

**TITLE:** OCCURRENCE OF HIGH ANTIMICROBIAL RESISTANCE RATES AND A PREVALENT GENETICALLY RELATED CLUSTER AMONG *SALMONELLA* INFANTIS STRAINS ISOLATED FROM HUMAN AND FOOD SOURCES IN BRAZIL

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**ABSTRACT:**

Salmonellosis caused by non-typhoidal *Salmonella* serovars has been among the most frequently reported foodborne infections worldwide. *Salmonella enterica* subs. *enterica* serovar Infantis (*S. Infantis*) is a non-specific host serovar, capable to infect multiple animal reservoirs besides humans that has been reported among the most isolated *Salmonella* serovars in Brazil. The aims of this study were to molecularly type and determine the phenotypic antimicrobial resistance of 73 *S. Infantis* strains isolated from humans (30) and food (43) in Brazil between 2013 and 2018. The genotypic diversity was accessed by Pulsed-Field Gel Electrophoresis (PFGE) using the enzyme XbaI. The antimicrobial susceptibility testing was performed by the disk diffusion method against 18 antimicrobials selected and tested according to the CLSI guidelines. PFGE grouped the strains into six groups and 52 PFGE-types, with a similarity  $\geq 49.6\%$ . The major group clustered 47 strains (64.4%) isolated from humans and food between 2013 and 2018 with a similarity  $> 64.2\%$ , and was subdivided into three subgroups, with a similarity  $\geq 71.0$  among them. No correlation regarding the years, sources, material or location of isolation was observed among these groups. Moreover, the strains presented resistance to ampicillin (42.5%), tetracycline (34.2%), piperacillin (31.5%), cefazolin (28.8%), nalidixic acid (27.4%), cefotaxime (24.7%), ceftriaxone (21.9%), chloramphenicol (19.2%), ceftazidime (11.0%), cefepime (11.0%), amoxicillin-clavulanic acid (9.6%), ceftiofloxacin (8.2%), trimethoprim-sulfamethoxazole (6.8%), streptomycin (6.8%), ciprofloxacin (2.7%), imipenem (2.7%), amikacin (1.4%) and gentamicin (1.4%). In addition, 23 strains (31.5%) of the total studied presented a multidrug-resistance (MDR) profile, being 19 strains isolated from food (26.0%) and four from humans (5.5%). In conclusion, the presence of a prevalent cluster comprising genetically related *S. Infantis* strains isolated from humans and food suggest that a possible contamination and/or transmission may have occurred between these sources. Moreover, the high antimicrobial resistance rates alert for the potential hazard that *S. Infantis* strains may represent for food safety and public health in Brazil.

**KEYWORDS:** antimicrobial resistance; molecular epidemiology; multidrug-resistance; PFGE; *Salmonella* Infantis.

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