TTLE: GENOTIPIC PROFILE OF *Salmonella* Typhimurium QUINOLONE RESISTANT ISOLATED FROM FOOD CHAIN IN BRAZIL

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ABSTRACT:
Salmonella spp. have a variety of animal reservoirs and routes of transmission that can result in human infection. *Salmonella* Typhimurium as the most important serotype in outpatients with acute diarrhea. The emergence and spread of antimicrobial-resistant *Salmonella* spp. originating from food of animal origin has become a serious health hazard worldwide. Quinolones, particularly fluoroquinolones, are among the most widely used antibiotics for treating salmonellosis in both human and veterinary infections. Plasmid-Mediated Quinolone Resistance (PMQR) has been increasingly reported in Enterobacteriaceae worldwide. The aim of this study is to evaluate the presence of PMQRs and the similarity profile of *Salmonella* ser. Typhimurium with resistance to quinolones/fluoroquinolones isolates from food chain in Brazil. A total of 63 *Salmonella* ser. Typhimurium (35originated from humans, 22 from food, 4 from environmental and 2 from animal origin) were evaluated by disk diffusion and broth microdilution assay for the nalidixic acid, ciprofloxacin, enrofloxacin, levofloxacin and ofloxacin. The PMQRs were detected by PCR amplification using primes for *qnr* genes (A, B, C, D and S), *aac (6')-Ib*, integrase and variable region of integron. The profile of genetic similarity were performed by PFGE. Among these 63 isolates 50 (79.4%) isolates were resistant to Ciprofloxacin, 50 (79.4%) to Enrofloxacin, 37 (58.7%) to Ofloxacin, 34 (54%) to Levofloxacin and 62 (98.4%) were resistant to Nalidixic Acid by microdilution test . The detection of resistance genes showed 4 isolates of human source with the *qnrB* gene, 1 isolate from food with *qnrS* gene, and 1 isolate from food with *qnrD* gene. None of the isolates presented the *qnrA* or *qnrC* genes. The *aac(6')-Ib* gene was detected in 14 isolates. Thirty-nine isolates showed the conserved integron region with 600 to 1000 bp variable region size identified. The isolates had their clonal profile obtained by PFGE through digestion with XbaI enzyme forming a dendrogram with 33 fingerprints classified in 4 clusters, with 63% homology. The detection of one pulse-type with 39,7% (25/63) isolates showed a resistance profile to all quinolones/fluoroquinolones in 84% (21/25).The monitoring over the spread of PMQR in *Salmonella* ser. Typhimurium is essential for the public health control considering its high involvement in gastroenteritis frames.

Keywords: *Salmonella* ser. Typhimurium; quinolone resistance; food chain; genotipic profile; PFGE