

TITLE: ANTIMICROBIAL RESISTANCE EVALUATION IN CIRCULATING AND EXOTIC ENTEROPATHOGENS IN THE FOOD CHAIN ISOLATED BETWEEN 2015 AND 2016

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ABSTRACT

Microorganisms that affect human health are intertwined with the cultural evolution of man. This means that the microbiota of a population may be constituted of pathogenic species, autochthonous and floating, change due to different factors which could represent a risk condition because those microorganisms will be naturally eliminated in our sanitary sewage systems. Rio de Janeiro is a touristic city which receives a high number of people from different cities in Brazil and from different countries. Considering the lack of knowledge of the health of this community, it is extremely important to evaluate the role that those people can represent to the resident people in the short, medium and long term.

Strains of *Escherichia coli* and *Salmonella* spp. sent from Public Health Laboratories and related to outbreaks of DTA in the period from 2015 to 2016 in different regions of the country, received for antigenic characterization and virulence capacity, and strains of *E. coli*, *Salmonella* spp. and *Aeromonas* sp. isolated from sewage samples collected in 2016 from four Sewage Stations and two Sewage Treatment Stations in the city of Rio de Janeiro had been evaluated and compared their phenotypic antimicrobial resistance and the presence of resistance genes by PCR. The results showed that among of 62 *E. coli* strains, 51.6% (32 strains) had a multiresistant profile, including resistance to 3rd generation cephalosporins. Among the 29 strains of *Salmonella* spp. isolated from AB, the highest percentages of resistance were observed for STR (37.9% - 11 strains), and strains of salmonella spp. isolates from food, the highest percentages of resistance were observed for NAL (78.6% - 22 strains).

Among the 53 strains of *Aeromonas* sp., 12 strains (22.6%) had a multiresistance profile, and the highest percentages were observed for NAL (98.1% - 52strains).

E. coli strains were previously submitted to PCR assay for mcr-1 gene, and 36 strains (58%) presented amplification products for this gene. Among the strains of *Salmonella* spp. isolated from food, resistance genes for QNRS were found in a strain.

The use of the laboratory tools allows a rapid diagnosis of the microorganisms as well as their subtyping, so that outbreaks determined by those with emergent and / or exotic characteristics can be recognized and controlled at an early stage, making it possible to minimize the magnitude of their dispersion.

Keywords Enteropathogens; Food Chain, antimicrobial resistance.