

Genetic Diversity and Antibiotic Resistance Patterns in a *Campylobacter* Population Isolated from Poultry Farms in Switzerland

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The diversity and genetic interrelation of *Campylobacter jejuni* and *C. coli* isolated from Swiss poultry were assessed by three independent typing methods. Samples were derived prior to slaughter from 100 randomly selected flocks (five birds per flock) raised on three different farm types. The observed flock prevalence was 54% in total, with 50% for conventional and 69% for free-range farms. Birds held on farms with a confined roaming area had the lowest prevalence of 37%. *Campylobacter* isolates were characterized by amplified fragment length polymorphism (AFLP), restriction fragment length polymorphism of *flaA* PCR fragments (*flaA*-RFLP), and disk diffusion testing for eight antimicrobial agents that are commonly used in veterinary or human medicine in Switzerland. Analysis of the genotypic results indicates that the *Campylobacter* population in Swiss poultry is genetically highly diverse. Nevertheless, occasionally, isolates with identical or nearly identical characteristics were isolated from different farms or farm types in different locations. Genetic typing by AFLP and *flaA*-RFLP was found to be complementary. The majority of isolates (67%) were susceptible to all tested antibiotics; however, single, double, and triple resistances were observed in 7%, 23%, and 2% of the strains, respectively. There was no correlation between genotype and antibiotic resistance. Surprisingly, sulfonamide resistance was frequently found together with streptomycin resistance. Our findings illustrate the results of common genetic exchange in the studied bacterial population.

The importance of *Campylobacter jejuni* as a human pathogen is generally accepted. This gram-negative, obligate microaerophilic, thermophilic bacterial species is ubiquitous and possesses the ability to colonize the intestinal mucosa of most warm-blooded animals. Birds are the preferred host for *C. jejuni*, where colonization occurs asymptotically. Human campylobacteriosis is the most common food-borne bacterial disease in many developed and developing countries (7), and the consumption or handling of poultry meat is a major risk factor contributing to approximately half of the infections (12). The reduction of the prevalence of *Campylobacter* in chicken products is, therefore, an effective way to reduce the risk of infection. To achieve this goal, the factors influencing *Campylobacter* prevalence at different points during its propagation from “stable to table” need to be clearly identified and their relevance needs to be evaluated using risk assessment models (13, 25).

The various DNA-based typing methods which have been developed for *Campylobacter* (32) are effective tools for identifying contamination sources and describing the population dynamics of any given microorganism. None of these methods is superior to describe the “true” evolutionary and epidemiological interrelations of a bacterial population. Studies ad-

ressing the pros and cons of bacterial typing schemes suggest that a combination of at least two methods is desirable in order to obtain significant discrimination and reliable strain identification (4, 32). This recommendation applies specifically to any bacterial species with a high diversity and a known weakly clonal population structure, such as *C. jejuni*.

The aim of our study was to describe the genetic interrelations of the *Campylobacter* population isolated from Swiss broilers. Taking the weak clonality of *C. jejuni* into account, we used three typing methods: amplified fragment length polymorphism (AFLP), based on the whole genome of a given organism; restriction fragment length polymorphism of *flaA* PCR fragments (*flaA*-RFLP), assessing polymorphisms in a single gene of *C. jejuni/C. coli*; and the phenotypic determination of antibiotic (AB) resistance. The latter phenotype can result from point mutations or the presence of (plasmids harboring) resistance genes. AFLP is considered to give relatively stable genotypes in *C. jejuni*, as it is insensitive to genome rearrangement and point mutation (5). RFLP analysis of *flaA* is valuable in short-term epidemiology of *Campylobacter* (26). Antibiotic resistance is of increasing concern and may be rapidly shared between populations with different genotypes. As *C. jejuni/C. coli* is naturally capable of taking up DNA, this applies to both plasmid-borne and chromosomally encoded resistance. The grouping based on cluster analysis carried out for each typing scheme was related to parameters identified as being relevant for risk assessment at the farm level. We focused on three factors: the housing system for broiler production, broiler flock size, and geographic location of the farm.

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