

**Title: Multilocus sequence typing of *Campylobacter coli* strains isolated from humans, food, animals and environment sources during 16 years in Brazil**

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**Abstract:** *Campylobacter coli* is an important causative agent of human diarrheal diseases worldwide. In Brazil, *C. coli* is not usually studied, therefore studies that molecularly characterize strains of this species are important. The aim of this study was to type *C. coli* strains isolated from clinical and non-clinical origins by multilocus sequence typing (MLST) and to assess the genetic diversity of them. A total of 20 *C. coli* strains isolated in Brazil from human feces (5), food (4) animals (7) and environment (4) between 1995 and 2011 was typed by MLST. The housekeeping genes *aspA*, *glnA*, *gltA*, *gly*, *pgm*, *tkt* and *uncA* were sequenced for each strain and a consensus sequence was obtained by Chromas Pro. The ST numbers were obtained in the *C. coli* database website (<http://pubmlst.org/campylobacter/>). The similarity diagram was constructed by eBURSTv3 software. The MLST analysis showed 18 different STs among the 20 strains studied. Only two STs (ST 1581 and ST 7370) were previously described in the *Campylobacter* spp. MLST database. Sixteen new STs (ST 7628, ST 7713, ST 7714, ST 7715, ST 7716, ST 7717, ST 7718, ST 7719, ST 7720, ST 7721, ST 7722, ST 7723, ST 7724, ST 7725, ST 7726 and ST 7727) that have not been described before were designated. Two strains one from animal and one from the environment were assigned to ST 7724 and two strains being one from human and one from food sources were designated as ST 7628. The remaining STs are composed exclusively by just one strain. Twelve STs belong to the 828 clonal complex (CC), the main CC of *C. coli* species and six STs were not related with any CC. The ST 7370 is double locus variant of the ST 825, the possible ST founder of the CC 828. The MLST data revealed a high genetic diversity among the 20 *C. coli* strains isolated from different sources during 16 years in Brazil and revealed its diversity compared to strains isolated in other countries of Europe, Japan, and USA, among others that are deposited in the MLST database. Furthermore, the existence of shared STs between strains isolated from human and food sources (ST 7628) and strains isolated from animal and environmental sources (ST 7724) suggest that a possible contamination may have occurred between clinical and non-clinical sources in this country.

**Keywords:** *Campylobacter coli*, MLST, Genotypic Similarity, Molecular Typing, Brazil

**Financial support:** CNPq and FAPESP