



## MOLECULAR CHARACTERISTICS OF ANTIBIOTIC RESISTANCE OF *SALMONELLA SPP.*, ISOLATED FROM FOOD PRODUCTS

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**Introduction.** The misuse of antibacterial drugs over the recent decades has resulted in antibiotic resistance as an increasing global threat. The widespread use of antimicrobial agents in human medicine, as well as in veterinary medicine for domestic and farm animals, and food production has caused the emergence of multidrug-resistant *S. enterica spp.*, including resistance to quinolones, fluoroquinolones and third generation cephalosporins, which are currently the drugs of choice for the treatment of severe salmonellosis, being one of the major global public health concerns. Thus, despite the great advances in food and drinking-water safety, salmonellosis is still considered one of the most common foodborne diseases worldwide. The purpose of this literature review was to analyse the genetic basis of antibiotic resistance in *Salmonella spp.*

**Material and methods.** This present paper analysed more than 30 scientific articles mostly retrieved from PubMed, EMBASE, HINARI databases. The most relevant data were included within the study review.

**Results.** *Salmonella spp.* belongs to the family Enterobacteriaceae, consisting of two main species, namely *S. bongori* and *S. enterica*, which are subdivided into more than 2500 serovars, based on antigenic differences in the lipopolysaccharide O antigen and two flagellin structures, most of them being recognized as potential human pathogens. Numerous researchers indicate that *S. enteritidis* is the most dominant serotype among the studied isolates. The study on antibiotic susceptibility shows a high level of multi-drug resistance to more than 3 drugs. A particularly high level of drug resistance was registered to tetracycline, fluoroquinolones (ciprofloxacin and nalidixic acid), ampicillin and trimethoprim-sulfamethoxazole. Many strains have shown concomitant resistance to ciprofloxacin and nalidixic acid, ampicillin and trimethoprim-sulfamethoxazole. Antimicrobial resistance genes have been identified to  $\beta$ -lactams (blaTEM, blaSHV, blaOXA, blaCTX-M and blaCMY), to tetracycline (tetA and tetB), to sulfonamide (sul1 and sul2), to chloramphenicol (from catA1 to cmlA) quinolone (qnrA, qnrB, qnrD, qnrS and qepA) and aminoglycoside (aac (6') - Ib, aac (3) - II and ant (2'') - I). The analysis of drug resistance determinants in isolated *S. enterica* strains will enable determining the presence and absence of particular genes or their various mutations, showing different resistance mechanisms to antibiotics. Changes have been recorded within the same gene across different geographic areas. The emergence of antibiotic resistance by mutation has been widely described and continues to be actively and comprehensively studied by scientists all over the world.

**Conclusions.** The results of many scientific papers have raised concerns about the emergence of multidrug-resistant *S. enterica*, especially to first-line drugs, as well as to third generation cephalosporins. The study of the molecular mechanisms of antimicrobial resistance confirms that these vary in *S. enterica*, depending on the geographic area and isolation environment. These findings provide the basis for further research of large-scale samples to better assess salmonellosis worldwide, as well as to consider the hygiene and infection control measures within the food industry, to prevent the spread of *Salmonella spp.* in food products.