

## ORIGINAL ARTICLE

# Genetic instability is associated with changes in the colonization potential of *Campylobacter jejuni* in the avian intestine

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*Campylobacter*, genotyping, instability.

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## Abstract

**Aims:** A panel of pulsed field gel electrophoresis (PFGE) type variants of *Campylobacter jejuni*, previously identified as of clonal origin, were investigated to determine whether genomic instability could be observed during competitive growth.

**Methods and Results:** Upon recovery from frozen storage, some variants had undergone alterations in PFGE profiles, but subsequent culture produced constant genotypes. Individual variants did not display differences in colonization potential when tested in orally challenged 1-day-old chickens. However, competitive colonization using mixtures of two or three PFGE types generally resulted, by 4 weeks postchallenge, in one predominant PFGE type in all birds. For some variant mixtures, a minor population of novel PFGE types was detected in individual birds. The creation of new variants appeared to be dependent on the extent of competition and of the individual host. Genomic rearrangements most likely explain this increase in genetic diversity, apparently without the involvement of natural transformation or plasmid acquisition. *In vitro* cultivation of mixed inoculations were again selected for particular variants; but genetic diversity was not generated, suggesting that the selection pressures *in vitro* differed from those active *in vivo*.

**Conclusion:** These observations support the hypothesis that by generating genetic diversity, *C. jejuni* can improve its phenotypic fitness to survive and colonize subsequent hosts.

**Significance and Impact of the Study:** The consequences of such observations for the development of campylobacter control strategies for poultry may be substantial.

## Introduction

*Campylobacter jejuni* is a major cause of human acute bacterial enteritis. Although this pathogen is considered to be largely food-borne, *C. jejuni* is ubiquitous in the environment and accurate source attribution is thus very important. For other organisms, the identification of sources relies on tracking strains through the environment. Such tracking is enabled by molecular epidemiology of strains identified by phenotypic or genotypic properties. The diversity of *C. jejuni* is well established

and detectable by both genotypic and phenotypic techniques and many such methods are routinely employed (Wassenaar and Newell 2000). However, the value of such molecular approaches in campylobacter epidemiology appears to be restricted by genomic instability (Wassenaar *et al.* 2000b). Genomic instability generates a weakly clonal bacterial population structure (Dingle *et al.* 2001) and is the result of genetic events such as intragenomic rearrangements and natural transformation followed by homologous recombination (Wassenaar *et al.* 2000b). Results of the latter mechanism have been observed in