

Fifteen years trends and serotype distribution of human *Salmonella* strains in central Italy (2008-2022)

Russini Valeria^{1,2}, Lucarelli Claudia³, Villa Laura³, Di Giamberardino Fabiola¹, Boria Pierpaolo¹, Vestri Annarita², De Marchis Maria Laura¹, Bossù Teresa¹

1. Istituto Zooprofilattico Sperimentale del Lazio e della Toscana "M. Aleandri" - Food Microbiology Unit, Rome, Italy

2. Specialization School of Public Health and Biometrics, Department of Public Health and Infectious Diseases, Sapienza University, Rome, Italy

3. Istituto Superiore di Sanità, Department of Infectious Diseases, Rome, Italy

Introduction

Salmonella enterica (S.) is one of the most common agents of foodborne infections and a risk for children, elder people and immunocompromised patients. S. is the first cause of foodborne outbreaks in the EU in 2021. The top five *Salmonella* serovars involved in human infections overall in 2021 were: S. Enteritidis (54.6%), S. Typhimurium (11.4%), monophasic S. Typhimurium (1,4,[5],12:i:-) (8.8%), S. Infantis (2.0%) and S. Derby (0.93%)[1].

Aims

Our study reports S. serovars prevalence and trends in clinical isolates in central Italy over 15 years (2008-2022).

Methods

S. strains were isolated by hospitals and private laboratories from patients in Lazio and Tuscany regions and sent to the Regional Reference Centre for Pathogenic Enterobacteria (CREP) and Regional Reference Laboratory for Foodborne Pathogens of Human Origin (LRPTAU) at IZSLT (Rome). Serotypes were identified through serum agglutination following the ISO 6579-3. The epidemiological information were collected at the time of sampling, as age, sex, sampling date and hospitalisation status. All metadata and a selection of isolates were shared with ISS according to the National Surveillance Enter-Net Italia program.

Results

A total of 5071 *Salmonella* isolates were reported during the study period, with a mean of 338 isolates per year. After a substantially stable trend, in the last six years the isolates collected by our laboratories are rising (from 230 in 2016 to 519 in 2022). A total of 158 different serovars of *Salmonella enterica* sub. *enterica* were identified, the other five subspecies (belonging to 15 groups) and the only other species of the genus. The five most common serovars were in order: S. Typhimurium var. monophasic, which showed an increase over the period, S. Typhimurium, S. Enteritidis, S. Napoli and S. Infantis. These five serotypes represent more than 70% of the total cases. The occurrence of S. Typhimurium var. monophasic increased compared to the biphasic one over the years with an evident inversed trend. Similar trends were shown on data collect in our laboratories from food, animals and environment samples. S. Enteritidis occurrence peaked in 2018, doubling its yearly average, suggesting the presence of an outbreak not officially identified. Serovar S. Napoli showed a substantial

stable trend, with a mean of 14 cases per year and *S. Infantis*, with 13 cases per year, showed its maximum in 2022 with 44 cases. Afterwards, *S. Derby* with a stable trend and *S. Brandenburg* that showed an increase, from 5 cases in 2008 to 18 cases in 2021 (11 in 2022). *S. Strathcona* occurrence showed a significant peak during 2019 with 23 cases, correlated to a European reported outbreak.

The average age of patients during the 15 years is increasing from average age of 19.2 (SD 24.3, median 7) to 33 (SD 31.1, median 19). The most affected age groups were 0-9 years (46.9%), 10-19 years (10.8%) 60-69 years and 70-79 years (7.3%, 7.4%, respectively).

No association was found between hospitalizations and the most prevalent serotypes. However, association was found between hospitalization and patients' sex, showing a 36% higher probability for male compared to female (OR=1.36, 95%CI 1.14, 1.62). The hospitalization rate was higher in the oldest patients (90+) and in the over-60 categories. However more of 38% of the hospitalised patients belonged to the youngest age class (0-9).

The distribution of sampling date shown the highly seasonality of the infection, with tops during the hot season (June-September). Unexpected peaks could represent specific foodborne outbreak occurred (Fig. 1, red circles). E.g., in January 2013 and in March-April 2017, an excess of *S. Typhimurium* var. monophasic and *S. Enteritidis* cases were reported. We also observed an unusual number of cases in summer 2009, due to a peak of isolation of *S. Typhimurium*. During summer 2022, a significant increase of cases was report and caused by *S. Enteritidis* (29 strains possibly related to a broiler clone) and *S. Typhimurium* var. monophasic (and to a lesser extent by *S. Infantis*, and *S. Napoli*). Most of these unexpected increases were not officially linked to national or multi-country outbreaks. Unlike European data, the reported cases did not decrease overall during the pandemic in 2020 and 2021, only a plummet is shown between March and May 2020, corresponding to the first Italian lockdown (Fig. 1, black circle).

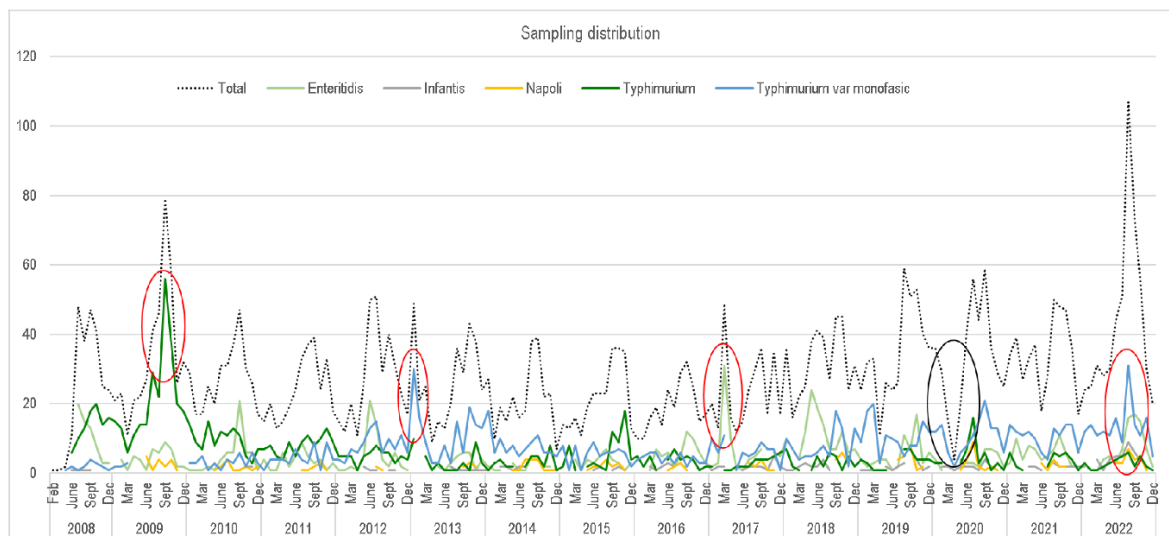


Figure 1. Sampling distribution of *Salmonella* isolates, showing the total and the detail of the five most frequent.

Conclusions

The results show that *Salmonella* infection is still a relevant risk in central Italy, with mostly *S. Typhimurium* and *S. Typhimurium* monophasic as the most frequent serovars, while in Europe the most widespread serovar during the last 15 years is *S. Enteritidis*, followed by *S. Typhimurium* and *Typhimurium* monophasic.

Even if the hospitalization rate is higher in the elderly population, the majority of cases in hospital concerning the children of 0-9 years old. Italian and European legislation still divides the serotypes into “relevant” and “non-relevant” for public health in the context of official food controls (laying hens and fresh chicken meat), considering relevant only *S. Typhimurium* (and var. monophasic) and *S. Enteritidis*. For breeding groups of *Gallus gallus* national plans considered relevant *S. Enteritidis*, *S. Typhimurium* (and var. monophasic), *S. Infantis*, *S. Virchow*, and *S. Hadar* (16 and 24 cases respectively in 15 years of surveillance) [2]. From the data collected, there was no evidence that only the relevant serotypes are causing human infection (e.g., *S. Napoli*). The observed trend suggests that the mean age of cases is rising, but no evidence seems to explain this trend.

Surveillance and digital reporting, even retrospective, are pivotal for long-term monitoring and outbreaks investigation and research. The analysed data show that there is still a need to improve communication about food safety, to prevent illness and hospitalization.

Bibliography

1. European Food Safety Authority and European Centre for Disease Prevention and Control, The European Union One Health 2021 Zoonoses Report. *EFSA J*, 2022; 20:7666
2. Leati M., Zaccherini A., Ruocco L., et al, The challenging task to select *Salmonella* target serovars in poultry: the Italian point of view. *Epidemiol Infect*, 2021; 149:e160