

**TITLE:** WHOLE-GENOME SEQUENCING REVEALS HIGH ANTIMICROBIAL RESISTANCE GENE FREQUENCY, PRESENCE OF PLASMIDS AND A PREVALENT GENETICALLY RELATED CLUSTER AMONG *Salmonella* Infantis ISOLATED IN BRAZIL

**AUTHORS:** VILELA, F.P.<sup>1</sup>; RODRIGUES, D.P.<sup>2</sup>; ALLARD, M.W.<sup>3</sup>; FALCÃO, J.P.<sup>1</sup>

**INSTITUTION:** <sup>1</sup>FACULDADE DE CIÊNCIAS FARMACÊUTICAS DE RIBEIRÃO PRETO - USP (AV. DO CAFÉ, S/N - FCFRP/USP, BLOCO S SALA 41 - 14040-903 - RIBEIRÃO PRETO - SP); <sup>2</sup>FUNDAÇÃO OSWALDO CRUZ (AV. BRASIL, 4365, PAVILHÃO ROCHA LIMA, 3º ANDAR - MANGUINHOS - 21040-900 - RIO DE JANEIRO - RJ); <sup>3</sup>U.S. FOOD AND DRUG ADMINISTRATION (5001 CAMPUS DRIVE, HFS-009, 20740-3835, COLLEGE PARK - MD)

**ABSTRACT:**

Non-typhoid *Salmonella* serovars have been among the main causes of foodborne infections worldwide. *Salmonella enterica* serovar Infantis (*S. Infantis*) is globally distributed and ubiquitous, associated with increasing antimicrobial resistance rates and capable to infect multiple food-producing animals and humans. The aims of this study were to characterize by whole-genome sequencing the genetic relatedness, verify the presence of plasmids and antimicrobial resistance gene content of *S. Infantis* strains isolated in Brazil. A total of 80 *S. Infantis* strains isolated from food (n=27), humans (n=19) and veterinary related sources (n=34) in Brazil from 2013 to 2018 were sequenced by the Illumina MiSeq 500 platform. The assemblies obtained were analyzed in the web-based tool CSI Phylogeny 1.4 to determinate the genetic relatedness of the strains through the single-nucleotide polymorphism (SNP) analysis, ResFinder 4.1 and AMRFinder for the frequency of antimicrobial resistance (AMR) genes and PlasmidFinder 2.1 for the presence of plasmids. SNP analysis grouped the strains studied into two major clusters, with the main cluster comprising 70% of the *S. Infantis* analyzed and displaying no clear distinction regarding the years, sources or places of isolation. The strains harbored the acquired AMR genes *aac(6')-Iaa* (100%), *aadA12* (2.5%), *aph(3'')-Ib* (1.3%) and *aph(6)-Id* (1.3%) for aminoglycosides; *bla<sub>TEM-1</sub>* (40%), *bla<sub>CTX-M-8</sub>* (11.3%) and *bla<sub>CMY-2</sub>* (10%) for  $\beta$ -lactams; *dfrA8* (37.5%) for diaminopyrimidine compounds; *tet(A)* (36.3%) for tetracyclines; *floR* (36.3%) for amphenicols; *sul2* (1.3%) for sulfonamide; and *mdsA* (100%) and *mdsB* (100%) for efflux pumps. Chromosomal point mutations Gln624→Lys (100%) in *gyrB*; Thr57→Ser (100%), Thr255→Ser (100%) and Val702→Ala (1.3%) in *parC*; Phe28→Leu (100%) and Leu40→Pro (100%) in *acrB*; and Asp28→Tyr (100%) in *pmrA*, which are also related to AMR resistance were also detected. In addition, the *S. Infantis* strains possessed plasmids of the incompatibility groups IncI1-I (23.8%), IncX1 (3.8%), IncFIB (1.3%), IncFII (1.3%), IncFII(29) (1.3%), IncR (1.3%), IncN (1.3%) and IncQ1 (1.3%). In conclusion, the possible presence of a prevalent *S. Infantis* subtype in Brazil and the high rates of genotypic AMR, associated with the presence of plasmids, reinforced the potential hazard that this serovar may represent for the public health and food safety fields.

**KEYWORDS:** antimicrobial resistance; molecular epidemiology; plasmids; *Salmonella*; SNP analysis.

**FUNDING AGENCY:** FAPESP and CAPES