TITLE: MOLECULAR CHARACTERIZATION AND RESISTANCE PROFILE OF *CAMPYLOBACTER JEJUNI* STRAINS ISOLATED FROM DIVERSE SOURCES OVER 20 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* has been underdiagnosed and understudied. Therefore, studies that molecularly characterize strains of this species isolated in this country are of great importance. The aims of this study were to genotype and to evaluate the resistance profile of *C. jejuni* strains isolated in Brazil. A total of 121 *C. jejuni* strains isolated from humans (51), animals (35), chicken meat (33) and sewage (02) between 1996 and 2016 in Brazil were genotyped by PFGE and *flaA*-SVR sequencing. Additionally, the resistance profile against ciprofloxacin, tetracycline, doxycycline and erythromycin was evaluated by Etest®. The dendrogram of genetic similarity of PFGE grouped the strains in three clusters with more than 46.9% of similarity. Cluster PFGE-A comprised 55 strains isolated from animals, humans, chicken meat and sewage. Cluster PFGE-B comprised 25 strains isolated from animals, humans and chicken meat. Cluster PFGE-C comprised 41 strains isolated from animals, humans, chicken meat and sewage. In the three PFGE clusters, 105 strains (86.8%) of clinical and non-clinical sources were grouped in subclusters with a similarity of ≥80%. The dendrogram of genetic similarity of *flaA*-SVR sequencing grouped the strains in two clusters with more than 80.9% of similarity. Cluster SVR-A comprised 20 strains isolated from animals, humans and sewage. Cluster SVR-B comprised 101 strains isolated from animals, humans, chicken meat and sewage. Regarding the resistance profile, 68 strains (56.2%) were resistant to at least one antimicrobial agent, being 19 strains (54.3%) isolated from animals, 24 strains (47.1%) isolated from humans and 25 strains (75.7%) isolated from chicken meat. Resistance to ciprofloxacin, doxycycline, tetracycline and erythromycin was observed in 53 (43.8%), 42 (34.7%), 42 (34.7%) and 06 (4.9%) strains, respectively. The results obtained by PFGE and *flaA*-SVR sequencing showed a high genomic similarity among some *C. jejuni* strains which may suggest that a possible contamination may have occurred among clinical and non-clinical sources during 20 years in Brazil and because of these, the existence of resistant strains becomes a concern.

Keywords: *Campylobacter jejuni*, PFGE, *flaA*-SVR sequencing, antimicrobial resistance profile.