

TITLE: SALMONELLA TYPHIMURIUM STRAINS FROM SWINE SHOWED GREATER GENOMIC DIVERSITY IN COMPARISON TO STRAINS ISOLATED FROM HUMANS AND FOODS IN BRAZIL

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ABSTRACT:

Salmonella enterica subsp. *enterica* serovar Typhimurium (*S. Typhimurium*) is an important zoonotic agent worldwide. In Brazil, *Salmonella* has been the first or second most common foodborne pathogen isolated from outbreaks in recent years and strains resistant to different antimicrobials have been reported. Despite its clinical importance, there are few published studies that have characterized the possible differences between Brazilian *S. Typhimurium* strains isolated from diverse sources by whole genome sequencing (WGS). Therefore, the aim of this work was to compare genetically *S. Typhimurium* strains isolated from clinical and non-clinical sources in Brazil from over 30 years using WGS data. A total of 117 *S. Typhimurium* strains isolated from humans (43), food (48) and swine (26) between 1983 and 2013 in Brazil were studied. The WGS was performed for all strains using the NextSeq 500 desktop sequencer with the NextSeq 500/500 high-output version 2 kit (Illumina) for 2×151 cycles according to the manufacturer's instructions at the U.S. Food and Drug Administration (FDA), College Park, Maryland, USA. Afterwards, the MLST typing was performed using the Center for Genomic Epidemiology platform, the prophages content were accessed by PHASTER and the presence of resistance genes related to efflux pump was verified by Comprehensive Antibiotic Resistance Database (CARD). For the 26 isolates from swine the sequence types (ST) 19 and ST1921 were the most prevalent ones; but the ST14, ST64, ST516 and ST639 were also detected. Previous results typed the 91 *S. Typhimurium* isolates from humans and foods as ST19, ST313, ST1921, ST3343 and ST1649. *S. Typhimurium* isolates from swine showed 6 (23.1%) unique prophages despite having a lower number of strains analysed in comparison to *S. Typhimurium* strains isolated from humans and food that presented 7 (16.3%) and 3 (6.25%) unique prophages, respectively. All the *S. Typhimurium* isolates contained the *acrA*, *acrB*, *macA*, *macB*, *mdtK*, *emrA*, *emrB*, *emrR* and *tolC* efflux pump genes. In conclusion, *S. Typhimurium* strains from swine showed greater diversity of STs and prophages in comparison to strains isolated from humans and foods. The pathogenic potential of *S. Typhimurium* strains was corroborated by the presence of exclusive prophages of this serovar involved in its virulence. The high number of resistance genes related to efflux pumps is worrying and may lead to therapeutic failures when clinical treatment is needed.

Keywords: *Salmonella Typhimurium*, humans, food, swine, efflux pump genes, prophages, MLST

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