

TITLE: VIRULENCE AND ANTIMICROBIAL RESISTANCE FEATURES OF WHOLE-GENOME SEQUENCED *Salmonella* Infantis STRAINS ISOLATED FROM CLINICAL AND FOOD SOURCES IN BRAZIL.

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ABSTRACT:

Non-typhoid *Salmonella* serovars have been considered as one of the main causes of bacterial foodborne infections worldwide. *Salmonella enterica* serovar Infantis (*S. Infantis*) is a zoonotic and globally distributed pathogen, associated with increasing antimicrobial resistance rates and capable to infect multiple food-producing animals and humans. The aims of this study were to evaluate by whole-genome sequencing data the occurrence of genomic features associated to virulence and antimicrobial resistance and to verify the genetic relatedness of *S. Infantis* strains isolated in Brazil. A total of 46 whole-genome sequenced *S. Infantis* strains isolated from food (n=27) and humans (n=19) in Brazil from 2013 to 2018 were analyzed in this study. The Comprehensive Antibiotic Resistance Database was used to search for efflux pump encoding genes (EPEGs) associated to antimicrobial resistance and NCBI's Pathogen Detection for heavy metal tolerance genes. VF Analyzer was used to search for virulence genes and SPIFinder 2.0 for *Salmonella* Pathogenicity Islands (SPIs). A core-genome multi-locus sequence typing (cgMLST) analysis was conducted using cgMLSTFinder 1.1 to determine the genomic relatedness of the strains. EPEGs *acrA*, *acrB*, *baeR*, *crp*, *emrB*, *emrR*, *hns*, *kdpE*, *kpnF*, *marA*, *marR*, *mdtK*, *msbA*, *rsmA*, *sdiA*, *soxR*, *soxS* were detected in 100% of the strains, *golS* in 98%, *mdfA* in 63% and *tet(A)* in 35%. All strains harbored arsenic (*arsR*) and golden (*golRT*) tolerance genes, while 35% additionally harbored a complete silver tolerance operon (*silABCDEFPRS*). A total of 146 virulence genes associated to fimbrial and non-fimbrial adherence, macrophage induction, magnesium uptake and type three secretion system regulators and effectors were detected, with at least 131 genes detected in all strains studied. All strains harbored nine SPIs (1, 2, 3, 4, 5, 9, 13, 14 and CF54). cgMLST grouped the 80 strains into four major clusters containing 11 to 37% of the strains studied, that were allocated regardless of the year or source of isolation. In conclusion, the high frequency and diversity of antimicrobial resistance genes and virulence factors in addition to the presence of clusters containing genetically related *S. Infantis* strains of food and human origin alerts for the possible necessity of more rigorous monitoring measures in the public health and food safety fields in Brazil.

KEYWORDS: antimicrobial resistance genes; molecular epidemiology; *Salmonella* Infantis; virulence genes; whole-genome sequencing.

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