Assessment of exposure of humans to *Campylobacter* spp. of animal origin in Switzerland

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Schlüsselwörter
Zoonoses, Campylobacter, dogs, cats, cattle, genotyping, AFLP

Problemstellung und Zielsetzung

Campylobacter is the most frequent food-born zoonotic pathogen in Switzerland. The aim of this project was to evaluate the contribution of different infection sources to human campylobacteriosis.

Material und Methoden

The project consisted of three sub-projects:
Analysis of existing information on Campylobacter in different animal species. Pets were identified as a potential source of human campylobacteriosis which had not been studied in Switzerland. Therefore, a prevalence and risk factor study on Campylobacter in dogs and cats was conducted.
Assessment of genetic relatedness of Campylobacter from human cases with isolates from different animal species. *C. jejuni* strains from humans, dogs, cats, cattle and poultry were analysed through AFLP genotyping, which allowed the assessment of possible interactions between hosts.
Establishment of a stochastic simulation model which integrates epidemiological and genotyping data to evaluate the relative importance of different infection sources to human campylobacteriosis. The exposure of humans to the potential risk factors traveling abroad, poultry consumption, contact with dogs and cats, and other sources were analysed for five different age groups.

Ergebnisse und Bedeutung

The prevalence of Campylobacter spp. in 634 dogs and 596 cats was 41.2% and 41.9%, respectively. Young animals (<=3 years) had significantly higher odds of carrying C. upsaliensis/C. helveticus than older animals (OR 1.8 - 3.3), whereas for *C. jejuni* carriage, the age was not a risk.
Among 243 apparently epidemiologically unrelated *C. jejuni* isolates, 136 different genotypes were identified, of which 48 were clusters grouping at least two isolates. A high degree of source mixing within the genotypes was observed, indicating the lack of host specificity of *C. jejuni*. By comparing isolates from different hosts, several *C. jejuni* strains were identified which remained identical over several years and in different species.
With the stochastic exposure model, the significance of the assessed exposure pathways was shown to differ considerably between age groups. With the included exposure pathways, 70% of the cases in young children and about 80% of the cases in the group of people aged from 20 to 34 years could be explained. Traveling abroad accounted for 53% of the cases in young adults, poultry for 24%, and pets for 3%.

Publikationen, Poster und Präsentationen

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***Projekt** 1.01.14*

***Projektdauer** June 2002 - December 2005*