

The Epidemiology of *Campylobacter* Infection in Dogs in the Context of the Risk of Infection to Humans

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Campylobacter is the most common bacterial cause of human gastroenteritis in England and Wales. Humans have frequent contact with dogs and dog faeces, and clearly where faecal pathogens such as *Campylobacter* are present there may be considerable opportunities for zoonotic transmission. Although there is epidemiological evidence of an association between *Campylobacter* in dogs and disease in humans, there is little information on specific risk factors for this.

This study investigates the prevalence and risk factors for *Campylobacter* carriage, and the molecular and spatial epidemiology of this infection in dogs, using a census-based study in a local community of 1278 houses in Cheshire, UK. Door-to-door interviews identified 260 dog-owning households with 327 dogs. These households were invited to participate further in the study by completing a questionnaire and providing a fresh faecal sample from their dog(s). Faecal samples were collected and immediately transported to the laboratory for processing. Three methods of *Campylobacter* spp. isolation were employed. Presumptive *Campylobacter* spp. colonies were confirmed by polymerase chain reaction (PCR), using the *Campylobacter* 16S rRNA gene as a target.

The majority of dogs sampled had no current signs of gastrointestinal disease. Currently 27% of samples have been confirmed positive for *Campylobacter* spp. Following speciation, further work using multilocus sequence typing will be used to determine the diversity within species of the isolates.

This study identifies a high prevalence of *Campylobacter* spp carriage in dogs. Given the close contact between many people and dogs, this route of transmission requires further investigation.