

Tracing and quantitative detection of *Campylobacter jejuni*

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Key words

real-time PCR, multilocus sequence typing (MLST), epidemiology

Aim of the study

Direct detection, identification and quantification of *C. jejuni* and *C. coli* from poultry by real-time PCR. Genotyping and antibiotic resistance towards quinolone and macrolide of *Campylobacter* isolates from poultry and human clinical cases to investigate their diversity and the role of poultry in human campylobacteriosis.

Material and methods

Swiss poultry neck skin and caeca samples collected in the framework of the 2008 “EU baseline study” were used in the project. The application of a newly developed *fusA* gene-based real-time PCR was directly tested on 351 neck skin samples. A total of 340 *Campylobacter* isolates from caeca and neck skin were genotyped (MLST, *flaB*, *rpoB*), antibiotic resistance towards macrolides (mutations in the 23S rRNA gene) and quinolones (mutations in *gyrA*) determined and later on compared with 136 human *C. jejuni* isolates from the same year.

Results and significance

The new real-time PCR assay proved to be a sensitive method for direct detection, quantification, and differentiation of *C. jejuni* and *C. coli* from poultry neck skin. A *Campylobacter* prevalence of 70% was determined with 60% of positive samples identified as *C. jejuni*, 10% as *C. coli* and 30% were positive for both. Genotyping and antibiotic resistance determination of poultry isolates showed a broad variety of types. Comparison of caecal and neck skin isolates indicated self-contamination from the flock during slaughter as the main source of *Campylobacter*. Antibiotic resistance against macrolides was low (3%) and only found in *C. coli* whereas resistance towards quinolones was found in 19% of *C. jejuni* and 28% of *C. coli* isolates. Genotypes found in human *C. jejuni* showed a significant overlap with those of poultry isolates. Quinolone resistance in human *C. jejuni* was much higher (38%) possibly resulting from therapeutic use of quinolones or reflecting infections acquired in other countries with elevated levels of quinolone resistance. The results provide a solid basis for further quantitative and qualitative analysis of *Campylobacter* in poultry by real-time PCR as well as for investigating more thoroughly source attribution of *Campylobacter*.

Publications, posters and presentations

- Schnider, A. (2009) Prevalence of *Campylobacter jejuni* and *Campylobacter coli* on Swiss broiler carcasses determined by comparative real-time PCR. Inaugural-Dissertation, Vetsuisse-Fakultät, Universität Bern.
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- Wirz, S. (2009) Genotypes and antibiotic resistance of *Campylobacter* isolates from Swiss broiler during 2008. Inaugural-Dissertation, Vetsuisse-Fakultät, Universität Bern.
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- Kittl, S. (2010) Comparison of genotypes and antibiotic resistance of *Campylobacter jejuni* from humans and slaughtered chickens in Switzerland. Inaugural-Dissertation, Vetsuisse-Fakultät, Universität Bern.
- Kuhnert, P. (2009) MLST and antibiotic resistance determination of Swiss *Campylobacter*. CRL-Campylobacter Workshop, Uppsala, Sweden 5.-7. October 2009 (Talk).
- The Annual meetings of SGM (Lausanne 2009, Zürich 2010) and at Swiss Molecular Microbiology Workshop SWIMM2010 (Gwattzentrum Thun) (Poster presentations).

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