

Title: MOLECULAR CHARACTERIZATION OF ANTIMICROBIAL RESISTANCE AND GENETIC DIVERSITY OF *SALMONELLA* SPP. STRAINS ISOLATED FROM NON-HUMAN SOURCES IN SÃO PAULO STATE

Authors: AMARANTE, A.F.; BERTANI, A.M.J.; DOS SANTOS, C.A.; DE ALMEIDA, E.A.; TIBACASAS, M.R.

Affiliation: INSTITUTO ADOLFO LUTZ, SÃO PAULO, SP (AVENIDA DR. ARNALDO, 355, 9º ANDAR, CEP 01246-902, SÃO PAULO – SP, BRAZIL).

Considered a highly important zoonosis, salmonellosis is one of the main foodborne diseases. The present study was carried out at the Bacteriology Center of Instituto Adolfo Lutz, in São Paulo, Brazil. 94 strains of *Salmonella* spp. from food, environment and animals were selected. The isolates received during the year 2020 were submitted to serotyping. The purpose of this work was to characterize these isolates using antimicrobial susceptibility testing and resistance genes from the known cephalosporins groups, such as *bla*_{CTX-M} (-2, -8, -15) and *bla*_{AmpC} (*bla*_{CMY-2}) detected by PCR. Molecular typing by PFGE was used to verify the genetic diversity of the strains, following the protocol standardized by the PulseNet network. The extended-spectrum beta-lactamases (ESBL) genes were detected in three strains (3.19%), identified as positive to genes *bla*_{CTX-M8} and *bla*_{CTX-M15} and 18 strains (19.14%) were positive to *bla*_{CMY-2}. For comparison reasons, only serotypes that had at least two isolates were included in the PFGE analysis: Anatum, Corvallis, Gallinarum, Heidelberg, Infantis, Mbandaka, Minnesota, Morehead, Muenchen, Newport, Oranienburg, Poona, Rissen, Saphra, Schwarzengrund, Typhimurium and S.II 42:r. The results were analyzed in BioNumerics software and the result was obtained by observing the restriction fragments after electrophoresis, comparing the restriction pattern between the analyzed samples. The PFGE analysis revealed that *S. Minnesota* strains were the most heterogeneous serotype, with nine restriction profiles presenting 43% of similarity between strains. *S. Heidelberg* and *S. Typhimurium* exhibited seven pulsetypes and presenting 63.3% and 45.4% of similarity, respectively. *Salmonella* *Infantis* showed 75.2% of similarity and *S. Muenchen* presenting 72.1% of similarity between strains. Three pulsetypes were found in Mbandaka, Newport and Schwarzengrund serotypes. Two restriction profiles were found in serotypes Anatum, Morehead, Oranienburg, Rissen, Saphra and S.II 42:r. *Salmonella* *Corvallis*, *Gallinarum* and *Poona* showed 100% of similarity. The data shows that among the serotypes that showed high genetic diversity, a clonal dispersion may be associated, impacting the measures of bacteria eradication, control and treatment. Furthermore, the resistance to beta-lactams found, reinforces the need for enhanced surveillance of the indiscriminate use of antibiotics in human and veterinary medicine and alert to prevent the emergence of resistant clones.

Keywords: *Salmonella*, antimicrobial resistance, ESBL, AmpC, genetic diversity.

Development Agency: Secretaria da Saúde do Estado de São Paulo