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***Campylobacter coli* from surface waters in regions with high and low livestock density**

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**Abstract:**

**Background/Objective:** Campylobacteriosis is a commonly reported bacterial zoonosis worldwide. In addition to livestock such as chickens, pigs and cattle, surface waters are also an important reservoir for *Campylobacter* spp. The pathways of *Campylobacter* entry into surface waters are poorly understood.

**Methods:** In order to better understand the influence of livestock density on *Campylobacter* input into the environment, a total of 201 water samples in regions with low and high livestock density were analysed for the presence of Campylobacter spp. in the period 2020-2022.

**Results:** Our data revealed a comparable *Campylobacter* prevalence of 18% in both regions. *C. coli* was predominantly detected in water samples from regions with low livestock density, whereas comparable proportions of *C. jejuni* and *C. coli* were detected in water samples from regions with high livestock density. *Campylobacter* spp. were isolated from 6 of the 7 livestock farms sampled in the high-density region, with *C. coli* detected in approx. 75% of the samples and *C. hyointestinales* in ca. 25% of the samples.

The genomes of the *C. coli* isolates were sequenced and analysed for typing purposes. All *C. coli* isolates from the livestock farms belonged to clade 1A. Although a high prevalence of *C. coli* was found in the farms, these genotypes could not be isolated from the surface water. The *C. coli* strains isolated from the water samples all belong to clades 1C, 2 and 3. The clade 1C strains were isolated in the region with high livestock density at river sites within a short distance from each other, and the clade 2 strains at the confluence of two lakes in a nature reserve. Clade 3 strains were detected in water samples from both the high and low livestock density regions.

Based on the genome sequences, higher rates of antimicrobial resistance genes, plasmids and prophages were detected in clade 1A strains (“livestock strains”) than in the environmental isolates.

**Conclusion:** Overall, genome sequence comparison of *C. coli* isolates indicates little or no discharge from the livestock farms to the surrounding surface waters. Further investigations are needed to clarify the source of *C. coli* input to the surface waters.

**Keywords:** *Campylobacter*, livestock, environment, surface water