Whole genome sequencing to investigate *Salmonella Gallinarum* isolates of recent fowl typhoid outbreaks in South Brazil.

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Fowl typhoid (FT) and pullorosis (PU) are avian diseases caused by *Salmonella Gallinarum* biovars Gallinarum and Pullorum. In Brazil, a governmental program (PNSA) was effective to control *S.* Gallinarum from 1994 to 2006, but more than 100 cases (mainly of FT) were reported in the last 10 years. Two possibilities were raised to explain FT resurgence: (i) virulence reversion of the live vaccine SG9R and (ii) failure in the farm biosecurity programs. In this study, we applied molecular biology assays (including whole-genome sequencing – WGS) to investigate *S.* Gallinarum strains of recent outbreaks in South Brazil. Eleven *S.* Gallinarum strains were isolated from poultry flocks with FT/PU in South Brazil from 2013 to 2015. *Salmonella* colonies were serotyped and tested to differentiate bv Gallinarum and Pullorum by specific PCR assays targeting *speC* and *glgC* genes. Intergenic sequence ribotyping (ISR) was also performed to observe intra-serotype differences. WGS of one *S.* Gallinarum strain (BR_RS12) was obtained with Illumina sequencing platform. A phylogenetic tree was generated by single nucleotide polymorphisms (SNPs) analysis. The results demonstrated that 6 isolates were from bv Gallinarum and 5 from bv Pullorum. ISR region analysis revealed that all bv Gallinarum isolates presented 100% of similarity with other reference strains of this biovar (including SG9R). On oppose, bv Pullorum isolates presented 2 different nucleotide sequences, divergent from the bv Gallinarum. In the phylogeny with the whole genome SNPs, BR_RS12 clustered in the same branch of one Brazilian field isolate from the 1990s (287/91) while all other Gallinarum genomes (including SG9R) clustered in another branch of the tree. These results support the hypothesis that the current field strains are not due to virulence reversion of the SG9R vaccine, but to bacteria maintained in some low-level biosecurity production flocks and backyard chickens.

**Key Words:** Salmonella, fowl typhoid, Pullorosis, whole genome, SNP