High diversity of genes and plasmids encoding resistance to third-generation cephalosporins and quinolones in clinical Escherichia coli from commercial poultry flocks in Italy

The aim was to investigate occurrence and diversity of plasmid-mediated resistance to third-generation cephalosporins (3GC) and quinolones in clinical Escherichia coli from 200 industrial poultry farms across Italy. E. coli was isolated from colibacillosis lesions in turkeys (n = 109), broilers (n = 98) and layers (n = 22) between 2008 and 2012. 3GC-resistant isolates were screened for extended-spectrum and AmpC β-lactamase (ESBL/AmpC), while all isolates were tested for plasmid-mediated quinolone resistance (PMQR) genes. ESBL/AmpC- and PMQR-positive isolates were typed by pulsed-field gel electrophoresis and antimicrobial susceptibility testing, and their plasmids were characterised by replicon typing, multilocus sequence typing, restriction fragment length polymorphism and conjugation. ESBL/AmpC genes (blaCTX-M-1, blaCTX-M-14, blaCTX-M-1, blaSHV-12, blaCMY-2) were detected in 7%, 9% and 4% of isolates from turkeys, broilers and layers, respectively. We identified seven ESBL/AmpC-encoding plasmid types, usually conjugative (78%), with a marked prevalence of IncI1/pST3 plasmids carrying blaCTX-M-1. PMQR occurred less frequently among isolates from turkeys (0.9%) compared to those from broilers (5%) and layers (4%). The PMQR genes qnrS, qnrB19 and oqxA/B were located on three plasmid types and two non-typeable plasmids, mostly (85%) conjugative. ESBL/AmpC- and PMQR-positive isolates were genetically unrelated and 64% of them were additionally resistant to aminoglycosides, sulfonamides and tetracyclines. Our data show that 3GC- and quinolone-resistant clinical E. coli in Italian poultry production represent a highly diverse population often resistant to most antimicrobials available for poultry. These findings underline the crucial need to develop new strategies for prevention and control of colibacillosis.
Multiplex PCR for detection of plasmid-mediated colistin resistance determinants, mcr-1, mcr-2, mcr-3, mcr-4 and mcr-5 for surveillance purposes

Background and aim: Plasmid-mediated colistin resistance mechanisms have been identified worldwide in the past years. A multiplex polymerase chain reaction (PCR) protocol for detection of all currently known transferable colistin resistance genes (mcr-1 to mcr-5, and variants) in Enterobacteriaceae was developed for surveillance or research purposes.

Methods: We designed four new primer pairs to amplify mcr-1, mcr-2, mcr-3 and mcr-4 gene products and used the originally described primers for mcr-5 to obtain a stepwise separation of ca 200 bp between ampli-cons. The primer pairs and amplification conditions allow for single or multiple detection of all currently described mcr genes and their variants present in Enterobacteriaceae. The protocol was validated testing 49 European Escherichia coli and Salmonella isolates.
of animal origin. Results: Multiplex PCR results in bovine and porcine isolates from Spain, Germany, France and Italy showed full concordance with whole genome sequence data. The method was able to detect mcr-1, mcr-3 and mcr-4 as singletons or in different combinations as they were present in the test isolates. One new mcr-4 variant, mcr-4.3, was also identified. Conclusions: This method allows rapid identification of mcr-positive bacteria and overcomes the challenges of phenotypic detection of colistin resistance. The multiplex PCR should be particularly interesting in settings or laboratories with limited resources for performing genetic analysis as it provides information on the mechanism of colistin resistance without requiring genome sequencing.
Cephalosporin-resistant Escherichia coli isolated from farm-workers and pigs in northern Vietnam

OBJECTIVE Antimicrobial-resistant bacteria may be transmitted between farm workers and livestock. This study aimed to determine and compare the prevalence and the genetic determinants of cefotaxime-resistant and ESBL-producing Escherichia coli in faecal isolates from workers and pigs at 100 farms in northern Vietnam.

METHODS Farmers were interviewed about antimicrobial usage in livestock. Escherichia coli isolated on MacConkey agar containing 2 mg/L of cefotaxime (CTX) were tested for susceptibility to different cephalosporins by disk diffusion and screened for occurrence of ESBL-encoding genes by PCR.

RESULTS Antimicrobial usage was widespread and included classes regarded of critical or high importance in human medicine. Dosages were 0.5-2 times higher than recommended and antimicrobials were often administered right until slaughter. Prevalence of CTX-resistant E. coli was 86% in farm workers and 89% in pigs. In 76% of farms, CTX-resistant E. coli were shared by pigs and farm workers. ESBL-producing E. coli were detected from pigs and workers at 66 and 69 farms, respectively. The ESBL phenotype was mainly mediated by CTX-M and to a lesser extent by TEM. Occurrence of bla\textit{CTX-M} was similar in E. coli from pigs (66.7%) and humans (68.5%).

CONCLUSION The high occurrence of ESBL-producing E. coli in pig farmers and pigs could present a risk for spill-over of these bacteria from pig farms into the community. Genomic studies are needed to elucidate reservoirs and transmission routes of ESBL-producing E. coli at livestock farms.
Vancomycin resistance in Enterococcus faecium isolated from Danish chicken meat is located on a pVEF4-like plasmid persisting in poultry for 18 years

The occurrence of vancomycin-resistant Enterococcus faecium (VREfm) in food has public health relevance since foodborne VREfm may colonize the gut of consumers and transfer vancomycin resistance genes to the indigenous gut microbiota. Therefore, we determined occurrence and elucidated genetic traits of VREfm in Danish retail chicken meat. Three out of 40 samples (7.5%) from two slaughterhouses yielded VREfm (vancomycin MIC > 32mg/L). This is the first report of VREfm in Danish retail poultry meat since 2010 (DANMAP). All three VREfm belonged to the sequence type ST32, cluster type CT1068. Using whole genome sequencing, we detected transposon Tn1546 harbouring the vanA operon encoding vancomycin resistance. The vanA operon was located on a 43.4kb plasmid highly similar (99.9% identity across 97.5% of the sequence) to pVEF4 which was observed in VREfm in Norwegian poultry in 1998 as well as in Danish poultry in 2010. The remarkable persistence of a pVEF4-like plasmid in enterococcal populations may be explained by the presence of two independent plasmid stability systems namely the ω/ε/ζ toxin-antitoxin system and the prgOPN gene cluster. Filter mating experiments showed that the pVEF4-like plasmid could transfer between E. faecium strains in vitro and that transfer occurred concomitantly with a larger, co-residing plasmid. The data presented here indicates that poultry meat constitutes a reservoir of VREfm and further investigations are needed to assess the risk of foodborne transmission to humans.

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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
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.

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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
Biochemical Characterization of CPS-1, a Subclass B3 Metallo-beta-Lactamase from a Chryseobacterium piscium Soil Isolate

CPS-1 is a subclass B3 metallo-beta-lactamase from a Chryseobacterium piscium isolate collected from soil, showing 68% amino acid identity to the GOB-1 enzyme. CPS-1 was overproduced in Escherichia coli Rosetta (DE3), purified by chromatography, and biochemically characterized. This enzyme exhibits a broad-spectrum substrate profile, including penicillins, cephalosporins, and carbapenems, which overall resembles those of L1, GOB-1, and acquired subclass B3 enzymes AIM-1 and SMB-1.
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Chromobacterium spp. harbour Ambler class A beta-lactamases showing high identity with KPC

Objectives: The origin of KPC is unknown. The aim of this study was to detect progenitors of KPC in silico and to functionally verify their beta-lactam hydrolysis activity.

Methods: The sequence of KPC-2 was used to mine the NCBI protein sequence database. The best non-KPC hits were analysed by amino acid (aa) alignment and phylogenetic tree construction. Genes encoding KPC-2 homologues were expressed in Escherichia coli. The carbapenemase activities of the recombinant strains were characterized by the CarbaNP test and UV spectrophotometry and MICs of selected beta-lactams were determined.

Results: Genes encoding the closest KPC-2 homologues were identified on the chromosome of Chromobacterium piscinae strain ND17 (CRP-1, 76% aa identity), Chromobacterium sp. C-61 (CRS-1, 70% aa identity) and Chromobacterium haemolyticum DSM19808 (CRH-1, 69% aa identity). All three Chromobacterium beta-lactamases were phylogenetically more related to KPC than to other Ambler class A beta-lactamases. The 27 bp region preceding the start codon of bla(CRP-1) displayed high nucleotide identity to the corresponding region upstream from bla(KPC) (74%). Heterologous expression of bla(CRP-1) and to a lesser extent of bla(CRH-1) in E. coli significantly increased the MICs of meropenem and most cephalosporins. The CarbaNP test was positive for both recombinant strains, but spectrophotometric analysis confirmed higher carbapenemase activity for CRP-1-producing clones.

Conclusions: The recovery of three class A beta-lactamases with up to 76% aa identity to KPC from distinct Chromobacterium species is highly indicative of the role played by this genus in the evolution of KPC.
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Erratum for Gudeta et al., The Soil Microbiota Harbors a Diversity of Carbapenem-Hydrolyzing beta-Lactamases of Potential Clinical Relevance (vol 60, pg 151, 2016)

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Expanding the Repertoire of Carbapenem-Hydrolyzing Metallo-ß-Lactamases by Functional Metagenomic Analysis of Soil Microbiota

Carbapenemases are bacterial enzymes that hydrolyze carbapenems, a group of last-resort ß-lactam antibiotics used for treatment of severe bacterial infections. They belong to three ß-lactamase classes based amino acid sequence (A, B, and D). The aim of this study was to elucidate occurrence, diversity and functionality of carbapenemase-encoding genes in soil microbiota by functional metagenomics. Ten plasmid libraries were generated by cloning metagenomic DNA from agricultural (n = 6) and grassland (n = 4) soil into Escherichia coli. The libraries were cultured on amoxicillin-containing agar and up to 100 colonies per library were screened for carbapenemase production by CarbaNP test. Presumptive carbapenemases were characterized with regard to DNA sequence, minimum inhibitory concentration (MIC) of ß-lactams, and imipenem hydrolysis. Nine distinct class B carbapenemases, also known as metallo-ß-lactamases (MBLs), were identified in six soil samples, including two subclass B1 (GRD23-1 and SPN79-1) and seven subclass B3 (CRD3-1, PEDO-1, GRD33-1, ESP-2, ALG6-1, ALG11-1, and DHT2-1). Except PEDO-1 and ESP-2, these enzymes were distantly related to any previously described MBLs (33 to 59% identity). RAphy analysis indicated that six enzymes (CRD3-1, GRD23-1, DHT2-1, SPN79-1, ALG6-1, and ALG11-1) originated from Proteobacteria, two (PEDO-1 and ESP-2) from Bacteroidetes and one (GRD33-1) from Gemmatimonadetes. All MBLs detected in soil microbiota were functional when expressed in E. coli, resulting in detectable imipenem-hydrolyzing activity and significantly increased MICs of clinically relevant ß-lactams. Interestingly, the MBLs yielded by functional metagenomics generally differed from those detected in the same soil samples by antibiotic selective culture, showing that the two approaches targeted different subpopulations in soil microbiota.

General information
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Host-Specific Patterns of Genetic Diversity among IncI1-I gamma and IncK Plasmids Encoding CMY-2 beta-Lactamase in Escherichia coli Isolates from Humans, Poultry Meat, Poultry, and Dogs in Denmark

CMY-2 is the most common plasmid-mediated AmpC beta-lactamase in Escherichia coli isolates of human and animal origin. The aim of this study was to elucidate the epidemiology of CMY-2-producing E. coli in Denmark. Strain and plasmid relatedness was studied in 93 CMY-2-producing clinical and commensal E. coli isolates collected from 2006 to 2012 from humans, retail poultry meat, broilers, and dogs. Multilocus sequence typing (MLST), antimicrobial susceptibility testing, and conjugation were performed in conjunction with plasmid replicon typing, plasmid multilocus sequence typing (pMLST), restriction fragment length polymorphism (RFLP), and sequencing of selected bla(CMY-2)-harboring plasmids. MLST revealed high strain diversity, with few E. coli lineages occurring in multiple host species and sample types. bla(CMY-2) was detected on plasmids in 83 (89%) isolates. Most (75%) of the plasmids were conjugative and did not (96%) cotransfer resistance to antimicrobials other than cephalosporins. The main replicon types identified were IncI1-I gamma (55%) and IncK (39%). Isolates from different host species mainly carried distinct plasmid subtypes. Seven of the 18 human isolates harbored IncI1-I gamma/sequence type 2 (ST2), IncI1-I gamma/ST12, or IncK plasmids highly similar to those found among animal isolates, even though highly related human and animal plasmids differed by nonsynonymous single nucleotide polymorphisms (SNPs) or insertion sequence elements. This study clearly demonstrates that the epidemiology of CMY-2 can be understood only by thorough plasmid characterization. To date, the spread of this beta-lactam resistance...
determinant in Denmark is mainly associated with IncK and IncI1-I gamma plasmids that are generally distributed according to host-specific patterns. These baseline data will be useful to assess the consequences of the increasing human exposure to CMY-2-producing E. coli via animal sources.

**IMPORTANCE**
CMY-2 is the most common plasmid-mediated AmpC beta-lactamase in Escherichia coli. This beta-lactamase is poorly inhibited by clavulanic acid and confers resistance to cephemycins, third-generation cephalosporins, and aztreonam. Furthermore, resistance to carbapenems has been reported in E. coli as a result of production of plasmid-encoded CMY-2 beta-lactamase in combination with decreased outer membrane permeability. The gene encoding CMY-2 generally resides on transferable plasmids belonging to different incompatibility groups. The prevalence of CMY-2-mediated cephalosporin resistance in E. coli varies significantly depending on the geographical region and host. This study demonstrates that the epidemiology of CMY-2 can be understood only by thorough plasmid characterization. To date, the spread of this beta-lactam resistance determinant in Denmark is mainly associated with IncK and IncI1-I gamma plasmids, which are generally distributed according to host-specific patterns. These data will be useful to assess the consequences of the increasing human exposure to CMY-2-producing E. coli via animal sources.
Human health risks associated with antimicrobial-resistant enterococci and Staphylococcus aureus on poultry meat

Enterococci and staphylococci are frequent contaminants on poultry meat. Enterococcus faecalis, Enterococcus faecium and Staphylococcus aureus are also well-known aetiologic agents of a wide variety of infections resulting in major healthcare costs. This review provides an overview of the human health risks associated with the occurrence of these opportunistic human pathogens on poultry meat with particular focus on the risk of food-borne transmission of antimicrobial resistance. In the absence of conclusive evidence of transmission, this risk was inferred using data from scientific articles and national reports on prevalence, bacterial load, antimicrobial resistance and clonal distribution of these three species on poultry meat. The risks associated with ingestion of antimicrobial-resistant enterococci of poultry origin comprise horizontal transfer of resistance genes and transmission of multidrug-resistant E faecalis lineages such as sequence type ST16. Enterococcus faecium lineages occurring in poultry meat products are distantly related to those causing hospital-acquired infections but may act as donors of quinupristin/dalfopristin resistance and other resistance determinants of clinical interest to the human gut microbiota. Ingestion of poultry meat contaminated with S. aureus may lead to food poisoning. However, antimicrobial resistance in the toxin-producing strains does not have clinical implications because food poisoning is not managed by antimicrobial therapy. Recently methicillin-resistant S. aureus of livestock origin has been reported on poultry meat. In theory handling or ingestion of contaminated meat is a potential risk factor for colonization by methicillin-resistant S. aureus. However, this risk is presently regarded as negligible by public health authorities. Clinical Microbiology and Infection (C) 2015 European Society of Clinical Microbiology and Infectious Diseases. Published by Elsevier Ltd. All rights reserved.

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Authors: Bortolaia, V. (Intern), Espinosa-Gongora, C. (Ekstern), Guardabassi, L. (Ekstern)
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Relation between tetR and tetA expression in tetracycline resistant Escherichia coli

Background: Tetracyclines are among the most used antibiotics in livestock worldwide. Resistance is widely disseminated in Escherichia coli, where it is generally mediated by tetracycline efflux pumps, such as TetA. Expression of tetracycline efflux pumps is tightly controlled by the repressor TetR, which has been shown to be tetracycline-responsive at sub-MIC tetracycline concentrations. The objective of this study was to investigate the effects of increasing tetracycline concentrations on the growth of TetA-producing E. coli, and to determine how expression of tetA and tetR related to each other in different growth phases in the presence of tetracycline. Results: A tetracycline resistant E. coli strain containing tetA and tetR on the chromosome was constructed and cultured in the presence of increasing concentrations of tetracycline. Expression of tetR and tetA was measured at four time points in different growth phases by quantitative real-time PCR. The TetA-producing E. coli exhibited prolonged lag phase with increasing concentrations of tetracycline, while expression of tetA and tetR increased and decreased, respectively, with increasing tetracycline concentration. The levels of tetA and tetR mRNA varied depending on growth phase, resulting in a gradual decrease of the tetA/tetR ratio from approximately 4 in the lag phase to approximately 2 in the stationary phase. Conclusion: This study shows that the expression of tetR and tetA is tetracycline concentration- and growth phase-dependent, contributing to improved understanding of the relationships between E. coli growth, tetracycline exposure and expression of tetracycline resistance.

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BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.472 SNIP 1.039 CiteScore 2.95
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The Soil Microbiota Harbors a Diversity of Carbapenem-Hydrolyzing beta-Lactamases of Potential Clinical Relevance

The origin of carbapenem-hydrolyzing metallo-beta-lactamases (MBLs) acquired by clinical bacteria is largely unknown. We investigated the frequency, host range, diversity, and functionality of MBLs in the soil microbiota. Twenty-five soil samples of different types and geographical origins were analyzed by antimicrobial selective culture, followed by phenotypic testing and expression of MBL-encoding genes in Escherichia coli, and whole-genome sequencing of MBL-producing strains was performed. Carbapenemase activity was detected in 29 bacterial isolates from 13 soil samples, leading to identification of seven new MBLs in presumptive Pedobacter roseus (PEDO-1), Pedobacter borealis (PEDO-2), Pedobacter kyungheensis (PEDO-3), Chryseobacterium piscium (CPS-1), Epilithonimonas tenax (ESP-1), Massilia oculi (MSI-1), and Sphingomonas sp. (SPG-1). Carbapenemase production was likely an intrinsic feature in Chryseobacterium and Epilithonimonas, as it occurred in reference strains of different species within these genera. The amino acid identity to MBLs described in clinical bacteria ranged between 40 and 69%. Remarkable features of the new MBLs included prophage integration of the encoding gene (PEDO-1), an unusual amino acid residue at a key position for MBL structure and catalysis (CPS-1), and overlap with a putative OXA beta-lactamase (MSI-1). Heterologous expression of PEDO-1, CPS-1, and ESP-1 in E. coli significantly increased the MICs of ampicillin, ceftazidime, cefpodoxime, cefoxitin, and meropenem. Our study shows that MBL producers are widespread in soil and include four genera that were previously not...
known to produce MBLs. The MBLs produced by these bacteria are distantly related to MBLs identified in clinical samples but constitute resistance determinants of clinical relevance if acquired by pathogenic bacteria.

**General information**

**State:** Published  
**Organisations:** University of Copenhagen  
**Authors:** Gudeta, D. D. (Ekstern), Bortolaia, V. (Intern), Amos, G. (Ekstern), Wellington, E. M. H. (Ekstern), Brandt, K. K. (Ekstern), Poirel, L. (Ekstern), Nielsen, J. B. (Ekstern), Westh, H. (Ekstern), Guardabassi, L. (Ekstern)  
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**Publication information**

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Web of Science (2016): Indexed yes  
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Scopus rating (2013): SJR 2.397 SNIP 1.42 CiteScore 4.67  
ISI indexed (2013): ISI indexed yes  
Web of Science (2013): Indexed yes  
BFI (2012): BFI-level 1  
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BFI (2011): BFI-level 1  
Scopus rating (2011): SJR 2.514 SNIP 1.578 CiteScore 5.02  
ISI indexed (2011): ISI indexed yes  
Web of Science (2011): Indexed yes  
BFI (2010): BFI-level 1  
Scopus rating (2010): SJR 2.412 SNIP 1.541  
Web of Science (2010): Indexed yes  
BFI (2009): BFI-level 1  
Scopus rating (2009): SJR 2.399 SNIP 1.648  
Web of Science (2009): Indexed yes  
BFI (2008): BFI-level 1  
Scopus rating (2008): SJR 2.327 SNIP 1.457  
Web of Science (2008): Indexed yes  
Scopus rating (2007): SJR 2.141 SNIP 1.493  
Web of Science (2007): Indexed yes  
Scopus rating (2006): SJR 2.315 SNIP 1.404  
Scopus rating (2005): SJR 2.285 SNIP 1.519
CTX-M-1 and CTX-M-15-producing Escherichia coli in dog faeces from public gardens

General information
State: Published
Organisations: University of Copenhagen
Authors: Damborg, P. (Ekstern), Kjelin Morsing, M. (Ekstern), Petersen, T. (Ekstern), Bortolaia, V. (Intern), Guardabassi, L. (Ekstern)
Number of pages: 4
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Main Research Area: Technical/natural sciences

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Scopus rating (2016): CiteScore 1.01 SJR 0.484 SNIP 0.775
Web of Science (2016): Indexed yes
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Scopus rating (2015): SJR 0.409 SNIP 1.445 CiteScore 0.98
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.644 SNIP 1.113 CiteScore 1.54
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.494 SNIP 1.001 CiteScore 1.41
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.57 SNIP 0.798 CiteScore 1.26
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.649 SNIP 0.99 CiteScore 1.42
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.541 SNIP 1.007
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.401 SNIP 0.698
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.33 SNIP 0.608
Scopus rating (2007): SJR 0.12 SNIP 0.539
Scopus rating (2006): SJR 0.155 SNIP 0.888
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.125 SNIP 0.142
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.114 SNIP 0
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.215 SNIP 0
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.382 SNIP 0.46
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.321 SNIP 0.769
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.11 SNIP 0.918
Web of Science (2000): Indexed yes
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Publication: Research - peer-review › Journal article – Annual report year: 2015
CTX-M-1 β-lactamase expression in Escherichia coli is dependent on cefotaxime concentration, growth phase and gene location.
blaCTX-M-1 mRNA expression and CTX-M-1 protein levels were dependent on cefotaxime concentration, growth phase and gene location. These results provide insight into the expression of cephalosporin resistance in CTX-M-1-producing E. coli, improving our understanding of the relationship between antimicrobial therapy and the expression of resistance mechanisms.
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.

**General information**

State: Published
Organisations: Department of Systems Biology, National Food Institute, Research Group for Genomic Epidemiology, Statens Serum Institut, University of Copenhagen
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Pages: 132-136
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Main Research Area: Technical/natural sciences

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The occurrence and diversity of vancomycin-resistant Enterococcus faecium (VREF) were investigated in 100 Danish broiler flocks 15 years after the avoparcin ban. VREF occurred in 47 flocks at low fecal concentrations detectable only by selective enrichment. Vancomycin resistance was prevalently associated with a transferable nontypeable plasmid lineage occurring in multiple E. faecium clones. Coselection of sequence type 842 by tetracycline use only partly explained the persistence of vancomycin resistance in the absence of detectable plasmid coresistance and toxin-antitoxin systems.
Quantitative assessment of faecal shedding of beta-lactam-resistant Escherichia coli and enterococci in dogs

Quantitative data on faecal shedding of antimicrobial resistant bacteria are crucial to assess the risk of transmission from dogs to other animals as well as humans. In this study we investigated prevalence and concentrations of beta-lactam-resistant Escherichia coli and enterococci in the faeces of 108 dogs presenting at a veterinary hospital in Denmark. The dogs had not been treated with antimicrobials for 4 weeks prior to the study. Total E. coli and enterococci were quantified by counts on MacConkey and Slanetz-Bartley, respectively. Resistant E. coli and enterococci were counted on the same media containing relevant antibiotic concentrations, followed by species identification using MALDI-TOF. Ampicillin- and cefotaxime-resistant E. coli were detected in 40% and 8% of the dogs, respectively, whereas approximately 15% carried ampicillin-resistant enterococci, mainly Enterococcus faecium. In the faeces of the carriers, the proportion of resistant strains in the total bacterial species population was on average 15% for both ampicillin-resistant E. coli (median faecal load $3.2 \times 10^4$ cfu/g) and E. faecium ($5.8 \times 10^2$ cfu/g), and 4.6% for cefotaxime-resistant E. coli ($8.6 \times 10^3$ cfu/g).

Cefotaxime resistance was associated with the presence of bla(CTX-M-1) ($n = 4$), bla(CMY-2) ($n = 4$) or multiple mutations in the promoter and coding region of chromosomal ampC ($n=1$). Altogether the results indicate that the risks of zoonotic transmission of beta-lactam-resistant bacteria via human exposure to canine faeces greatly vary amongst individual dogs and are influenced by unidentified factors other than recent antimicrobial use. (C) 2015 Elsevier B.V. All rights reserved.

General information
State: Published
Organisations: University of Copenhagen
Authors: Espinosa-Gongora, C. (Ekstern), Qaswar Ali Shah, S. (Ekstern), Jessen, L. R. (Ekstern), Bortolaia, V. (Intern), Langebaek, R. (Ekstern), Bjornvad, C. R. (Ekstern), Guardabassi, L. (Ekstern)
Number of pages: 5
Pages: 298-302
High diversity of plasmids harbouring blaCMY-2 among clinical Escherichia coli isolates from humans and companion animals in the upper Midwestern USA

Objectives: To determine the population structure and genetic relatedness of plasmids encoding CMY-2 β-lactamase in clinical Escherichia coli from humans and companion animals within a defined geographical area. Methods: In total, 42 human and 73 companion animal isolates displaying an AmpC phenotype were isolated at a regional diagnostic reference laboratory in the upper Midwestern USA during 2009-11. Following PCR screening for transferable AmpC genes and plasmid transformation, blaCMY-2-positive plasmids were characterized by S1 nuclease PFGE, PCR-based replicon typing, antimicrobial susceptibility testing of transformants, conjugation experiments, plasmid multilocus sequence typing and restriction fragment length polymorphism. Results: blaCMY-2 occurred in 6 (14%), 56 (86%) and 6 (75%) isolates from humans, dogs and cats, respectively. Usually plasmids carrying blaCMY-2 were conjugative (78%) and did not contain additional resistance genes (82%). The replicon types were IncI1 (52%), IncAC (13%), IncFII (10%), IncI2 (5%), IncL/M (3%), IncB/O (2%) or non-typeable (15%). Related IncI1/ST12 plasmids were detected in one human and five canine isolates, while the remaining plasmids did not show similarity across host species. A novel epidemiological linkage of blaCMY-2 with IncL/M plasmids and a new CMY gene variant (blaCMY-108) were found in human isolates. Conclusions: This study is one of the first One Health attempts to compare plasmids encoding CMY-2 β-lactamase among clinical isolates from humans and companion animals in the same region. The results indicate an unforeseen heterogeneity of plasmid backgrounds and suggest limited exchange between the two populations, in which blaCMY-2 occurred at very different frequencies and was harboured by distinct plasmid types. © The Author 2014. Published by Oxford University Press on behalf of the British Society for Antimicrobial Chemotherapy. All rights reserved.

General information
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The aim of this study was to evaluate the population dynamics of CTX-M-producing Enterobacteriaceae in individual pigs on a farm positive for CTX-M-14-producing Escherichia coli. Fecal samples were collected once around the farrowing time from five sows and four times along the production cycle from two of their respective offspring. Multiple colonies per sample were isolated on cefotaxime-supplemented MacConkey agar with or without prior enrichment, resulting in 98 isolates identified by matrix-assisted laser desorption ionization-time of flight mass spectrometry and tested for bla(CTX-M). CTX-M-positive isolates (n = 86) were typed by pulsed-field gel electrophoresis (PFGE). Plasmids harboring bla(CTX-M) were characterized in 22 representative isolates by replicon typing and restriction fragment length polymorphism. Based on the PFGE results, all individuals shed unrelated CTX-M-14-producing E. coli strains during the course of life. Concomitant shedding of CTX-M-2/97-producing Proteus mirabilis or Providencia rettgeri was observed in two sows and two offspring. At least two genetically unrelated CTX-M-producing E. coli strains were isolated from approximately one-fourth of the samples, with remarkable differences between isolates obtained by enrichment and direct plating. A clear decrease in strain diversity was observed after weaning. Dissemination of bla(CTX-M-14) within the farm was attributed to horizontal transfer of an IncK plasmid that did not carry additional resistance genes and persisted in the absence of antimicrobial selective pressure. Assessment of strain diversity was shown to be influenced by the production stage from which samples were collected, as well as by the isolation method, providing useful information for the design and interpretation of future epidemiological studies of CTX-M-producing Enterobacteriaceae in pig farms.

General information
State: Published
Organisations: University of Copenhagen
Authors: Hansen, K. H. (Ekstern), Bortolaia, V. (Intern), Damborg, P. (Ekstern), Guardabassi, L. (Ekstern), Goodrich-Blair, H. (ed.) (Ekstern)
Number of pages: 7
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Publication date: 2014
Main Research Area: Technical/natural sciences

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BFI (2018): BFI-level 2
VanO, a new glycopeptide resistance operon in environmental Rhodococcus equi isolates

We describe here the sequence and gene organization of a new glycopeptide resistance operon (vanO) in Rhodococcus equi from soil. The vanO operon has low homology to enterococcal van operons and harbors a vanHOX cluster transcribed in the direction opposite that of the vanS-vanR regulatory system and composed of three open reading frames with unknown function. This finding has clinical interest, since glycopeptides are used to treat R. equi infections and resistance has been reported in clinical isolates. Copyright © 2014, American Society for Microbiology. All Rights Reserved.

General information
State: Published
Organisations: University of Copenhagen
Authors: Gudeta, D. D. (Ekstern), Moodley, A. (Ekstern), Bortolaia, V. (Intern), Guardabassi, L. (Ekstern)
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Scopus rating (2016): CiteScore 4.21 SJR 2.21 SNIP 1.312
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Scopus rating (2015): SJR 2.322 SNIP 1.365 CiteScore 4.28
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Scopus rating (2014): SJR 2.349 SNIP 1.431 CiteScore 4.45
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Scopus rating (2013): SJR 2.397 SNIP 1.42 CiteScore 4.67
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The first attempt of an active integrated laboratory-based Salmonella surveillance programme in the north-eastern region of Nigeria

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

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, University of Ilorin, University of Maiduguri
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.41
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.57
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.56
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.69
ISI indexed (2013): ISI indexed yes
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BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.51
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BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.55
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Characterization of Isolates of Salmonella enterica Serovar Stanley, a Serovar Endemic to Asia and Associated with Travel

Salmonella enterica serovar Stanley (S. Stanley) is a common serovar in Southeast Asia and was the second most common serovar implicated in human salmonellosis in Thailand in the years 2002 to 2007. In contrast, this serovar is relatively uncommon in Europe. The objective of this study was to characterize a collection of S. Stanley strains isolated from Thai (n = 62), Danish (n = 39), and French (n = 24) patients to gain a broader understanding of the genetic diversity, population dynamics, and susceptibility to antimicrobials. All isolates were characterized by pulsed-field gel electrophoresis and antimicrobial susceptibility testing. The molecular mechanisms of resistance to extended-spectrum cephalosporins and plasmid-mediated resistance to quinolones were characterized by PCR and sequencing. Plasmid profiling, replicon typing, and microarray analysis were used to characterize the genetic mechanisms of antimicrobial resistance in 10 extended-spectrum cephalosporinase-producing isolates. Considerable genetic diversity was observed among the isolates characterized with 91 unique XbaI pulsed-field gel electrophoresis (PFGE) patterns, including 17 distinct clusters consisting of two to seven indistinguishable isolates. We found some of the S. Stanley isolates isolated from patients in Europe were acquired during travel to Southeast Asia, including Thailand. The presence of multiple plasmid lineages carrying the extended-spectrum cephalosporinase-encoding bla\textit{CMY-2} gene in S. Stanley isolates from the central part of Thailand was confirmed. Our results emphasize that Thai authorities, as well as authorities in other countries lacking prudent use of antimicrobials, should improve the ongoing efforts to regulate antimicrobial use in agriculture and in clinical settings to limit the spread of multidrug-resistant Salmonella isolates and plasmids among humans and pigs in Thailand and abroad.
The 9th EURL-AR Proficiency Testing Salmonella and Campylobacter 2010

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Karlsmose, S. (Intern), Hendriksen, R. S. (Intern), Bortolaia, V. (Intern), Aarestrup, F. M. (Intern)
Number of pages: 73
Publication date: Jun 2011

Publication information
Population Genetics of Vibrio cholerae from Nepal in 2010: Evidence on the Origin of the Haitian Outbreak

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

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

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Northern Arizona University, National Public Health Laboratory, Translational Genomics Research Institute
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Main Research Area: Technical/natural sciences

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ISSN (Print): 2150-7511
Ratings:
Potential Pathogenicity and Host Range of Extended-Spectrum β-Lactamase-Producing Escherichia coli Isolates from Healthy Poultry

Thirty of 33 epidemiologically unrelated extended-spectrum β-lactamase (ESBL)-producing Escherichia coli isolates from healthy poultry lacked the virulence genes commonly associated with human-pathogenic strains. The main zoonotic risk is associated with the broad host range of avian E. coli belonging to sequence type complex 10 and of IncN and IncI1 plasmids carrying blaCTX-M or blaSHV.

General information

State: Published
Organisations: University of Copenhagen
Authors: Bortolaia, V. (Intern), Larsen, J. (Ekstern), Damborg, P. (Ekstern), Guardabassi, L. (Ekstern)
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General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Hendriksen, R. S. (Intern), Karlsmose, S. (Intern), Bortolaia, V. (Intern), Jensen, A. B. (Intern), Aarestrup, F. M. (Intern)
Distribution and possible transmission of ampicillin- and nalidixic acid-resistant Escherichia coli within the broiler industry

This study was performed to determine the origin and transmission of beta-lactam- and (fluoro)quinolone-resistant Escherichia coli in healthy, untreated broiler flocks. We focused on the dynamics of bacteria resistant to critically important antimicrobials for public and veterinary health in view of the possible link between antimicrobial resistant bacteria in farm animals and humans. By processing faecal samples collected with the sock method in broiler parent and broiler flocks, E. coli resistant to ampicillin and nalidixic acid were frequently isolated, while resistance to ciprofloxacin was detected at a very low frequency, and resistance to cephalosporins was not detected. Similarly, resistance to ampicillin and nalidixic acid were the only phenotypes detected in a collection of clinical E. coli isolates associated with first-week-mortality in broiler parent chicks. Although antimicrobial resistant E. coli were genetically diverse by means of amplified fragment length polymorphism (AFLP) typing, indistinguishable isolates were present in different flocks, including isolates from broiler parent chicks, broiler parents and broilers. In the absence of apparent selective pressure, the genotypic heterogeneity that we describe is likely the consequence of multiple introductions of antimicrobial resistant bacteria into the production system. The confinement under which broilers are raised limits the possibilities of bacterial transmission among different flocks. Our findings are consistent with vertical transmission of ampicillin- and nalidixic acid-resistant E. coli through the broiler production system. The persistence of antimicrobial resistant E. coli in healthy, untreated chicken flocks emphasises the need of careful evaluation of therapeutic options at any level of the broiler production. (C) 2009 Elsevier B.V. All rights reserved.
LIFE, Escherichia coli, antimicrobial resistance, Poultry, Vertical transmission, AFLP, Microbiology, Veterinary (all), Antimicrobial resistance, ampicillin, beta lactam antibiotic, cefotaxime, ceftiofur, cephalosporin derivative, ciprofloxacin, nalidixic acid, quinoline derived antiinfective agent, amplified fragment length polymorphism, antibiotic resistance, article, bacterial transmission, bacterium isolation, broiler, chicken, controlled study, feces analysis, genetic heterogeneity, genetic selection, genotype, minimum inhibitory concentration, mortality, nonhuman, phenotype, poultry farming, vertical transmission, veterinary medicine, Ampicillin, Ampicillin Resistance, Amplified Fragment Length Polymorphism Analysis, Animals, Anti-Bacterial Agents, Chickens, Drug Resistance, Bacterial, Escherichia coli Infections, Feces, Genotype, Microbial Sensitivity Tests, Nalidixic Acid, Phenotype, Poultry Diseases, Animalia, Bacteria (microorganisms), MICROBIOLOGY, VETERINARY, QUINOLONE RESISTANCE, HUMANS, SALMONELLA, DENMARK, DANISH, FECES, PIGS, Biochemistry studies - General, Pathology - Therapy, Pharmacology - General, Physiology and biochemistry of bacteria, Medical and clinical microbiology - General and methods, Medical and clinical microbiology - Bacteriology, Chemotherapy - General, methods and metabolism, Chemotherapy - Antibacterial agents, cephalosporin, Bacteria, Eubacteria, Microorganisms, Animals, Birds, Chordates, Nonhuman Vertebrates, Vertebrates

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10.1016/j.vetmic.2009.10.024
Source: FindIt
Source-ID: 70139
Publication: Research - peer-review › Journal article – Annual report year: 2010
High Diversity of Extended-Spectrum β-Lactamases in Escherichia coli Isolates from Italian Broiler Flocks

We characterized 67 Escherichia coli isolates with reduced susceptibility to cefotaxime or ceftiofur obtained from healthy broilers housed in five Italian farms. The blaCTX-M-1, blaCTX-M-32 and blaSHV-12 β-lactamase genes were identified on IncI1, IncN, or IncFIB plasmids. Considerable genetic diversity was detected among the extended-spectrum β-lactamase (ESBL)-producing isolates, and we identified indistinguishable strains in unrelated farms and indistinguishable plasmids in genetically unrelated strains. The detection of highly mobile plasmids suggests a potential animal reservoir for β-lactamase genes.

General information
State: Published
Organisations: University of Copenhagen
Authors: Bortolaia, V. (Intern), Guardabassi, L. (Ekstern), Trevisani, M. (Ekstern), Bisgaard, M. (Ekstern), Venturi, L. (Ekstern), Bojesen, A. M. (Ekstern)
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BFI (2015): BFI-level 1
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

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

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
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

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
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

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

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

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

European Committee on Antimicrobial Susceptibility Testing (External organisation)
Period: 2016 → …
Valeria Bortolaia (Member)
National Food Institute
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 Aloitiabi, University of Copenhagen, Denmark
Degree of recognition: International
Activity: Examinations and supervision › Supervisor activities

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

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
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
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

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 Copehnagen, Denmark
Activity: Examinations and supervision › Supervisor activities

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)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International

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

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

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

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

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

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