8 Summary

Prevalence, antimicrobial resistance and genotyping (AFLP) of thermophilic *Campylobacter* spp. in broiler flocks and analysis of risk factors for *Campylobacter* colonisation at flock level

From May 2004 to July 2005, 279 broiler flocks of different production types were tested for the presence of thermophilic *Campylobacter* spp. Of each flock caecal content of ten chickens was tested. All *Campylobacter* isolates were additionally identified by multiplex- PCR. 79 *Campylobacter* isolates were tested for susceptibility to eight antimicrobial agents and combinations by microbroth dilution and 236 *Campylobacter* isolates were genotyped by AFLP- analysis, too. To identify potential risk factors for the presence of *Campylobacter* spp. at flock level, 75 farms were analysed using farm and flock specific information obtained from questionnaires.

Of all investigated broiler flocks *Campylobacter* spp. was detected in 44%. The *Campylobacter* prevalence varied between different slaughter houses. *C. jejuni* was the most prevalent species (77%) followed by *C. coli* (23%). An association of *Campylobacter* colonisation with increasing age at slaughter was not observed. In one slaughterhouse more *C. coli* positive flocks were observed. A longer fattening duration and different sources of infections are possible explanations. Higher prevalence was mainly associated with summer and fall.

Within- flock prevalence varied from 10% to 100%. In 33% of the *Campylobacter* positive flocks all ten caecal probes were positive. Differences in time of infection and in the ability of *Campylobacter* strains to colonize chickens are possible reasons.

Flocks of conventional and Louisiana broiler houses harboured in most cases *C. jejuni*, whereas *C. coli* was the predominant species in flocks from free range or organic farming. Different sources of infection, differences in slaughter age and different *Campylobacter* strains could explain this distribution of *Campylobacter* species.

Comparing results of pooled and single probes, 93% of *Campylobacter* positive single probes were detected using pooled probes. Reasons for that were probably low within-flock prevalence and a low quantitative level of *Campylobacter* spp. Such a result is tolerable because of less investigation of material and time.

The biochemical results were in accordance with results of the multiplex- PCR.

Of the 79 (61 *C. jejuni*, 18 *C. coli*) chicken isolates 30% (31% bzw. 28%) were ampicillin resistant, 13% (8% bzw. 28%) were resistant against a combination of ampicillin and sulbactam, 10% (8% bzw. 17%) were ceftazidime resistant, 41% (39%

bzw. 44%) were ciprofloxacin and nalidixic acid resistant und 30% (30% bzw. 33%) were tetracycline resistant. All strains were susceptible against gentamicin. All *C. jejuni* strains were susceptible against erythromycin, whereas 28% of *C. coli* strains were resistant.

From 61 *C. jejuni*- isolates and 18 *C. coli* isolates 34 AFLP- cluster respectively 11 AFLP- cluster were identified, demonstrating the genetic diversity of *Campylobacter* spp. isolated from poultry. However, the presence of identical AFLP- genotypes in different flocks and various time intervals demonstrates stability of *Campylobacter* strains under certain environmental conditions. Dominant and reiterating AFLP-genotypes in successive flocks show the presence of persistent sources of *Campylobacter* spp. in the environment. Colonisation with sporadic isolates was also found.

Campylobacter negative flocks followed *Campylobacter* positive flocks demonstrating, that it is possible to prevent a *Campylobacter* infection. The presence of *Campylobacter* positive simultaneously with *Campylobacter* negative flocks on a farm makes a vertical transmission improbable. Different *Campylobacter* species within a flock and in successive flocks may be caused by different sources of infections and describe the dynamic of colonisation.

Three risk factors for *Campylobacter* colonisation were identified. Free range and organic broiler flocks showed a significantly higher *Campylobacter* prevalence. A possible reason could be a higher risk of contamination from natural sources. Significantly more *Campylobacter* positive flocks were also observed in flocks with a size up to 15.000 and more than 25.000 chickens. Different production and management systems are possible explanations. Additionally, flocks using nipple drinkers with trays were significantly more frequently infected with *Campylobacter* spp. in contrast to flocks using nipple drinkers without trays. Other variables like hygiene measures, age, resting period and water sources showed no significant effect on the *Campylobacter* prevalence.

The results of this study show a seasonal variation in the presence of *Campylobacter* spp. in broiler flocks, with higher prevalence mainly associated with the summer and fall season. *Campylobacter* prevalence was dependent on production system and flock management. Introduction of control programmes to minimize *Campylobacter* colonization could help producers to reduce *Campylobacter* infections by the application of strict biosecurity measures. However, a total elimination of

Campylobacter spp. is not expected, therefore adequate consumer information on proper handling of poultry meat is needed.