

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

AUTHORS: BERTANI, A.M.J.¹; SANTOS, C.A.¹; ALMEIDA, E.A.¹; CUNHA, M.P.V.²; CAMARGO, C.H.¹; TIBA-CASAS, M.R.¹.

INSTITUTION: 1- INSTITUTO ADOLFO LUTZ, SÃO PAULO, SP (AVENIDA DR. ARNALDO, 351, 9º ANDAR, CEP 01246-902, SÃO PAULO-SP, BRAZIL); 2- FACULDADE DE MEDICINA VETERINÁRIA E ZOOTECNIA, UNIVERSIDADE DE SÃO PAULO (AVENIDA PROF. ORLANDO MARQUES DE PAIVA, 87, CEP 05508-010, SÃO PAULO- SP, BRAZIL).

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 (*bla*_{CTX-M-2}, *bla*_{CTX-M-8}, *bla*_{CTX-M-15} and *bla*_{CMY-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 *Xba*I 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 *bla*_{CMY-2}, IncHI2 in *bla*_{CTX-M-2}, IncI1 and IncF were positive to *bla*_{CTX-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 *bla*_{CTX-M-8} and *bla*_{CTX-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 *bla*_{CMY-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 *bla*_{CTX-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.

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