Characterization of virulence of strains of *Salmonella spp*. isolated from a slaughter plant.

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Abstract:

Salmonella spp. is an enteric bacterium, responsible for severe foodborne infections and it´s one of the main agents involved in outbreaks worldwide. According to the serovar involved, the concentration of the inoculum, the virulence factors expressed by the agent and the immune status of the host, the infection can cause result a mild gastrentestinal infection to systemic infection. The virulence of *Salmonella* is multifactorial and complex, requiring the expression of several genes encoding toxins, adhesins, invasins, among others. This study aimed to investigate the presence of several genes involved in virulence strains (*invA, sopB, sopD, sipA, sipB, sipD, ssaR, sifA, spvB, sitC, tolC, flgK, fljB* and *flgL*). Forty *Salmonella* previously isolated from mats in a poultry slaughtering plant were used and their DNA was extracted by boiling for 10 minutes, followed by centrifugation at 13.000g/5 minutes and the supernatant was used for PCR reaction. The incubation was performed in a thermocycler, using the parameters of an initial cycle at 94 for 5 minutes initial denaturation, followed by 35 cycles of 94 ° C / 30s. The annealing temperatures were specific to each primer, followed by 72 ° C / 30s and a final extension temperature was 72 ° C for 4 minutes. The products were visualized on 1.5% agarose gel, stained with Sybr Safe. All 40 strains analyzed presented gene *invA, sipB, sipD, ssaR, sifA, sitC, tolC, flgK, fljB* and *flgL.* The genes *sopB* and *sipA* were observed in 37 strains (92.5%) and *sopD,* in 36 (90%). The gene less frequent was *spvB,* present in only 13 isolates (32.5%). In conclusion, the high prevalence of virulence markers indicates a high pathogenic potential of these strains. The study of these genes allows the understanding of the full potential of these bacteria causing infection as well as their characterization, contributing to tracking the bacterium.

Keywords: PCR, *Salmonella*, virulence genes

Fomentation agency: Capes