

## ORIGINAL ARTICLE

# Phenon cluster analysis as a method to investigate epidemiological relatedness between sources of *Campylobacter jejuni*

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## Keywords

amplified fragment length polymorphism, *Campylobacter jejuni*, molecular epidemiology, source identification, zoonoses.

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## Abstract

**Aims:** To develop a method for assessing the relative epidemiological significance of possible infection sources for human campylobacteriosis.

**Methods and Results:** Using fluorescent amplified fragment length polymorphism (AFLP), 243 apparently epidemiologically unrelated *Campylobacter jejuni* isolates were genotyped (77 human, 46 cattle, 49 pet and 71 poultry isolates). In total 136 different phenons were identified, of which 48 were clusters grouping at least two isolates. Isolates from different sources were frequently clustered together, underlining the high degree of source mixing and the lack of host specificity of *C. jejuni*. The phenons were classified into different phenon types according to the sources of the isolates they contained. The occurrence of these phenon types was analysed using an area-proportional Euler diagram to describe epidemiological relatedness among *C. jejuni* isolates. Group separation statistics revealed that 43% of analysed human isolates expressed maximum similarity to other human isolates, 9% to cattle isolates, 21% to pet isolates and 27% to poultry isolates; these results were in accordance with the pattern observed in the phenon cluster analysis.

**Conclusions:** Based on the grouping of strains into molecular similarity clusters, ecological patterns between sources can be investigated.

**Significance and Impact of the Study:** This approach is a new methodological contribution to establish the relative epidemiological significance of concurrent infection sources.

## Introduction

Zoonotic disease agents that are transmissible from animals to man have been acknowledged as a major threat for public health. *Campylobacter jejuni*, a common zoonotic agent, is found in a large number of animal species, for example, in poultry, cattle, sheep, pets and wild animals (Adak *et al.* 1995; Wolfs *et al.* 2001; Neimann *et al.* 2003; Damborg *et al.* 2004; Friedman *et al.* 2004). In order to take preventive action against zoonotic diseases in humans, the relative significance of exposure from various possible sources needs to be understood. For

those organisms that comprise host-specific subpopulations, such as serotypes, this can be readily achieved. An example is *Salmonella enterica*, where a source account method based on phage typing was developed to assess the relative importance of infection sources (Hald *et al.* 2004). However, host-dependent subpopulations have not been convincingly demonstrated for *C. jejuni*, and serotypes do not correlate to virulence or host specificity for this organism. Hence, a different approach is necessary to identify the major transmission routes. The importance of infection sources, especially the contact with carrier animals, has been subject to major speculation. In addition