

TITLE: DETECTION OF GENES ASSOCIATED TO RESISTANCE TO CARBAPENEMS IN *Salmonella* spp. ISOLATED IN THE PERIOD 2014 TO 2017

AUTHORS: FESTIVO, M.L.^{1 2}; AMPARO, L.F.V.¹; IASBIK, L.L.F.¹; PRIBUL, B.R.¹; COSTA, R.G.¹; RODRIGUES, E.C.P. ¹; RODRIGUES, D.P.¹.

INSTITUTION: ¹LABORATÓRIO DE REFERÊNCIA NACIONAL DE ENTEROBACTÉRIAS/IOC/FIOCRUZ (AV. BRASIL, 4365, CEP 2104-360, MANGUINHOS, RIO DE JANEIRO – RJ, BRAZIL; ²UNIVERSIDADE FEDERAL DO ESTADO DO RIO DE JANEIRO/UNIRIO/PPGBMC (FREI CANECA, 94, CEP 2021 – 1010, CENTRO, RIO DE JANEIRO – RJ, BRAZIL)

ABSTRACT

Salmonella spp. represents one of the most important pathogens associated with gastroenteritis. Its epidemiology is complex, considering its capacity to implant and disseminate in different ecological niches. The emergence of strains resistant to carbapenems is also a major problem in Public Health, considering its use as a therapeutic option in the treatment of resistant *Salmonella* spp. infections commonly used as 3rd generation cephalosporin and fluoroquinolones. The present study aimed to evaluate the profile of antimicrobial susceptibility to carbapenems in *Salmonella* spp. isolated from different sources (Environmental, Food, Animal and Human) and determine the genetic mechanism of resistance. A total of 46 strains with resistance or intermediate susceptibility to carbapenems isolated from the period 2014 to 2017 were selected and submitted to PCR methodology using the *bla*KPC, *bla*IMP, *bla*VIM, *bla*NDM and *bla*OXA48 genes. The susceptibility profile was confirmed by the disc diffusion method and minimum inhibitory concentration (CLSI), with resistance percentages equivalent to 67.3% (31/46) for Imipenem (IMP) and Meropenem (MEN) and 4.3% (2/46) for Ertapenem (ERT) and intermediate profile of 32.6% (15/46) for IMP; 17.3% (8/46) for men and 11.1% (4/46) for ERT. PCR detected that 93.4% (43/46) were positive for one or more genes with the highest values for the *bla*VIM gene (82.6% - 38/46), in all years evaluated in different *Salmonella* spp. circulating in Brazil, including the most prevalent serovars: *S. Typhimurium*, *S. Heidelberg*, *S. Saintpaul*, *S. Infantis* and *S. Hadar*. The percentage to *bla*Oxa48 was 6.5% (3/46) in *S. Heidelberg* isolated from 2015 and 2016. It is noteworthy that a strain of *S. Mbandaka* isolated in 2015 presented the genes *bla*IMP, *bla*VIM and *bla*OXA48. The results confirm the importance of continuous monitoring of *Salmonella* spp., considering the capacity of implantation and environmental dispersion of microorganisms with multiple resistance between bacteria of different taxonomic and ecological groups, through mobile genetic elements determining a clinical and epidemiological impact for human medicine and veterinary.

Key-words: *Salmonella* spp., antimicrobial resistance, carbapenems