

**TITLE:** VIRULENCE FACTORS PROFILES OF *Salmonella* spp. ISOLATED FROM SWINE LYMPH NODES: A GENOMIC APPROACH

**AUTHORS:** TAVARES R.M.; SOUZA W.F.; POSSEBON, F.S.; VIANA, C.; NERO, L.A.; YAMATOGLI R.S.

**INSTITUTION:** UNIVERSIDADE FEDERAL DE VIÇOSA (AVENIDA PETER HENRY ROLFS, S/N - CAMPUS UNIVERSITÁRIO, 36570-900 VIÇOSA - MG, BRAZIL)

**ABSTRACT:**

*Salmonella* is a Gram-negative bacterium, that encompass a diversity of serovars that cause disease in humans and animals, considered an important foodborne pathogen. Although the genus *Salmonella* possess similar genetic traits, variation in DNA content, such as virulence factors, accounts for the difference in the severity of the disease. These *Salmonella* features have been largely identified through whole-genome sequencing which provides insights in molecular epidemiological studies. Thus, this study aimed to analyze the genome population of 27 *Salmonella* strains, isolated from swine mesenteric lymph nodes obtained in three different States of Brazil (Minas Gerais, São Paulo and Paraná) representing 10 different serovars (*S. Derby*, *S. Bredeney*, *S. Typhimurium*, *S. I.4,5,12:i:-*, *S. Panamá*, *S. Cerro*, *S. Give*, *S. Bovismorbificans*, *S. London*, *S. Infantis*). The genomes were annotated using PROKKA 1.14.5 software, compared with OrthoFinder and BLAST tool to analyze a total of 142 genes, these genes were selected according to their function and region, including 9 different pathogenic islands (SPI-1, SPI-2, SPI-3, SPI-4, SPI-5, SPI-6, SPI-7, SPI-11 and CS54). The genomic comparison revealed an overall high degree of similarity, concerning the presence of major virulence factors throughout the isolates, showing high conservation of important islands (SPI-1, SPI-2 and SPI-3), which at least one gene from the 9 different islands present on the isolates from different serotypes and locations. SPI-6 genes (*pagN* and *pagC*) were the most prevalent found, 27/27 and 26/27 respectively and SPI-7 genes (*pilV* and *pilR*) were the least found 4/27 and 2/27 respectively. *S. Serro*, *S. Give*, *S. Derby* isolates from Minas Gerais presented the smaller amount of virulence genes, while *S. Typhimurium* and *S. I.4,5,12:i:-* from São Paulo and Paraná presented majority of genes investigated, and higher potential to develop the disease. This comparative genomic overview highlights the importance WGS studies and brings new insights in pathogenic islands, reinforcing data from the literature about main serovars involved in outbreaks.

**Keywords:** foodborne pathogen, microbiology, *Salmonella*, SPI, Whole-genome.

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