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 Smal 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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