

Dynamics of *Campylobacter jejuni* shedding in a broiler flock experimentally infected with two different strains

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Campylobacter is the main cause of gastroenteritis in industrialized countries and poultry its principal reservoir and source for human infection. When *Campylobacter* enters a flock infection spreads rapidly colonizing most of the animals in the flock shortly afterwards. Animals remain infected throughout their productive life shedding the bacterium in their faeces. With the aim to monitor spreading of different *Campylobacter jejuni* strains in a flock, 600 one-day-old male Ross 308 broilers were allocated in floor pens bedded with ca. 5 cm of wood shavings and reared following standard commercial practices. At 15-day-old, 120 chickens were inoculated by oral gavage with a dose of 10^5 cfu of a mixture of 2 *C. jejuni* strains, the collection strain CNET099 (sequence type 267, clonal complex 283) and a field strain isolated from chicken C303 (sequence type 572, clonal complex 206). Faecal pool samples and cloacal swab samples from chickens, as well as samples from the drinking water and the air, were obtained weekly until the end of their productive life (42 days of age). Animal and environmental samples were analysed for the presence of *C. jejuni* by culture on the *Campylobacter* selective chromogenic medium CASA (BioMérieux) and real-time PCR. Environmental samples remained culture negative throughout the experiment but 6 days after inoculation the infection was widespread in the flock. Based on the difference between both inoculated strains in terms of quinolone resistance (CNET099, Sensitive; C303, Resistant) their spread was monitored by real-time PCR SNP mutation detection in the *gyrA* gene (C257T) [1]. Six days post-inoculation, the field strain was already slightly more prevalent and during the following 2 weeks it was detected in over 80% of the samples. At the end of the experiment the proportion was 70% vs. 30% for the field strain. Mixed infections were detected at some point in 8.5% of the cloacal swabs individually tested. In the majority of the inoculated animals that were repeatedly sampled, the field strain was the only detected; but in one third of the animals a transition between one strain to the other was observed. Although birds were not under any selective pressure, further MLST genotyping analyses are to be carried out to rule out the small possibility that the quinolone resistance determinant used here to differentiate both strains was transferred between the strains during colonization. If confirmed, these results showed that the field strain C303 was more widely disseminated in the flock and more heavily shed by chicken. Pending analysis of caecal content samples will allow us to compare colonization levels of both strains and associate them with the dissemination patterns observed.

Keywords: *Campylobacter jejuni*; broilers, experimental infection; shedding

References

- [1] Oporto, B., Juste, R.A. and Hurtado, A. (2009) Phenotypic and genotypic antimicrobial resistance profiles of *Campylobacter jejuni* isolated from cattle, sheep and free-range poultry faeces. International Journal of Microbiology 2009, 456573.