

TITLE: CHARACTERIZATION OF VIRULENCE GENES PRESENTS IN SPI1 AND SPI2 IN *Salmonella* ser. Enteritidis AND *Salmonella* ser. Typhimurium ISOLATED FROM FOOD, HUMAN AND ANIMAL SOURCES.

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ABSTRACT

Salmonella spp. are found worldwide and recognized as zoonotic microorganisms transmitted by food and its transmission and pathogenesis represent relevant public health problem. The serovars *S. Enteritidis* has been global cause of enterocolitis, have been associated with intensive poultry farming and egg production and the serovar *S. Typhimurium* being one of the main serovar varieties isolated from humans, animals and food, both are prevalent in Brazil and in many countries in the world. *Salmonella enterica* encodes numerous pathogenic islands (SPI). SPI-1 and SPI-2 are the most studied and contribute to the invasion of the epithelial cell layer and survival within systemic tissues. In the present study six *Salmonella enteric* serovar Enteritidis and 34 *Salmonella enteric* serovar Typhimurium strains resistant to 3rd generation Cephalosporins, Fluoroquinolone and Carbapenem isolated from food, human and animal sources, received for serological identification in the laboratory of Enterobacteria/IOC/FIOCRUZ, from different states of Brazil, between 2015 to 2017. Was evaluated their virulence profile by amplification of the polymerase chain reaction (PCR) identification of the following genes *slyA*, *orgA*, *invEA*, *phopQ*, *mgtC*, *invEA*, *stn*, *spvC*. Among the total analyzed *Salmonella enteric* serovar Enteritidis were selected 6 strains from food (1 strain) and human (5 strains) sources, of which 80 % have positive signal to *slyA*, *orgA*, *invEA*, *phopQ*, *mgtC* and *stn* genes and 66.7% to *spvC* gene. With respect to *Salmonella enterica* serovar Typhimurium 33 strains were selected from food (7 strains), Animal (13 strains) and human (13 strains) of which 100% *phopQ*, 97% *mgtC* and *osrA*, 91% *slyA*, 88% *invEA*, 85% *stn*, 21% *spvC* gene. The serovar *S. Enteritidis* is a successful *Salmonella* strain with the apparent ability to adapt to different hosts and transmission niches when and where specialization opportunities arise. Those information can provide a further means to identify problems, especially in *Salmonella* spp. which is worrisome and represent a hazard to animal and human health

Keywords: *Salmonella* spp, PCR, SPI