manner while allowing for transparent synergies and trade-offs (in implementing the measures). A policy-oriented foresight should be carried out to provide policy based evidence for the applicability of the proposed adaptation and mitigation measures.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Authors: Wambui, J. M. (Ekstern), Karuri, E. G. (Ekstern), Ojiambo, J. A. (Ekstern), Njage, P. M. K. (Intern)
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Scopus rating (2016): SJR 0.535 SNIP 0.856 CiteScore 2.17
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ISI indexed (2013): ISI indexed yes
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ISI indexed (2012): ISI indexed yes
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A decision support system for the control of Campylobacter in chickens at farm level using data from Denmark
The control of Campylobacter in poultry is considered a public health priority and some intervention strategies have been implemented in Denmark. Nonetheless, Campylobacter infection in poultry can still be considerable particularly during the summer when the most promising Campylobacter control strategy seems to be the use of fly screens. The use of cost-effective vaccines against Campylobacter is also desirable. In order to control Campylobacter, poultry producers need to make crucial decisions under conditions of uncertainty. With the aim of assisting poultry producers in decision making regarding Campylobacter control strategies, the objective of the present study was to produce a decision support system that integrated knowledge and used a Bayesian approach to handle uncertainty. This decision support system integrated epidemiological data, microbiological considerations, financial information and potential control strategies (the use of fly screens and hypothetrical vaccines). In conclusion, results from model and sensitivity analyses indicated that the financial variables (cost–benefit functions) and the effectiveness of the different control strategies drove the results.

General information
State: Published
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 of 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.
An Approach to Cluster EU Member States into Groups According to Pathways of Salmonella in the Farm-to-Consumption Chain for Pork Products

The aim of the project as the cluster analysis was to in part to develop a generic structured quantitative microbiological risk assessment (QMRA) model of human salmonellosis due to pork consumption in EU member states (MSs), and the objective of the cluster analysis was to group the EU MSs according to the relative contribution of different pathways of Salmonella in the farm-to-consumption chain of pork products. In the development of the model, by selecting a case study MS from each cluster the model was developed to represent different aspects of pig production, pork production, and consumption of pork products across EU states. The objective of the cluster analysis was to aggregate MSs into groups of countries with similar importance of different pathways of Salmonella in the farm-to-consumption chain using available, and where possible, universal register data related to the pork production and consumption in each country. Based on MS-specific information about distribution of (i) small and large farms, (ii) small and large slaughterhouses, (iii) amount of pork meat consumed, and (iv) amount of sausages consumed we used nonhierarchical and hierarchical cluster analysis to group the MSs. The cluster solutions were validated internally using statistic measures and externally by comparing the clustered MSs with an estimated human incidence of salmonellosis due to pork products in the MSs. Finally, each cluster was characterized qualitatively using the centroids of the clusters.

General information
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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Authors: Vigre, H. (Intern), Coutinho Calado Domingues, A. R. (Intern), Pedersen, U. B. (Intern), Hald, T. (Intern)
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BFI (2014): BFI-level 1
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Scopus rating (2013): SJR 1.067 SNIP 1.563 CiteScore 2.1
ISI indexed (2013): ISI indexed yes
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BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.725 SNIP 1.707 CiteScore 2.15
ISI indexed (2011): ISI indexed yes
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BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.741 SNIP 1.526
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BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.64 SNIP 1.39
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Scopus rating (2008): SJR 0.673 SNIP 1.461
Scopus rating (2007): SJR 0.78 SNIP 1.441
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.818 SNIP 1.458
Scopus rating (2005): SJR 0.717 SNIP 1.42
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.711 SNIP 1.208
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.636 SNIP 1.331
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Salmonella is an important cause of bacterial foodborne infections in Denmark. To identify the main animal-food sources of human salmonellosis, risk managers have relied on a routine application of a microbial subtyping-based source attribution model since 1995. In 2013, multiple locus variable number tandem repeat analysis (MLVA) substituted phage typing as the subtyping method for surveillance of S. Enteritidis and S. Typhimurium isolated from animals, food, and humans in Denmark. The purpose of this study was to develop a modeling approach applying a combination of serovars, MLVA types, and antibiotic resistance profiles for the Salmonella source attribution, and assess the utility of the results for the food safety decisionmakers. Full and simplified MLVA schemes from surveillance data were tested, and model fit and consistency of results were assessed using statistical measures. We conclude that loci schemes STTR5/STTR10/STTR3 for S. Typhimurium and SE9/SE5/SE2/SE1/SE3 for S. Enteritidis can be used in microbial subtyping-based source attribution models. Based on the results, we discuss that an adjustment of the discriminatory level of the subtyping method applied often will be required to fit the purpose of the study and the available data. The issues discussed are also considered highly relevant when applying, e.g., extended multi-locus sequence typing or next-generation sequencing techniques.
Apramycin treatment affects selection and spread of a multidrug-resistant Escherichia coli strain able to colonize the human gut in the intestinal microbiota of pigs

The effect of apramycin treatment on transfer and selection of an Escherichia coli strain (E. coli 912) in the intestine of pigs was analyzed through an in vivo experiment. The strain was sequenced and assigned to the sequence type ST101 and serotype O11. It carried resistance genes to apramycin/gentamicin, sulphonamide, tetracycline, hygromycin B, β-lactams and streptomycin [aac(3)-IV, sul2, tet(X), aph(4), bla TEM-1 and strA/B], with all but tet(X) located on the same conjugative plasmid. Nineteen pigs were randomly allocated into two inoculation groups, one treated with apramycin (pen 2) and one non-treated (pen 3), along with a non-inoculated control group (pen 1). Two pigs of pen 2 and 3 were inoculated intragastrically with a rifampicin resistant variant of the strain. Apramycin treatment in pen 2 was initiated immediately after inoculation. Strain colonization was assessed in the feces from all pigs. E. coli 912 was shown to spread to non-inoculated pigs in both groups. The selective effect did not persist beyond 3 days post-treatment, and the strain was not detected from this time point in pen 2. We demonstrated that E. coli 912 was able to spread between pigs in the same pen irrespective of treatment, and apramycin treatment resulted in significantly higher counts compared to the non-treated group. This represents the first demonstration of how antimicrobial treatment affects spread of resistant bacteria in pig production. The use of apramycin may lead to enhanced spread of gentamicin-resistant E. coli. Since gentamicin is a first-choice drug for human bacteremia, this is of concern.

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Authors: Herrero-Fresno, A. (Ekstern), Zachariasen, C. (Ekstern), Hansen, M. H. (Ekstern), Hendriksen, R. S. (Intern), Nielsen, S. S. (Ekstern), Olsen, J. E. (Ekstern)
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Scopus rating (2014): SJR 1.189 SNIP 1.197 CiteScore 2.46
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BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.353 SNIP 1.457 CiteScore 3.13
ISI indexed (2013): ISI indexed yes
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BFI (2009): BFI-level 2
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Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.557 SNIP 2.009
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.745 SNIP 2.184
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.348 SNIP 1.946
Scopus rating (2005): SJR 0.879 SNIP 1.593
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.782 SNIP 1.302
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.729 SNIP 1.076
Scopus rating (2002): SJR 0.8 SNIP 1.191
Scopus rating (2001): SJR 0.629 SNIP 1.081
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.575 SNIP 0.994
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A Quantitative Microbiological Risk Assessment for Salmonella in Pigs for the European Union

A farm-to-consumption quantitative microbiological risk assessment (QMRA) for Salmonella in pigs in the European Union has been developed for the European Food Safety Authority. The primary aim of the QMRA was to assess the impact of hypothetical reductions of slaughter-pig prevalence and the impact of control measures on the risk of human Salmonella infection. A key consideration during the QMRA development was the characterization of variability between E.U. Member States (MSs), and therefore a generic MS model was developed that accounts for differences in pig production, slaughterhouse practices, and consumption patterns. To demonstrate the parameterization of the model, four case study MSs were selected that illustrate the variability in production of pork meat and products across MSs. For the case study MSs the average probability of illness was estimated to be between 1 in 100,000 and 1 in 10 million servings given consumption of one of the three product types considered (pork cuts, minced meat, and fermented ready-to-eat sausages). Further analyses of the farm-to-consumption QMRA suggest that the vast majority of human risk derives from infected pigs with a high concentration of Salmonella in their feces (≥10^4 CFU/g). Therefore, it is concluded that interventions should be focused on either decreasing the level of Salmonella in the feces of infected pigs, the introduction of a control step at the abattoir to reduce the transfer of feces to the exterior of the pig, or a control step to reduce the level of Salmonella on the carcass post-evisceration.

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Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
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BFI (2014): BFI-level 1
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Scopus rating (2013): SJR 1.067 SNIP 1.563 CiteScore 2.1
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ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.725 SNIP 1.707 CiteScore 2.15
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.741 SNIP 1.526
Web of Science (2010): Indexed yes
A risk-based approach for evaluation of hygiene performance at pig slaughter

In Denmark, the pig slaughterhouses have a daily input of pigs infected and/or contaminated with Salmonella, and the slaughter hygiene has major influence on the level of Salmonella contamination on the meat leaving the slaughterhouse. However, the relationship between the effect of improved hygiene performance and the consequential reduction of human health risk has not been estimated so far. In this study, swab samples from 2702 pig carcasses were collected, originally for other purposes, from five large Danish slaughterhouses in a period from 2005 to 2007, covering all seasons of the year. The samples were analysed quantitatively for E. coli and semi-quantitatively for Salmonella. A positive association between the number of E. coli on carcasses and the prevalence of Salmonella positive carcasses was shown. For carcasses positive for Salmonella, a positive association was also shown between the number of E. coli and the number of Salmonella on the carcass. As no biological association has been reported between faecal shedding of E. coli and presence of Salmonella, the relationship was considered to be associated with the level of faecal contamination. The positive association between E. coli and Salmonella was used as basis for developing a quantitative risk assessment model for Salmonella, using the level E. coli as model input. The model output associated the hygiene performance with a relative risk estimate of human salmonellosis. The overall objective was to develop a decision support tool that can be used to support risk-based hygiene interventions in pig slaughterhouses.

General information
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Organisations: National Food Institute, Research Group for Microbial Food Safety, Research Group for Risk-Benefit, Research Group for Genomic Epidemiology
Authors: Bollerslev, A. M. (Intern), Nauta, M. (Intern), Hald, T. (Intern), Hansen, T. B. (Intern), Aabo, S. (Intern)
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  Web of Science (2018): Indexed yes
  BFI (2019): BFI-level 1
  Web of Science (2019): Indexed yes
  BFI (2020): BFI-level 1
  Web of Science (2020): Indexed yes
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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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Scopus rating (2016): CiteScore 4.21 SJR 2.24 SNIP 1.527
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.203 SNIP 1.513 CiteScore 4.06
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.303 SNIP 1.772 CiteScore 4.61
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.416 SNIP 1.782 CiteScore 4.7
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.157 SNIP 1.654 CiteScore 4.35
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.235 SNIP 1.745 CiteScore 4.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.09 SNIP 1.642
Assessing the Effectiveness of On-Farm and Abattoir Interventions in Reducing Pig Meat–Borne Salmonellosis within E.U. Member States

As part of the evidence base for the development of national control plans for Salmonella spp. in pigs for E.U. Member States, a quantitative microbiological risk assessment was funded to support the scientific opinion required by the EC from the European Food Safety Authority. The main aim of the risk assessment was to assess the effectiveness of interventions implemented on-farm and at the abattoir in reducing human cases of pig meat–borne salmonellosis, and how the effects of these interventions may vary across E.U. Member States. Two case study Member States have been chosen to assess the effect of the interventions investigated. Reducing both breeding herd and slaughter pig prevalence were effective in achieving reductions in the number of expected human illnesses in both case study Member States. However, there is scarce evidence to suggest which specific on-farm interventions could achieve consistent reductions in either breeding herd or slaughter pig prevalence. Hypothetical reductions in feed contamination rates were important in reducing slaughter pig prevalence for the case study Member State where prevalence of infection was already low, but not for the high-prevalence case study. The most significant reductions were achieved by a 1- or 2-log decrease of Salmonella contamination of the carcass post-evisceration; a 1-log decrease in average contamination produced a 90% reduction in human illness. The intervention analyses suggest that abattoir intervention may be the most effective way to reduce human exposure to Salmonella spp. However, a combined farm/abattoir approach would likely have cumulative benefits. On-farm intervention is probably most effective at the breeding-herd level for high-prevalence Member States; once infection in the breeding herd has been reduced to a low enough level, then feed and biosecurity measures would become increasingly more effective.

General information
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Authors: Hill, A. A. (Ekstern), Simons, R. L. (Ekstern), Swart, A. N. (Ekstern), Kelly, L. (Ekstern), Hald, T. (Intern), Snary, E. L. (Ekstern)
Number of pages: 15
Association of Panton Valentine Leukocidin (PVL) genes with methicillin resistant Staphylococcus aureus (MRSA) in Western Nepal: a matter of concern for community infections (a hospital based prospective study)

Methicillin resistant Staphylococcus aureus (MRSA) is a major human pathogen associated with nosocomial and community infections. Panton Valentine leukocidin (PVL) is considered one of the important virulence factors of S. aureus responsible for destruction of white blood cells, necrosis and apoptosis and as a marker of community acquired MRSA. This study was aimed to determine the prevalence of PVL genes among MRSA isolates and to check the reliability of PVL as marker of community acquired MRSA isolates from Western Nepal. A total of 400 strains of S. aureus were collected from clinical specimens and various units (Operation Theater, Intensive Care Units) of the hospital and 139 of these had been confirmed as MRSA by previous study. Multiplex PCR was used to detect mecA and PVL genes. Clinical data as well as antimicrobial susceptibility data was analyzed and compared among PVL positive and negative MRSA isolates. Out of 139 MRSA isolates, 79 (56.8 %) were PVL positive. The majority of the community acquired MRSA (90.4 %) were PVL positive (Positive predictive value: 94.9 % and negative predictive value: 86.6 %), while PVL was detected only in 4 (7.1 %) hospital associated MRSA strains. None of the MRSA isolates from hospital environment was found positive for the PVL genes. The majority of the PVL positive strains (75.5 %) were isolated from pus samples. Antibiotic resistance among PVL negative MRSA isolates was found higher as compared to PVL positive MRSA. Our study showed high prevalence of PVL among community acquired MRSA isolates. Absence of PVL among MRSA isolates from hospital environment indicates its poor association with hospital acquired MRSA and therefore, PVL may be used a marker for community acquired MRSA. This is first study from Nepal, to test PVL among MRSA isolates from hospital environment.

General information
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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Tribhuvan University, Banaras Hindu University, Manipal College of Medical Sciences
Authors: Bhatta, D. R. (Ekstern), Cavaco, L. (Intern), Nath, G. (Ekstern), Kumar, K. (Ekstern), Gaur, A. (Ekstern), Gokhale, S. (Ekstern), Bhatta, D. R. (Ekstern)
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Scopus rating (2015): SJR 1.505 SNIP 1.204 CiteScore 2.91
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.538 SNIP 1.391 CiteScore 3.14
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.449 SNIP 1.411 CiteScore 3.23
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.523 SNIP 1.323 CiteScore 3.48
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.539 SNIP 1.43 CiteScore 3.6
ISI indexed (2011): ISI 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 down-sampled 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.
Projects:
Benchmarking of methods for identification of antimicrobial resistance genes in bacterial whole genome data
Benchtop Whole-Genome Sequencing for Identification of Nosocomial Outbreaks in Tanzania

**General information**

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Organisations: Department of Systems Biology, Center for Biological Sequence Analysis, National Food Institute, Research Group for Genomic Epidemiology, Kilimanjaro Christian Medical Centre, University of Copenhagen
Authors: Sonda, T. (Ekstern), Kumburu, H. (Ekstern), Zwetselaar, M. V. (Ekstern), Ahrenfeldt, J. (Intern), Alifrangis, M. (Ekstern), Lund, O. (Intern), Kibiki, G. (Ekstern), Aarestrup, F. M. (Intern)
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- BFI (2016): BFI-level 1
- Scopus rating (2016): SJR 1.799 SNIP 1.394 CiteScore 2.54
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 2.093 SNIP 1.519 CiteScore 2.5
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 2.154 SNIP 1.625 CiteScore 3.13
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 2.445 SNIP 1.992 CiteScore 3.61
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 2.486 SNIP 1.644 CiteScore 3.25
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 3.029 SNIP 1.653 CiteScore 3.41
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 2.305 SNIP 1.518
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 1.615 SNIP 1.366
- BFI (2008): BFI-level 1
- Scopus rating (2008): SJR 2.093 SNIP 1.181
- Scopus rating (2007): SJR 1.534 SNIP 1.41
- Scopus rating (2006): SJR 1.851 SNIP 1.482
- Scopus rating (2005): SJR 1.504 SNIP 1.191
- Scopus rating (2004): SJR 0.991 SNIP 1.192
- Scopus rating (2003): SJR 0.96 SNIP 1.27
- Scopus rating (2002): SJR 1.322 SNIP 1.364
- Scopus rating (2001): SJR 1.353 SNIP 1.411
- Scopus rating (2000): SJR 1.151 SNIP 1.218
- Scopus rating (1999): SJR 1.181 SNIP 1.532

Original language: English

DOIs:
Characterization of the Human Risk of Salmonellosis Related to Consumption of Pork Products in Different E.U. Countries Based on a QMRA

In response to the European Food Safety Authority's wish to assess the reduction of human cases of salmonellosis by implementing control measures at different points in the farm-to-consumption chain for pork products, a quantitative microbiological risk assessment (QMRA) was developed. The model simulated the occurrence of Salmonella from the farm to consumption of pork cuts, minced meat, and fermented ready-to-eat sausage, respectively, and a dose-response model was used to estimate the probability of illness at consumption. The QMRA has a generic structure with a defined set of variables, whose values are changed according to the E.U. member state (MS) of interest. In this article we demonstrate the use of the QMRA in four MSs, representing different types of countries. The predicted probability of illness from the QMRA was between 1 in 100,000 and 1 in 10 million per serving across all three product types. Fermented ready-to-eat sausage imposed the highest probability of illness per serving in all countries, whereas the risks per serving of minced meat and pork chops were similar within each MS. For each of the products, the risk varied by a factor of 100 between the four MSs. The influence of lack of information for different variables was assessed by rerunning the model with alternative, more extreme, values. Out of the large number of uncertain variables, only a few of them have a strong influence on the probability of illness, in particular those describing the preparation at home and consumption.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Technical University of Denmark, National Institute of Public Health and the Environment, Animal Health and Veterinary Laboratories Agency
Authors: Vigre, H. (Intern), Barfoed, K. (Ekstern), Swart, A. N. (Ekstern), Simons, R. R. L. (Ekstern), Hill, A. A. (Ekstern), Snary, E. L. (Ekstern), Hald, T. (Intern)
Number of pages: 15
Pages: S31-S45
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Risk Analysis
Volume: 36
Issue number: 3
ISSN (Print): 0272-4332
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.21 SJR 0.955 SNIP 1.458
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.305 SNIP 1.521 CiteScore 2.51
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.352 SNIP 1.61 CiteScore 2.2
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.067 SNIP 1.563 CiteScore 2.1
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.763 SNIP 1.612 CiteScore 2.12
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.725 SNIP 1.707 CiteScore 2.15
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
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.
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.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, University of Antwerp, European Bioinformatics Institute
Authors: Xavier, B. B. (Ekstern), Das, A. J. (Ekstern), Cochrane, G. (Ekstern), De Ganck, S. (Ekstern), Kumar-Singh, S. (Ekstern), Aarestrup, F. M. (Intern), Goossens, H. (Ekstern), Malhotra-Kumar, S. (Ekstern)
Number of pages: 9
Pages: 851-859
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Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Clinical Microbiology
Volume: 54
Issue number: 4
ISSN (Print): 0095-1137
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.14 SNIP 1.417
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.204 SNIP 1.448 CiteScore 3.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.205 SNIP 1.538 CiteScore 3.84
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.414 SNIP 1.646 CiteScore 4.18
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.114 SNIP 1.632 CiteScore 4.11
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.336 SNIP 1.698 CiteScore 4.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.303 SNIP 1.727
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.173 SNIP 1.694
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.239 SNIP 1.621
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.202 SNIP 1.689
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.187 SNIP 1.642
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.012 SNIP 1.655
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.678 SNIP 1.701
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.845 SNIP 1.855
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.947 SNIP 1.722
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.076 SNIP 1.808
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.945 SNIP 1.938
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.851 SNIP 2.036

Original language: English
DOIs:
DANMAP 2015: Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark

General information
State: Published
Organisations: National Food Institute, Division of Risk Assessment and Nutrition, Research Group for Genomic Epidemiology, Research Group for Microbial Food Safety, Statens Seruminstitute, State Serum Institute, Statens Serum Institut
Number of pages: 142
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Original language: English
Series: Dansk Veterinaertidsskrift
ISSN: 1600-2032
Main Research Area: Technical/natural sciences
Electronic versions:
DANMAP_2015.pdf
Links:
http://www.danmap.org/~media/Projekt%20sites/Danmap/DANMAP%20reports/DANMAP%20%202015/DADD%20pigs%20DANMAP%202015.ashx
Source: PublicationPreSubmission
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Danske dyrlægers brug af Antibiotikavejledning til familiedyr: en spørgeskemaundersøgelse

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen
Authors: Lilja, Z. (Ekstern), Møller Sørensen, T. (Ekstern), Kristensen, M. (Ekstern), Hald, T. (Intern), Damborg, P. P. (Ekstern), Jessen, L. R. (Ekstern)
Pages: 18-25
Publication date: 2016
Main Research Area: Technical/natural sciences

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Journal: Dansk Veterinaertidsskrift
Volume: 99
Issue number: 10
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BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
Detection of plasmid-mediated colistin resistance (mcr-1) in E. coli isolated from pig caecum in Austria

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, National Reference Laboratory for Antimicrobial Resistance
Authors: Jelovcan, S. (Ekstern), Leekitcharoenphon, P. (Intern), Weissensteiner, G. (Ekstern), Hendriksen, R. S. (Intern), Lassnig, H. (Ekstern), Allerberger, F. (Ekstern), Springer, B. (Ekstern)
Number of pages: 1
Pages: 44
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Main Research Area: Technical/natural sciences

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Journal: International Journal of Infectious Diseases
Volume: 53
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Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2016): CiteScore 2.51 SJR 1.237 SNIP 1.232
Scopus rating (2015): CiteScore 2.24 SJR 1.2 SNIP 1.097
Scopus rating (2014): CiteScore 2.1 SJR 1.031 SNIP 1.11
Scopus rating (2013): CiteScore 2.32 SJR 1.03 SNIP 1.278
Scopus rating (2012): CiteScore 2.27 SJR 0.982 SNIP 1.485
Scopus rating (2011): CiteScore 1.68 SJR 0.769 SNIP 1.059
Scopus rating (2010): SJR 0.825 SNIP 1.283
Scopus rating (2009): SJR 0.843 SNIP 1.403
Scopus rating (2008): SJR 0.826 SNIP 1.184
Scopus rating (2007): SJR 0.987 SNIP 1.138
Scopus rating (2006): SJR 0.788 SNIP 0.996
Scopus rating (2005): SJR 0.723 SNIP 0.851
Scopus rating (2004): SJR 0.489 SNIP 0.75
Scopus rating (2003): SJR 0.445 SNIP 0.536
Scopus rating (2002): SJR 0.515 SNIP 0.675
Scopus rating (2001): SJR 0.565 SNIP 0.818
Scopus rating (2000): SJR 0.437 SNIP 0.672
Scopus rating (1999): SJR 0.271 SNIP 0.47
Original language: English
Electronic versions:
1_s2.0_S1201971216313340_main.pdf
DOIs:
10.1016/j.ijid.2016.11.116
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Source-ID: 2350140247
Effect of slaughterhouse and day of sample on the probability of a pig carcass being Salmonella-positive according to the Enterobacteriaceae count in the largest Brazilian pork production region

Sources of contamination of carcasses during slaughter include infected pigs as well as environmentally related sources. There are many microbial indicators that can be used in the processing of food to assess food hygiene and the safety of food processing. The presence of some microbial indicators can be viewed as a result of direct or indirect contamination of a food with fecal material. The presence of Enterobacteriaceae is often used as a hygiene indicator, as they are found both in the environment and in the intestine of warm-blooded animals. An association between Salmonella isolation and Enterobacteriaceae count (EC) on pre-chill carcasses has been described, however the impact of slaughterhouse and the day of sampling on the occurrence of Salmonella has not been previously investigated. To this end, mixed logistic regressions (MLRs) with random effects and fixed slopes were performed to assess the change in EC and its correlation with Salmonella occurrence using two data sets. The first describes the EC and Salmonella isolation in 60 pork carcasses in one slaughterhouse sampled at 11 different slaughter steps, including the carcass as a random effect. The second describes the EC and Salmonella isolation on 1150 pre-chill carcasses sampled in 13 slaughterhouses over 230 sampling days, and the model combined two random intercepts, slaughterhouse and date of sampling nested with slaughterhouse (day/slaughterhouse). Statistically significant associations (p <0.0001) between the log of the EC and Salmonella occurrence were found in all models. Nevertheless, although a strong association was found between Enterobacteriaceae and Salmonella contamination in pork carcasses, this association was not constant, given that there was a high variation in the probability of a carcass being positive for Salmonella according to the EC mainly between days of samples. The effect of the day of sampling on Salmonella prevalence was so large that the predictive value of the EC count for Salmonella isolation on a daily basis was compromised. It is possible that on some days batches with a high prevalence of Salmonella carriers shedding a high number of Salmonella were slaughtered. On these days, the potential for contamination/cross-contamination of carcasses will be so large that even hygienic slaughter, confirmed by the low EC on carcasses, will not be able to prevent the presence of Salmonella on some carcasses. The results of this study demonstrate that, despite the statistically significant association found, it may be difficult to predict when hygiene failure measured via EC actually indicates Salmonella contamination, and neither the inverse.

General information
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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Research Group for Risk-Benefit, Ministério da Agricultura, Universidade Federal do Rio Grande do Sul, Embrapa Suínos e Aves
Number of pages: 9
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Publication date: 2016
Main Research Area: Technical/natural sciences

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ISSN (Print): 0168-1605
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BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.97 SJR 1.462 SNIP 1.554
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.628 SNIP 1.694 CiteScore 4.02
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.501 SNIP 1.711 CiteScore 3.62
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.602 SNIP 1.86 CiteScore 3.8
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
For many societally important science-based decisions, data are inadequate, unreliable or non-existent, and expert advice is sought. In such cases, procedures for eliciting structured expert judgments (SEJ) are increasingly used. This raises questions regarding validity and reproducibility. This paper presents new findings from a large-scale international SEJ study intended to estimate the global burden of foodborne disease on behalf of WHO. The study involved 72 experts distributed over 134 expert panels, with panels comprising thirteen experts on average. Elicitations were conducted in five languages. Performance-based weighted solutions for target questions of interest were formed for each panel. These weights were based on individual expert's statistical accuracy and informativeness, determined using between ten and fifteen calibration variables from the experts' field with known values. Equal weights combinations were also calculated. The main conclusions on expert performance are: (1) SEJ does provide a science-based method for attribution of the global burden of foodborne diseases; (2) equal weighting of experts per panel increased statistical accuracy to acceptable levels, but at the cost of informativeness; (3) performance-based weighting increased informativeness, while retaining accuracy; (4) due to study constraints individual experts' accuracies were generally lower than in other SEJ studies, and (5) there was a negative correlation between experts' informativeness and statistical accuracy which attenuated as accuracy improved, revealing that the least accurate experts drive the negative correlation. It is shown, however, that performance-based weighting has the ability to yield statistically accurate and informative combinations of experts'
judgments, thereby offsetting this contrary influence. The present findings suggest that application of SEJ on a large scale is feasible, and motivate the development of enhanced training and tools for remote elicitation of multiple, internationally-dispersed panels.

**General information**

State: Published

Organisations: National Food Institute, Research Group for Genomic Epidemiology, University of Bristol, Delft University of Technology, Utrecht University

Authors: Aspinall, W. P. (Ekstern), Cooke, R. M. (Ekstern), Havelaar, A. H. (Ekstern), Hoffmann, S. (Ekstern), Hald, T. (Intern)

Number of pages: 14

Publication date: 2016

Main Research Area: Technical/natural sciences

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Journal: P L o S One

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BFI (2018): BFI-level 1

Web of Science (2018): Indexed yes

BFI (2017): BFI-level 1

Web of Science (2017): Indexed yes

BFI (2016): BFI-level 1

Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092

Web of Science (2016): Indexed yes

BFI (2015): BFI-level 1

Scopus rating (2015): SJR 1.414 SNIP 1.131 CiteScore 3.32

Web of Science (2015): Indexed yes

BFI (2014): BFI-level 1

Scopus rating (2014): SJR 1.545 SNIP 1.141 CiteScore 3.54

Web of Science (2014): Indexed yes

BFI (2013): BFI-level 1

Scopus rating (2013): SJR 1.74 SNIP 1.147 CiteScore 3.94

ISI indexed (2013): ISI indexed yes

Web of Science (2013): Indexed yes

BFI (2012): BFI-level 1

Scopus rating (2012): SJR 1.945 SNIP 1.142 CiteScore 4.15

ISI indexed (2012): ISI indexed yes

Web of Science (2012): Indexed yes

BFI (2011): BFI-level 1

Scopus rating (2011): SJR 2.369 SNIP 1.23 CiteScore 4.58

ISI indexed (2011): ISI indexed no

Web of Science (2011): Indexed yes

BFI (2010): BFI-level 1

Scopus rating (2010): SJR 2.631 SNIP 1.161

Web of Science (2010): Indexed yes

BFI (2009): BFI-level 1

Scopus rating (2009): SJR 2.473 SNIP 0.985

Web of Science (2009): Indexed yes

BFI (2008): BFI-level 1

Scopus rating (2008): SJR 2.323 SNIP 0.96

Web of Science (2008): Indexed yes

Scopus rating (2007): SJR 1.289 SNIP 0.525

Web of Science (2007): Indexed yes
Explanation and Elaboration Document for the STROBE-Vet Statement: Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary Extension

The STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement was first published in 2007 and again in 2014. The purpose of the original STROBE was to provide guidance for authors, reviewers and editors to improve the comprehensiveness of reporting; however, STROBE has a unique focus on observational studies. Although much of the guidance provided by the original STROBE document is directly applicable, it was deemed useful to map those statements to veterinary concepts, provide veterinary examples and highlight unique aspects of reporting in veterinary observational studies. Here, we present the examples and explanations for the checklist items included in the STROBE-Vet Statement. Thus, this is a companion document to the STROBE-Vet Statement Methods and process document, which describes the checklist and how it was developed.

General information
State: Published
Organisations: National Veterinary Institute, National Food Institute, Research Group for Genomic Epidemiology
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Main Research Area: Technical/natural sciences

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Journal: Zoonoses and Public Health
Volume: 63
Issue number: 8
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Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.3 SJR 1.068 SNIP 0.979
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.256 SNIP 1.103 CiteScore 2.27
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.026 SNIP 0.951 CiteScore 1.97
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.905 SNIP 1.039 CiteScore 2.24
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.049 SNIP 1.226 CiteScore 2.35
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.928 SNIP 1.129 CiteScore 2.05
Explanation and Elaboration Document for the STROBE-Vet Statement: Strengthening the Reporting of Observational Studies in Epidemiology-Veterinary Extension

The STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement was first published in 2007 and again in 2014. The purpose of the original STROBE was to provide guidance for authors, reviewers, and editors to improve the comprehensiveness of reporting; however, STROBE has a unique focus on observational studies. Although much of the guidance provided by the original STROBE document is directly applicable, it was deemed useful to map those statements to veterinary concepts, provide veterinary examples, and highlight unique aspects of reporting in veterinary observational studies. Here, we present the examples and explanations for the checklist items included in the STROBE-Vet statement. Thus, this is a companion document to the STROBE-Vet statement methods and process document (JVIM_14575 “Methods and Processes of Developing the Strengthening the Reporting of Observational Studies in Epidemiology—Veterinary (STROBE-Vet) Statement” undergoing proofing), which describes the checklist and how it was developed.

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State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology
Number of pages: 33
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Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Veterinary Internal Medicine
Volume: 30
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BFI (2018): BFI-level 2
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.
As we are approaching the twentieth anniversary of PulseNet, a network of public health and regulatory laboratories that has changed the landscape of foodborne illness surveillance through molecular subtyping, public health microbiology is undergoing another transformation brought about by so-called next-generation sequencing (NGS) technologies that have made whole-genome sequencing (WGS) of foodborne bacterial pathogens a realistic and superior alternative to traditional subtyping methods. Routine, real-time, and widespread application of WGS in food safety and public health is on the horizon. Technological, operational, and policy challenges are still present and being addressed by an international and multidisciplinary community of researchers, public health practitioners, and other stakeholders.
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 315S 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.
Heavy metal and disinfectant resistance genes among livestock-associated methicillin-resistant Staphylococcus aureus isolates

Livestock associated methicillin-resistant Staphylococcus aureus (LA-MRSA) has emerged in animal production worldwide. Most LA-MRSA in Europe belong to the clonal complex (CC)398. The reason for the LA-MRSA emergence is not fully understood. Besides antimicrobial agents used for therapy, other substances with antimicrobial activity applied in animal feed, including metal-containing compounds might contribute to their selection. Some of these genes have been found in various novel SCCmec cassettes. The aim of this study was to assess the occurrence of metal-resistance genes among a LA-S. aureus collection (n = 554, including 542 MRSA and 12 methicillin-susceptible S. aureus (MSSA)) isolated from livestock and food thereof. Most LA-MRSA isolates (76%) carried at least one metal-resistance gene. Among the LA-MRSA CC398 isolates (n = 456), 4.8%, 0.2%, 24.3% and 71.5% were positive for arsA (arsenic compounds), cadD (cadmium), copB (copper) and czrC (zinc/cadmium) resistance genes, respectively. In contrast, among the LA-MRSA non-CC398 isolates (n = 86), 1.2%, 18.6% and 16.3% were positive for the cadD, copB and czrC genes, respectively, and none were positive for arsA. Of the LA-MRSA CC398 isolates, 72% carried one metal-resistance gene, and the remaining
harboured two or more in different combinations. Differences between LA-MRSA CC398 and non-CC398 were statistically significant for \textit{arsA} and \textit{czeC}. The \textit{czeC} gene was almost exclusively found (98\%) in the presence of SCCmec V in both CC398 and non-CC398 LA-MRSA isolates from different sources. Regarding the LA-MSSA isolates (n = 12), some (n = 4) were also positive for metal-resistance genes. This study shows that genes potentially conferring metal-resistance are frequently present in LA-MRSA.

**General information**

State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Federal Institute for Risk Assessment, Istituto Zooprofilattico Sperimentale delle Regioni Lazio e Toscana, Ghent University, Universidad Complutense
Authors: Argudin, M. A. (Ekstern), Lauzat, B. (Ekstern), Kraushaar, B. (Ekstern), Alba, P. (Ekstern), Cavaco, L. (Intern), Butaye, P. (Ekstern), Porrero, M. C. (Ekstern), Battisti, A. (Ekstern), Tenhagen, B. (Ekstern), Fetsch, A. (Ekstern), Guerra, B. (Ekstern)
Pages: 88–95
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**

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- Web of Science (2018): Indexed yes
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- BFI (2016): BFI-level 2
- Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 2
- Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 2
- Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 2
- Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 2
- Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 2
- Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
- ISI indexed (2011): ISI indexed yes
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 2
- Scopus rating (2010): SJR 1.371 SNIP 1.476
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 2
- Scopus rating (2009): SJR 1.29 SNIP 1.472
- Web of Science (2009): Indexed yes
- BFI (2008): BFI-level 2
- Scopus rating (2008): SJR 1.169 SNIP 1.3
- Web of Science (2008): Indexed yes
- Scopus rating (2007): SJR 1.043 SNIP 1.322
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.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen
Authors: Knudsen, B. E. (Intern), Bergmark, L. (Intern), Munk, P. (Intern), Lukjancenko, O. (Intern), Priemé, A. (Ekstern), Aarestrup, F. M. (Intern), Pamp, S. J. (Intern)
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Main Research Area: Technical/natural sciences

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Web of Science (2017): Indexed yes
Web of Science (2016): Indexed yes
Original language: English
16S rRNA gene profiling, DNA isolation, Metagenomics, Microbial ecology, Microbiome, Next-generation sequencing
Influence of Thawing Methods and Storage Temperatures on Bacterial Diversity, Growth Kinetics, and Biogenic Amine Development in Atlantic Mackerel

Limited knowledge is currently available on the influence of fish thawing and subsequent storage conditions on bacterial growth kinetics, succession, and diversity alongside the production of biogenic amines. This study aimed to address these factors during the thawing and subsequent storage of mackerel. Thawing was either done fast in 18 degrees C water for 2 h or slowly at 30 degrees C overnight. Subsequent storage was at 30 degrees C (ambient) for 36 h and 2 to 5 degrees C (refrigerated) for 12 days. The cultivation methods used were total viable counts, hydrogen sulfide producing bacteria, and Pseudomonas. Maximum growth rate, population density, and lag time were fitted on the counts using the Baranyi model. The bacterial diversity and succession were based on sequencing of 16S rRNA amplicons, and biogenic amines were quantified on high-pressure liquid chromatography UV. The results show that lag time of hydrogen sulfide producing bacteria was significantly affected by both thawing methods, and further, the interaction between thawing and storage significantly affected the maximum growth rate of these bacteria. However, the maximum growth rate of Pseudomonas was higher during refrigerated storage compared with storage at ambient temperature. Total viable counts showed longer lag time and reduced growth rate under refrigerated storage. Higher bacterial diversity was correlated to slow thawing and storage at ambient temperature compared with slow thawing and refrigerated storage. Overall, Acinetobacter and Psychrobacter genera were the dominant bacterial populations. The amine levels were low and could not be differentiated along the thawing and storage approaches, despite a clear increase in bacterial load, succession, and diversity. This corresponded well with the low abundance of biogenic amine producing bacteria, with the exception of the genus Proteus, which was 8.6% in fast-thawed mackerel during storage at ambient temperature. This suggests that the decarboxylation potential is dependent on both microbial load and microbial community structure.
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.

**General information**

**State:** Published

**Organisations:** National Food Institute, Research Group for Genomic Epidemiology, Research Group for Diagnostic Engineering, University of Ilorin, University of Abuja, Institut Pasteur
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.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Department of Systems Biology
Authors: Roer, L. (Intern), Hendriksen, R. S. (Intern), Leekitcharoenphon, P. (Intern), Lukjancenko, O. (Intern), Kaas, R. S. (Intern), Hasman, H. (Intern), Aarestrup, F. M. (Intern)
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restriction-modification systems, evolution, Salmonella phylogenetic analysis, next-generation sequencing, whole-genome sequencing
Electronic versions:
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DOIs:
10.1128/mSystems.00009-16
Source: FindIt
Source-ID: 2305998441
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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 (I-2) 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.

**General information**

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Organisations: Department of Systems Biology, Center for Biological Sequence Analysis, National Food Institute, Research Group for Genomic Epidemiology, Kilimanjaro Christian Medical Centre, University of Copenhagen, KCRI Kilimanjaro Clinical Research Institute

Authors: Sonda, T. (Ekstern), Kumburu, H. (Ekstern), van Zwetselaar, M. (Ekstern), Alifrangis, M. (Ekstern), Lund, O. (Intern), Kibiki, G. (Ekstern), Aarestrup, F. M. (Intern)

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Scopus rating (2013): SJR 0.601 SNIP 0.997 CiteScore 2.2

Original language: English

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**Methods and processes of developing the Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary (STROBE-Vet) statement**

Background: Reporting of observational studies in veterinary research presents challenges that often are not addressed in published reporting guidelines.Objective: To develop an extension of the STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement that addresses unique reporting requirements for observational studies in veterinary medicine related to health, production, welfare, and food safety Design: Consensus meeting of experts.Setting: Mississauga, Canada.Participants: Seventeen experts from North America, Europe, and Australia.Methods: Experts, completed a pre-meeting survey about whether items in the STROBE statement should be added to or modified to address unique issues related to observational studies in animal species with health, production, welfare, or food safety outcomes. During the meeting, each STROBE item was discussed to determine whether or not re-wording was recommended and whether additions were warranted. Anonymous voting was used to determine consensus.Results: Six items required no modifications or additions. Modifications or additions were made to the STROBE items 1 (title and abstract), 3 (objectives), 5 (setting), 6 (participants), 7 (variables), 8 (data sources-measurement), 9 (bias), 10 (study size), 12 (statistical methods), 13 (participants), 14 (descriptive data), 15 (outcome data), 16 (main results), 17 (other analyses), 19 (limitations), and 22 (funding).Conclusion: The methods and processes used were similar to those used for other extensions of the STROBE statement. The use of this STROBE statement extension should improve reporting of observational studies in veterinary research by recognizing unique features of observational studies involving food-producing and companion animals, products of animal origin, aquaculture, and wildlife.
Methods and processes of developing the Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary (STROBE-Vet) statement

Background: The reporting of observational studies in veterinary research presents many challenges that often are not adequately addressed in published reporting guidelines. Objective: To develop an extension of the STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement that addresses unique reporting requirements for observational studies in veterinary medicine related to animal health, production, welfare, and food safety. Design: A consensus meeting of experts was organized to develop an extension of the STROBE statement to address observational studies in veterinary medicine with respect to animal health, animal production, animal welfare, and food safety outcomes. Setting: Consensus meeting May 11–13, 2014 in Mississauga, Ontario, Canada. Participants: Seventeen experts from North America, Europe, and Australia attended the meeting. The experts were epidemiologists and biostatisticians, many of whom hold or have held editorial positions with relevant journals. Methods: Prior to the meeting, 19 experts completed a survey about whether they felt any of the 22 items of the STROBE statement should be modified and if items should be added to address unique issues related to observational studies in animal species with health, production, welfare, or food safety outcomes. At the meeting, the participants were provided with the survey responses and relevant literature concerning the reporting of veterinary observational studies. During the meeting, each STROBE item was discussed to determine whether or not re-wording was recommended, and whether additions were warranted. Anonymous voting was used to determine whether there was consensus for each item change or addition.

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Scopus rating (2016): CiteScore 2.2 SJR 1.185 SNIP 1.329
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.26 SNIP 1.23 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.267 SNIP 1.421 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.247 SNIP 1.552 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Methods and Processes of Developing the Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary (STROBE-Vet) Statement

**Background:** The reporting of observational studies in veterinary research presents many challenges that often are not adequately addressed in published reporting guidelines. **Objective:** To develop an extension of the STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement that addresses unique reporting requirements for observational studies in veterinary medicine related to health, production, welfare, and food safety. **Design:** A consensus meeting of experts was organized to develop an extension of the STROBE statement to address observational studies in veterinary medicine with respect to animal health, animal production, animal welfare, and food safety outcomes. **Setting:** Consensus meeting May 11–13, 2014 in Mississauga, Ontario, Canada. **Participants:** Seventeen experts from North America, Europe, and Australia attended the meeting. The experts were epidemiologists and biostatisticians, many of whom hold or have held editorial positions with relevant journals. **Methods:** Prior to the meeting, 19 experts completed a survey about whether they felt any of the 22 items of the STROBE statement should be modified and if items should be added to address unique issues related to observational studies in animal species with health, production, welfare, or food safety outcomes. At the meeting, the participants were provided with the survey responses and relevant literature concerning the reporting of veterinary observational studies. During the meeting, each STROBE item was discussed to determine whether or not re-wording was recommended, and whether additions were warranted. Anonymous voting was used to determine whether there was consensus for each item change or addition. **Results:** The
consensus was that six items needed no modifications or additions. Modifications or additions were made to the STROBE items numbered: 1 (title and abstract), 3 (objectives), 5 (setting), 6 (participants), 7 (variables), 8 (data sources/measurement), 9 (bias), 10 (study size), 12 (statistical methods), 13 (participants), 14 (descriptive data), 15 (outcome data), 16 (main results), 17 (other analyses), 19 (limitations), and 22 (funding). Limitation: Published literature was not always available to support modification to, or inclusion of, an item. Conclusion: The methods and processes used in the development of this statement were similar to those used for other extensions of the STROBE statement. The use of this extension to the STROBE statement should improve the reporting of observational studies in veterinary research related to animal health, production, welfare, or food safety outcomes by recognizing the unique features of observational studies involving food-producing and companion animals, products of animal origin, aquaculture, and wildlife.

General information
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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Ontario Veterinary College, Iowa State University, University of Prince Edward Island, Cornell University, University of Bern, University of Southern Denmark, University of Copenhagen, Royal Veterinary College, Center for Food Safety and Applied Nutrition, University of Saskatchewan, University of Sydney
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Web of Science (2017): Indexed Yes
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Scopus rating (2016): SJR 1.354 SNIP 1.359 CiteScore 2.06
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.206 SNIP 1.247 CiteScore 2.09
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.261 SNIP 1.494 CiteScore 2.08
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.529 SNIP 1.681 CiteScore 2.24
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.301 SNIP 1.524 CiteScore 2.08
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.598 SNIP 1.502 CiteScore 1.98
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.611 SNIP 1.693
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.479 SNIP 1.589
Methods and Processes of Developing the Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary (STROBE-Vet) Statement

The reporting of observational studies in veterinary research presents many challenges that often are not adequately addressed in published reporting guidelines. A consensus meeting of experts was organized to develop an extension of the STROBE statement to address observational studies in veterinary medicine with respect to animal health, animal production, animal welfare and food safety outcomes. The consensus meeting was held 11-13 May 2014 in Mississauga, Ontario, Canada. Seventeen experts from North America, Europe and Australia attended the meeting. The experts were epidemiologists and biostatisticians, many of whom hold or have held editorial positions with relevant journals. Prior to the meeting, 19 experts completed a survey about whether they felt any of the 22 items of the STROBE statement should be modified and whether items should be added to address unique issues related to observational studies in animal species with health, production, welfare or food safety outcomes. At the meeting, the participants were provided with the survey responses and relevant literature concerning the reporting of veterinary observational studies. During the meeting, each STROBE item was discussed to determine whether or not re-wording was recommended, and whether additions were warranted. Anonymous voting was used to determine whether there was consensus for each item change or addition. The consensus was that six items needed no modifications or additions. Modifications or additions were made to the STROBE items numbered as follows: 1 (title and abstract), 3 (objectives), 5 (setting), 6 (participants), 7 (variables), 8 (data sources/measurement), 9 (bias), 10 (study size), 12 (statistical methods), 13 (participants), 14 (descriptive data), 15 (outcome data), 16 (main results), 17 (other analyses), 19 (limitations) and 22 (funding). Published literature was not always available to support modification to, or inclusion of, an item. The methods and processes used in the development of this statement were similar to those used for other extensions of the STROBE statement. The use of this extension to the STROBE statement should improve the reporting of observational studies in veterinary research related to animal health, production, welfare or food safety outcomes by recognizing the unique features of observational studies involving food-producing and companion animals, products of animal origin, aquaculture and wildlife.

General information

State: Published
Organisations: National Veterinary Institute, National Food Institute, Research Group for Genomic Epidemiology, University of Guelph, Iowa State University, University of Prince Edward Island, Cornell University, University of Bern, University of Southern Denmark, Ontario Veterinary College, Royal Veterinary College, Center for Food Safety and Applied Nutrition, University of Saskatchewan, University of Sydney, University of Copenhagen
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Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.3 SJR 1.068 SNIP 0.979
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.256 SNIP 1.103 CiteScore 2.27
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.026 SNIP 0.951 CiteScore 1.97
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.905 SNIP 1.039 CiteScore 2.24
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.049 SNIP 1.226 CiteScore 2.35
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.928 SNIP 1.129 CiteScore 2.05
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.863 SNIP 1.147
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.773 SNIP 1.165
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.606 SNIP 0.883
Scopus rating (2007): SJR 0.71 SNIP 1.083
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.64 SNIP 0.911
Scopus rating (2005): SJR 0.682 SNIP 0.906
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.554 SNIP 0.957
Scopus rating (2003): SJR 0.332 SNIP 0.588
Scopus rating (2002): SJR 0.388 SNIP 0.685
Scopus rating (2001): SJR 0.377 SNIP 0.682
Scopus rating (2000): SJR 0.36 SNIP 0.702
Scopus rating (1999): SJR 0.333 SNIP 0.633
Original language: English
Reporting guidelines, animal, observational study, veterinary
Methods and Processes of Developing the Strengthening the Reporting of Observational Studies in Epidemiology—Veterinary (STROBE-Vet) Statement

Reporting of observational studies in veterinary research presents challenges that often are not addressed in published reporting guidelines. Our objective was to develop an extension of the STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement that addresses unique reporting requirements for observational studies in veterinary medicine related to health, production, welfare, and food safety. We conducted a consensus meeting with 17 experts in Mississauga, Canada. Experts completed a premeeting survey about whether items in the STROBE statement should be modified or added to address unique issues related to observational studies in animal species with health, production, welfare, or food safety outcomes. During the meeting, each STROBE item was discussed to determine whether or not rewording was recommended, and whether additions were warranted. Anonymous voting was used to determine consensus. Six items required no modifications or additions. Modifications or additions were made to the STROBE items 1 (title and abstract), 3 (objectives), 5 (setting), 6 (participants), 7 (variables), 8 (data sources and measurement), 9 (bias), 10 (study size), 12 (statistical methods), 13 (participants), 14 (descriptive data), 15 (outcome data), 16 (main results), 17 (other analyses), 19 (limitations), and 22 (funding). The methods and processes used were similar to those used for other extensions of the STROBE statement. The use of this STROBE statement extension should improve reporting of observational studies in veterinary research by recognizing unique features of observational studies involving food-producing and companion animals, products of animal origin, aquaculture, and wildlife.

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State: Published
Organisations: National Veterinary Institute, National Food Institute, Research Group for Genomic Epidemiology, University of Guelph, Iowa State University, University of Prince Edward Island, Cornell University, University of Bern, University of Southern Denmark, University of Copenhagen, University of London, U.S. Food and Drug Administration, University of Saskatchewan, University of Sydney
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.68 SJR 0.759 SNIP 0.82
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.96 SNIP 1.031 CiteScore 2.03
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.91 SNIP 0.957 CiteScore 1.94
Web of Science (2014): Indexed yes
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Non-plastic food contact materials: classification of chemicals using predictive models

General information

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Research Group for Analytical Food Chemistry, Istituto di Ricerche Farmacologiche Mario Negri
Authors: Boriani, E. (Intern), Pieke, E. N. (Intern), Wedebye, E. B. (Intern), Benfenati, E. (Ekstern), Granby, K. (Intern), Hald, T. (Intern)
Number of pages: 1
On the need for integrating LCA into decision making

The need for sustainable solutions has gained attention both in academia and industry research due to increasing demands of human beings, which are incompatible with limitations in resources availability. Several methods, such as Life Cycle Assessment (LCA), were developed in the past decades to assess the environmental profile of products and services. However, when decision makers have several alternatives at hand to solve a problem, environmental performance is not the only criterion for choosing the best alternative. Other criteria such as risks and economical costs and benefits that are associated with the alternatives will also influence the final choice. Sometimes the most environmentally sustainable alternative may not be the safest or cheapest one. How to make a balanced decision considering environmental performance together with other criteria is not straightforward.

Decision analysis is broadly used to help decision makers identify the best solution among alternatives. The decision is based on expected utility generation, which incorporates consequences (or impacts) associated with each alternative. Depending on the research field and goal of the study, the included consequences can be e.g. environmental impacts, property damages from natural hazards and/or human health impacts. We examined the current decision analysis practice as it is applied in different research fields. The review shows that generally environmental impacts are considered less often than the other consequences. Meanwhile, LCA has been applied in many research fields to assess a wide range of environmental impacts associated with products or services. There is a huge potential for integrating LCA into other decisions analysis tools to include assessments of the environmental profile of alternatives. This will provide the possibility of systematical inclusion of environmental considerations in the decision making process, thus facilitating a more holistic decision. However, due to different scopes and purposes of LCA and other decision analysis tools, the integration is not straightforward. The lack of consistency in e.g. system boundaries and handling of uncertainty needs to be carefully managed.

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, University Paris-Est Anses  
Authors: Henri, C. (Ekstern), Félix, B. (Ekstern), Guillier, L. (Ekstern), Leekitcharoenphon, P. (Intern), Michelon, D. (Ekstern), Mariet, J. (Ekstern), Aarestrup, F. M. (Intern), Mistou, M. (Ekstern), Hendriksen, R. S. (Intern), Roussel, S. (Ekstern)  
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Quantitative Microbiological Risk Assessment and Source Attribution for Salmonella: Taking it Further

General information
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Authors: Snary, E. L. (Ekstern), Swart, A. N. (Ekstern), Hald, T. (Intern)
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Web of Science (2016): Indexed yes
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Scopus rating (2015): SJR 1.305 SNIP 1.521 CiteScore 2.51
BFI (2014): BFI-level 1
Recipient Determinants Affecting Conjugational Promiscuity in 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 kolistin 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 kontrolleer spredningen af antibiotika resistens. Plasmider er et af de mobile elementer kan udveksle DNA mellem bakterier, og er en udbredt mægler i spredningen af antibiotika resistens fra en donor til en recipient.

recipient gener hos Salmonella enterica der har betydning for god eller dårlig udveksling af DNA. For undertype
Salmonella Enteritidis er 33 gen kandidater ved at blive yderligere undersøgt og verifieret.
Dette Ph.d. studie har øget viden indenfor RM systemer, deres indflydelse på overførsel af DNA via celle-celle kontakt, og
deres betydning i udviklingen af bakterier. Yderligere har studiet indikeret at der findes gener hos modtageren af DNA,
 som kan kontrollere overførslen. Ph.d. studiet efterlader store muligheder for at finde gener der er involveret i optaget af
plasmider og antibiotika resistens.

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Authors: Roer, L. (Intern), Aarestrup, F. M. (Intern), Hasman, H. (Intern)
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Research Synthesis Methods in an Age of Globalized Risks: Lessons from the Global Burden of Foodborne Disease
Expert Elicitation
We live in an age that increasingly calls for national or regional management of global risks. This article discusses the
contributions that expert elicitation can bring to efforts to manage global risks and identifies challenges faced in conducting
expert elicitation at this scale. In doing so it draws on lessons learned from conducting an expert elicitation as part of the
World Health Organizations (WHO) initiative to estimate the global burden of foodborne disease; a study commissioned by the
Foodborne Disease Epidemiology Reference Group (FERG). Expert elicitation is designed to fill gaps in data and
research using structured, transparent methods. Such gaps are a significant challenge for global risk modeling.
Experience with the WHO FERG expert elicitation shows that it is feasible to conduct an expert elicitation at a global scale,
but that challenges do arise, including: defining an informative, yet feasible geographical structure for the elicitation;
defining what constitutes expertise in a global setting; structuring international, multidisciplinary expert panels; and
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Authors: Hald, T. (Intern), Angulo, F. (Ekstern), Bin Hamzah, W. M. (Ekstern), Bellinger, D. (Ekstern), Black, R. (Ekstern),
de Silva, N. (Ekstern), Doepfer, D. (Ekstern), Havelaar, A. (Ekstern), Gibb, H. (Ekstern), Kasuga, F. (Ekstern), Lake, R.
(Ekstern), Rokni, M. B. (Ekstern), Speybroeck, N. (Ekstern), Aspinall, W. (Ekstern), Cooke, R. (Ekstern), Hoffmann, S.
(Ekstern), DeVleesschauwer, B. (Ekstern), Pires, S. M. (Intern)
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Selective enrichment of ESBL, AmpC and carbapenemase producing E. coli in meat and cecal samples - additional validation for poultry samples

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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Authors: Cavaco, L. (Intern), Hendriksen, R. S. (Intern), Agersø, Y. (Intern), Svendsen, C. A. (Intern), Nielsen, H. (Ekstern), Guerra, B. (Ekstern), Peran, R. (Ekstern), Hasman, H. (Ekstern)
Number of pages: 1
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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.
Spatial patterns of Antimicrobial Resistance Genes in Danish Pig Farms

Samples from 687 Danish pig farms were collected at five finisher slaughterhouses in February and March 2015. Faecal samples from five pigs per farm were collected randomly at the slaughter line and pooled into one sample per farm. DNA was extracted from the pooled samples and the level of seven antimicrobial resistance genes, ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W), was quantified by a high-throughput qPCR. It was evaluated whether the sample method resulted in a study population representative of Danish pig farms with finishers where it was found that the study population was biased towards farms having more finisher and a higher productivity. Spatial cluster analyses were performed in SaTScan®. The results showed significant spatial clusters for ermF, ermB, sulII and tet(W) whereas no significant clusters were found for sulI, tet(M) and tet(O).

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The 18th EURL-AR Proficiency Test - Enterococci, Staphylococci and E. coli 2015

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Authors: Cavaco, L. (Intern), Karlsmose Pedersen, S. (Intern), Hendriksen, R. S. (Intern), Aarestrup, F. M. (Intern)
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The 19th EURL-AR Proficiency Test Salmonella, Campylobacter and genotypic characterisation 2015

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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Authors: Karlsmose Pedersen, S. (Intern), Cavaco, L. (Intern), Hendriksen, R. S. (Intern), Aarestrup, F. M. (Intern)
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The 1st EURL-AR Proficiency Test on selective isolation of E. coli with presumptive ESBL or AmpC phenotypes from meat or caecal samples - 2015

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Authors: Cavaco, L. (Intern), Karlsmose Pedersen, S. (Intern), Hendriksen, R. S. (Intern), Aarestrup, F. M. (Intern)
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The External Quality Assurance System of the WHO Global Foodborne Infections Network, 2014

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

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Authors: Hendriksen, R. S. (Intern), Karlsmose Pedersen, S. (Intern), Roer, L. (Intern), Frimann, J. M. (Intern), Aarestrup, F. M. (Intern)
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The impact of farmers’ participation in field trials in creating awareness and stimulating compliance with the World Health Organization’s farm-based multiple-barrier approach

The results of a study aimed as assessing the extent to which urban vegetable farmers’ participation in field trials can impact on their awareness and engender compliance with the World Health Organization’s farm-based multiple-barrier approach are presented in this paper. Both qualitative and quantitative approaches have been used in this paper. One hundred vegetable farmers and four vegetable farmers’ associations in the Kumasi Metropolis in Ghana were covered. The individual farmers were grouped into two, namely: (1) participants and (2) non-participants of the farm-based multiple-barrier approach field trials. The results of the study show that participation in the field trials has statistically significant effects on farmers’ awareness of the farm-based multiple-barrier approach. Compliance has, however, been undermined by the farmers’ perception that the cost of compliance is more that the benefits. Policy tools that can address these constraints have been recommended in the paper.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, DHI Denmark, Kwame Nkrumah University of Science and Technology
Authors: Amponsah, O. (Ekstern), Vigre, H. (Intern), Schou, T. W. (Ekstern), Braimah, I. (Ekstern), Abaidoo, R. C. (Ekstern)
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Main Research Area: Technical/natural sciences

Publication information
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.
The policy implications of urban open space commercial vegetable farmers' willingness and ability to pay for reclaimed water for irrigation in Kumasi, Ghana

The acute waste management problems, coupled with the proliferation of small scale industries in many developing countries, make low quality water treatment before use inevitable in the long run. These industries have the potential to discharge effluent containing chemicals and heavy metals into the environment. The indiscriminate use of pharmaceutical products by households in many of these countries is another source of health concern. Low quality water treatment in these countries has however been hampered by the high cost of infrastructure provision and maintenance. Cost-sharing among stakeholders appears to be a promising strategy to finance and maintain the wastewater treatment infrastructure. In this study therefore, the willingness and ability of urban open space commercial vegetable farmers to pay for reclaimed water for irrigation purposes has been assessed. One hundred open space commercial vegetable farmers and four vegetable farmers' associations were selected and interviewed in Kumasi in Ghana using semi-structured interview schedules and interview guides respectively. The results of the study show that approximately three out of every five vegetable farmers were willing to pay for reclaimed water for irrigation. The results further show that the probability of being willing to pay by farmers who agreed that the current water they used for irrigation was harmful is approximately 5.3 times greater than that of those who did not. The analysis of the farmers' ability to pay revealed that all the farmers would be capable of paying for reclaimed water at a price of US$0.11/m³. This has implications for land tenure security and vegetable consumers' willingness to pay higher prices for the produce.
Two listeria outbreaks caused by smoked fish consumption using whole-genome sequencing for outbreak investigations

Listeria monocytogenes may contaminate and persist in food production facilities and cause repeated, seemingly sporadic, illnesses over extended periods of time. We report on the investigation of two such concurrent outbreaks. We compared patient isolates and available isolates from foods and food production facilities by use of whole-genome sequencing and subsequent multilocus sequence type and single nucleotide polymorphism analysis. Outbreak cases shared outbreak strains, defined as Listeria monocytogenes isolates belonging to the same sequence type with fewer than five single nucleotide polymorphism differences. We performed routine food consumption interviews of L. monocytogenes patients and compared outbreak cases with sporadic cases. Two outbreaks were defined, each consisting of ten outbreak cases in the period 2013-15. Seven outbreak cases and a fetus in gestational week 38 died. Listeria monocytogenes isolates from cold smoked or gravad fish products or their two respective production environments were repeatedly found to belong to the outbreak strains. Outbreak cases more often than sporadic cases stated that they consumed the relevant fish products, odds ratio 10.7. Routine collection and typing of food isolates was key to solving the outbreaks. Furthermore, these outbreaks illustrate the value of whole-genome sequencing for outbreak definition and investigation. Whole-genome sequencing combined with epidemiological investigations provided the discriminatory power to recognize low-intensity, extended time-period outbreaks and link them to food products from two different contaminated production facilities with sufficient strength for food authorities to intervene on. Cold smoked and gravad fish constitute risk products and may be responsible for more listeriosis cases than previously recognized.

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Organisations: National Food Institute, Research Group for Analytical and Predictive Microbiology, Research Group for Genomic Epidemiology, Statens Serum Institut, Danish Veterinary and Food Administration
Authors: Gillesberg Lassen, S. (Ekstern), Ethelberg, S. (Ekstern), Björkman, J. T. (Ekstern), Jensen, T. (Ekstern), Serensen, G. (Intern), Kvistholm Jensen, A. (Ekstern), Muller, L. (Ekstern), Nielsen, E. M. (Ekstern), Mølbak, K. (Ekstern)
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Variation in the effect of carcass decontamination impacts the risk for consumers

- The variation of decontamination has an effect on consumer risk reduction.
- The effect of variation on risk is lower when mean log reduction is high.
- The effect of variation on risk also depends on initial carcass contamination.
- The effect of decontamination should be expressed as consumer risk reduction.

General information
Whole genome sequencing as a tool for phylogenetic analysis of clinical strains of Mitis group streptococci

Identification of Mitis group streptococci (MGS) to the species level is challenging for routine microbiology laboratories. Correct identification is crucial for the diagnosis of infective endocarditis, identification of treatment failure, and/or infection relapse. Eighty MGS from Danish patients with infective endocarditis were whole genome sequenced. We compared the phylogenetic analyses based on single genes (recA, sodA, gdh), multigene (MLSA), SNPs, and core-genome sequences. The six phylogenetic analyses generally showed a similar pattern of six monophyletic clusters, though a few differences were observed in single gene analyses. Species identification based on single gene analysis showed their limitations when more strains were included. In contrast, analyses incorporating more sequence data, like MLSA, SNPs and core-genome analyses, provided more distinct clustering. The core-genome tree showed the most distinct clustering.

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Organisations: Department of Systems Biology, Center for Biological Sequence Analysis, Department of Bio and Health Informatics, National Food Institute, Research Group for Genomic Epidemiology, Slagelse Hospital, University of Copenhagen, Roskilde University, Odense University Hospital, Vejle Hospital, Odense Universitetshospital
Authors: Rasmussen, L. H. (Ekstern), Dargis, R. (Ekstern), Iversen, K. H. (Intern), Christensen, J. J. (Ekstern), Skovgaard, O. (Ekstern), Justesen, U. S. (Ekstern), Rosenvinge, F. S. (Ekstern), Moser, C. (Ekstern), Lukjancenko, O. (Intern), Rasmussen, S. (Intern), Nielsen, X. C. (Ekstern)
Number of pages: 11
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Volume: 35
Issue number: 10
Whole-genome Sequencing Used to Investigate a Nationwide Outbreak of Listeriosis Caused by Ready-to-eat Delicatessen Meat, Denmark, 2014

Listeriosis is a serious foodborne infection. Outbreaks of listeriosis occur rarely, but have often proved difficult to solve. In June 2014, we detected and investigated a listeriosis outbreak in Denmark using patient interviews and whole-genome sequencing (WGS). We performed WGS on Listeria monocytogenes isolates from patients and available isolates from ready-to-eat foods and compared them using single-nucleotide polymorphism (SNP) analysis. Case patients had L. monocytogenes with ≤3 SNPs (the outbreak strain) isolated in September 2013-December 2014. Through interviews, we established case patients’ food and clinical histories. Food production facilities were inspected and sampled, and we performed trace-back/trace-forward of food delivery chains. In total, 41 cases were identified; 17 deaths occurred (41%).
An isolate from a delicatessen meat (spiced meat roll) from company A was identical to the outbreak strain. Half of the patients were infected while hospitalized/institutionalized; institutions were supplied food by company A. The outbreak strain was repeatedly isolated from further samples taken within this company and within companies in its distribution chain. Products from company A were traced and recalled from >6000 food establishments, after which the outbreak ended. Ready-to-eat spiced meat roll from a single production facility caused this outbreak. The product, served sliced and cold, is popular among the elderly; serving it at hospitals probably contributed to the high case-fatality rate. WGS used for patient isolates and isolates from food control inspections, coupled with routine epidemiological follow-up, was instrumental in swiftly locating the source of infections, preventing further illnesses and deaths.

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Organisations: National Food Institute, Research Group for Diagnostic Engineering, Research Group for Genomic Epidemiology, Research Group for Microbial Food Safety and Quality, Statens Serum Institut, Department of Danish Veterinary and Food Administration, State Serum Institute
Authors: Kvistholm Jensen, A. (Ekstern), Nielsen, E. M. (Ekstern), Björkman, J. T. (Ekstern), Jensen, T. (Ekstern), Müller, L. (Ekstern), Persson, S. (Ekstern), Bjerager, G. (Ekstern), Perge, A. (Ekstern), Krause, T. G. (Ekstern), Kiil, K. (Ekstern), Sørensen, G. (Intern), Andersen, J. K. (Intern), Mølbak, K. (Ekstern), Ethelberg, S. (Ekstern)
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Scopus rating (2014): SJR 5.132 SNIP 3.43 CiteScore 6.11
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Scopus rating (2013): SJR 4.651 SNIP 3.303 CiteScore 6.37
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Scopus rating (2012): SJR 4.482 SNIP 3.201 CiteScore 6.25
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Web of Science (2012): Indexed yes
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BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.944 SNIP 3.115
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 3.4 SNIP 2.926
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Scopus rating (2008): SJR 3.397 SNIP 2.6
Scopus rating (2007): SJR 2.927 SNIP 2.45
World Health Organization Estimates of the Relative Contributions of Food to the Burden of Disease Due to Selected Foodborne Hazards: A Structured Expert Elicitation

Background
The Foodborne Disease Burden Epidemiology Reference Group (FERG) was established in 2007 by the World Health Organization (WHO) to estimate the global burden of foodborne diseases (FBDs). This estimation is complicated because most of the hazards causing FBD are not transmitted solely by food; most have several potential exposure routes consisting of transmission from animals, by humans, and via environmental routes including water. This paper describes an expert elicitation study conducted by the FERG Source Attribution Task Force to estimate the relative contribution of food to the global burden of diseases commonly transmitted through the consumption of food.

Methods and Findings
We applied structured expert judgment using Cooke's Classical Model to obtain estimates for 14 subregions for the relative contributions of different transmission pathways for eleven diarrheal diseases, seven other infectious diseases and one chemical (lead). Experts were identified through international networks followed by social network sampling. Final selection of experts was based on their experience including international working experience. Enrolled experts were scored on their ability to judge uncertainty accurately and informatively using a series of subject-matter specific 'seed' questions whose answers are unknown to the experts at the time they are interviewed. Trained facilitators elicited the 5th, and 50th and 95th percentile responses to seed questions through telephone interviews. Cooke's Classical Model uses responses to the seed questions to weigh and aggregate expert responses. After this interview, the experts were asked to provide 5th, 50th, and 95th percentile estimates for the 'target' questions regarding disease transmission routes. A total of 72 experts were enrolled in the study. Ten panels were global, meaning that the experts should provide estimates for all 14 subregions, whereas the nine panels were subregional, with experts providing estimates for one or more subregions, depending on their experience in the region. The size of the 19 hazard-specific panels ranged from 6 to 15 persons with several experts serving on more than one panel. Pathogens with animal reservoirs (e.g. non-typhoidal Salmonella spp. and Toxoplasma gondii) were in general assessed by the experts to have a higher proportion of illnesses attributable to food than pathogens with mainly a human reservoir, where human-to-human transmission (e.g. Shigella spp. and Norovirus) or waterborne transmission (e.g. Salmonella Typhi and Vibrio cholerae) were judged to dominate. For many pathogens, the foodborne route was assessed relatively more important in developed subregions than in developing subregions. The main exposure routes for lead varied across subregions, with the foodborne route being assessed most important only in two subregions of the European region.

Conclusions
For the first time, we present worldwide estimates of the proportion of specific diseases attributable to food and other major transmission routes. These findings are essential for global burden of FBD estimates. While gaps exist, we believe the estimates presented here are the best current source of guidance to support decision makers when allocating resources for control and intervention, and for future research initiatives.
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Accounting for Campylobacter biology and epidemiology in source attribution modelling

General information
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Diarrhoeal diseases are major contributors to the global burden of disease, particularly in children. However, comprehensive estimates of the incidence and mortality due to specific aetiologies of diarrhoeal diseases are not available. The objective of this study is to provide estimates of the global and regional incidence and mortality of diarrhoeal diseases caused by nine pathogens that are commonly transmitted through foods. We abstracted data from systematic reviews and, depending on the overall mortality rates of the country, applied either a national incidence estimate approach or a modified Child Health Epidemiology Reference Group (CHERG) approach to estimate the aetiology-specific incidence and mortality of diarrhoeal diseases, by age and region. The nine diarrhoeal diseases assessed caused an estimated 1.8 billion (95% uncertainty interval [UI] 1.1-3.3 billion) cases and 599,000 (95% UI 472,000-802,000) deaths worldwide in 2010. The largest number of cases were caused by norovirus (677 million; 95% UI 468-1,153 million), enterotoxigenic Escherichia coli (ETEC) (233 million; 95% UI 154-380 million), Shigella spp. (188 million; 95% UI 94-379 million) and Giardia lamblia (179 million; 95% UI 125-263); the largest number of deaths were caused by norovirus (213,515; 95% UI 171,783-266,561), enteropathogenic E. coli (121,455; 95% UI 103,657-143,348), ETEC (73,041; 95% UI 55,474-96,984) and Shigella (64,993; 95% UI 48,966-92,357). There were marked regional differences in incidence and mortality for these nine diseases. Nearly 40% of cases and 43% of deaths caused by these nine diarrhoeal diseases occurred in children under five years of age. Diarrhoeal diseases caused by these nine pathogens are responsible for a large disease burden, particularly in children. These aetiology-specific burden estimates can inform efforts to reduce diarrhoeal diseases caused by these nine pathogens commonly transmitted through foods.
An OXA-48-producing Escherichia coli isolated from a Danish patient with no hospitalization abroad

Carbapenemase-producing organisms are disseminating globally and are now emerging as a worrying threat in Scandinavia. Before August 2013, OXA-48-producing organisms had not been detected in Danish patients. Here we report the isolation of an ST746 OXA-48-producing Escherichia coli with the plasmid pOXA-48a carrying the bla(OXA-48) gene isolated from a Danish patient without history of hospitalization abroad. The patient reported tourist travel to Egypt and Turkey. The potential acquisition of carbapenemase-producing organisms by ingestion of contaminated food is discussed.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Aarhus University Hospital
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Assessing low quality water use policy framework: Case study from Ghana

We bought to understand the factors that have undermined the effective implementation of the low quality water reuse provision in Ghana’s Irrigation Policy. Two Strategic Environmental Assessment tools (i.e. compatibility matrix and sustainability test) were used for the policy analyses. The analyses identified neither conflicts nor sustainability issues which could undermine the effective implementation of the policy in Ghana. Rather, its effective implementation was found to be the result of the lack of supportive legislation, regulations and guidelines. Furthermore, most of the institutions, which have been identified as key stakeholders for the policy implementation, not only lack the commitment to implement the policy but also perceive low quality water reuse as a practice that can endanger public health. We conclude that effective implementation of the low quality water reuse policy requires an integration of the policy into the broader water resources management context supported with legislation and regulations which spell out clearly institutional responsibilities, and rewards and punishments for compliance or otherwise. (C) 2015 Elsevier B.V. All rights reserved.
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, bla(CTX-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.

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BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.07 SNIP 0.756
Web of Science (2010): Indexed yes
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Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.067 SNIP 0.827
Scopus rating (2007): SJR 1.095 SNIP 0.859
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.091 SNIP 0.851
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.984 SNIP 0.798
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Scopus rating (2004): SJR 0.989 SNIP 0.723
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Web of Science (2002): Indexed yes
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Web of Science (2001): Indexed yes
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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 13 MSSA and 5 MRSA isolates belonging to 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
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Organisations: National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen
Authors: Seier-Petersen, M. A. (Intern), Nielsen, L. N. (Intern), Ingmer, H. (Ekstern), Aarestrup, F. M. (Intern), Agersø, Y. (Intern)
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BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.945 SNIP 0.999 CiteScore 2.48
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Scopus rating (2013): SJR 1.252 SNIP 1.144 CiteScore 2.87
ISI indexed (2013): ISI indexed yes
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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, Myxinidin, 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

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Authors: Ebbensgaard, A. E. (Intern), Mordhorst, H. (Intern), Overgaard, M. T. (Ekstern), Nielsen, C. G. (Ekstern), Aarestrup, F. M. (Intern), Hansen, E. B. (Intern), Mergaert, P. (ed.) (Ekstern)
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DANMAP 2014 - Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark
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.
Development of Spatial Distribution Patterns by Biofilm Cells

Confined spatial patterns of microbial distribution are prevalent in nature, such as in microbial mats, soil communities, and water stream biofilms. The symbiotic two-species consortium of *Pseudomonas putida* and *Acinetobacter* sp. C6, originally isolated from a creosote-polluted aquifer, has evolved a distinct spatial organization in the laboratory that is characterized by an increased fitness and productivity. In this consortium, *P. putida* is reliant on microcolonies formed by *Acinetobacter* sp. C6 — to which it attaches. Here we describe the processes that lead to the microcolony-pattern by *Acinetobacter* sp. C6. Ecological spatial pattern analyses revealed that the microcolonies were not entirely randomly distributed, and instead arranged in a uniform pattern. Detailed time-lapse confocal microscopy at the single cell level demonstrated that the spatial pattern was the result of an intriguing self-organization: Small multicellular clusters moved along the surface to fuse with one another to form microcolonies. This active distribution capability was dependent on environmental factors (carbon source, oxygen) and historical contingency (formation of phenotypic variants). The findings of this study are discussed in the context of species distribution patterns observed in macroecology, and we summarize observations about the processes involved in co-adaptation between *P. putida* and *Acinetobacter* sp. C6. Our results contribute to an understanding of spatial species distribution patterns as they are observed in nature, as well as the ecology of engineered communities that have the potential for enhanced and sustainable bioprocessing capacity.
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BFI (2015): BFI-level 2
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Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.857 SNIP 1.384 CiteScore 4.02
Web of Science (2014): Indexed yes
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Scopus rating (2013): SJR 1.899 SNIP 1.414 CiteScore 4.25
ISI indexed (2013): ISI indexed yes
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BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.975 SNIP 1.429 CiteScore 4.29
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BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.914 SNIP 1.455 CiteScore 4.12
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Scopus rating (2010): SJR 1.887 SNIP 1.436
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Scopus rating (2008): SJR 2.156 SNIP 1.572
Web of Science (2008): Indexed yes
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Web of Science (2003): Indexed yes
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Web of Science (2002): Indexed yes
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Draft Genome Sequences of Sanguibacteroides justesenii, gen. nov., sp. nov., Strains OUH 308042T (= ATCC BAA-2681T) and OUH 334697 (= ATCC BAA-2682), isolated from Blood Cultures from Two Different Patients

We announce here the draft genome sequences of Sanguibacteroides justesenii, gen. nov., sp. nov., strains OUH 308042T (= DSM 28342T = ATCC BAA-2681T) and OUH 334697 (= DSM 28341 = ATCC BAA-2682), isolated from blood cultures from two different patients and composed of 51 and 39 contigs for totals of 3,385,516 and 3,410,672 bp, respectively.

General information
State: Published
Organisations: Division of Epidemiology and Microbial Genomics, National Food Institute, Research Group for Genomic Epidemiology, Odense University Hospital
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EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2015. Scientific Opinion on an alternative method for the hygienic treatment of bovine colostrum through a series of filtration steps

An alternative method to the HTST treatment (High Temperature Short Time pasteurisation at 72 °C for at least 15 seconds or equivalent pasteurisation effect achieving a negative reaction to a phosphatase test), approved for the treatment of bovine colostrum (Category 3 material), was assessed. The purpose of the alternative method, based on a series of filtration steps, is the production of Colostrinov, a product whose main ingredient is bovine colostrum, to be used for foal nutrition. Since the filtration techniques used are known to eliminate particles of the size of bacteria, fungi and protozoa from liquids, it is reasonable to assume that the microfiltration process reduces these contaminants to a level at least equivalent to the treatment required by the legislation. Owing to their small size, viruses are not retained by the mechanical effect of the filters but they may be retained by physico-chemical interactions with the surface of the filter, depending on the surface properties of the viruses and those of the filter, as well as on the properties of the surrounding liquid. From the information provided by the applicant, it cannot be concluded whether or not the microfiltration process reduces the relevant viral contaminants to a level at least equivalent to a single HTST treatment as required by the legislation.

General information
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EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2015. Scientific Opinion on the development of a risk ranking toolbox for the EFSA BIOHAZ Panel

Eight tools relevant to risk ranking of biological hazards in food were identified and assessed using two case studies. Differences in their performance were observed, related to the risk metrics, data requirements, ranking approach, model type, model variables and data integration. Quantitative stochastic models are the most reliable for risk ranking. However, this approach needs good characterisation of input parameters. The use of deterministic models that ignore variability may result in risk ranking errors. The ordinal scoring approaches in semi-quantitative models provide ranking with more errors than the deterministic approaches. FDA (Food and Drug Administration)-iRISK was identified as the most appropriate tool for risk ranking of microbiological hazards. The Burden of Communicable Diseases in Europe (BCoDE) toolkit can be used in combination with the outputs from FDA-iRISK or as a top-down tool to rank pathogens. Uncertainty needs to be addressed and communicated to decision makers and stakeholders as one of the outcomes of the risk ranking process. Uncertainty and variability can be represented by means of probability distributions. Techniques such as the NUSAP (numeral, unit, spread, assessment and pedigree) approach can also be used to prioritise factors for sensitivity and scenario analysis or stochastic modelling. Quantitative risk ranking models are preferred over semi-quantitative models. When data and time constraints do not allow quantitative risk ranking, semi-quantitative models could be used, but the limitations of these approaches linked to the selection and integration of the ordinal scores should be made explicit. Decision trees should be used only to show how decisions are made about classifying food–pathogen combinations into broad categories. BCoDE and FDA-iRISK, in combination with a network of available predictive microbiology tools, databases and information sources, can form a risk ranking toolbox and be applied based on a “fit for purpose” approach supporting timely and transparent risk ranking.

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EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2015. Scientific Opinion on the public health risks related to the consumption of raw drinking milk

Raw drinking milk (RDM) has a diverse microbial flora which can include pathogens transmissible to humans. The main microbiological hazards associated with RDM from cows, sheep and goats, horses and donkeys and camels were identified using a decision tree approach. This considered evidence of milk-borne infection and the hazard being present in the European Union (EU), the impact of the hazard on human health and whether there was evidence for RDM as an important risk factor in the EU. The main hazards were Campylobacter spp., Salmonella spp., shigatoxin-producing Escherichia coli (STEC), Brucella melitensis, Mycobacterium bovis and tick-borne encephalitis virus, and there are clear links between drinking raw milk and human illness associated with these hazards. A quantitative microbiological risk assessment for these hazards could not be undertaken because country and EU-wide data are limited. Antimicrobial resistance has been reported in several EU countries in some of the main bacterial hazards isolated from raw milk or associated equipment and may be significant for public health. Sale of RDM through vending machines is permitted in some EU countries, although consumers purchasing such milk are usually instructed to boil the milk before consumption, which would eliminate microbiological risks. With respect to internet sales of RDM, there is a need for microbiological, temperature and storage time data to assess the impact of this distribution route. Intrinsic contamination of RDM with pathogens can arise from animals with systemic infection as well as from localised infections such as mastitis. Extrinsic contamination can arise from faecal contamination and from the wider farm environment. It was not possible to rank control options as no single step could be identified which would significantly reduce risk relative to a baseline of expected good practice, although potential for an increase in risk was also noted. Improved risk communication to consumers is recommended.

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Emergence of a Clonal Lineage of Multidrug-Resistant ESBL-Producing Salmonella Infantis Transmitted from Broilers and Broiler Meat to Humans in Italy between 2011 and 2014

We report the spread of a clone of multidrug-resistant (MDR), ESBL-producing (blaCTX-M-1) Salmonella enterica subsp. enterica serovar Infantis, in the Italian broiler chicken industry and along the food-chain. This was first detected in Italy in 2011 and led to human infection in Italy in 2013-2014. A set (n = 49) of extended-spectrum cephalosporin (ESC)-resistant (R) isolates of S. Infantis (2011-2014) from humans, food-producing animals and meat thereof, were studied along with a selected set of earlier and more recent ESC-susceptible (ESC-S) isolates (n = 42, 2001-2014). They were characterized by macrorestriction-PFGE analysis and genetic environment of ESC-resistance. Isolates representative of PFGE-patterns and origin were submitted to Whole Genome Sequencing. The emerging ESC-R clone, detected mainly from broiler
chickens, broiler meat and humans, showed a minimum pattern of clinical resistance to cefotaxime, tetracycline, sulfonamides, and trimethoprim, beside ciprofloxacin microbiological resistance (MIC 0.25 mg/L). All isolates of this clone harbored a conjugative megaplasmid (~280-320 Kb), similar to that described in ESC-susceptible S. Infantis in Israel (pESI-like) in 2014. This megaplasmid carried the ESBL gene blaCTX-M-1, and additional genes [tet(A), sul1, dfrA1 and dfrA14] mediating cefotaxime, tetracycline, sulfonamide, and trimethoprim resistance. It also contained genes conferring enhanced colonization capability, virulence (fimbriae, yersiniabactin), resistance and fitness (qacE1, mer) in the intensive-farming environment. This emerging clone of S. Infantis has been causing infections in humans, most likely through the broiler industry. Since S. Infantis is among major serovars causing human infections in Europe and is an emerging nontyphoidal Salmonella globally, further spread of this lineage in primary productions deserves quick and thorough risk-management strategies.

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- Scopus rating (2014): SJR 1.545 SNIP 1.141 CiteScore 3.54  
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Evaluation of methods for enrichment of carbapenemase-producing E. coli in pork meat and cecal samples of porcine and bovine origin: EV0266

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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.

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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.

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Authors: Noor Uddin, G. M. (Ekstern), Larsen, M. H. (Ekstern), Christensen, H. (Ekstern), Aarestrup, F. M. (Intern), Phu, T. M. (Ekstern), Dalsgaard, A. (Ekstern)
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Identification of a Pseudomonas aeruginosa co-producing NDM-1, VIM-5 and VIM-6 metallo-betalactamases in Denmark using Whole-Genome Sequencing

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Authors: Wang, M. (Ekstern), Borris, L. C. (Ekstern), Aarestrup, F. M. (Intern), Hasman, H. (Intern)
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Limited similarity between plasmids encoding CTX-M-1 β-lactamase in Escherichia coli from humans, pigs, cattle, organic poultry layers and horses in Denmark

CTX-M-1 is a common extended-spectrum β-lactamase (ESBL) in Escherichia coli from animals and is often detected among human clinical isolates. The objective of this study was to investigate the epidemiological relationship between CTX-M-1-producing E. coli isolated from patients and animals in Denmark between 2006 and 2010. In total, 65 CTX-M-1-producing isolates from patients (n=22), pigs (n=21), cattle (n=4), organic poultry layers (n=3) and horses (n=15) were typed by pulsed-field gel electrophoresis (PFGE). Plasmids harbouring blaCTX-M-1 were characterised by S1 PFGE, PCR-based replicon typing, plasmid multilocus sequence typing, restriction fragment length polymorphism, and sequencing. Human and animal strains were unrelated based on PFGE. IncI1 was more common in human isolates (13/22) than in animal isolates (7/43), whereas the opposite trend was observed for IncN (5/22 human isolates and 24/43 animal isolates). Full characterisation of the plasmids harbouring blaCTX-M-1 revealed host-specific patterns in the distribution of plasmid types, with specific IncI1, IncN and IncH1 plasmid subtypes being predominant in humans, livestock and horses, respectively. Three indistinguishable human, bovine and porcine IncI1/ST49 plasmids had high nucleotide sequence homology and differed by the presence of IS66 elements in the bovine plasmid and the absence of one gene within the microcin-encoding operon in the human plasmid. In conclusion, this work suggests a minor contribution by animals to the occurrence of CTX-M-1 in human E. coli infections in Denmark during the study period.
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. bla\(_{CTX-M}\)) carried on airplanes from South Asia compared to North America. Presence of *Salmonella enterica* and norovirus were also detected in higher amounts from South Asia, whereas *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.
Methodological Framework for World Health Organization Estimates of the Global Burden of Foodborne Disease

The Foodborne Disease Burden Epidemiology Reference Group (FERG) was established in 2007 by the World Health Organization to estimate the global burden of foodborne diseases (FBDs). This paper describes the methodological framework developed by FERG’s Computational Task Force to transform epidemiological information into FBD burden estimates. The global and regional burden of 31 FBDs was quantified, along with limited estimates for 5 other FBDs, using Disability-Adjusted Life Years in a hazard- and incidence-based approach. To accomplish this task, the following workflow was defined: outline of disease models and collection of epidemiological data; design and completion of a database template; development of an imputation model; identification of disability weights; probabilistic burden assessment; and estimating the proportion of the disease burden by each hazard that is attributable to exposure by food (i.e., source attribution). All computations were performed in R and the different functions were compiled in the R package ‘FERG’. Traceability and transparency were ensured by sharing results and methods in an interactive way with all FERG members throughout the process. We developed a comprehensive framework for estimating the global burden of FBDs, in which methodological simplicity and transparency were key elements. All the tools developed have been made available and can be translated into a user-friendly national toolkit for studying and monitoring food safety at the local level.
Performance, compliance and reliability of Waste stabilization pond: Effluent discharge quality and environmental protection agency standards in Ghana

Measuring performance has been arguably, one of the metric with many facets with different school of thoughts, as there exist different approaches of measuring it. Several of the existing approaches measure such metric by comparison with standards esherined in policy documents and as a result, takes less look to its compliance and reliability of values being matched to an established standards. This study seeks to integrate reliability and compliance into measuring of performance of Waste Stabilization Pond (WSP) and Treatment Plant (TP) as well as to generate the appropriate standard chart tables using the Ghana Environmental Protection Agency (EPA) approved discharge values for physico-chemical and some biological parameters to account for these shortfalls on over reliance of EPA discharge standards. Probability distribution density function was applied on the lognormal distribution function to establish the relationship between the statistical coefficient of variation and the coefficient of reliability based on rth moment about the origin in the moment of generation function to generate the functions of the mean and standard deviation, properties of the standard Z normal distribution were used to establish the coefficient of reliability relationship depending on the coefficient of variation influenced by the standard of deviation. Discharge values of Physico-chemical Parameters measured from the WSP were found be performing acceptably based on the EPA standards, whereas only four of the TP were acceptable. Discharge Values of physico-chemical and biological parameters which are found to be accepted under comparison with EPA standards were found to have compliance levels below what is generally accepted for Waste Stabilization Ponds (WSP) designed compliance. Based on these shortcomings, reference charts were develop to serve as reference points in assessing the various characteristics of compliance and performance of WSPs in Ghana on (28) physico-chemical and biological parameters. These charts are intended to make it easier to assess the performance of WSPs and its corresponding reliability and compliance level to compensate for overreliance on EPA standards alone.

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Authors: Owusu-Ansah, E. D. J. (Intern), Sampson, A. (Ekstern), Amponsah, S. K. (Ekstern), Abaidoo, R. C. (Ekstern), Hald, T. (Intern)
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Proficiency Testing for Bacterial Whole Genome Sequencing: An End-User Survey of Current Capabilities, Requirements and Priorities

The advent of next-generation sequencing (NGS) has revolutionised public health microbiology. Given the potential impact of NGS, it is paramount to ensure standardisation of ‘wet’ laboratory and bioinformatic protocols and promote comparability of methods employed by different laboratories and their outputs. Therefore, one of the ambitious goals of the Global Microbial Identifier (GMI) initiative (http://www.globalmicrobialidentifier.org/) has been to establish a mechanism for
inter-laboratory NGS proficiency testing (PT). This report presents findings from the survey recently conducted by Working Group 4 among GMI members in order to ascertain NGS end-use requirements and attitudes towards NGS PT. The survey identified the high professional diversity of laboratories engaged in NGS-based public health projects and the wide range of capabilities within institutions, at a notable range of costs. The priority pathogens reported by respondents reflected the key drivers for NGS use (high burden disease and ‘high profile’ pathogens). The performance of and participation in PT was perceived as important by most respondents. The wide range of sequencing and bioinformatics practices reported by end-users highlights the importance of standardisation and harmonisation of NGS in public health and underpins the use of PT as a means to assuring quality. The findings of this survey will guide the design of the GMI PT program in relation to the spectrum of pathogens included, testing frequency and volume as well as technical requirements. The PT program for external quality assurance will evolve and inform the introduction of NGS into clinical and public health microbiology practice in the post-genomic era.

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, flIA, 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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Web of Science (2015): Indexed yes
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ISI indexed (2011): ISI indexed yes
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Scopus rating (2010): SJR 2.303 SNIP 1.727
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Scopus rating (2007): SJR 2.202 SNIP 1.689
Web of Science (2007): Indexed yes
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Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.678 SNIP 1.701
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.845 SNIP 1.855
Web of Science (2003): Indexed yes
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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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Scopus rating (2004): SJR 2.824 SNIP 1.559
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Risikorangering af sygdomsfremkaldende mikroorganismer i frisk frugt og grønt: Frugt og grønt indsatser 2013-2016

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Division of Epidemiology and Microbial Genomics
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.

General information
State: Published
Organisations: Division of Epidemiology and Microbial Genomics, National Food Institute, Research Group for Genomic Epidemiology
Authors: Aarestrup, F. M. (Intern)
Number of pages: 13
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Philosophical Transactions of the Royal Society B: Biological Sciences
The use of third and fourth generation cephalosporins affects the occurrence of extended-spectrum cephalosporinase-producing Escherichia coli in Danish pig herds
Extended-spectrum cephalosporinase resistance is currently the fastest emerging antimicrobial resistance problem worldwide; however, evidence documenting the effect of potential risk factors is limited. The main objective of this study was to investigate the effect of using third and fourth generation cephalosporins on the occurrence of extended-spectrum cephalosporinase-producing Escherichia coli (ESC-Ec) in Danish pig herds. Conventional, integrated, medium to large herds were selected based on information from the Danish Central Husbandry Register and two groups were formed based on the use of third and fourth generation cephalosporins within a specified period, namely, 20 herds with no cephalosporin use (non-exposed) and 19 herds with frequent use (exposed). Data on prescribed antimicrobials were obtained from the National database (VetStat). Management data were obtained through a questionnaire. At the herd level, three pooled faecal samples were collected from sows with their piglets (farrowing pens), weaners, and finishers. ESC-Ec were then identified using selective enrichment. Because several of the herds only had a low number of weaners and/or finishers, analysis was only performed on samples from the farrowing pens. Logistic regression showed a significant effect of using cephalosporins-III/IV on the occurrence of ESC-Ec in the farrowing pens, even when adjusted for use of other antimicrobials 1 year prior to sampling. No confounding effect was identified in relation to management data. The relative risk ESC-Ec in exposed compared to non-exposed was 4.7 (95% confidence interval 2.0–11.5), confirming that regular use of cephalosporins-III/IV was a significant risk factor for the occurrence of ESC-Ec.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Division of Epidemiology and Microbial Genomics, Danish Agriculture and Food Council
Authors: Dalhoff Andersen, V. (Intern), Jensen, V. F. (Intern), Vigre, H. (Intern), Andreasen, M. (Ekstern), Agersø, Y. (Intern)
Number of pages: 6
Pages: 345-350
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Journal
Volume: 204
Issue number: 3
ISSN (Print): 1090-0233
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.78 SJR 1.008 SNIP 1.138
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.95 SNIP 1.045 CiteScore 1.61
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.917 SNIP 1.09 CiteScore 1.7
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.034 SNIP 1.307 CiteScore 1.91
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.041 SNIP 1.626 CiteScore 2.09
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.09 SNIP 1.412 CiteScore 2
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.042 SNIP 1.464
Web of Science (2010): Indexed yes
Threat of multidrug resistant Staphylococcus aureus in Western Nepal

ObjectiveTo determine the prevalence of methicillin resistant Staphylococcus aureus (MRSA) and antimicrobial susceptibility patterns of the isolates from Manipal Teaching Hospital, Pokhara, Nepal. MethodsThis study was conducted over a period of 11 months (September 2012–August 2013) at the Manipal Teaching Hospital, Pokhara, Nepal. A total of 400 isolates were collected from various clinical specimens including hospital units (operation theaters and intensive care units). Antibiotic susceptibility testing was performed by Kirby-Bauer disc diffusion method. Primary screening for MRSA was performed using disc diffusion test by cefoxitin (30 μg) and oxacillin (1 μg) disc, further confirmation was done by detection of mecA gene using PCR. ResultsOut of 400 Staphylococcus aureus strains, 139 (34.75%) were found to be MRSA. Among the MRSA isolates, 74 (53.2%) were from inpatient departments, 58 (41.7%) of the isolates were from outpatients and 7 (5.0%) isolates were from hospital units (operation theaters and intensive care units). Majority of MRSA (73.38%) isolates were multidrug resistant while less than 15% were resistant to amikacin, clindamycin and tetracycline. None of the isolate was resistant to vancomycin. Inducible clindamycin resistance was found in 54 (25.47%) isolates. ConclusionsThis study showed a high prevalence of MRSA in our hospital. There is need of regular surveillance of antibiotic resistance, standardization of laboratory methods for detecting methicillin resistance and performing antibiotic susceptibility testing in developing countries like Nepal. Hospital acquired infections including prevalence of MRSA can be minimized by appropriate hygienic measures in patient care and management and by antibiotic stewardship. Screening of erythromycin resistant isolates would minimize clinical failures associated with clindamycin therapy.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Tribhuvan University, Banaras Hindu University, Manipal College of Medical Sciences
Authors: Bhatta, D. R. (Ekstern), Cavaco, L. (Intern), Nath, G. (Ekstern), Gaur, A. (Ekstern), Gokhale, S. (Ekstern), Bhatta, D. R. (Ekstern)
Number of pages: 5
Pages: 617-621
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Asian Pacific Journal of Tropical Disease
Volume: 5
Issue number: 8
ISSN (Print): 2222-1808
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2016): SJR 0.261 SNIP 0.653 CiteScore 1.32
Scopus rating (2015): SJR 0.274 SNIP 0.794 CiteScore 1.02
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 0.345 SNIP 0.815 CiteScore 1.01
Unique and conserved genome regions in Vibrio harveyi and related species in comparison with the shrimp pathogen Vibrio harveyi CAIM 1792

Vibrio harveyi CAIM 1792 is a marine bacterial strain that causes mortality in farmed shrimp in north-west Mexico, and the identification of virulence genes in this strain is important for understanding its pathogenicity. The aim of this work was to compare the V. harveyi CAIM 1792 genome with related genome sequences to determine their phylogenetic relationship and explore unique regions in silico that differentiate this strain from other V. harveyi strains. Twenty-one newly sequenced genomes were compared in silico against the CAIM 1792 genome at nucleotide and predicted proteome levels. The proteome of CAIM 1792 had higher similarity to those of other V. harveyi strains (78%) than to those of the other closely related species Vibrio owensii (67%), Vibrio rotiferianus (63%) and Vibrio campbellii (59%). Pan-genome ORFans trees showed the best fit with the accepted phylogeny based on DNA-DNA hybridization and multi-locus sequence analysis of 11 concatenated housekeeping genes. SNP analysis clustered 34/38 genomes within their accepted species. The pangenomic and SNP trees showed that V. harveyi is the most conserved of the four species studied and V. campbellii may be divided into at least three subspecies, supported by intergenomic distance analysis. blastp atlases were created to identify unique regions among the genomes most related to V. harveyi CAIM 1792; these regions included genes encoding glycosyltransferases, specific type restriction modification systems and a transcriptional regulator, LysR, reported to be involved in virulence, metabolism, quorum sensing and motility.
Validation of methods for enrichment of ESBL and AmpC producing E. coli in meat and cecal samples: P0995

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Federal Institute for Risk Assessment, European Commission
Authors: Hasman, H. (Intern), Agersø, Y. (Intern), Cavaco, L. (Intern), Svendsen, C. A. (Intern), San Jose, M. (Ekstern), Fisher, J. (Ekstern), Schnogor, S. (Ekstern), Jahn, S. (Ekstern), Guerra, B. (Ekstern), Peran, R. (Ekstern)
Number of pages: 1
Publication date: 2015
Event: Abstract from 25th European Congress of Clinical Microbiology and Infectious Diseases, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions: 7369963_P0995.pdf
Source: PublicationPreSubmission
Source-ID: 110765984
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

What Can We Learn from a Metagenomic Analysis of a Georgian Bacteriophage Cocktail?
Phage therapy, a practice widespread in Eastern Europe, has untapped potential in the combat against antibiotic-resistant bacterial infections. However, technology transfer to Western medicine is proving challenging. Bioinformatics analysis could help to facilitate this endeavor. In the present study, the Intesti phage cocktail, a key commercial product of the Eliava Institute, Georgia, has been tested on a selection of bacterial strains, sequenced as a metagenomic sample, de novo assembled and analyzed by bioinformatics methods. Furthermore, eight bacterial host strains were infected with the cocktail and the resulting lysates sequenced and compared to the unamplified cocktail. The analysis identified 23 major phage clusters in different abundances in the cocktail, among those clusters related to the ICTV genera T4likevirus, T5likevirus, T7likevirus, Chilikevirus and Twortlikevirus, as well as a cluster that was quite distant to the database sequences and a novel Proteus phage cluster. Examination of the depth of coverage showed the clusters to have different abundances within the cocktail. The cocktail was found to be composed primarily of Myoviridae (35%) and Siphoviridae (32%), with Podoviridae being a minority (15%). No undesirable genes were found.

General information
State: Published
Organisations: Department of Systems Biology, Center for Biological Sequence Analysis, National Food Institute, Research Group for Genomic Epidemiology, Department of Microbiology, Technical University of Denmark, Eliava Institute of Bacteriophages, Microbiology and Virology, Eliava Biopreparations LTD, The Evergreen State College
Number of pages: 20
Pages: 6570-6589
Publication date: 2015
Main Research Area: Technical/natural sciences
Publication information
Journal: Viruses
Volume: 7
Issue number: 12
ISSN (Print): 1999-4915
Ratings:
Web of Science (2018): Indexed yes
Web of Science (2017): Indexed Yes
Scopus rating (2016): CiteScore 3.6 SJR 1.699 SNIP 1.018
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 1.834 SNIP 1.059 CiteScore 3.74
Web of Science (2015): Indexed yes
Antimicrobial consumption in animals

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Division of Risk Assessment and Nutrition
Authors: de Knegt, L. (Intern), Borck Høg, B. (Intern), Bager, F. (Intern)
Pages: 23-30
Publication date: 2014

Host publication information
Title of host publication: DANMAP 2013: Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark
Publisher: Statens Serum Institut
Chapter: 4
Series: Dansk Veterinærtidsskrift
ISSN: 1600-2032
Main Research Area: Technical/natural sciences
Electronic versions:
Danmap_2013.pdf
Publication: Research › Book chapter – Annual report year: 2015

EFSA (European Food Safety Authority) and ECDC (European Centre for Disease Prevention and Control), 2014. The European Union Summary Report on Trends and Sources of Zoonoses, Zoonotic Agents and Food-borne Outbreaks in 2012

Zoonoses are infections and diseases that are naturally transmissible, directly or indirectly, for example via contaminated foodstuffs, between animals and humans. The severity of these diseases in humans varies from subclinical infection or mild symptoms to life-threatening conditions. In order to prevent zoonoses from occurring, it is important to identify which animals and foodstuffs are the main sources of infection. For this purpose information aimed at protecting human health is collected and analysed from all European Union Member States.

In 2012, 27 Member States submitted information on the occurrence of zoonoses, zoonotic agents and food-borne outbreaks to the European Commission and the European Food Safety Authority. Furthermore, information on cases of zoonoses reported in humans was provided by the European Centre for Disease Prevention and Control. In addition, three European countries that were not European Union Member States provided information. The European Food Safety Authority and the European Centre for Disease Prevention and Control jointly analysed the data, the results of which are published in this annual European Union Summary Report, which covers 15 zoonoses and food-borne outbreaks.

In 2012, the notification rate and confirmed number of cases of human campylobacteriosis in the European Union decreased compared with 2011. Human campylobacteriosis, however, continued to be the most commonly reported zoonosis with 214,268 confirmed cases. The number of confirmed cases of campylobacteriosis in the European Union has followed a significant increasing trend in the last five years (2008-2012), along with a clear seasonal trend. The proportion of Campylobacter-positive food and animal samples remained mainly at levels similar to previous years, with the occurrence of Campylobacter continuing to be high in broiler meat.

The number of salmonellosis cases in humans decreased by 4.7 % compared with 2011. A statistically significant decreasing trend in the European Union was observed over the period 2008-2012. In total, 91,034 confirmed human cases were reported in 2012. It is assumed that the observed reduction in salmonellosis cases is mainly a result of the
A total of 5,363 food-borne outbreaks were reported in the European Union, resulting in 55,453 human cases, 5,118 hospitalisations and 41 deaths. Most of the reported outbreaks were caused by Salmonella, bacterial toxins, viruses and Campylobacter. The most important food sources of the outbreaks were eggs and egg products, followed by mixed food and fish and fish products. Overall, 16 waterborne outbreaks were reported in 2012, caused by calicivirus, verocytotoxigenic E. coli, Cryptosporidium parvum and rotavirus.

General information
Quality scores for 32,000 genomes

Background
More than 80% of the microbial genomes in GenBank are of ‘draft’ quality (12,553 draft vs. 2,679 finished, as of October, 2013). We have examined all the microbial DNA sequences available for complete, draft, and Sequence Read Archive genomes in GenBank as well as three other major public databases, and assigned quality scores for more than 30,000 prokaryotic genome sequences.

Results
Scores were assigned using four categories: the completeness of the assembly, the presence of full-length rRNA genes, tRNA composition and the presence of a set of 102 conserved genes in prokaryotes. Most (~88%) of the genomes had quality scores of 0.8 or better and can be safely used for standard comparative genomics analysis. We compared genomes across factors that may influence the score. We found that although sequencing depth coverage of over 100x did not ensure a better score, sequencing read length was a better indicator of sequencing quality. With few exceptions, most of the 30,000 genomes have nearly all the 102 essential genes.

Conclusions
The score can be used to set thresholds for screening data when analyzing “all published genomes” and reference data is either not available or not applicable. The scores highlighted organisms for which commonly used tools do not perform well. This information can be used to improve tools and to serve a broad group of users as more diverse organisms are sequenced. Unexpectedly, the comparison of predicted tRNAs across 15,000 high quality genomes showed that anticodons beginning with an ‘A’ (codons ending with a ‘U’) are almost non-existent, with the exception of one arginine codon (CGU); this has been noted previously in the literature for a few genomes, but not with the depth found here.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Department of Systems Biology, Center for Biological Sequence Analysis
Authors: Land, M. L. (Ekstern), Hyatt, D. (Ekstern), Jun, S. (Ekstern), Kora, G. H. (Ekstern), Hauser, L. J. (Ekstern), Lukjancenko, O. (Intern), Ussery, D. (Intern)
Number of pages: 10
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Standards in Genomic Sciences
Volume: 9
Issue number: 20
ISSN (Print): 1944-3277
Ratings:
Web of Science (2018): Indexed yes
Web of Science (2017): Indexed Yes
Scopus rating (2016): CiteScore 1.26 SJR 0.481 SNIP 0.452
Relative human risk of Salmonella Enteritidis in table eggs

General information
State: Published
Organisations: National Food Institute, Division of Risk Assessment and Nutrition, Research Group for Genomic Epidemiology
Authors: Korsgaard, H. (Intern), Struve, T. (Intern), Hald, T. (Intern), Vigre, H. (Intern)
Pages: 20-22
Publication date: 2014

Host publication information
Title of host publication: Annual Report on Zoonoses in Denmark 2013
Place of publication: Søborg
Publisher: National Food Institute, Technical University of Denmark
Editors: Vedel Sørensen, A. I., Helwigh, B., Müller, L.
Chapter: 4
Main Research Area: Technical/natural sciences

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 pan genome was found to consist of 16,373 genes. 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**
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Department of Systems Biology, Center for Biological Sequence Analysis
Authors: Kaas, R. S. (Intern), Aarestrup, F. M. (Intern), Ussery, D. (Intern), Lund, O. (Intern)
Number of pages: 126
Publication date: 2014

**Publication information**
Place of publication: Kgs. Lyngby
Publisher: Technical University of Denmark (DTU)
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:

PhD_Thesis_Rolf_Sommer_Kaas_numbered.pdf
Publication: Research › Ph.D. thesis – Annual report year: 2015

**The global establishment of a highly-fluoroquinolone resistant *Salmonella enterica* serotype Kentucky ST198 strain**

While the spread of *Salmonella enterica* serotype Kentucky resistant to ciprofloxacin across Africa and the Middle-East has been described recently, the presence of this strain in humans, food, various animal species (livestock, pets, and wildlife) and in environment is suspected in other countries of different continents. Here, we report results of an in-depth molecular epidemiological study on a global human and non-human collection of S. Kentucky (*n* = 70). We performed Xba I-pulsed field gel electrophoresis and multilocus sequence typing, assessed mutations in the quinolone resistance-determining regions, detected β-lactam resistance mechanisms, and screened the presence of the *Salmonella* genomic island 1 (SGI1). In this study, we highlight the rapid and extensive worldwide dissemination of the ciprofloxacin-resistant S. Kentucky ST198-X1-SGI1 strain since the mid-2000s in an increasingly large number of contaminated sources, including
the environment. This strain has accumulated an increasing number of chromosomal and plasmid resistance determinants and has been identified in the Indian subcontinent, Southeast Asia and Europe since 2010. The second substitution at position 87 in GyrA (replacing the amino acid Asp) appeared helpful for epidemiological studies to track the origin of contamination. This global study provides evidence leading to the conclusion that high-level resistance to ciprofloxacin in S. Kentucky is a simple microbiological trait that facilitates the identification of the epidemic clone of interest, ST198-X1-SGI1. Taking this into account is essential in order to detect and monitor it easily and to take rapid measures in livestock to ensure control of this infection.

General information

State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen, Institut Pasteur, Universite Paris-Est, Chittagong Veterinary and Animal Sciences University, Federal Institute for Risk Assessment, National Veterinary Research Institute, Robert Koch Institute, University of Sydney, Institut Pasteur du Maroc, University of Ibadan, FINALAB, French National Centre for Scientific Research
Authors: Le Hello, S. (Ekstern), Bekhit, A. (Ekstern), Granier, S. A. (Ekstern), Barua, H. (Ekstern), Beutlich, J. (Ekstern), Zajac, M. (Ekstern), Münch, S. (Ekstern), Sintchenko, V. (Ekstern), Bouchrif, B. (Ekstern), Fashae, K. (Ekstern), Pinsard, J. L. (Ekstern), Sontag, L. (Ekstern), Fabre, L. (Ekstern), Garnier, M. (Ekstern), Guibert, V. (Ekstern), Howard, P. (Ekstern), Hendriksen, R. S. (Intern), Christensen, J. P. (Ekstern), Biswas, P. K. (Ekstern), Cloeckaert, A. (Ekstern), Rabsch, W. (Ekstern), Wasyi, D. (Ekstern), Doublet, B. (Ekstern), Weill, F. X. (Ekstern)
Number of pages: 1
Pages: 395
Publication date: 2013
Main Research Area: Technical/natural sciences

Publication Information
Journal: Frontiers in Microbiology
Volume: 4
ISSN (Print): 1664-302X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.16 SJR 1.731 SNIP 1.172
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.878 SNIP 1.208 CiteScore 4.15
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.861 SNIP 1.16 CiteScore 3.76
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.751 SNIP 0.951 CiteScore 3.56
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.415 SNIP 0.725 CiteScore 2.78
ISI indexed (2012): ISI indexed no
Scopus rating (2011): SJR 0.626 SNIP 0.187
Web of Science (2011): Indexed yes
Original language: English
S. Kentucky, ST198, SGI1, QRDR, MDR Salmonella Dissemination, Poultry
Electronic versions:
fmicb_04_00395.pdf
DOIs:
10.3389/fmicb.2013.00395
Source: FindIt
Source-ID: 258223605
Publication: Research - peer-review › Journal article – Annual report year: 2013
Projects:

Bekæmpelse af ESBL producerende, colistin og multiresistente Salmonella og E. coli
National Food Institute
Research Group for Genomic Epidemiology
University of Copenhagen
Period: 01/09/2016 → 31/12/2016
Number of participants: 1
ESBL, colistin, phage
Project participant:
Bortolaia, Valeria (Intern)
Project

Comparison of ADDs used in VetStat with primary data on usage doses obtained at visits in 20 Danish pig herds
Master project
National Food Institute
Research Group for Genomic Epidemiology
Period: 01/08/2016 → 06/01/2017
Number of participants: 1
antimicrobial usage, VetStat, Epidemiology, pigs
Main Supervisor:
Hald, Tine (Intern)
Project

COMPARE WG 1, Task 1.2: Development of a novel approach for food chain risk assessment based on NGS data
National Food Institute
Research Group for Genomic Epidemiology
Period: 01/02/2016 → 31/12/2018
Number of participants: 1
microbial risk assessment, whole genome sequencing, machine learning, listeria
Supervisor:
Hald, Tine (Intern)
Project

Establishing Next Generation sequencing Ability for Genomic analysis in Europe.
National Food Institute
Research Group for Genomic Epidemiology
Period: 29/01/2016 → 29/01/2018
Number of participants: 1
Acronym: ENGAGE
Project ID: -GP/EFSA/AFSCO/2015/01
Project participant:
Hendriksen, Rene S. (Intern)

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).

**National Food Institute**

Research Group for Genomic Epidemiology

National Institute for Public Health and the Environment (RIVM) Bilthoven The Netherlands

Erasmus Medical Center

World Health Organization

Period: 01/01/2016 → …

Number of participants: 2

Project participant:

Hendriksen, Rene S. (Intern)

Project Manager, organisational:

Aarestrup, Frank Møller (Intern)

**Symposium on Gut Microbiota and Host Metabolic Health**

The idea with the symposium is to invite four esteemed foreign speakers within the field of Gut Microbiota and Metabolic Health, who can thereby inspire and interact with Danish senior researchers as well as young Danish scientists. Additionally, the symposium will be used as a platform to disseminate the new results from the 3G Center and related research. This will contribute to the continuous development of Danish research as a major international player within this field of science.

National Food Institute

Research Group for Gut Microbiology and Immunology

Research Group for Genomic Epidemiology

Spanish National Research Council

Louvain Drug Research Institute

Wageningen IMARES

Cornell University

Period: 01/07/2015 → 30/06/2017

Number of participants: 3

gut, microbiota, diabetes

Acronym: Novo_Gut Symposium

Project Coordinator:

Licht, Tine Rask (Intern)

Bang-Berthelsen, Iben (Intern)

Project Coordinator:

Skiby, Jeffrey Edward (Intern)

**Financing sources**

Source: Private funding (private)

Name of research programme: Novo Nordisk fonden

Amount: 130.00 Danish Kroner

Year of approval: 2015

**Global Decision Support Initiative**

Holistic approach to decision analysis considering both risk and sustainability

National Food Institute

Research Group for Genomic Epidemiology

Period: 01/01/2015 → …

Number of participants: 1
risk assessment, sustainability assessment, decision support

Acronym: GDSI

Project participant:
Hald, Tine (Intern)

Project

Collaborative Management Platform for Detection and Analyses of (Re-) Emerging and Foodborne Outbreaks in Europe

COMPARE aims to harness the rapid advances in molecular technology to improve identification and mitigation of emerging infectious diseases and foodborne outbreaks

National Food Institute
Research Group for Genomic Epidemiology
Erasmus University Medical Centre
Statens Serum Institut
Friedrich Loeffler Institute
Agence nationale de la sécurité sanitaire, alimentation, environnement et travail
Robert Koch Institute
European Molecular Biology Laboratory
Istituto Superiore di Sanita
National Institute of Public Health and the Environment
Animal and Plant Health Agency
University of Edinburgh
Ubiversitaetsklinikum Bonn (UK-Bonn)
Universiteit van Amsterdam
Universiteit Antwerpen
Artemis One Health Research
University of Cambridge
Stiftung Tierarztiische Hochschule Hannover
Universidad de Castilla-La Mancha
Fondation Merieux
Aristotelio Panepistimio Thessalonikis
IFREMER
Erasmus Universiteit
Australian National University
Magyar Tudomanyos Akademia Wigner Fizikai Kutatokozpont
Civic Consulting
Responisble Technology

University of Bologna
Leibniz-Institut DSMZ
Wellcome Trust Sanger Institute

Period: 01/12/2014 → 30/11/2019
Number of participants: 3

genomic epidemiology, risk-based molecular surveillance, bioinformatics, Next generation sequencing

Acronym: COMPARE

Project ID: Horizon 2020
Number of related Ph.D. students: 1
Contact person:
Carlsson, Susanne (Intern)
Project Manager, organisational:
Skiby, Jeffrey Edward (Intern)
Project Coordinator:
Aarestrup, Frank Møller (Intern)

Financing sources
Source: EU research programme (public)
Name of research programme: Horizon 2020
Amount: 20,800,000.00 Euro
Year of approval: 2014

Relations
Publications:
Benchmarking of methods for identification of antimicrobial resistance genes in bacterial whole genome data
Two listeria outbreaks caused by smoked fish consumption-using whole-genome sequencing for outbreak investigations
A Bacterial Analysis Platform: An Integrated System for Analysing Bacterial Whole Genome Sequencing Data for Clinical
Diagnostics and Surveillance
Spatiotemporal Analysis of the Genetic Diversity of Seal Influenza A(H10N7) Virus, Northwestern Europe
Emergence of a Clonal Lineage of Multidrug-Resistant ESBL-Producing Salmonella Infantis Transmitted from Broilers and
Broiler Meat to Humans in Italy between 2011 and 2014
Meta-genomic analysis of toilet waste from long distance flights; a step towards global surveillance of infectious diseases
and antimicrobial resistance

EURL-AR: EU Reference Laboratory – Antimicrobial Resistance
The National Food Institute was in 2006 appointed EU Reference Laboratory for antimicrobial resistance (EURL-AR) by
the European Commission. It is the responsibility of the EURL-AR to provide scientific advice to the Commission on
matters in relation to antimicrobial resistance.
In particular it is the responsibility of the EURL-AR to provide scientific advice in relation to the organisation,
implementation and evaluation of monitoring schemes for antimicrobial resistance.

National Food Institute
Research Group for Genomic Epidemiology
Period: 01/06/2014 → 31/12/2014
Number of participants: 5
EURL-AR, EU Reference Laboratory, Antimicrobial Resistance, EU Reference Laboratory
Project participant:
Hendriksen, Rene S. (Intern)
Karlsmose Pedersen, Susanne (Intern)
Cavaco, Lina (Intern)
Other:
Carlsson, Susanne (Intern)
Project Manager, academic:
Aarestrup, Frank Møller (Intern)

Financing sources
Source: EU research programme (public)
Name of research programme: European Commision
Amount: 517,000.00 Euro

Relations
Activities:
EU conference " farmers and Veterinarians together to tackle antimicrobial resistance"
The 6th AMR EFSA Network meeting
EURL-AR Training Course: Methods required by The EU Legislation (2013/652/Eu)
Antimicrobial resistance and susceptibility testing, definitions and methods
European Union Reference Laboratory, Antimicrobial Resistance – Annual Workshop
The EURLs directors meeting
EFFORT: Ecology from farm to fork of microbial drug resistance and transmission
EFFORT will study the complex epidemiology and ecology of antimicrobial resistance and the interactions between bacterial communities, commensals and pathogens in animals, the food chain and the environment. This will be conducted by a combination of epidemiological and ecological studies using newly developed molecular and bio-informatics technologies. EFFORT will include an exposure assessment of humans from animal and environmental sources. The ecological studies on isolates will be verified by in vitro and in vivo studies. Moreover, real-life intervention studies will be conducted with the aim to reduce the use of antimicrobials in veterinary practice. Focus will be on understanding the eco-epidemiology of antimicrobial resistance from animal origin and based on this, predicting and limiting the future evolution and exposure to humans of the most clinically important resistance by synthesising different sources of information in our prediction models.

Through its results, the EFFORT research will provide scientific evidence and high quality data that will inform decision makers, the scientific community and other stakeholders about the consequences of AMR in the food chain, in relation to animal health and welfare, food safety and economic aspects. These results can be used to support political decisions and to prioritise risk management options along the food chain.

National Food Institute
Research Group for Genomic Epidemiology
Period: 01/12/2013 → 30/11/2018
Number of participants: 4
EFFORT, Ecology, from farm to fork, microbial drug resistance, transmission
Project participant:
Hald, Tine (Intern)
Knudsen, Berith Elkær (Intern)
Other:
Carlsson, Susanne (Intern)
Project Manager, academic:
Aarestrup, Frank Møller (Intern)

Financing sources
Source: EU research programme (public)
Name of research programme: EU FP7
Amount: 1,450,568.00 Euro

REINSURE: Revolutionizing Infectious disease surveillance
National Food Institute
Research Group for Genomic Epidemiology
Department of Systems Biology
DHI
Period: 30/05/2013 → 29/05/2017
Number of participants: 3
Project participant:
Bergmark, Lasse (Intern)
Other:
Carlsson, Susanne (Intern)
Project Manager, academic:
Aarestrup, Frank Møller (Intern)

Financing sources
Source: Private funding (private)
Name of research programme: Villum Fonden
Web address: http://villumfonden.dk/C12576AB0041A865/0/4C05C456014EDFD5C1256E9F00371B87?OpenDocument
Amount: 4,980,551.00 Danish Kroner
Whole genome based diagnostics and investigations
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.

National Food Institute
Research Group for Genomic Epidemiology
Department of Systems Biology
Center for Biological Sequence Analysis
University of Copenhagen
Kilimanjaro Christian Medical Centre
Period: 01/01/2013 → 31/12/2016
Number of participants: 5
Epidemiology, Health, Infections, Vaccines, Research
Contact person:
Hammer, Vibeke Dybdahl (Intern)
Project participant:
Hasman, Henrik (Intern)
Lund, Ole (Intern)
Other:
Carlsson, Susanne (Intern)
Project Coordinator:
Aarestrup, Frank Møller (Intern)

Financing sources
Source: Public research programme (public)
Name of research programme: Danida
Web address: http://drp.dfcentre.com/
Amount: 8,639,400.00 Danish Kroner
Year of approval: 2012

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 horisontal genoverførsel. Undersøgelserne vil specielt fokusere på at kortlægge de egenskaber, som bevirkere, 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 eger disse bakteriers evne til at tilpasse og udvikle sig. En sådan viden vil kunne bruges til at udvikle strategier til at stoppe udvikling af antibiotikaresistens hos sygdomsfremkaldende bakterier, samt gøre det muligt at forudsige potentialet 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.

National Food Institute
Research Group for Genomic Epidemiology
University of Copenhagen
Period: 01/01/2012 → 31/12/2015
Number of participants: 4
ADAP, Adaptability, promiscuity, commensal, microorganisms
Project participant:
Hasman, Henrik (Intern)
Roer, Louise (Intern)
Other:
Carlsson, Susanne (Intern)
Project Manager, academic:
Aarestrup, Frank Møller (Intern)

Financing sources
Source: Public research council
Name of research programme: Det Frie Forskningsråd
Web address: http://ufm.dk/forskning-og-innovation/rad-og-udvalg/det-frie-forskningsrad
Amount: 4,890,449.00 Danish Kroner

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.

National Food Institute
Research Group for Genomic Epidemiology
Period: 01/09/2011 → 
Number of participants: 2
Acronym: GMI
Project participant:
Hendriksen, Rene S. (Intern)
Project Manager, organisational:
Aarestrup, Frank Møller (Intern)

APUA: Animal Production without Antibiotics

National Food Institute
Research Group for Genomic Epidemiology
Aalborg University
University of Copenhagen
ISI Food Protection APS
BioMar A/S
**Intricate: Infectious Triggers of Chronic Autoimmunity**

The INTRICATE project has four specific aims, namely to:

1. Use novel high-throughput antigen array technology and well-characterized patient cohorts to determine whether acute infection with specific microorganisms triggers the induction or re-activation of AASV; and to ascertain whether antibody responses to microbial proteins cross-react with native or epigenetically modified self-proteins.

2. Elucidate the reasons why dysbiotic expansion of S. aureus in nasal sinuses and upper airways is linked to localised and systemic granulomatous vasculitis in AASV; and in particular to analyse the roles of microbial superantigens and the local adaptive immune response to them.

3. Analyse the mechanisms of molecular mimicry in transgenic mice expressing the human forms of LAMP-2, PR3 and MPO – the major targets of autoantibodies in AASV – by determining whether infection with bacteria that express molecular mimics induce AASV and, if so, to define under which circumstances they do so.

4. Characterise disease-associated genes identified in the European Vasculitis Genetics Consortium's genome wide association study (GWAS) of AASV and to examine their effect on gene expression and function; and to determine whether the genetic variants that predispose to AASV have been maintained in the gene pool because of a beneficial effect on resistance to infection.

National Food Institute

Research Group for Genomic Epidemiology

Technical University of Denmark

Medizinische Universität Wien

Max-Planck-Gesellschaft zur Foerderung der Wissenschaften

Universitätsklinikum Bonn Germany

Mayo Clinic College of Medicine

Academisch Ziekenhuis Groningen

University of Cambridge

The Board of Trustees of the Leland Stanford Junior University United States

EMC Microcollections GmbH

Hycult Biotechnology b.v.

Gesellschaft für Ablauforganisation GmbH & Co. KG

**Financing sources**

Source: EU research programme (public)
Name of research programme: EU FP7 Health 2010
CGE: Center for Genomic Epidemiology

The cost of sequencing a bacterial genome is $50 and is expected to decrease further in the near future and the equipment needed cost less than $150,000. Thus, within a few years all clinical microbiological laboratories will have a sequencer in use on a daily basis. The price of genome sequencing is already so low that whole genome sequencing will also find worldwide application in human and veterinary practices as well as many other places where bacteria are handled. In Denmark alone this equals more than 1 million isolates annually in 15-20 laboratories and globally up to 1-2 billion isolates per year. The limiting factor will therefore in the future 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, 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.

National Food Institute
Research Group for Genomic Epidemiology

Department of Systems Biology

Center for Biological Sequence Analysis
Period: 01/04/2010 → 30/09/2016
Number of participants: 5
Genomic Epidemiology, genome, CGE

Project participant:
Hasman, Henrik (Intern)
Hendriksen, Rene S. (Intern)
Lund, Ole (Intern)

Other:
Carlsson, Susanne (Intern)

Project Manager, academic:
Aarestrup, Frank Møller (Intern)

Financing sources
Source: Public research programme (public)
Name of research programme: Innovationsfonden
Web address: http://innovationsfonden.dk/da
Amount: 11,246,579.00 Danish Kroner

WHO Advisory Group on Integrated Surveillance of Antimicrobial Resistance (AGISAR)

WHO AGISAR was established in December 2008 to support WHO's effort to minimize the public health impact of antimicrobial resistance associated with the use of antimicrobials in food animals. The Group comprises over 30 internationally renowned experts in a broad range of disciplines relevant to antimicrobial resistance, appointed following a web-published call for advisers and a transparent selection process.

National Food Institute
Research Group for Genomic Epidemiology

Period: 15/12/2009 → …
Number of participants: 1
Acronym: AGISAR

Project participant:
Hendriksen, Rene S. (Intern)
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.

Department of Systems Biology
National Institute of Aquatic Resources
National Food Institute
Research Group for Genomic Epidemiology
University of Copenhagen
Hvidovre Hospital

DHI
Period: 01/01/2009 → 01/05/2015
Number of participants: 2
Biocides, Resistance, Biocides resistance
Other:
Carlsson, Susanne (Intern)
Project Manager, academic:
Aarestrup, Frank Møller (Intern)

Financing sources
Source: Other public support (public)
Name of research programme: Innovationsfonden
Web address: http://innovationsfonden.dk/da
Amount: 14,993,406.00 Danish Kroner

Activities:

Carbapenemase epidemiology in bacteria of animal and environmental origin: the One Health prospective
Period: 8 Jun 2018
Valeria Bortolaia (Guest lecturer)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International

Related event
ASM Microbe 2018
07/06/2018 → 11/06/2018
Atlanta, United States
Activity: Talks and presentations › Conference presentations

International Journal of Food Microbiology (Journal)
Period: 2017
Ana Sofia Ribeiro Duarte (Reviewer)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International

Related journal
International Journal of Food Microbiology
0168-1605
Central database
Activity: Research › Peer review of manuscripts

10th International Conference on Predictive Modelling in Food (Event)
Period: 26 Sep 2017 → 29 Sep 2017
Ana Sofia Ribeiro Duarte (Reviewer)
National Food Institute
Research Group for Genomic Epidemiology
Description
Member of Scientific Committee
Degree of recognition: International
Related event
10th International Conference on Predictive Modelling in Food: ICPMF10
26/09/2017 → 29/09/2017
Cordoba, Spain
Activity: Research › Peer review of manuscripts

Genome dynamics of vancomycin-resistant Enterococcus faecium in clinical samples
Period: 1 Aug 2017 → 1 Feb 2018
Valeria Bortolaia (Supervisor)
National Food Institute
Research Group for Genomic Epidemiology
Description
Master project by Yasmin Kamel
Degree of recognition: International
Activity: Examinations and supervision › Supervisor activities

EU capacity building projects: ENGAGE and COMPARE
Period: 12 Jul 2017
Valeria Bortolaia (Guest lecturer)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International
Related event
Genomics in foodborne pathogen surveillance and outbreak investigation: INNUENDO summer course
12/07/2017 → 13/07/2017
Vitoria-Gasteiz, Spain
Activity: Talks and presentations › Conference presentations

Phenotype prediction using WGS data: resistome and virulome
Period: 12 Jul 2017
Valeria Bortolaia (Guest lecturer)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International
Related event
Genomics in foodborne pathogen surveillance and outbreak investigation: INNUENDO summer course
12/07/2017 → 13/07/2017
Vitoria-Gasteiz, Spain
23836 Quantitative Microbiological Risk Assessment
Period: Jun 2017
Ana Sofia Ribeiro Duarte (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Course Lecturer

Related event

23836 Quantitative Microbiological Risk Assessment 2017
01/06/2017 → 30/06/2017
Denmark
Activity: Other

TEACH FOOD -Developing a teacher's community of practice
Period: 23 May 2017 → 24 May 2017
Lene Duedahl-Olesen (Speaker)
Håkan Vigre (Other)
Lars Bøge Jensen (Other)
Pernille Hammar Andersson (Other)
National Food Institute
Research Group for Analytical Food Chemistry
Research Group for Genomic Epidemiology
Research Group for Microbial Food Safety
Office for Study Programmes and Student Affairs

Description
Oral Presentation and paper
Degree of recognition: International
Documents:
TEACH FOOD abstract

Related event

ETALEE 2017: Exploring Teaching for Active Learning in Engineering Education 2017
23/05/2017 → 24/05/2017
Odense, Denmark
Activity: Talks and presentations › Conference presentations

Silent vanA in Enterococcus faecium from Danish pigs
Period: 22 May 2017 → 2 Jun 2017
Valeria Bortolaia (Main supervisor)
National Food Institute
Research Group for Genomic Epidemiology

Description
Internship of Hans Murillo in relation to the One Health course held at University of Copenhagen, Denmark
Degree of recognition: National
Activity: Examinations and supervision › Supervisor activities

Applied Bioinformatics & Public Health Microbiology
Period: 17 May 2017 → 19 May 2017
Valeria Bortolaia (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Related event

Applied Bioinformatics & Public Health Microbiology
17/05/2017 → 19/05/2017
Cambridge, United Kingdom
Activity: Attending an event › Participating in or organising a conference

Tar-Eating Bacterial Duo may Transform Toxic Compounds into New Usable Materials
Period: 16 May 2017
Sünje Johanna Pamp (Participant)
Department of Biotechnology and Biomedicine
Department of Bio and Health Informatics
National Food Institute
Research Group for Genomic Epidemiology

Description
Danish researchers have sequenced and analyzed the genome of a bacterium that can feed off coal tar. It lives in symbiosis with another bacterium that can recycle its partner’s waste. Researchers hope that this sustainable bacterial duo can transform toxic substances into useful materials. Nevertheless, mapping the genome also led to an unpleasant surprise.

Interview person.
Degree of recognition: International
Documents:
Tar-eating bacterial duo may transform toxic compounds into new usable materials | Sciencenews.dk
Links:
Activity: Other

Applying LCA in decision making- the need and the future perspective
Period: 10 May 2017
Yan Dong (Speaker)
Simona Miraglia (Other)
Stefano Manzo (Other)
Stylianos Georgiadis (Other)
Hjalte Jomo Danielsen Sørup (Other)
Elena Boriani (Other)
Tine Hald (Other)
Sebastian Thøns (Other)
Michael Zwicky Hauschild (Other)
Department of Management Engineering
Quantitative Sustainability Assessment
Centre for oil and gas – DTU
Transport DTU
Transport Modelling
Department of Applied Mathematics and Computer Science
Statistics and Data Analysis
Department of Environmental Engineering
Urban Water Systems
National Food Institute
Research Group for Genomic Epidemiology
Department of Civil Engineering
Section for Structural Engineering
Documents:
Abstra
Applying LCA in policy decision making_Final
Links:
https://brussels.setac.org/welcome/

Related event

SETAC Europe: 27th Annual Meeting – Environmental Quality Through Transdisciplinary Collaboration
07/05/2017 → 13/07/2017
Brussels, Belgium
Activity: Talks and presentations › Conference presentations

One Health International Summer Course 2017
Period: 8 May 2017 → 18 Aug 2017
Tine Hald (Organizer)
Maria Vang Johansen (Organizer)
Liza Rosenbaum Nielsen (Panel member)
Lars Erik Larsen (Organizer)
Anders Dalsgaard (Organizer)
National Food Institute
Research Group for Genomic Epidemiology
National Veterinary Institute
Virology

Description
One Health International Summer Course 2017
5-week elearning part + 1-week on campus part, a total of 5 ECTS
Degree of recognition: International

Related event

One Health International Summer Course 2017
08/05/2017 → 18/08/2017
Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Teaching Quantitative Microbial Risk Assessment - Better Training for Safer Food (BTSF)
Period: 8 May 2017 → 12 May 2017
Ana Sofia Ribeiro Duarte (Guest lecturer)
National Food Institute
Research Group for Genomic Epidemiology

Related event

Teaching Quantitative Microbial Risk Assessment - Better Training for Safer Food (BTSF)
08/05/2017 → 12/05/2017
Czech Republic
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities
Applying LCA in decision making - the need and the future perspective

Period: 7 May 2017 → 11 May 2017

Yan Dong (Guest lecturer)
Simona Miraglia (Guest lecturer)
Stefano Manzo (Guest lecturer)
Stylianos Georgiadis (Guest lecturer)
Hjalte Jomo Danielsen Sarup (Guest lecturer)
Elena Boriani (Guest lecturer)
Tine Hald (Guest lecturer)
Sebastian Thöns (Guest lecturer)
Michael Zwicky Hauschild (Guest lecturer)

Department of Management Engineering
Quantitative Sustainability Assessment

Department of Civil Engineering
Transport DTU
Transport Modelling

Department of Applied Mathematics and Computer Science
Statistics and Data Analysis

Department of Environmental Engineering
Urban Water Systems
National Food Institute
Research Group for Genomic Epidemiology
Section for Structural Engineering

Description
There is nowadays a need of including sustainable considerations in the policy and decision making. Sound decision making requires evidence-based support, i.e. decision analysis to help decision makers in identifying the best alternative based on the associated impacts. Decision analysis includes four steps: 1) structure decision problem; 2) assess possible impacts associated with alternatives; 3) determine stakeholder preferences and 4) evaluate alternatives. Decision analysis can be performed applying different tools, such as cost-benefit analysis (CBA), risk assessment, and life cycle assessment (LCA).

LCA is a decision analysis tool that focuses on environmental impacts. One limit is that LCA is based on defined impact categories and therefore does not provide information for those impacts and consequences out of the LCA scope. However, the LCA framework closely follows the decision analysis scheme and has the potential to be integrated with other decision analysis tools to enhance their assessment of environmental impacts.

To understand why LCA is needed in the policy decision context, we looked into the decision support for policy in several disciplines. Taking sustainable transport policy as an example, the traditional decision analysis tool for choosing the best alternative is CBA. CBA mainly analyses socio-economic impacts, such as travel time savings and costs, while only some environmental impacts are considered; i.e. the damage costs of greenhouse gas emissions, particulate matters, SOx, NOx and noise. Therefore, current transport policy making rarely reflect a full environmental profile of the suggested alternatives. Making decisions based on incomplete information may lead to sub-optimal solutions, especially where the environment is a major concern. There is a growing attention of conducting LCA in transport. Some identified environmental hotspots, such as consumer and household behavior, which may be the focus for future policies. Others assess the environmental impacts associated with building infrastructures and vehicle use. These studies verify that LCA can successfully quantify the environmental profile of alternatives in transport policy, if the relevant physical changes, e.g. vehicle travel distance and new infrastructures, are well-defined. However, before integrating LCA with other decision analysis methods for decision support, the study system, objectives, scopes, evaluation metrics and uncertainty handling need to be aligned.

Degree of recognition: International

Links:
https://brussels.setac.org/

Related event
SETAC Europe: 27th Annual Meeting – Environmental Quality Through Transdisciplinary Collaboration
07/05/2017 → 13/07/2017
Brussels, Belgium
Activity: Talks and presentations › Conference presentations

**Source attribution: Translating science into public health action**
Period: 29 Mar 2017 → 31 Mar 2017
Tine Hald (Keynote speaker)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International

**Related event**

2017 Annual Meeting of SVEPM 2017, 29-31 March, Inverness, Scotland
29/03/2017 → 31/03/2017
Scotland, United Kingdom
Activity: Talks and presentations › Conference presentations

**Burden of disease and source attribution**
Period: 16 Mar 2017
Tine Hald (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
Teaching vet students at the One Health differentiation
Degree of recognition: Local

**Related external organisation**

University of Copenhagen
Bülowsvej 17, 1780, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Waldemir Santiago Neto**
Start date: 3 Mar 2017 → 15 Sep 2017
Tine Hald (Host)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
External research stay for PhD study
Degree of recognition: International
Activity: Hosting a guest lecturer

**ESVAC annual network meeting**
Period: 2 Mar 2017 → 3 Mar 2017
Valeria Bortolaia (Participant)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International

**Related event**

ESVAC annual network meeting
01/03/2016 → 02/03/2016
London, United Kingdom
Activity: Attending an event › Participating in or organising a conference
Prediction of antibiotic resistance phenotypes from whole genome sequence data of clinically relevant bacteria
Period: 27 Feb 2017 → 10 Jul 2017
Valeria Bortolaia (Main supervisor)
National Food Institute
Research Group for Genomic Epidemiology

Description
Bachelor project by Mohammed Nateqi
Degree of recognition: International
Activity: Examinations and supervision › Supervisor activities

Epidemiology and control of Taenia solium in Africa
Period: 24 Feb 2017
Tine Hald (External examiner)
National Food Institute
Research Group for Genomic Epidemiology

Description
PhD thesis
Degree of recognition: International
Activity: Examinations and supervision › Internal examination

First meeting of the One Health Network on Antimicrobial Resistance
Period: 23 Feb 2017
Valeria Bortolaia (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Related event
First meeting of the One Health Network on Antimicrobial Resistance
23/02/2017 → 23/02/2017
Activity: Attending an event › Participating in or organising a conference

Descriptive study of antibiotic resistance and resistance determinants in indicator E. coli from Danish and imported meat and Danish animals using whole genome sequencing (WGS) and phenotypic resistance determination
Period: 21 Feb 2017
Tine Hald (Supervisor)
National Food Institute
Research Group for Genomic Epidemiology

Description
Supervisor and co-examiner of Master thesis, Master in Food Quality and Safety
Degree of recognition: National
Activity: Examinations and supervision › Supervisor activities

Master i Fødevarekvalitet og - sikkerhed
Period: 31 Jan 2017 → 28 Apr 2017
Tine Hald (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

Description
Tine Hald responsible for a module on Risk Assessment of Foodborne Hazards (9 ECTS)
Degree of recognition: National

Related external organisation

University of Copenhagen
Bülowsvej 17, 1780, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Bacterial factors determining changes in epidemiology of cephalosporin-resistant Escherichia coli in Danish poultry
Period: 30 Jan 2017 → 14 Jun 2017
Valeria Bortolaia (Main supervisor)
National Food Institute
Research Group for Genomic Epidemiology

Description
Bachelor project by Anna Mortensen
Degree of recognition: International
Activity: Examinations and supervision › Supervisor activities

ENGAGE Interim meeting 2017
Period: 23 Jan 2017
Rene S. Hendriksen (Organizer)
National Food Institute
Research Group for Genomic Epidemiology

Description
ENGAGE Interim meeting 2017

Related event

ENGAGE Interim meeting 2017
23/01/2017 → 23/01/2017
Parma, Italy
Activity: Attending an event › Participating in or organising a conference

WHO/PAHO Meeting on the Application of WHO Whole Genome Sequencing as a Tool to Strengthen FBD Surveillance and Response in Developing Countries
Period: 10 Jan 2017 → 13 Jan 2017
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
WHO/PAHO Meeting on the Application of WHO Whole Genome Sequencing as a Tool to Strengthen FBD Surveillance and Response in Developing Countries
Washington DC, USA, 10-13 January 2017

Related event

WHO/PAHO Meeting on the Application of WHO Whole Genome Sequencing as a Tool to Strengthen FBD Surveillance and Response in Developing Countries
10/01/2017 → 13/01/2017
Washington DC, United States
Activity: Attending an event › Participating in or organising a conference

Molecular epidemiological studies of Campylobacter isolated from different sources in New Zealand between 2005 and 2015.
Period: 1 Jan 2017 → 4 Mar 2017
Tine Hald (External examiner)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
PhD thesis
Degree of recognition: International
Activity: Examinations and supervision › Internal examination

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**27th European Congress of Clinical Microbiology and Infectious Diseases (ECCMID) (Event)**
Period: 2016 → …
Valeria Bortolaia (Member)
National Food Institute
Research Group for Genomic Epidemiology

**Related event**

**27th European Congress of Clinical Microbiology and Infectious Diseases (ECCMID)**
22/04/2017 → 25/04/2017
Vienna, Austria
Activity: Membership › Membership in review committee

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**Antibiotic induced transmission of antibiotic resistance in Escherichia coli**
Period: 2016 → …
Valeria Bortolaia (Supervisor)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
Co-supervision of PhD student Gang Liu, University of Copenhagen, Denmark
Degree of recognition: International
Activity: Examinations and supervision › Supervisor activities

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**European Committee on Antimicrobial Susceptibility Testing (External organisation)**
Period: 2016 → …
Valeria Bortolaia (Member)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
EUCAST Subcommittee on MIC distributions and ECOFFs. European Committee on Antimicrobial Susceptibility Testing (EU)

**Related external organisation**

**European Committee on Antimicrobial Susceptibility Testing**
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

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**Public health risks linked to antimicrobial-resistant enterococci in meat**
Period: 2016 → …
Valeria Bortolaia (Supervisor)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
Co-supervisor of PhD student Sulaiman Mohammed I Aloitabi, University of Copenhagen, Denmark
2nd Meeting of the Global AMR Surveillance System (GLASS) Collaborating Platform,
Period: 15 Dec 2016 → 16 Dec 2016
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
2nd Meeting of the Global AMR Surveillance System (GLASS) Collaborating Platform,

Related event

Meeting of the WHO Collaborating Centres to support AMR activities globally
Period: 13 Dec 2016 → 14 Dec 2016
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Meeting of the WHO Collaborating Centres to support AMR activities globally

Related event

EURL-AR Training Course: Methods required by The EU Legislation (2013/652/Eu)
Period: 7 Dec 2016 → 9 Dec 2016
Rene S. Hendriksen (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

Description
Selective isolation, quantification, identification and susceptibility testing of ESBL-, Ampc- and carbapenemase-producing E. coli 7 - 9 December 2016

7 - 9 December 2016

Related event

EURL-AR Training Course: Methods required by The EU Legislation (2013/652/Eu)
07/12/2016 → 09/12/2016
Kgs. Lyngby, Denmark
Activity: Talks and presentations › Conference presentations

Global surveillance of antimicrobial resistance in sewage
Period: 7 Dec 2016
Rene S. Hendriksen (Invited speaker)
National Food Institute
Research Group for Genomic Epidemiology

Description
Symposium: "AMR IN Pakistan: Current Situation and Future Approaches", scheduled for the 7-8th December, 2016. Karachi, Pakistan

by videolink

Related event
Symposium: "AMR IN Pakistan: Current Situation and Future Approaches"
07/12/2016 → 08/12/2016
Karachi, Pakistan
Activity: Talks and presentations › Conference presentations

The EURs directors meeting
Period: 2 Dec 2016
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
The EURs directors meeting

Related event
The EURs directors meeting
02/12/2016 → 02/12/2016
Brussels, Belgium
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Antimicrobial resistance as a global threat
Period: 1 Dec 2016
Valeria Bortolaia (Guest lecturer)
National Food Institute
Research Group for Genomic Epidemiology

Description
The Annual Finnish Veterinary Congress 2017

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

COMPARE WP2 meeting
Period: 16 Nov 2016
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
COMPARE WP2 meeting, November 16 2016, RKI, Berlin, Germany.

Related event
COMPARE WP2 meeting
16/11/2016 → 16/11/2016
Berlin, Germany
**6th AMR Network meeting**  
Period: 10 Nov 2016 → 11 Nov 2016  
Rene S. Hendriksen (Lecturer)  
National Food Institute  
Research Group for Genomic Epidemiology

**Description**  
10-11 November 2016, EFSA, Parma, Italy.

**Related event**

**The 6th AMR EFSA Network meeting**  
Period: 10 Nov 2016 → 11 Nov 2016  
Rene S. Hendriksen (Speaker)  
National Food Institute  
Research Group for Genomic Epidemiology

**Description**  
The 6th AMR EFSA Network meeting on 10-11 November 2016, EFSA, Parma, Italy

**Related event**

**Attributing the disease burden to different food groups - will it be easier in the future**  
Period: 7 Nov 2016  
Tine Hald (Speaker)  
National Food Institute  
Research Group for Genomic Epidemiology

**Related event**

**New Science for Food Safety: supporting food chain transparency for improved health**  
07/11/2016 → 10/11/2016  
Singapore, Singapore  
Activity: Talks and presentations › Conference presentations

**To serve and detect" EURL-AR and WHO CC activities: EURL-AR and WHO CC activities**  
Period: 7 Nov 2016  
Rene S. Hendriksen (Lecturer)  
National Food Institute  
Research Group for Genomic Epidemiology

**Description**  
DTU Kompetenceudvikling i forskningsbaseret rådgivning (FBR) - RDTU

**Related external organisation**
**Unknown external organisation**

**Activity:** Talks and presentations › Conference presentations

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**Expert Commission on Addressing the Contribution of Livestock to the Antibiotic Resistance Crisis (External organisation)**

**Period:** 15 Oct 2016 → …

Valeria Bortolaia (Participant)

National Food Institute

Research Group for Genomic Epidemiology

**Description**

This Expert Commission is charged with reviewing federal efforts to date on addressing antibiotic use, including unnecessary use, in animal agriculture, and developing a roadmap for progress for the coming months and years. To that end, the Expert Commission’s primary goal is to develop a short report for release in early 2017 that includes key recommendations for U.S. policymakers, their staff and other key stakeholders in the U.S. government. The report will primarily focus on recommendations on improving and strengthening existing public policy and regulations, as well as new policy ideas and possibly, recommendations for research priorities. Secondary audiences of the report will include journalists who cover antibiotic resistance and the general public.

Degree of recognition: International

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**Related external organisation**

**Expert Commission on Addressing the Contribution of Livestock to the Antibiotic Resistance Crisis**

**Activity:** Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

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**EFSA ENGAGE Workshop**

**Period:** 10 Oct 2016 → 11 Oct 2016

Rene S. Hendriksen (Organizer)

National Food Institute

Research Group for Genomic Epidemiology

**Description**

Speaker

EFSA ENGAGE Workshop 10-11 October 2016 in Warsaw, Poland.

**Related event**

**EFSA ENGAGE Workshop**

10/10/2016 → 11/10/2016

Warsaw, Poland

**Activity:** Attending an event › Participating in or organising a conference

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**Differential fitness of avian CTX-M-1- and CMY-2-encoding plasmids in Escherichia coli**

**Period:** Sep 2016 → Dec 2016

Valeria Bortolaia (Supervisor)

National Food Institute

Research Group for Genomic Epidemiology

**Description**

Special course by Anna Kathrine Bach Mortensen

Degree of recognition: National

**Activity:** Examinations and supervision › Supervisor activities

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**Global Surveillance**

**Period:** 29 Sep 2016

Tine Hald (Speaker)

National Food Institute
Research Group for Genomic Epidemiology

Description
Taking advantage of developments in genomics and data-sharing
Degree of recognition: National

Related event

XVII SIDILV Congress
28/09/2016 → 29/09/2016
Pacengo di Lazise (VR), Italy
Activity: Talks and presentations › Conference presentations

The Global Burden of Foodborne Disease
Period: 28 Sep 2016
Tine Hald (Keynote speaker)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: National

Related event

XVII SIDILV Congress
28/09/2016 → 29/09/2016
Pacengo di Lazise (VR), Italy
Activity: Talks and presentations › Conference presentations

WHO informal WGS training course meeting,
Period: 5 Sep 2016 → 6 Sep 2016
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
WHO informal WGS training course meeting, Milan, Italy, Sep 5-6 2016.

Related event

WHO informal WGS training course meeting,
05/09/2016 → 06/09/2016
Milan, Italy
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

The ESBL/AmpC resistome in Escherichia coli from pigs and pig farmers, Vietnam
Period: 1 Sep 2016 → 15 May 2017
Valeria Bortolaia (Supervisor)
National Food Institute
Research Group for Genomic Epidemiology

Description
Co-supervisor of Master student Jing-Yuan Wang (China Agricultural University) in collaboration with Anders Dalsgaard, University of Copenhagen, Denmark
Activity: Examinations and supervision › Supervisor activities

The Global Burden of Foodborne diseases
Period: 6 Jul 2016
Tine Hald (Speaker)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: Local

Related event
Internal seminar for EFSA staff
06/07/2016 → 06/07/2017
Parma, Italy
Activity: Talks and presentations › Conference presentations

Online Course "Antimicrobial resistance- theory and methods"
Period: 7 Jun 2016 → …
Lina Cavaco (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

Description
Lina Cavaco acted as coordinator and instructor
Links:
https://www.coursera.org/learn/antimicrobial-resistance

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Risk assessment of Salmonella in broiler farms with slaughter and sale at the farm
Period: 1 Jun 2016 → 2 Sep 2016
Tine Hald (Consultant)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: National

Related external organisation
Fødevarestyrelsen
Glostrup, Denmark
Activity: Public and private sector consultancy › Consultancy

Cephalosporin resistance in the Danish chicken meat production chain
Period: 20 May 2016
Valeria Bortolaia (Speaker)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: National

Related event
Third annual meeting of the University of Copenhagen Research Centre for control of antibiotic resistance (UC-CARE)
20/05/2016 → 20/05/2016
Activity: Talks and presentations › Conference presentations

GLOBAL MEETING OF WHO COLLABORATING CENTRES ON FOOD SAFETY AND OTHER STAKEHOLDERS
Period: 16 May 2016 → 17 May 2016
Valeria Bortolaia (Participant)
Related event

GLOBAL MEETING OF WHO COLLABORATING CENTRES ON FOOD SAFETY AND OTHER STAKEHOLDERS
16/05/2016 → 17/05/2016
Geneva, Switzerland
Activity: Attending an event › Participating in or organising a conference

University of Edinburgh
Period: 12 May 2016 → 27 May 2016
Tine Hald (Visiting researcher)

National Food Institute
Research Group for Genomic Epidemiology
Activity: Visiting an external institution › Visiting another research institution

One Health International Summer Course 2016
Period: 9 May 2016 → 23 Aug 2016
Tine Hald (Organizer)
Maria Vang Johansen (Organizer)
Liza Rosenbaum Nielsen (Organizer)
Lars Erik Larsen (Organizer)
Anders Dalsgaard (Organizer)

National Food Institute
Research Group for Genomic Epidemiology
National Veterinary Institute
Virology

Description
One Health International Summer Course 2016
5-week elearning part + 1-week on campus part, a total of 5 ECTS
Degree of recognition: International

Related event

One Health International Summer Course 2016
09/05/2016 → 23/08/2016
Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Impact of Antimicrobial Usage in Food Production
Period: 27 Apr 2016
Tine Hald (Speaker)
National Food Institute
Research Group for Genomic Epidemiology

Description
Presentation given for the Food Forum
Degree of recognition: International

Related external organisation

The National Academies of Science, Engineering and Medicine
10th EUR-AL-AR Workshop 2016
Period: 14 Apr 2016 → 15 Apr 2016
Lina Cavaco (Organizer)
National Food Institute
Research Group for Genomic Epidemiology

Description
10th EUR-AL-AR workshop

Related event

European Union Reference Laboratory, Antimicrobial Resistance – Annual Workshop
Period: 14 Apr 2016 → 15 Apr 2016
Rene S. Hendriksen (Organizer)
National Food Institute
Research Group for Genomic Epidemiology

Description
European Union Reference Laboratory, Antimicrobial Resistance – Annual Workshop April 14-15, 2016, Kgs. Lyngby, Denmark

Related event

World Health Organization's estimates of the relative contributions of food to the burden of disease due to selected foodborne hazards: a structured expert elicitation
Period: 11 Apr 2016
Tine Hald (Speaker)
National Food Institute
Research Group for Genomic Epidemiology

Related event

Food Safety and Food Security Workshop: COST meeting, IS1304, Network on Structured Expert Elicitation
11/04/2016 → 13/04/2016
Dubrovnik, Croatia
Activity: Talks and presentations › Conference presentations

26th European Congress of Clinical Microbiology and Infectious Diseases (ECCMID 2016)
Period: 9 Apr 2016 → 12 Apr 2016
Lina Cavaco (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Poster presenter

ECCMID 2016

Related event

26th European Congress of Clinical Microbiology and Infectious Diseases (ECCMID 2016)
Period: 09/04/2016 → 12/04/2016
Amsterdam, Netherlands
Activity: Attending an event › Participating in or organising a conference

Plasmids without frontiers: animal contribution to plasmid-mediated antimicrobial resistance problems in human medicine
Period: 9 Apr 2016
Valeria Bortolaia (Guest lecturer)
National Food Institute
Research Group for Genomic Epidemiology

Description
26th European Congress of Clinical Microbiology and Infectious Diseases (ECCMID). Amsterdam, NL. 9-12 April 2016. Plasmids without frontiers: animal contribution to plasmid-mediated antimicrobial resistance problems in human medicine

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

AMEG group for the update of the opinion in colistin (External organisation)
Period: 5 Apr 2016
Lina Cavaco (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Body type: EMA

Related external organisation

AMEG group for the update of the opinion in colistin
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

WHO AGISAR Thematic Working Groups (TGW) Meetings
Period: 4 Apr 2016 → 6 Apr 2016
Rene S. Hendriksen (Organizer)
National Food Institute
Research Group for Genomic Epidemiology

Description
WHO AGISAR Thematic Working Groups (TGW) Meetings; Laboratory Methods and Antimicrobial Susceptibility Testing and Data Integration, Bangkok, Thailand 4-6 April 2016

Related event

WHO AGISAR Thematic Working Groups (TGW) Meetings: Laboratory Methods and Antimicrobial Susceptibility Testing and Data Integration
Period: 04/04/2016 → 06/04/2016
Bangkok, Thailand
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.
WHO Global Workshop on Strengthening Integrated Surveillance of Foodborne Diseases and Antimicrobial Resistance through the Whole Genome Sequencing
Period: 4 Apr 2016 → 8 Apr 2016
Rene S. Hendriksen (Organizer)
National Food Institute
Research Group for Genomic Epidemiology

Description
Facilitator / speaker

Related event
WHO Global Workshop on Strengthening Integrated Surveillance of Foodborne Diseases and Antimicrobial Resistance through the Whole Genome Sequencing
04/04/2016 → 08/04/2016
Bangkok, Thailand
Activity: Attending an event › Participating in or organising a conference

Owusu Amponsah
Start date: 1 Apr 2016 → 21 Jun 2016
Håkan Vigre (Host)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International
Activity: Hosting a guest lecturer

TEACH FOOD seminars
Period: Mar 2016 → …
Lene Duedahl-Olesen (Organizer)
Lars Bogø Jensen (Organizer)
Håkan Vigre (Organizer)
National Food Institute
Research Group for Analytical Food Chemistry
Research Group for Microbial Food Safety
Research Group for Genomic Epidemiology

Description
Workshops on Teaching and Learning for teachers every March and September at DTU FOOD
Degree of recognition: Local

Related event
TEACH FOOD seminars: biannual workshops on Teaching and Learning
18/03/2016 → …
Lyngby, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Annual Meeting of the Dutch Society for Microbiology
Period: 22 Mar 2016
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Annual Meeting of the Dutch Society for Microbiology,
Related event

**Annual Meeting of the Dutch Society for Microbiology**
22/03/2016 → 22/03/2016
Arnhem, Netherlands
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Molecular tools for surveillance of antimicrobial resistance**
Period: 22 Mar 2016
Rene S. Hendriksen (Invited speaker)
National Food Institute
Research Group for Genomic Epidemiology
Description

Related event

**Annual Meeting of the Dutch Society for Microbiology**
22/03/2016 → 22/03/2016
Arnhem, Netherlands
Activity: Talks and presentations › Conference presentations

**On the pathogenesis of infections associated with percutaneous orthopaedic implants (External organisation)**
Period: 22 Mar 2016
Lina Cavaco (Participant)
National Food Institute
Research Group for Genomic Epidemiology
Description
Half-time PhD seminar Magdalena Zaborowska. Biomatcell Center for Biomaterials Department of Biomaterials, Institute of Clinical Sciences, Sahlgrenska Academy at University of Gothenburg

Committee for evaluation of Half time seminar, review of report and publications and participation in public defense. The half-time seminar does not just fill the function of control station for the project's advancement, but is also a PhD course that gives 5 HECs. This somewhat influences the task of the evaluation committee.
Degree of recognition: International

Related external organisation

**On the pathogenesis of infections associated with percutaneous orthopaedic implants**
Activity: Membership › Membership in review committee

**Trace back and trace forward in foodborne outbreak investigations**
Period: 15 Mar 2016
Tine Hald (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International

Related event

**SVEPM: Annual meeting 2016: Held a workshop on outbreak investigation**
15/03/2016 → 18/03/2016
Elsinore, Denmark
Activity: Talks and presentations › Conference presentations
H2020 COMPARE General Meeting,
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
H2020 COMPARE General Meeting,

Related event

H2020 COMPARE General Meeting,
08/03/2016 → 10/03/2016
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Gram negatives; Enterobacteriaceae and other -Proteobacteriaceae
Period: 4 Mar 2016
Rene S. Hendriksen (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

Description
DTU course 23258; General Medical Microbiology.

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

ESVAC annual stakeholders meeting
Period: 2 Mar 2016
Lina Cavaco (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
ESVAC annual stakeholders meeting

Related event

ESVAC annual stakeholders meeting
02/03/2016 → 02/03/2016
London, United Kingdom
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

ESVAC annual network meeting
Period: 1 Mar 2016 → 2 Mar 2016
Lina Cavaco (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
ESVAC annual network meeting, European Medicines Agency, Lina Cavaco participated as EURL-AR representative

Related event
ESVAC annual network meeting
01/03/2016 → 02/03/2016
London, United Kingdom
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Antimicrobials advice ad-hoc Group (AMEG), European Medicines Agency (External organisation)
Period: 26 Feb 2016 → Jun 2016
Lina Cavaco (Participant)
National Food Institute
Research Group for Genomic Epidemiology
Description
The AMEG is composed of representatives and experts from the EMA’s Committee for Medicinal Products for Veterinary Use (CVMP) and Committee for Medicinal Products for Human Use (CHMP) as well as the CVMP Antimicrobials Working Party and the CHMP Infectious Diseases Working Party, from the European Food Safety Authority (EFSA), the European Centre for Disease Prevention and Control (ECDC) and the Joint Interagency Antimicrobial Consumption and Resistance Analysis Report (JIACRA). Lina Cavaco is participating as EURL-AR representative work group reconvened based on follow up on the finding of plasmid mediated colistin resistance

Related external organisation
Antimicrobials advice ad-hoc Group (AMEG), European Medicines Agency
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Antimicrobial Resistance in Bacteria from Livestock and Companion Animals (Journal)
Period: Jan 2016 → Mar 2017
Lina Cavaco (Editor)
National Food Institute
Research Group for Genomic Epidemiology
Description
Book to be published by ASM press and to be edited by Frank Aarestrup, Stefan Schwarz, Jianzhong Shen and Lina Cavaco

Related journal
Antimicrobial Resistance in Bacteria from Livestock and Companion Animals
Local database
Activity: Research › Editor of unfinished research anthology/collection

EFSA ENGAGE
Period: 29 Jan 2016
Rene S. Hendriksen (Organizer)
National Food Institute
Research Group for Genomic Epidemiology
Description
Speaker
EFSA ENGAGE kick off meeting
Related event
EFSA ENGAGE
29/01/2016 → 29/01/2016
Parma, Italy
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.
Colloquium "Statistical Methods in Empiric Research"
Period: 26 Jan 2016
Ana Sofia Ribeiro Duarte (Invited speaker)
National Food Institute
Research Group for Genomic Epidemiology

Description
A new method to fit a distribution to microbial counts: making sense of zeroes
Degree of recognition: International

Related external organisation
Bundesinstitut für Risikobewertung
Berlin, Germany
Activity: Talks and presentations › Conference presentations

Project management for researchers at DTU
Period: 25 Jan 2016 → 18 May 2016
Lina Cavaco (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Project management course for researchers at DTU

Related event

Project management for researchers at DTU
25/01/2016 → 18/05/2016
Lyngby, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Project management for researchers at DTU
Period: 25 Jan 2016 → 18 May 2016
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Module 1 25th and 26th January 2016, Module 2 7th and 8th March 2016, Module 3 18th and 19th April 2016, Module 4 17th and 18th May 2016,

Project Management for researchers at DTU: Module 1 -4

Related event

Project management for researchers at DTU
25/01/2016 → 18/05/2016
Lyngby, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

The Global Burden of Foodborne Disease
Period: 20 Jan 2016
Tine Hald (Speaker)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: Local

Related event

Internal meeting for FVST staff
20/01/2016 → 20/01/2016
Glostrup, Denmark
Activity: Talks and presentations › Conference presentations

26th European Congress of Clinical Microbiology and Infectious Diseases (ECCMID) (Event)
Period: 2015 → …
Valeria Bortolaia (Member)
National Food Institute
Research Group for Genomic Epidemiology

Description
Reviewer of conference abstracts

Related event

26th European Congress of Clinical Microbiology and Infectious Diseases (ECCMID)
09/04/2016 → 12/04/2016
Amsterdam, Netherlands
Activity: Membership › Membership in review committee

Antimicrobial resistance and susceptibility testing, definitions and methods
Period: 2015 → 2017
Lina Cavaco (Lecturer)
National Food Institute
Division of Epidemiology and Microbial Genomics
Research Group for Genomic Epidemiology

Description
Coursera e-learning platform "Antimicrobial resistance and susceptibility testing, definitions and methods"

Related event

Antimicrobial resistance and susceptibility testing, definitions and methods
23/04/2015 → …
Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

European Society for Clinical Microbiology and Infectious Diseases (ECCMID) (Event)
Period: 2015 → …
Valeria Bortolaia (Member)
National Food Institute
Research Group for Genomic Epidemiology

Description
Reviewer of grant proposals

Related event

European Society for Clinical Microbiology and Infectious Diseases (ECCMID)
31/10/2015 → 30/11/2015
Activity: Membership › Membership in review committee
Modelling of horizontal transfer of extended-spectrum beta-lactamases (ESBLs) in the gut microbiota
Period: 2015 → …
Valeria Bortolaia (Supervisor)
National Food Institute
Research Group for Genomic Epidemiology
Description
Co-supervisor of PhD student Mehreen Anjum, University of Copenhagen, Denmark
Degree of recognition: International
Activity: Examinations and supervision › Supervisor activities

Source Attribution Estimates of the Relative Contributions to the Burden of Disease due to selected Foodborne Hazards: a WHO Expert Elicitation
Period: 15 Dec 2015 → 16 Dec 2015
Tine Hald (Speaker)
National Food Institute
Research Group for Genomic Epidemiology
Description
FERG symposium, held in Amsterdam
Degree of recognition: International
Documents:
FERGsymposiumabstractbook
Related external organisation
World Health organization and RIVM (National Institute for Public Health)
Royal Netherlands Academy of Arts and Sciences, Amsterdam, Netherlands
Activity: Talks and presentations › Conference presentations

Head of assessment committee
Period: 3 Dec 2015
Håkan Vigre (Internal examiner)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International
Activity: Examinations and supervision › Internal examination

-Steering committee of PhD student Clémentine Henri
Period: 24 Nov 2015
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology
Description
Steering committee of PhD student Clémentine Henri
Related event
-Steering committee of PhD student Clémentine Henri
24/11/2015 → 24/11/2015
Paris, France
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.
Karakterisering multi-resistente Salmonella Typhi ved helgenom sekventering
Period: 18 Nov 2015
Rene S. Hendriksen (Speaker)
National Food Institute
Research Group for Genomic Epidemiology

Related event
DANMAP-seminar /Europæisk Antibiotikadag
18/11/2015 → 18/11/2015
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

-EFSA 5th AMR Network meeting
Period: 12 Nov 2015 → 13 Nov 2015
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology
Description
EFSA 5th AMR Network meeting
Related event
-EFSA 5th AMR Network meeting
12/11/2015 → 13/11/2015
Parma, Italy
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

-EFSA 5th AMR Network meeting
Period: 12 Nov 2015
Rene S. Hendriksen (Speaker)
National Food Institute
Research Group for Genomic Epidemiology
Description
Confirmatory testing in relation to reporting antimicrobial resistance in animal and food - Commission implementing decision; Sanco /652 and Update on activities of the EURL on AMR
Related event
-EFSA 5th AMR Network meeting
12/11/2015 → 13/11/2015
Parma, Italy
Activity: Talks and presentations › Conference presentations

Estimates of the relative contributions to the burden of disease due to selected foodborne hazards: A World Health Organization Expert Elicitation
Period: 5 Nov 2015
Tine Hald (Speaker)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International
Documents:
Abstract EE FERG ISVEE 2015 submitted new
Related event
**Animal contribution to ESBL-producing Escherichia coli and MRSA infections in humans**

**Period:** 29 Oct 2015

Valeria Bortolaia (Guest lecturer)

National Food Institute

Research Group for Genomic Epidemiology

**Related event**

**Symposium on Selection and Spread of Antibiotic Resistances in Agro-Ecosystems and Food Production Environments**

29/10/2015 → 29/10/2015

Fribourg, Switzerland

Activity: Talks and presentations › Conference presentations

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**TEACH FOOD seminar**

**Period:** 29 Oct 2015 → 30 Oct 2015

Lene Duedahl-Olesen (Organizer)

Lars Bogø Jensen (Organizer)

Håkan Vigre (Organizer)

Pernille Hammar Andersson (Organizer)

Sofie Katrine Lorentzen (Organizer)

National Food Institute

Research Group for Analytical Food Chemistry

Research Group for Microbial Food Safety

Research Group for Genomic Epidemiology

Office for Study Programmes and Student Affairs

Office for HR

Office for Finance and Accounting

**Description**

Seminar for teachers at DTU FOOD

Degree of recognition: Local

**Related event**

**TEACH FOOD seminar: seminar for DTU FOOD teachers**

29/10/2015 → 30/10/2015

Hvalsø, Denmark

Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

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**EU conference " farmers and Veterinarians together to tackle antimicrobial resistance"**

**Period:** 23 Oct 2015

Lina Cavaco (Participant)

National Food Institute

Research Group for Genomic Epidemiology

**Description**

EU conference " farmers and Veterinarians together to tackle antimicrobial resistance"

**Related event**
EU conference "farmers and Veterinarians together to tackle antimicrobial resistance"
23/10/2015 → 23/10/2015
Brussels, Belgium
Activity: Attending an event › Participating in or organising a conference

-WHO GLASS, the Implementation of the WHO global antimicrobial resistance surveillance system (GLASS)
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology
Description
WHO GLASS, the Implementation of the WHO global antimicrobial resistance surveillance system (GLASS)
Related event
-WHO GLASS, the Implementation of the WHO global antimicrobial resistance surveillance system (GLASS)
22/10/2015 → 23/10/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Characterization of clonal complexes of Listeria monocytogenes strains of food origin in France: MVN meeting
Period: 9 Oct 2015
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology
Description
Characterization of clonal complexes of Listeria monocytogenes strains of food origin in France: MVN meeting
co-author of the abstact / poster
Related event
Characterization of clonal complexes of Listeria monocytogenes strains of food origin in France: MVN meeting
09/10/2015 → …
France
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

 Hvordan bruger vi risikovurdering i forskellige sammenhæng?
Period: 4 Sep 2015
Håkan Vigre (Speaker)
National Food Institute
Research Group for Genomic Epidemiology
Description
Presentation at Dyrlægerens Dag - Mikrobiologisk Risiko Analyse
Related event
Dyrlægernes Dag 2015: Dyrlægen i risikosamfundet
04/09/2015 → 04/09/2015
Activity: Talks and presentations › Conference presentations

23836 Quantitative Microbiological Risk Assessment
Period: Jun 2015
Ana Sofia Ribeiro Duarte (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Course Lecturer

Related event

23836 Quantitative Microbiological Risk Assessment 2015
01/06/2015 → 30/06/2015
Denmark
Activity: Other

Owusu Amponsah
Start date: 19 Jun 2015 → 19 Dec 2015
Håkan Vigre (Host)
National Food Institute
Research Group for Genomic Epidemiology

Description
Hosting Phd student Owusu Amponsah from Department of Planning, Kwame Nkrumah University of Science and Technology, Ghana. Research project SAWAFO
Degree of recognition: International
Activity: Hosting a guest lecturer

-WHO AGISAR 6 meeting
Period: 10 Jun 2015 → 12 Jun 2015
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
WHO AGISAR 6 meeting

Related event

-WHO AGISAR 6 meeting
10/06/2015 → 12/06/2015
Seoul, Korea, Republic of
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

-WHO AGISAR 6 meeting
Period: 10 Jun 2015
Rene S. Hendriksen (Speaker)
National Food Institute
Research Group for Genomic Epidemiology

Description
Whole Genome Sequencing and integrated surveillance of antimicrobial resistance: "Opportunities and challenges

Related event

-PathoNGen-Trace, Progress Meeting
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
PathoNGen-Trace, Progress Meeting

Related event

-PathoNGen-Trace, Progress Meeting
18/05/2015 → 19/05/2015
Berlin, Germany
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

8th GMI meeting
Period: 11 May 2015
Rene S. Hendriksen (Speaker)
National Food Institute
Research Group for Genomic Epidemiology

Description
Proficiency testing - Progress report 2015

Related event

-8th the Global Microbial Identifier meeting
Beijing, China
Activity: Talks and presentations › Conference presentations

-Better Training Safer Food
Håkan Vigre (Organizer)
National Food Institute
Research Group for Genomic Epidemiology

Description
Better Training for Safer Food - Mikrobiological Risk Assessment
One week training course in the EU program better training for safer food.
Training coordinator
Degree of recognition: International
Related event

**Better Training Safer Food**
04/05/2015 → 08/05/2015
Tallinn, Estonia
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Course in Microbiological Risk Assessment**
Leonardo de Knegt (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
Better Training Safer Food course for QMRA held in Tallinn, Estonia.

Related event

**Better Training Safer Food**
04/05/2015 → 08/05/2015
Tallinn, Estonia
Activity: Talks and presentations › Conference presentations

**Better Training for Safer Food - Risk Analysis**
Period: 3 May 2015 → 5 May 2015
Tine Hald (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
Tutor at course

Related external organisation

**BTSF, Tallin**
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**25th European Congress of Clinical Microbiology and Infectious Diseases**
Period: 25 Apr 2015 → 28 Apr 2015
Lina Cavaco (Participant)
National Food Institute
Division of Epidemiology and Microbial Genomics
Research Group for Genomic Epidemiology

Related event

**25th European Congress of Clinical Microbiology and Infectious Diseases**
25/04/2015 → 28/04/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising a conference

**25th European Congress of Clinical Microbiology and Infectious Diseases**
Period: 25 Apr 2015 → 28 Apr 2015
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology
Description
25th ECCMID - European Congress of Clinical Microbiology and Infectious Diseases,

Related event
25th European Congress of Clinical Microbiology and Infectious Diseases
25/04/2015 → 28/04/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

9th EURL-AR Workshop 2015
Period: 23 Apr 2015 → 24 Apr 2015
Lina Cavaco (Participant)
National Food Institute
Division of Epidemiology and Microbial Genomics
Research Group for Genomic Epidemiology

Related event
9th EURL-AR Workshop 2015
23/04/2015 → 24/04/2015
Lyngby, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

European Union Reference Laboratory Antimicrobial Resistance and FWD ECDC, – Joint Annual Workshop 2015
Period: 23 Apr 2015 → 25 Apr 2015
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
European Union Reference Laboratory Antimicrobial Resistance and FWD ECDC, – Joint Annual Workshop 2015

Related event
European Union Reference Laboratory Antimicrobial Resistance and FWD ECDC, – Joint Annual Workshop 2015
23/04/2015 → 25/04/2015
Kgs. Lyngby, Denmark
Activity: Attending an event › Participating in or organising a conference

Emmanuel de-Graft Johnson Owusu-Ansah
Start date: 17 Apr 2015 → 15 Oct 2015
Tine Hald (Host)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International
Activity: Hosting a guest lecturer

EU FVO training course on AMR
Period: 15 Apr 2015 → 16 Apr 2015
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
EU FVO training course on AMR
Related event

EU FVO training course on AMR
15/04/2015 → 16/04/2015
Kgs. Lyngby, Denmark
Activity: Attending an event › Participating in or organising a conference

One Health International Summer Course 2015
Period: 13 Apr 2015 → 21 Aug 2015
Tine Hald (Organizer)
Maria Vang Johansen (Organizer)
Liza Rosenbaum Nielsen (Organizer)
Lars Erik Larsen (Organizer)
Anders Dalsgaard (Organizer)
National Food Institute
Research Group for Genomic Epidemiology
National Veterinary Institute
Virology

Description
One Health International Summer Course 2015
6-week elearning part + 2 week on campus part, a total of 5 ECTS
Degree of recognition: International

Related event

Gram negatives: Enterobacteriaceae and other -Proteobacteriaceae
Period: 23 Mar 2015
Rene S. Hendriksen (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

Description
DTU course 23258; General Medical Microbiology

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

H2020 EU Compare Kick-off Meeting
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
H2020 EU Compare Kick-off Meeting

Related event
**Course in Microbiological Risk Assessment**

*Period:* 2 Mar 2015  
*Leonardo de Knegt* (Lecturer)  
*National Food Institute  
*Research Group for Genomic Epidemiology*  

**Description**  
Better Training Safer Food course for QMRA held in Berlin, Germany.

**Related event**

**Better Training Safer Food**  
*02/03/2015 → 06/03/2015*  
*Berlin, Germany*  
*Activity:* Talks and presentations › Conference presentations  
*Ana Sofia Ribeiro Duarte* (Guest lecturer)

**Teaching Quantitative Microbial Risk Assessment - Better Training for Safer Food (BTSF)**

*Period:* 2 Mar 2015 → 6 Mar 2015  
*Ana Sofia Ribeiro Duarte* (Guest lecturer)  
*National Food Institute  
*Research Group for Genomic Epidemiology*  

**Degree of recognition:** International

**Related event**

**Teaching Quantitative Microbial Risk Assessment - Better Training for Safer Food (BTSF)**  
*02/03/2015 → 06/03/2015*  
*Germany*  
*Activity:* Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Complutense University**

*Period:* Feb 2015  
*Ana Sofia Ribeiro Duarte* (Visiting researcher)  
*National Food Institute  
*Research Group for Genomic Epidemiology*  

**Degree of recognition:** International  
*Activity:* Visiting an external institution › Visiting another research institution

**Lecturing in the education "Master i Fødevarekvalitet og -sikkerhed" at Copenhagen University**

*Period:* 2 Feb 2015 → 24 Mar 2015  
*Håkan Vigre* (Lecturer)  
*National Food Institute  
*Research Group for Genomic Epidemiology*  

**Description**  
Lecturing in the course Mikrobiologisk og Kemisk fødevaresikkerhed  
*Degree of recognition:* National

**Related external organisation**

**University of Copenhagen**  
Bülowsvej 17, 1780, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Training in Microbiological Risk Assessment: EDES training on Microbiological Risk Assessment**
Period: 19 Jan 2015 → 23 Jan 2015
Ana Sofia Ribeiro Duarte (Speaker)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
Training in Microbiological Risk Assessment: EDES training on Microbiological Risk Assessment - Mauritius
Degree of recognition: International

**Related event**

**Training in Microbiological Risk Assessment: EDES training on Microbiological Risk Assessment**
19/01/2015 → 23/01/2015
Mauritius
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Master i Fødevarekvalitet og -sikkerhed**
Period: 1 Jan 2015 → 20 Dec 2015
Tine Hald (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
Tine Hald responsible for a module on Risk Assessment of Foodborne Hazards (9 ECTS) and a module on Foodborne Outbreak Investigation (4 ECTS)
Degree of recognition: National

**Related external organisation**
University of Copenhagen
Bülowsvej 17, 1780, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Epidemiology and Infection (Journal)**
Period: 2014
Ana Sofia Ribeiro Duarte (Reviewer)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International

**Related journal**
Epidemiology and Infection
0950-2688
Central database
Activity: Research › Peer review of manuscripts

**Food Microbiology (Journal)**
Period: 2014
Ana Sofia Ribeiro Duarte (Reviewer)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International

Related journal

Food Microbiology
0740-0020

Central database
Activity: Research › Peer review of manuscripts

-12th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases
Period: 12 Dec 2014
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
co-author

Largest Vibrio cholera outbreak in Cameroon history studied using whole genome sequencing

Related event

-12th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases
11/12/2014 → 13/12/2014
Bangkok, Thailand
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

WHO Workshop on introduction to microbial whole genome sequencing and analysis for microbiologists
Period: 9 Dec 2014
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description

WHO Workshop on introduction to microbial whole genome sequencing and analysis for microbiologists

Related event

WHO Workshop on introduction to microbial whole genome sequencing and analysis for microbiologists
09/12/2014 → 09/12/2014
Bangkok, Thailand
Activity: Attending an event › Participating in or organising a conference

- **Surveillance of Antimicrobial Resistance for Local and Global Action**
  Period: 2 Dec 2014 → 3 Dec 2014
  Rene S. Hendriksen (Participant)
  National Food Institute
  Research Group for Genomic Epidemiology
  **Description**
  Surveillance of Antimicrobial Resistance for Local and Global Action
  **Related event**
  - **Surveillance of Antimicrobial Resistance for Local and Global Action**
    02/12/2014 → 03/12/2014
    Stockholm, Sweden
    Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

- **7th Meeting on Global Microbial Identifier**
  Period: 11 Sep 2014 → 12 Sep 2014
  Rene S. Hendriksen (Participant)
  National Food Institute
  Research Group for Genomic Epidemiology
  **Description**
  7th Meeting on Global Microbial Identifier
  **Related event**
  - **7th Meeting on Global Microbial Identifier**
    York, United Kingdom
    Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

- **7th Meeting on Global Microbial Identifier**
  Period: 11 Sep 2014
  Rene S. Hendriksen (Speaker)
  National Food Institute
  Research Group for Genomic Epidemiology
  **Description**
  Ring trials and QA/QC - Progress report
  **Related event**
  - **7th Meeting on Global Microbial Identifier**
    York, United Kingdom
    Activity: Talks and presentations › Conference presentations

- **Pathogen Genomics: Application in Plant Health**
  Period: 10 Sep 2014
  Rene S. Hendriksen (Participant)
  National Food Institute
  Research Group for Genomic Epidemiology
Description
Pathogen Genomics: Application in Plant Health

Related event

-Pathogen Genomics: Application in Plant Health
10/09/2014 → 10/09/2014
York, United Kingdom
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Description
Genome sequencing – the ultimate answer to global real time genotyping and surveillance

Related event

-Pathogen Genomics: Application in Plant Health
Period: 10 Sep 2014
Rene S. Hendriksen (Speaker)
National Food Institute
Research Group for Genomic Epidemiology

Description
WHO WPRO training course
Period: 30 Jul 2014 → 1 Aug 2014
Rene S. Hendriksen (Organizer)
National Food Institute
Research Group for Genomic Epidemiology

Description
WHO WPRO National Workshop on Syndromic Surveillance and Testing of Enteric Pathogens (Next Generation Sequencing)

Related event

WHO WPRO training course: WHO WPRO National Workshop on Syndromic Surveillance and Testing of Enteric Pathogens
30/07/2014 → 01/08/2014
Hanoi, Viet Nam
Activity: Attending an event › Participating in or organising a conference

Description
Course lecturer

Related event

23836 Quantitative Microbiological Risk Assessment
Period: Jun 2014
Ana Sofia Ribeiro Duarte (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Course lecturer

Related event

23836 Quantitative Microbiological Risk Assessment 2014
01/06/2014 → 30/06/2014
Denmark
Activity: Other
-EFSA Scientific Colloquium on WGS of food-borne pathogens for public health protection
Period: 16 Jun 2014 → 17 Jun 2014
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
EFSA Scientific Colloquium on WGS of food-borne pathogens for public health protection

Related event
-Global Foodborne Infections Network (GFN) Stakeholder Meeting
Period: 11 Jun 2014 → 13 Jun 2014
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Global Foodborne Infections Network (GFN) Stakeholder Meeting

Related event
A genomic dissection of travel associated ESBL producing Salmonella Typhi originating from the Philippines - A one-off occurrence or threat to the effective treatment of typhoid fever.
Period: 4 Jun 2014
Rene S. Hendriksen (Speaker)
National Food Institute
Research Group for Genomic Epidemiology

Related event
European Union Reference Laboratory, Antimicrobial Resistance – Annual Workshop 2014
Period: 7 Apr 2014 → 8 Apr 2014
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
European Union Reference Laboratory, Antimicrobial Resistance – Annual Workshop
EU WG AMR
Period: 27 Mar 2014
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
EU WG AMR

Related event

Supervision of PhD students at DTU
Period: 25 Mar 2014
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Supervision of PhD students at DTU

Related event

Supervision of PhD students at DTU
25/03/2014 → 25/03/2014
Kgs- Lyngby, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Gram negatives: Enterobacteriaceae and other -Proteobacteriaceae
Period: 13 Mar 2014
Rene S. Hendriksen (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

Description
DTU course 23258; General Medical Microbiology.

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Supervision of PhD students at DTU
Period: 5 Mar 2014 → 20 May 2014
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology
Description
3 time one day course

Supervision of PhD students at DTU

Related event

Supervision of PhD students at DTU
05/03/2015 → 20/05/2015
Kgs. Lyngby, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Collateral damage of disaster relief: introduction of pandemic cholera in Haiti
Period: 3 Mar 2014
Rene S. Hendriksen (Invited speaker)
National Food Institute
Research Group for Genomic Epidemiology

Related event

-Field Epidemiology Scientific Meeting – Public Health England
03/03/2014 → 03/03/2014
Birmingham, United Kingdom
Activity: Talks and presentations › Conference presentations

Description
Field Epidemiology Scientific Meeting – Public Health England

Related event

-Field Epidemiology Scientific Meeting – Public Health England
Period: 3 Mar 2014
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Teaching & Learning (UDtU Module 1)
Period: 21 Jan 2014 → 24 Jan 2014
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Related event

Teaching & Learning (UDtU Module 1)
21/01/2015 → 24/01/2015
Kgs. Lyngby, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

-DG SANCO Meeting with the Directors of the EU reference laboratories in the food, feed and animal health sectors
Period: 17 Jan 2014
Rene S. Hendriksen (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
DG SANCO Meeting with the Directors of the EU reference laboratories in the food, feed and animal health sectors

Related event
-DG SANCO Meeting with the Directors of the EU reference laboratories in the food, feed and animal health sectors
17/01/2014 → 17/01/2014
Bussels, Belgium
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Ana Sofia Ribeiro Duarte (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Poster presentation - Making sense of zeros: impact on human health risk estimates
Degree of recognition: International

Related event
MedVetNet Association International Scientific Conference 2013: One health, one medicine: sharing challenges for combating zoonoses
24/06/2013 → 25/06/2013
Lyngby, Denmark
Activity: Attending an event › Participating in or organising a conference

Origin and evolution of clinically important antimicrobial resistance genes
Period: 2012 → 2015
Valeria Bortolaia (Supervisor)
National Food Institute
Research Group for Genomic Epidemiology

Description
Co-supervisor of PhD student Dereje Dadi Gudeta, University of Copenhagen, DK
Degree of recognition: International
Activity: Examinations and supervision › Supervisor activities

Plasmid-mediated cephalosporin resistance in human and animal Escherichia coli
Period: 2012 → 2015
Valeria Bortolaia (Supervisor)
National Food Institute
Research Group for Genomic Epidemiology

Description
Co-supervisor of PhD student Katrine Hartung Hansen, University of Copenhagen, DK
Degree of recognition: International
Activity: Examinations and supervision › Supervisor activities

23rd International ICFMH Symposium, FoodMicro 2012
Period: 3 Sep 2012 → 7 Sep 2012
Ana Sofia Ribeiro Duarte (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Poster presentation - Fitting a distribution to microbial counts: Making sense of zeros
Degree of recognition: International

Related event
23rd International ICFMH Symposium, FoodMicro 2012
03/09/2012 → 07/09/2012
Istanbul, Turkey
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

University of Tasmania
Period: Mar 2012 → May 2012
Ana Sofia Ribeiro Duarte (Visiting researcher)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International
Activity: Visiting an external institution › Visiting another research institution

Master i Fødevarekvalitet og -sikkerhed
Period: 1 Jan 2012 → 20 Dec 2012
Tine Hald (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology
Description
Tine Hald responsible for a module on Risk Assessment of Foodborne Hazards (9 ECTS) and a module on Foodborne Outbreak Investigation (4 ECTS)
Degree of recognition: National

Related external organisation
University of Copenhagen
Bülowsvej 17, 1780, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

EFSA expert panel on Biological Hazard (External organisation)
Period: 1 Jun 2009 → 1 Jun 2015
Tine Hald (Participant)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International

Related external organisation
EFSA expert panel on Biological Hazard
European Food Safety Authority, Parma, Italy
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

WHO-FERG Foodborne Disease Burden Epidemiology Reference Group (External organisation)
Period: 1 Jan 2007 → …
Tine Hald (Participant)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
Core member of the WHO's Foodborne Disease Burden Epidemiology Reference Group (FERG)
Degree of recognition: International

**Related external organisation**
WHO-FERG Foodborne Disease Burden Epidemiology Reference Group
World Health Organization, Geneva, Switzerland
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

**Prizes:**

**Best Oral Presentation**
Ana Sofia Ribeiro Duarte (Recipient)
National Food Institute, Research Group for Genomic Epidemiology

**Details**
Awarded date: 2010
event: Food Denmark Congress 2010
Prize: Prizes, scholarships, distinctions

**F1000 - Exceptional: Development of Spatial Distribution Patterns by Biofilm Cells (AEM Vol. 81(18)).**
Sünje Johanna Pamp (Recipient)
National Food Institute, Research Group for Genomic Epidemiology

**Description**
Article: Development of Spatial Distribution Patterns by Biofilm Cells, Applied and Environmental Microbiology, 2015 (DOI: 10.3410/f.72596154,793509444), has been recommended in F1000Prime as being of special significance in its field by F1000 Faculty Member Robert Palmer.

**Details**
Awarded date: 8 Sep 2015
Granting Organisations: Faculty of 1000 Ltd
Prize: Prizes, scholarships, distinctions

**F1000Prime - Tolerance to the antimicrobial peptide colistin in Pseudomonas aeruginosa biofilms is linked to metabolically active cells (Mol.Microbiol. Vol. 68(1)).**
Sünje Johanna Pamp (Recipient)
National Food Institute, Research Group for Genomic Epidemiology

**Description**
This study demonstrates that difficulties in treating infections caused by biofilm-forming bacteria may be due to differential sensitivities of metabolically distinct subpopulations of bacterial cells in the biofilm. The authors show that combination therapy, with antibiotics targeting each distinct subpopulation, may be a successful treatment strategy for infections of biofilm-forming bacteria [...].

Synergistic effects of antibiotics are well known, and this paper presents one interesting explanation: distinct subpopulations of cells in a biofilm that are susceptible to different classes of drugs [...].

This paper highlights the importance of studying distinct and well-defined sub-populations of cells in a physiologically relevant context.

**Details**
Awarded date: 15 May 2008
Prize: Prizes, scholarships, distinctions

**Selected by Editors: Microbial Community Assembly and Spatial Ecology (AEM Vol. 81(18)): Articles of Significant Interest**
Sünje Johanna Pamp (Recipient)
National Food Institute, Research Group for Genomic Epidemiology
The principles and mechanisms that govern multicellular community assembly are incompletely understood. Haagensen et al. (p. 6120 – 6128 [doi: 10.1128/AEM.01614-15]) integrated high-resolution time-lapse microscopy with ecological spatial pattern analysis to characterize microbial community assembly and spatial organization. Their work revealed that small multicellular clusters can move, interact with each other, and fuse to form symmetric patterns of larger multicellular assemblages. Knowledge about microbial spatial ecology is central to our understanding of the structure and function of environmental, host-associated, and synthetic microbial communities. Moreover, the observed formation of primordial cell groups and their aggregation to higher-level structures may be a model for studying the emergence of multicellular life.

Details
Awarded date: Sep 2015
Granting Organisations: ASM - Applied Environmental Microbiology
Prize: Prizes, scholarships, distinctions

Press clippings:

Resistensovervågning
Rene S. Hendriksen
30/05/2017
National Food Institute, Research Group for Genomic Epidemiology

Media coverage (1)

Resistensovervågning i Danmark
30/05/2017
Politikens Forlag, Denmark, Other
Andreas Lindqvist
Rene S. Hendriksen
National Food Institute, Research Group for Genomic Epidemiology
Press / Media

ENGAGE project
Rene S. Hendriksen
19/05/2017
National Food Institute, Research Group for Genomic Epidemiology

Media coverage (1)

Idéen bag ENGAGE
19/05/2017
EFSA (International), Denmark, Other
Christian Dominic
Rene S. Hendriksen
National Food Institute, Research Group for Genomic Epidemiology
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

WHO's prioritéringsliste for R&D
Frank Møller Aarestrup
28/02/2017
National Food Institute, Research Group for Genomic Epidemiology

**Media coverage (1)**

**WHO's prioriteringsliste for R&D**
28/02/2017
Videnskab.dk (National), Denmark, Web
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology

**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

**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

**Antibiotika vægtning**
Frank Møller Aarestrup
17/02/2017
National Food Institute, Research Group for Genomic Epidemiology

**Media contribution (1)**

**Antibiotika vægtning**
17/02/2017
Landbrugsmidierne, Web
Mette Boas
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology

**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

Cephalosporiner og differentieret gult kort  
Rene S. Hendriksen  
04/01/2017  
National Food Institute, Research Group for Genomic Epidemiology  
Media contribution (1)

Cephalosporiner og differentieret gult kort  
04/01/2017  
DR Nyhederne, Radio  
Kristian Sloth  
Rene S. Hendriksen  
National Food Institute, Research Group for Genomic Epidemiology  
Press / Media

DTU Fødevareinstituttets rådgivning af Fødevarestyrelsen om MRSA  
Frank Møller Aarestrup  
17/11/2016  
National Food Institute, Research Group for Genomic Epidemiology  
Media contribution (1)

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  
Media contribution (1)

Debatindlæg om MRSA og andre former for resistens  
09/10/2016  
Politiken, Print  
Frank Møller Aarestrup  
National Food Institute, Research Group for Genomic Epidemiology  
Press / Media

MRSA bekæmpelse  
Frank Møller Aarestrup  
19/09/2016  
Subject  
MRSA bekæmpelse  
National Food Institute, Research Group for Genomic Epidemiology  
Media contribution (1)

MRSA bekæmpelse  
19/09/2016
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

Ifm MRSA-dokumentar
Frank Møller Aarestrup
14/09/2016

Subject
Er der blevet lagt pres på mig?
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

Ifm MRSA-dokumentar
14/09/2016
Politiken, Web
Maj Bak Madsen
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
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

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

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
TV2, Television
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology
Press / Media

I relation til DTU presse-meddelse: Mapping foods' DNA can reveal fraud'
Rene S. Hendriksen
30/08/2016

Subject
I relation til DTU presse-meddelse: Mapping foods' DNA can reveal fraud'
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

I relation til DTU presse-meddelse: Mapping foods' DNA can reveal fraud'
30/08/2016
FoodQualityNews.com, Web
Joseph James Whitworth
Rene S. Hendriksen
National Food Institute, Research Group for Genomic Epidemiology
Press / Media

WGS capable of revealing food fraud but limitations identified
Rene S. Hendriksen
30/08/2016
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

WGS capable of revealing food fraud but limitations identified
30/08/2016
FoodQualityNews.com , Web
Rene S. Hendriksen
National Food Institute, Research Group for Genomic Epidemiology
Press / Media
Døden kom med nødhjælpen
Rene S. Hendriksen
30/06/2016

Description
no 18/2016

Subject
Cholera in Haiti
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

Døden kom med nødhjælpen
30/06/2016
Illustreret Videnskab, Web
Rene S. Hendriksen
National Food Institute, Research Group for Genomic Epidemiology

Press / Media

The Haiti /Nepal Cholera connection
Rene S. Hendriksen
30/06/2016

Subject
The Haiti /Nepal Cholera connection
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

The Haiti /Nepal Cholera connection
30/06/2016
Illustreret Videnskab, Print
Antje Poulsen
Rene S. Hendriksen
National Food Institute, Research Group for Genomic Epidemiology

Press / Media

Resistens, MRSA, mv
Frank Møller Aarestrup
08/02/2016

Subject
Resistens, MRSA, mv
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)

Resistens, MRSA, mv
08/02/2016
DR, Television
george larsen, Poul-Erik Heilbutt
Frank Møller Aarestrup
National Food Institute, Research Group for Genomic Epidemiology

Press / Media

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
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

Media contribution (1)

Reduktion i forbrug
Frank Møller Aarestrup
04/08/2015

Subject
Reduktion i forbrug
National Food Institute, Research Group for Genomic Epidemiology

Media contribution (1)