

TITLE: PHYLOGENETIC AND GENOTYPIC ANALYSIS OF CTX-M-2-PRODUCING *SALMONELLA* MUEENCHEN IN CLINICAL ISOLATES FROM BRAZIL.

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Antimicrobial resistance in foodborne pathogens is a major concern for public health safety, as the incidence of *Salmonella* isolates with resistance to multiple drugs is rapidly increasing globally, including the beta-lactam resistance. Of concern is the increased incidence of infections caused by extended-spectrum-lactamase (ESBL)-producing organisms, including *Salmonella* spp., being that beta-lactams are used in salmonellosis treatment in children. The emergence of CTX-M-type ESBL-producing *Salmonella* spp. has been reported in clinical cases, animals, and food samples worldwide. CTX-M-2-producing *S. Muenchen* was considered, until then, infrequent in Brazil. However, the occurrence of this beta-lactamase producing serovar has increased over the years. In total, seven clinical isolates identified as *S. Muenchen* ST112 were included in this study belonging to 2012-2015 period. DNA was extracted using the Wizard Genomic DNA Purification kit (Promega). Whole-genome shotgun sequencing was performed using an Ion Torrent S5. Read trimming and assembly were performed using CLC Genomics Workbench v.11.0.1 software. For genotypic analysis, online tools of the Center for Genomic Epidemiology were used to determine *in silico* serotype and MLST, resistance genes, and plasmid classification <https://cge.cbs.dtu.dk/services/>. The *bla*_{CTX-M-2} gene was located in an IncHI2 plasmid (~200 Kb). Transferable resistance genes to aminoglycosides (*aac(6')-Iaa*, *aac(3)-VIa*, *aph(3')-Ia* and *aadA1*), sulfonamide (*sul1*), tetracycline (*tetA*) and quaternary ammonium compounds (*qacE*) were found. Some isolated also carried the *qnrB19* gene (fluoroquinolone resistance) on the plasmid. For phylogenetic analysis, we employed the core genome analysis (cgMLST), for identifying variations in the whole genome sequences of our isolates along with the 294 *S. Muenchen* sequences available in the Enterobase database (2021, august) available at <https://enterobase.warwick.ac.uk>. It was used the commercial software BioNumerics version 8.0 (Applied Maths, Sint-Martens-Latem, Belgium). We generated a minimum spanning tree based on core-genome single-nucleotide polymorphisms. The isolates were closely related to ST112 *S. Muenchen* isolates from human and environment in the USA and United Kingdom. Our study reinforces the importance of intensifying the monitoring of antimicrobial resistance in *Salmonella* isolates that carry the *bla*_{CTX-M-2} gene since this variant was predominant in this serovar.

Keywords: *Salmonella*, ESBL, CTX-M-2, cgMLST

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