

TITLE: MOLECULAR CHARACTERIZATION OF *SALMONELLA* 1,4, [5],12:I:- STRAINS ISOLATED IN BRAZIL DURING 37 YEARS.

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ABSTRACT:

Salmonella 1,4, [5],12:i:- is among the main serovars related to gastroenteritis in humans and animals in different countries. In Brazil, there was an increase in the isolation of *S.*1,4, [5],12:i:- strains from human and non-human samples in the 1990s, becoming one of the most prevalent serovars in this country. Therefore, studies that seek to molecularly characterize strains of this serovar are of great importance. The aims of this study were to genotype by pulsed-field gel electrophoresis (PFGE) and investigate the frequency of virulence-associated genes by Polymerase Chain Reaction (PCR) in *S.* 1,4, [5],12:i strains :- isolated from different sources in this country. A total of 60 strains of *S.* 1,4,[5],12:i:- isolated from humans and food between 1983 and 2020 in the States of São Paulo, Mato Grosso, Santa Catarina and Minas Gerais were studied. For PFGE, genomic DNA was digested with 40U of *Xba*I and the fragments resolved in a CHEF-DRIII apparatus. Data were analyzed by BioNumerics 7.6 version software and the dendrogram constructed by UPGMA method and DICE similarity coefficient. All the 60 strains studied presented the genes *invA*, *sopB* e *sopE2*. The genes *sopD*, *spvB* e *ssaR* were detected in 55 (91,7%) strains. The gene *flgK* was found in 59 (98,3%) strains, the gene *sipD* in 58 (96,7%) strains, the gene *flgL* in 56 (93,3%) strains, the gene *sipA* in 54 (90%) strains, and the gene *sifA* in 52 (86,7%). The gene *fljB* was not detected in any strains of *S.* 1,4,[5],12:i:- studied. The dendrogram of genetic similarity of PFGE grouped the strains in two clusters, designated A and B. The cluster A contained two strains isolated in 1987 and 1992 with 75% of similarity. The cluster B contained 57 (95%) strains and it was subdivided into subgroups B1 and B2. The subgroup B1 contained 53 (93%) strains isolated between 1983-2020 with above 81,9% of similarity and the subgroup B2 contained 4 (7%) strains isolated between 1985-2002 with above 75,4% similarity. Among clusters A and B strains the similarity was 73% and one strain was not grouped in any cluster. The pathogenic potential of the strains studied was reinforced by the high prevalence of the majority of virulence-associated genes searched. The PFGE results suggest that one prevalent subtype of *S.*1,4, [5],12:i:- that differed little genotypically, prevailed during 37 years in different States of Brazil.

Keywords: *Salmonella* monophasic, virulence genes, PFGE, molecular typing.

Financial support: CAPES and FAPESP