TITLE: MOLECULAR CHARACTERIZATION OF PLASMIDS ENCODING CTX-M β-LACTAMASES AND AmpC CEPhALOSPORINASE AMONG SALMONELLA spp


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ABSTRACT:

Salmonella spp. are one of the major enteropathogens that cause outbreaks of foodborne diseases, sporadic gastroenteritis, and extraintestinal infections. In recent years, the dissemination of extended-spectrum β-lactamases and AmpC-type beta-lactamases in Salmonella spp. strains have emerged worldwide and are currently portrayed as a major public health problem. Resistance by these mechanisms in Salmonella until then were considered relatively rare, however, the number of cases reported for several serotypes of Salmonella carrying genes of ESBL and AmpC mediated by mobile genetic elements, such as the plasmids increased. In this study, 45 strains of Salmonella isolated from clinical and non-human infections with plasmid-mediated beta-lactam resistance genes (blaCTX-M-2, blaCTX-M-8, blaCTX-M-15 and blaCMY-2) were characterized by PCR-based inc/rep typing method. Genetic relatedness among strains within the same serotypes was determined by Pulsed field gel electrophoresis (PFGE) using the Xba1 enzyme following the standardized protocol for Pulsenet pathogens. The genetic profiles were analyzed with BioNumerics software (Applied Maths, Belgium). The results obtained from the 45 plasmids revealed that cephalosporin resistant strains were IncI1 (n=21), IncF (n=3), IncHI2 (n=3), IncL/M (n=1), IncA/C (n=1) and sixteen non-typeable plasmids of Salmonella strains. Inc I1 was found in positive strains for the blaCMY-2 gene, IncHI2 in blaCTX-M-2, Inc1 and IncF were positive to blaCTX-M-8 strains. The PFGE analysis revealed that among the Typhimurium serotype (n=5) the genetic relatedness was 70.9% of similarity, and we found blaCTX-M-8 and blaCTX-M-15 genes associated with this serotype. For the Heidelberg serotype (n=16), the genetic relatedness was 81.8% of similarity and all of them carrying blaCMY-2 gene, while for the Muenchen serotype (n=10), we found that serotype was genetically related, presenting 96.1% of similarity and all of them carrying blaCTX-M-2 gene. These results suggest the circulation of closely related strains between human and non-human sources, besides of then, the presence of recurrent and epidemic plasmid groups in non-epidemiologically related isolates reinforce the need for improved continuous surveillance of antimicrobial resistance in isolates from human sources and alert to avoid possible failures in the antimicrobial treatment of severe invasive salmonellosis.

Keywords: Salmonella spp., beta-lactams resistance, plasmids, PCR-based replicon typing, PFGE.

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