

**TITLE:** MOLECULAR EPIDEMIOLOGY OF *SALMONELLA ENTERICA* SEROVAR TYPHIMURIUM ISOLATES DETECTED BY PFGE: COMPARISON OF ISOLATES FROM WILD ANIMALS, HUMAN AND FOOD IN BRAZIL.

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## **ABSTRAC**

Most *Salmonella* infections are caused by eating contaminated food, especially food from animal origins and, *Salmonella enterica* serovar Typhimurium (*S. Typhimurium*) is one of the prevalent serotypes associated with foodborne illness. Salmonellosis is an infectious disease of global concern that is transmitted between species, sometimes by a vector, from animals other than humans to humans or from humans to other animals. Indeed, *Salmonella* spp. are able to infect a wide range of domestic and wild animal species. Infectious pathogens of wildlife origin have gained interest and are considered to be of increasing global importance, mainly because of their role in livestock health and productivity, as well as their zoonotic potential. In order to better understand the origin and dissemination of this pathogen, the specific aim of our study was to assess the genetic relatedness of *S. Typhimurium* strains isolated from humans, environmental and foods with strains isolated from wild animals captured in Rio de Janeiro, 2011 and Rio Grande do Sul, 2016. Bacteria were phenotypically characterized using standard microbiological techniques and the genetic relatedness of isolates was investigated using pulsed-field gel electrophoresis (PFGE). 290 *Salmonella* Typhimurium strains (215 from human source, 64 from food, 7 from environment and 4 from wild animal) were characterized. PFGE results showed a total of 111 pulsotypes. Our cluster analysis revealed 15 pulsotypes with close genetic relationship to range of 90% similarities between some human strains comparing with wild animal isolates. Wild animal strain isolated in 2011 from Rio de Janeiro showed similarities of 100% with human strain from Santa Catarina in 2012. The strains from Rio Grande do Sul isolated in 2016 in wild animal showed similarities of 100% with food strains from Bahia, 2009 and Rio Grande do Sul, 2014 and human (Rio Grande do Sul, 2010 and 2013). Similarities of 96% with human e food strains from Distrito Federal, Goiás, Minas Gerais, Rio Grande do Sul and Santa Catarina, between 2009

and 2013. The evaluation by Pulsed-field gel electrophoresis demonstrated that the *S. Typhimurium* isolates in this study belonged to a few, sometimes clonal, strains. This suggests the role of wild animals as carriers and faecal spreaders of *S. Typhimurium* in the environment should not be neglected as they can act as good sentinel species implicated in food contamination, and in human infections.

**Keywords:** *Salmonella*, PFGE, epidemiology, wild animal

**Development Agencies:** FIOCRUZ