TITLE: MOLECULAR SUBTYPING OF PLASMID-MEDIATED QUINOLONE RESISTANCE IN *SALMONELLA* STRAINS.

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Salmonella spp are the most frequent causative agents of foodborne disease. Clinical manifestations of human infections with Salmonella spp. cause from mild to severe gastroenteritis intestinal and extra-intestinal infections such as bacteremia, sepsis and including typhoid fever. Antimicrobial therapy is essential meningitis, immunocompromised patients, the elderly or children, or in severe and invasive cases caused by Salmonella, and ciprofloxacin (fluorquinolone) is recommended as the drug of first choice for treatment. The resistance to fluorquinolones is still rare in Salmonella spp. However, in recent decades the emergence and spread of resistance to nalidixic acid associated with reduced susceptibility to ciprofloxacin among Salmonella serotypes, have become of great interest public health. The multidrug resistance in Salmonella has been increased due to the indiscriminate use of antimicrobial agents in the treatment and prophylaxis human and veterinary medicine. In this study, 43 Salmonella strains harboring plasmid-mediated quinolone resistance genes (oqxA/B, qnrB19 and aac(6') lbcr) from human infections cases and non-human origin (mostly food) were evaluated. We verified that 20 transconjugants/transformants strains had from 1 to 3 plasmids of low and high molecular weight (up to approximately 98kb), using the technique S1-PFGE. PCR-based replicon typing detected the presence of six IncF, two IncL/M, and five Incl1 replicons in Salmonella transconjugants strains. Some transconjugants strains were non typeable. These results suggest the presence of recurrent and common plasmids in epidemiological unrelated Salmonella isolates of different serotypes and PMQR genes isolated, suggesting the successful spread of these genetic determinants.

Keywords: Salmonella, PCR-based replicon typing, quinolone resistance.

Development agency: FAPESP, Secretaria de Saúde do Estado de São Paulo