

TITLE: wgMLST ANALYSIS AND ANTIMICROBIAL RESISTANCE GENES OF *Campylobacter jejuni* STRAINS ISOLATED FROM HUMANS AND FOOD 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 importance. The aims of this study were to assess the phylogenetic relationship and to evaluate the molecular resistance profile of *C. jejuni* strains isolated in Brazil. A total of 79 *C. jejuni* strains isolated from humans (47) and food (32) in four States of Brazil were genotyped by whole genome multi locus sequence typing using PGADB-builder. Additionally, the presence of resistance genes as well as points of mutation in the *gyrA* and in the 23S rRNA were evaluated *in silico* using ResFinder. By wgMLST all the *C. jejuni* strains studied were distributed in six clades. Clade A comprised 15 strains isolated from humans and food in Sao Paulo and Minas Gerais. Clade B was composed of 26 strains isolated from humans and food in Sao Paulo, Minas Gerais, Rio Grande do Sul and Rio de Janeiro. Clade C contained six strains isolated from humans and food in Minas Gerais and Rio de Janeiro. Clade D comprised 12 strains isolated from humans and food in Sao Paulo, Minas Gerais and Rio de Janeiro. Clade E was composed of 10 strains isolated from humans in Sao Paulo and Rio de Janeiro. Clade F contained 10 strains isolated from humans in Sao Paulo and Rio de Janeiro. Regarding the resistance profile, 65 strains showed at least one resistance gene or one point of mutation. Five genes were found in the 79 *C. jejuni* strains from Brazil, being, *bla*_{OXA-61} presented in 31 (39.2%), *bla*_{OXA-184} in 7 (8.9%), *tet*(O) in 29 (36.7%), *aadE* in 3 (3.8%) and *aph*(3')III in 6 (7.6%) strains. The point of mutation T86I in the *gyrA* gene was observed in 38 (48.1%) strains and 4 (5.1%) strains presented the point of mutation A2075G in the 23S rRNA. In conclusion, the results obtained by wgMLST showed that the *C. jejuni* studied in each group were similar among themselves, suggesting potential for transmission between human and food over the course of 20 years in different States of the Southeast and South regions in Brazil and because of this, the prevalence of some resistant genes and/or points of mutation found in the strains studied becomes a concern.

KEYWORDS: *Campylobacter jejuni*, wgMLST, resistance genes and points of mutation.

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