

# Subtyping of *Campylobacter* spp to the identification of foodborne sources and to the development of targeted control strategies

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## Schlüsselwörter

Campylobacter; typing; antibiotic resistance; data base; monitoring

## Problemstellung und Zielsetzung

*Campylobacter* is a worldwide disseminated zoonosis which causes gastroenteritis in humans and severe cases require antibiotic treatment. The *Campylobacter* population in both animals and humans in Switzerland should be characterized using different genotyping methods and the antibiotic resistance should be determined. A database containing these information should be created and be accessible for further epidemiological studies.

## Material und Methoden

*Campylobacter* strains were isolated from humans, poultry, pigs, cats, dogs, cattle, zoo animals and water, identified using biochemical methods and differentiated by genotyping using AFLP, PFGE and RFLP. Antibiotic resistance profile was determined by disk diffusion and broth dilution techniques. The mechanisms of resistance were determined by sequence analyses. The data base was created using Bionumerics.

## Ergebnisse und Bedeutung

*C. jejuni* was the dominant *Campylobacter* species and could be detected in every source. *C. coli* was the most frequent species in pigs, and was less frequent in humans, poultry, pets and zoo animals. *C. upsaliensis* was mainly found in pets, and rarely in humans and zoo animals. A few *C. lari* were found in humans, pets, cattle, as *C. concisus* in pets, and *C. hyointestinalis* in cattle. AFLP was found to be the most appropriate genotyping method to distinguish between specific strains, whereas RFLP is suitable for the analysis of a large amount of strains. Genotyping methods revealed a weak clonality between *Campylobacter* of the same species.

Resistance to ampicillin, amoxicillin, ciprofloxacin, tetracycline, streptomycin and sulfonamides were found in *Campylobacter* isolates from poultry. In *C. coli* isolates from pigs, resistance to ciprofloxacin and erythromycin was explained by the presence of a point mutation in the *gyrA* and 23S rRNA genes, respectively. There was no correlation between *Campylobacter* genotype and antibiotic resistance.

This study reflects the current *Campylobacter* population in Switzerland and allowed to create a database. Further surveillance of *Campylobacter* including antibiotic resistance is necessary to prevent outbreaks caused by multidrug resistant strains.

## Publikationen, Poster und Präsentationen

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