

ORIGINAL ARTICLE

## Comparison of *Campylobacter fla*-SVR genotypes isolated from humans and poultry in three European regions

T.M. Wassenaar<sup>1</sup>, A. Fernández-Astorga<sup>2</sup>, R. Alonso<sup>2</sup>, V.T. Marteinson<sup>3</sup>, S.H. Magnússon<sup>3</sup>, A.B. Kristoffersen<sup>4</sup> and M. Hofshagen<sup>4</sup>

<sup>1</sup> Molecular Microbiology and Genomics Consultants, Zotzenheim, Germany

<sup>2</sup> Inmunología, Microbiología y Parasitología, Facultad de Farmacia, Universidad del País Vasco, Paseo de la Universidad 7, Vitoria-Gasteiz, Spain

<sup>3</sup> Mátis, Skúlagöta 4, Reykjavík, Iceland

<sup>4</sup> Veterinærinstituttet, Pb 750 Sentrum, Oslo, Norway

### Keywords

*Campylobacter*, *fla*-SVR, genetic diversity, genotyping, poultry.

### Correspondence

Trudy M. Wassenaar, Molecular Microbiology and Genomics Consultants, Tannenstrasse 7, 55576 Zotzenheim, Germany.  
E-mail: trudy@mmgc.eu

2009/0199: received 2 February 2009, revised 27 May 2009 and accepted 1 June 2009

doi:10.1111/j.1472-765X.2009.02678.x

### Abstract

**Aims:** The genetic diversity of *Campylobacter* isolated from human infection and from poultry was assessed in strains originating in three different European regions in order to compare these two hosts and to investigate European regional differences.

**Methods and Results:** Randomly chosen isolates originated from Norway, Iceland and Basque Country in Spain were genotyped by sequencing of the short variable region (SVR) of *flaA*. A total of 293 strains were investigated, c. 100 per country with half originated from either host. The results indicate extensive diversity in both hosts and identified differences in the nature and distribution of genotypes between the countries. These differences could in part be related to geographical location, in that *Campylobacter* genotypes from Iceland and Norway were more similar to each other than either was to Basque Country.

**Conclusions:** Differences between the countries exceeded the observed differences between human and poultry isolates within a country.

**Significance and Impact of the Study:** Regional differences are extensive and should not be ignored when comparing genotyping data originating from different international studies.

### Introduction

The genetic diversity of *Campylobacter jejuni* and *Campylobacter coli* from humans and poultry is well established. Whatever genotyping method is applied, invariably a large diversity is observed, the degree of which seems mostly determined by the discriminatory power of the method (Wassenaar and Newell 2000). In most studies, overlap of genotypes was observed for human and poultry isolates, but nearly always that overlap was incomplete so that human- and poultry-specific genotypes were also observed (see for instance, Moore *et al.* 2003; Siemer *et al.* 2005; Fang *et al.* 2006; Zorman *et al.* 2006; Keller *et al.* 2007; Lévesque *et al.* 2008).

The method of multi-locus sequence typing (MLST) is most appropriate to study population biology of bacterial

subpopulations in various environments (Maiden *et al.* 1998; Maiden 2006) and has been developed for *Campylobacter* as well (Dingle *et al.* 2001). However, this method is elaborate and expensive and investigates the alleles of a limited number of housekeeping genes that are under negative selective pressure. Although this gives valuable information about the population structure of investigated samples, it is of limited use for short-term, localized epidemiological studies. In the latter case, a cheap and easy genotyping method determining alleles of virulence or colonization factors would be appropriate. Determination of the sequence of a short variable region (SVR) in the gene encoding flagellin A, called *fla*-SVR, fits these requirements (Meinersmann *et al.* 1997).

In this study, we compare and contrast *Campylobacter* isolates by *fla*-SVR genotyping, obtained from the human