

AN EIGHT-YEAR MONITORING (2011–2019) OF SALMONELLA SEROVARS ISOLATED FROM DIFFERENT SOURCES IN SOUTHERN ITALY.

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INTRODUCTION

According to the 2020 EFSA Report, *Salmonella* spp. represents one of the most diffused food pathogens worldwide (1). It has been reported that the most common *Salmonella* detected in foods are *S. Enteritidis*, *S. Typhimurium*, *S. 1,4,[5],12:i:-*, *S. Infantis* and *S. Derby*; while, in humans, *S. Newport*, *S. Stanley*, *S. Kentucky*, *S. Virchow* and *S. Agona* are also present (2). The inappropriate use of antibiotics to control *Salmonella* spp. infections has led to the spread of antimicrobial resistance (AMR). In addition, several studies have demonstrated the relationship between *Salmonella* serovars and antimicrobial resistance. The monitoring of AMR represents an efficient tool for evaluating the rapid changes in the microbial population (3), and immediately modifying national and European treatment guidelines. The aim of this study was to isolate and characterise the resistance profile of *Salmonella* isolated from different sources (human, food and environment) over about a decade (2011–2019).

METHODOLOGY

A total of 728 *Salmonella* spp. strains isolated from different matrices were grouped together as follows: 326 human, 148 environment and 254 food. The time interval of the study ranged from 2011 to 2019. All strains were from southern Italy (Campania and Calabria regions) and were analysed by the official laboratory for *Salmonella* serotyping of the Campania region (southern Italy). All isolates were serotyped according to the Kauffman–White scheme by means of agglutination with specific anti-sera for O (Statens Serum Institute–DK) and H antigens (Difco, Franklin Lakes, NJ, USA). The identification of the monophasic variant of *S. Typhimurium* was assessed by means of molecular assay.

The Antibiotic Susceptibility Test was carried out according to the disk diffusion method, following the Clinical and Laboratory Standards Institute (CLSI) recommendations. The result was indicated as MDR (multidrug-resistant) when the strain was resistant to at least

three classes of antibiotic. In human samples, the ASSuT profile (Ampicillin, Streptomycin, Sulphonamide and Tetracycline) was considered an “alert profile” for human health.

RESULTS

The serotyping data allowed us to identify the 326 strains isolated from humans: 97 (29.7 %) *S. Typhimurium*, 93 (28.5 %) *S. Typhimurium* monophasic variant, 61 (19 %) *S. Enteritidis* and 24 (7.4 %) *S. Napoli*. Of the 97 *S. Typhimurium* strains, 38 showed the antibiotic resistance profile ASSuT, while 24 showed an MDR profile. Of the 93 *S. Typhimurium* monophasic variant strains 71 showed the ASSuT profile and 15 showed an MDR profile. Of the 61 *S. Enteritidis* strains, only 4 showed an MDR profile. Finally, only one strain of *S. Napoli* showed an MDR profile.

With regard to the samples isolated from the environment, 148 *Salmonella* strains were identified: 34 (23 %) *S. Napoli*, 15 (10.1 %) *S. Typhimurium*, 15 (10.1 %) *S. Fischerhuette* and 9 (6.1 %) *S. Diarizonae*. Three *S. Typhimurium* and two *S. Fischerhuette* strains showed an MDR profile. No strains of *S. Napoli* and *S. Diarizonae* showed an MDR profile.

As regards the food matrices, 254 *Salmonella* strains were identified: 31 (12.2 %) *S. Typhimurium* monophasic variant, 57 (22.4 %) *S. Typhimurium*, 18 (7.1 %) *S. Enteritidis* and 14 (5.5 %) *S. Derby*. Of the above *Salmonella* strains, 26 *S. Typhimurium* monophasic variant, 37 *S. Typhimurium*, one *S. Enteritidis* and 7 *S. Derby* showed an MDR profile.

DISCUSSION

This study has focused on evaluating the antimicrobial resistance of several *Salmonella* serotypes isolated from different sources (environment, food, and humans) to 16 antimicrobial substances. Data have shown the different antimicrobial resistance profiles of the *Salmonella* spp. isolated from three sources.

Data have allowed us to conclude that, among the different *Salmonella* serovars isolated, *S. Typhimurium* and its monophasic variant were the most common and representative *Salmonella* among the food and human isolates. All the isolates showed an MDR profile (ranging from 4 to 8 antimicrobial molecules). This evidence is also supported by several studies [4][5][6][7].

With regard to the samples isolated from the environment, only three *S. Typhimurium* strains were isolated and a resistance to 4 or 5 antimicrobial molecules was observed.

Our data could support the hypothesis that - in humans - the principal transmission of the resistant *Salmonella typhimurium* strain could be associated with the consumption of food of animal origin, which represents the principal reservoir of this pathogen.