

## TEN-YEARS OF INTEGRATED APPROACH IN SURVEILLANCE OF FOOD-BORNE SALMONELLA IN PIEDMONT REGION, 2011-2020

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Foodborne zoonotic diseases and multi-drug resistance are of global concern for public health. Nontyphoid serotypes of *Salmonella enterica* subsp. *enterica* are the second most reported cause of food-borne outbreaks in Europe [1]. Disease incidence in humans have generally declined in recent years thanks to improvements in veterinary health associated to both *Salmonella* occurrence and rational use of antibiotics [2]. Due to the existing interrelations between animals, humans and environment a multidisciplinary One Health approach in *Salmonella* surveillance might ensure a high food safety level and reduce the risk of pathogen transmission to humans. We aim at investigating the geographical and temporal distributions of *Salmonella* infection in humans, farmed animals and wildlife in Piedmont region over the 2011-2020 period, identifying serotypes involved and evaluating their antimicrobial-resistance profiles. All isolates were identified and serotyped according to ISO/TR 6579; then antimicrobial resistance, against 18 molecules in human and environmental isolates and 12 molecules in animals' isolates, was evaluated by the Kirby-Bauer method according to Clinical and Laboratory Standard Institute guidelines. To achieve a good representativeness of the geographic distribution of the infections in farmed and wild animals, poultry and cattle livestock and red fox, roe deer and wild boar species were considered. We successfully characterized 4,440 isolates from symptomatic human patients requiring clinical care in different inpatient facilities across Piedmont region. Our results showed clear differences in pathogen infections by age and gender strata, being male children (<9 years-old) the most affected class. The two livestock populations showed similar levels of *Salmonella* prevalence: however, we detected differences according to farming methods and productive orientations, with organic poultry (P=22.2; 95% CI=14.1-32.2), layer hens' production (P=14.8; 95% CI= 11.3-18.9) and dairy cattle (P=21.1; 95% CI=14.5-29.9), showing the largest pathogen occurrence. In wildlife species, *Salmonella* infections were restricted to only few geographic areas, and prevalence was particularly relevant in red fox (P=7.8%; 95% CI=4.7-12.1), compared with wild boar (P=4.4%; 95% CI=1.6-9.3) and roe deer (P=2.5%; 95% CI=1.0-5.0). Phenotypic analyses uncovered a great variety of *Salmonella* serotypes, especially in humans (n=151) and poultry (n=34). *Salmonella* Typhimurium monophasic variant 1,4,[5],12:i:- was the most prevalent serotype involved in human infections, *S. Typhimurium* prevailed in cattle and wildlife and *S. Enteritidis* in poultry. Among these serotypes, the highest number of multidrug resistant strains were observed for *S. Typhimurium* monophasic variant 1,4,[5],12:i:- of human origin (up to 11 antibiotics); in particular, more than 70% of these strains were resistant to some antibiotics used in clinical practice (tetracycline, ampicillin and streptomycin). High levels of antimicrobial resistance also occurred in isolates from poultry (up to 9 antibiotics), cattle (up to 12 antibiotics) and wild species (up to 8 antibiotics).

Our study provides a broad picture of the epidemiology of nontyphoid salmonellosis in Piedmont region during the last decade. We underline the importance of adopting a multidisciplinary approach to develop effective strategies to comprehensively respond to salmonellosis and antibiotic resistance globally.

[1] EFSA and ECDC. The European Union One Health 2019 Zoonoses Report. EFSA Journal 2021

[2] EIP-AGRI Focus Group. Reducing antimicrobial use in poultry farming. Final report 2021.