

TITLE: ANTIMICROBIAL RESISTANCE AND MOLECULAR TYPING OF *Salmonella* 1,4, [5],12:i:- ISOLATED IN THE STATE OF SÃO PAULO BETWEEN 1983 AND 2020

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ABSTRACT:

Salmonellosis is one of the main foodborne diarrheagenic diseases, with a worldwide estimate of 93.8 million cases each year. *Salmonella* 1,4, [5],12:i:-, a monophasic variant of *Salmonella* Typhimurium, has been one of the most prevalent serovars associated with human foodborne outbreaks and septicemia cases in Brazil. Therefore, studies that seek to characterize genotypically and phenotypically strains of this serovar are of great importance. The aims of this study were to molecularly type and determine the phenotypic antimicrobial resistance profiles of *S.* 1,4, [5],12:i:- strains isolated from diverse sources in Brazil. A total of 113 *S.* 1,4, [5],12:i:- strains isolated from humans (99), animals (7), food (5) and the environment (2) between 1983 and 2020 in São Paulo State were studied. For PFGE, the genomic DNAs were digested with *Xba*I enzyme, and the fragments resolved in a CHEF-DRIII apparatus. Data were analyzed by BioNumerics software and the dendrogram constructed by UPGMA method and DICE similarity coefficient. The antimicrobial susceptibility testing was performed by the disk diffusion method and 13 antimicrobials were tested. The PFGE dendrogram allocated the strains in five clusters, designated PFGE-A, PFGE-B, PFGE-C, PFGE-D and PFGE-E. The main clusters were PFGE-A and PFGE-B. The cluster PFGE-A contained 52 strains isolated from humans, food, animals, and the environment between 1983-2020 with 81.7% of genetic similarity. The cluster PFGE-B contained 34 strains isolated from humans, food, and animals between 1985-2020 with 84.2% of genetic similarity. Moreover, the strains presented resistance to ampicillin (51.33%), nalidixic acid (39.82%), tetracycline (38.05%), gentamicin (27.43%), trimethoprim-sulfamethoxazole (12.39%), chloramphenicol (11.50%), ciprofloxacin (7.96%), levofloxacin (7.96%), amoxicillin-clavulanic acid (4.42%), cefotaxime (3.54%), cefepime (2.65%), imipenem and ceftazidime (0.88%). In addition, 39 (34.51%) strains of the total studied presented a multidrug-resistance (MDR) profile. In conclusion, the PFGE results suggested that most of the strains studied belonged to two main clusters that have been prevailing in the São Paulo State, Brazil. Finally, the significant rates of MDR strains found is alarming and worrying once it may lead to failure when antimicrobial treatment is required.

Keywords: Monophasic *Salmonella*; PFGE; molecular typing; antimicrobial resistance profiles.

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