Antimicrobial Resistance Evolution to 3rd generation of Cephalosporins and Fluoroquinolones in *Salmonella* spp Isolated from Food Chain.

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Salmonella is an important public health problem and represent one of the main causes of foodborne disease in humans. The microorganism is commonly found in the intestines of different animals and can be transmitted to people by foods. Another public health concern is the emergence of antibiotic resistant strains of *Salmonella*. Infections caused by MDR *Salmonella* may increase morbidity and mortality and require use of expensive drugs. This study includes *Salmonella* strains which have been submitted to National Reference Laboratory-NRL / Laboratory of Enterobacteria in Brazil from 2010 to 2014, to identify the serovars and the evolution of antimicrobial resistance.

All strains isolated from human source and foods involved in outbreaks have been sent by PHL and, from other sources, by public and private Institutions.

Susceptibility test was determined by disk diffusion test, according to the CLSI, in a total strains from human and food outbreak, and from other sources with alleatory selection (±10%).

From a total of 52,002 strains identified *S*.Typhimurium was the prevalent sorovar followed by *S*.Enteritidis until 2011. From 2012 to 2014 *S*.Typhimurium and, *S*.Infantis ranked among the 10 most prevalent serovars.

A total of 7,441 strains have been tested for susceptibility and showed MDR $\bar{x}$35.8%. Resistance among strains from food production animal showed reduced percentage of *S*.Minnesota from 2010-2014 (46.7% to 30%) and increase from 2010-2014 in *S*.Typhimurium (52.8% to 60.9%), *S.*Infantis (11.8% to 28.9%) and highest percentage in *S*.Heidelberg (80% to 88.7%). Different clusters of *S.* Heidelberg were observed in strains isolated from different years, sources and geographic areas when subtyped by pulsed-field gel electrophoresis.

Among 45 strains resistant to 3rd generation cephalosporins, PCR revealed of CTX$_{-M}$ and *bla*$_{CMY}$ genes among 37 strains. From 55 strains resistant to fluoroquinolones 48.1% were positive to gyrB, 20% to Qnr, 36.2% to integrase and one strain (1.8%) of aac(3”)IIa.

The surveillance of *Salmonella* serovars from human and non-human source is an important tool at a national level which may enhance our understanding of the epidemiology of this zoonotic microorganism and show how is vital the control on the use of antimicrobials in food producing animal which can represent a source to transmit for human.

Keywords: Salmonella, antimicrobial resistance, 3rd Cephalosporins, Fluoroquinolone, food chain