

TITLE: ANTIBIOTIC RESISTANCE PROFILE AND ANTIBIOTIC RESISTANCE GENES IN *Salmonella* PREVALENT SEROVARS ISOLATED FROM FOOD CHAIN IN BRAZIL: COMPARATIVE DATA FROM 2013 AND 2015

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ABSTRACT:

Among the etiologic agents involved in foodborne diseases, *Salmonella* spp. is present in large parts of the world, and its transmission and pathogenesis represent relevant public health problems. In addition to the high incidence, a worrying factor has been the increase in antimicrobial resistance which is the result of the indiscriminate use of drugs in human and veterinary medicine. In the present study, it was selected the resistant strains to cephalosporins and fluoroquinolones (3rd to 4th generations), obtained from the evaluation of antimicrobial susceptibility to a panel of 12 drugs belonging to different classes. This was carried out among 17449 of the total number of strains received for conclusive identification by the Laboratory of Enterobacteria / IOC / FIOCRUZ, between 2013 and 2015, isolated from different food chain sources, sent by public and private institutions. Were evaluated by amplification of the polymerase chain reaction (PCR) of the *bla_{CMY}*, *bla_{CTX-M}*, *acc(6')-Ib*, and integrase and integron genes among the 10 prevalent serovars, 2758 strains of *S. Heidelberg*, 1,283 of *S. Typhimurium*, 484 of *S. Enteritidis*. Among the beta-lactams, there was resistance to one or more drugs, of which cephalosporins of 2nd and 3rd generation, cefoxitin 310 (6.8%) and ceftazidime 356 (7.8%) and resistance to ciprofloxacin, was observed in 151 (3.3%) of the strains. The PCR results showed one *S. Typhimurium* strain from human source with, amplified product for *bla_{CMY}* and amplified product to integrase into seven strains *S. Typhimurium* and one of *S. Enteritidis* isolated from human origin too. Finally, 27 strains were investigated for the presence of integron and 17 strains (63%) presented amplification products. The misuse of antimicrobial agents in human and veterinary medicine or as growth promoter in food animals can potentially lead to widespread dissemination of antimicrobial resistance in *Salmonella* and other pathogens via mobile genetic elements. Many researches indicate in the last two decades the occurrence of MDR strains in different *Salmonella* serovars. Nowadays, interest in antimicrobial resistance in *Salmonella* has increased. The emergence and persistence of antibiotic resistance in *Salmonella* spp. is worrisome as it can pose a risk to animal and human health.

KEYWORDS: *Salmonella*, Antimicrobial Resistance, Genes of Resistance, Applied Microbiology, Public Health.

DEVELOPMENT AGENCY: CNPq; FIOTEC