TITLE: GENOMIC ANALYSIS OF *SALMONELLA* TYPHIMURIUM STRAINS ISOLATED FROM SWINE REVEALED A HIGH DIVERSITY AMONG THEM

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ABSTRACT:

Salmonella enterica serovar Typhimurium is able to infect different hosts, such as humans, swine, horses, birds, and sheep, among others. In humans it is a major cause of gastroenteritis worldwide. In countries such as Brazil, China and Germany it has been reported as the main serovar isolated from swine carcasses. Specifically, in Brazil there are few published studies that molecularly characterized this serovar isolated from swine. The aim of this study was to analyze the complete genome of six strains isolated from swine in the Santa Catarina State in Brazil. Our research group performed the whole genome sequence (WGS) of six *S.* Typhimurium strains using the NextSeq (Illumina). The genomic analysis performed included the six genomes of the strains studied and 40 *S.* Typhimurium genomes from different sources sequenced previously and available at the NCBI database. For all the 46 genomes, a phylogenetic tree was constructed using the Gegenees software. For the six swine genomes and one *S.* Typhimurium LT2 reference genome it was made an analysis of gene synthesis by the Mauve software. Furthermore, the comparison of the six genomes with a specific strain was made by the BRIG software. We observed a high diversity among the six *S.* Typhimurium strains of this study and in comparison with the 40 additional *S.* Typhimurium genomes available at NCBI. In addition, through Mauve's analysis, it was possible to observe that the six genomes of this study isolated from the swine showed a considerable number of different regions of inversions and deletions. Furthermore, this high diversity observed may be explained by the presence of genomic islands and transposases in the six genomes studied. It was also observed a great diversity and a high number of deletions in each of the studied strains in relation to the reference *S.* Typhimurium LT2 strain, using the BRIG software. The data obtained showed that the *S.* Typhimurium genomes analyzed presented a low degree of similarity among each other demonstrating the efficiency of genomic analysis for discriminating a monomorphic genus such as *Salmonella*. Moreover it might be suggested that there have been more than one subtype of *S.* Typhimurium contaminating swines in Brazil.

Keywords: *Salmonella* Typhimurium, genomic analyses, phylogeny, swines.