TITLE: VIRULENCE GENOTYPIC PROFILE OF *SALMONELLA* GALLINARUM

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SUMMARY:

Salmonella enterica subspecies enterica serovar Gallinarum biovar Gallinarum, named *Salmonella* Gallinarum (SG), is the most pathogenic serovar that infects birds and responsible for the development of avian typhus. It mainly attacks chickens but its virulence genes are still poorly understood. Thus, this work aimed to delineate a genotypic profile for SG. For that, 15 strains of SG were obtained from commercial poultry reared in Brazil, previously isolated and confirmed according to MAPA with confirmation of the biovar by microarray assays. The genotype profile was characterized by the search of 27 genes associated with virulence (invA, hILA, lpfA, lpfC, sefA, agfA, spvC, spvB, pefA, sopE, avrA, sivH, orgA, prgH, psaN, tolC, sipB, sitC, PgC, msgA, spiA, iRON, sopB, cdtB, sifA, sseL, stn) using PCR. DNA extraction was performed by heat treatment protocol and the reactions of amplification in Swift MaxPro® thermocycler, with the samples submitted to cycles of denaturation, annealing and extension. After the amplification, the electrophoresis was performed in 1.5% agarose gel stained with ethidium bromide. The analysis of the amplified products was made by visualization of the corresponding bands in ultraviolet light transducer MacroVue® and digital photo documentation. The genes invA, hILA, avrA, sefA, lpfA, agfA, slVH, slPA, pagC, msgA, prgH, orgA, tolC, sifA, sopB, sseL, stn were detected in all samples, whereas genes CdtB, pefA were not observed in any of them. The sopE and spvB genes were verified in 80% (12/15) of the isolates, whereas the spvC gene was detected in 20% (3/15) of the samples. The sipB, spaN, lpfC genes were determined in 86.67% (13/15) of the isolates and the ironN and sitC genes were detected in 13.34% (2/15) and 66.67% (10/15) respectively. The detection of these virulence genes in SG is one of the initial steps to assist in the understanding of the function of each SG gene and the characterization of the virulence of the isolates present in the poultry chain, aiming to improve pathogen control programs in this sector.

Keywords: Salmonella Gallinarum, poultry, virulence genes, PCR