

Muenster, Germany). Clusters were generated using the minimum spanning tree (MST) algorithm.

Results: In total, 111 STEC O91 patient isolates were analyzed by WGS. MST analysis of these isolates was based on 4671 genes, pairwise ignoring missing values, and resulted in five clusters (< 300 alleles differing) and six singletons. MLST⁺-based clustering was concordant with classical MLST and serotyping. Most common ST were ST33 (67 samples), associated with serotypes O91:H14, H⁻ and Hnt and ST442 (28 samples), associated with serotype O91:H21. These two serotypes represent two main clusters in MST with a distance of at least 2379 alleles among each other. One sample out of the O91:H14 cluster was isolated from a patient suffering from HUS, while eight samples out of the O91:H21 cluster were associated with HUS. The chance to develop severe illness and HUS manifestation is significantly higher in patients infected with the cluster representing serotype O91:H21 (Odds Ratio: 37.3).

Conclusion: WGS allows a detailed clustering of STEC O91 and prediction of severity of clinical disease (symptoms). Current investigations address a deeper evolutionary analysis and subclustering of O91 serotypes to elucidate their phylogenetic origin.

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420/ZOV

Human pathogenic *Clostridium difficile* strains in companion animals detected in a Germany-wide survey.

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Introduction: In humans *Clostridium (C.) difficile* infections (CDI) can vary from symptomless carriage to life-threatening intestinal disease. The recent changes in epidemiology of CDI with an increasing incidence and severity are of particular concern. Although virulent strains affecting humans have also been isolated from various animal species, epidemiological data on *C. difficile* in companion animals are scarce, limiting the risk assessment of possible interspecies transmission.

Objectives: This study aimed to collect first national data on occurrence and genotypic variation of *C. difficile* in dogs, cats and their owners and define risk factors associated with colonization or CDI.

Materials & Methods: From July 2012 to August 2013, a Germany-wide survey was conducted sampling companion animals and their owners. Capillary gel electrophoresis based PCR ribotyping, Multilocus VNTR Analysis (MLVA) and PCR detection of toxin genes A, B and the binary toxin were used to characterise isolated *C. difficile* strains.

Results: A total of 1,435 faecal samples could be acquired from 415 different households with 40.7% of human and 59.3% of animal origin. The *C. difficile* isolation rates were 2.91% (17/584) and 2.94% (25/851) for human and animal samples, respectively. Typing revealed twelve resp. eight different PCR ribotypes in isolates from humans resp. companion animals. Three of the animal ribotypes could also be isolated from human samples (014/0, 010 and the highly virulent ribotype 078). Moreover ribotypes 027 and 078 were isolated in dogs. These ribotypes are considered highly virulent in humans. Within two households identical ribotypes were isolated from two partner animals (in both cases 014/0), whereas no *C. difficile* pair from owner and pet sharing the same household could be detected. The risk assessment revealed known risk factors for colonization or CDI in humans (antibiotic intake and age). In companion animals risk factors positively associated with *C. difficile* colonization/CDI were the contact to a human suffering from diarrhoea, intake of antibiotics

or proton pump inhibitors, age, acute disease, inappetence, and diarrhoea.

Conclusion: *C. difficile* isolation rates are low in companion animals and their owners in Germany. Well known human ribotypes including virulent ribotypes 027 and 078 also occur in dogs and suggest a common infection source, zoonotic transmission or both. Future case-control studies should be implemented to get insight into the risk of zoonotic *C. difficile* infections.

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421/ZOV

A combined case control and MLST source attribution study of human *Campylobacter* infections in Germany

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Background: *Campylobacter* infection is the most commonly reported bacterial gastroenteritis in Germany, but its epidemiology remains incompletely understood. To investigate the risk factors for *Campylobacter* infections and the routes of transmission in Germany, we have performed a case control study combined with molecular strain typing (MLST) and source attribution analysis in the framework of the FBI-Zoo network.

Methods: We conducted the study in selected districts of four German federal states. Case patients were recruited through local health authorities (Nov 2011-Feb 2014). Controls were randomly selected from population registries. All participants completed a questionnaire. *Campylobacter* isolates of a subset of case patients were cultured and further analyzed by MLST of seven housekeeping genes. Using the questionnaires, we conducted univariate logistic regression analyses (SVA), adjusted for age group, sex, and federal state, and multivariate logistic regression analyses (MVA).

Results: In the SVA, travelling abroad was determined to be a statistically significant risk factor (OR 1.11 (95% CI: 1.06-1.17; p-value <0,001; study population: 1814 cases, 3983 controls). For further source-directed analyses, we excluded cases that had travelled abroad. Consumption of chicken meat, preparation of poultry meat in the household, eating out, contact to chickens or ducks/geese, and the use of antacids were identified, among others, as risk factors in SVA. Being a vegetarian, consumption of beef, fresh fruit, vegetables, or herbs were negatively associated with disease. For children <5 years contact with animals (dogs, birds, chickens, ducks/geese), playing in a sand box, and using a pacifier were additional risk factors. Results of MVA will also be presented.

MLST was performed for 614 patient isolates and 543 isolates from animals (338) and food sources (205) that had been collected in the geographical and temporal context of the study. Several new *Campylobacter* sequence types (STs) were uncovered and currently dominant STs in humans, animals and food were identified.

MLST data combined with detailed source information of current animal and food strains were then combined for a source attribution analysis of the human isolates using Bayesian inference on an asymmetric island model. The main sources attributed to human *Campylobacter* infection overall, and specifically with *C. jejuni*, were consumption of chicken and contact with pets. The main source attributed to human *C. coli* infection was consumption of pork meat.

Conclusions: This first analysis of *Campylobacter* cases and controls in Germany in combination with molecular typing and source attribution confirmed that chicken meat consumption and its