

Title: Genotypic diversity and pathogenic potential of *Campylobacter jejuni* strains isolated from different sources during 16 years in Brazil

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Abstract:

Campylobacter jejuni is an important causative agent of human diarrheal diseases worldwide. Specifically, in Brazil *C. jejuni* is not usually studied, therefore studies that molecularly characterize strains of this species are of great importance. The aims of this study were to genotype *C. jejuni* strains by Pulsed field gel electrophoresis (PFGE) and investigate the presence of some virulence-associated genes by PCR. A total of 76 *C. jejuni* strains isolated from humans (34), animals (21), food (20) and the environment (01) between 1996 and 2012 in Brazil were studied. The presence of 16 virulence-associated genes was searched by PCR. For PFGE, genomic DNA was digested with 40U of *Sma*I and the fragments resolved in a CHEF-DRIII apparatus. Data were analyzed by BioNumerics 5.1 version software and the dendrogram constructed by UPGMA method and DICE similarity coefficient. All the 76 strains studied presented the genes *flaA*, *flhA*, *cadF*, *docA*, *cdtA*, *cdtB*, *cdtC*, *iamA*, *ciaB*, *racR* and *crsA*. The gene *pldA* was found in 75 (98.7%) strains. The gene *dnaJ* was found in 74 (97.4%) strains. The gene *sodB* was found in 73 (96%) strains. The gene *wlaN* was found in 11 (14.4%) strains and the gene *virB* was found in only one (1.3%) strain. The dendrogram of genetic similarity of PFGE grouped the strains in three clusters, designated A, B and C. Cluster A comprised 45 strains isolated from animals, humans, food and the environment. Cluster B comprised 16 strains isolated from animals, humans and food. Cluster C comprised 15 strains isolated from animals and humans. In the three clusters, strains of clinical and non-clinical sources were grouped in subclusters with a similarity of more than 80%. A genomic diversity of more than 44.6% was observed among all the strains. The Discriminatory Index of PFGE was 0.977. It is possible to conclude that the PFGE confirmed the heterogeneity of the *C. jejuni* studied. However, the high similarity (>80%) among some strains of animals, humans, the environment and food may suggest that a possible contamination occurred between these clinical and non-clinical sources in Brazil. The high frequency of the majority of the virulence-associated genes searched highlighted the pathogenic potential of those strains.

Keywords: *Campylobacter jejuni*, molecular typing, PFGE, pathogenic potential.

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