ANTIMICROBIAL RESISTANCES OF *SALMONELLA* STRAINS ISOLATED FROM HUMAN, WILD BOAR, AND ENVIRONMENTAL SAMPLES FROM 2018 TO 2020 IN THE NORTHWEST OF ITALY

Valeria Listort , Aitor Garcia-Vozmediano, Monica Pitti, Cristiana Maurella, Daniela Adriano, Carlo Ercolini, Monica Dellepiane, Lisa Guardone, Elisabetta Razzuoli

Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta
Corresponding author: V. Listorti (valeria.listorti@izsto.it)

Salmonellosis is the second most common zoonosis reported in Europe in 2020 [1], and antimicrobial resistance (AMR) in foodborne pathogens such as *Salmonella* is a major concern for public health safety [2]. The interface between the environment, wild animals and humans contributes to the emergence of antimicrobial resistant bacteria [3]. Integrated surveillance of AMR is one of the top priorities of the European Union [4]. From a one-health perspective, this study aimed to investigate the serotypes and antimicrobial resistance profiles of *Salmonella* spp. strains circulating in humans, environment and wild boars in Liguria region from 2018 to 2020. A total of 517 *Salmonella* spp. strains were analysed. In details: Sixty strains were isolated from liver of wild boars hunted in Liguria, according to ISO 6579:2002/COR. 1, 2004, 193 environmental strains have been previously isolated and 264 human strains were conferred by different hospitals in Liguria, isolated from patients showing clinical signs referred to salmonellosis. Serotype identification was carried out in accordance to ISO/TR 6579-3, 2014. Antimicrobial resistance was evaluated in 415 typed isolates using the Kirby-Bauer method according to Clinical and Laboratory Standard Institute guidelines. Human and environmental isolates were tested against to 18 molecules and isolates from wild boar against 12 molecules. *S.* Typhimurium monophasic variant 1.4.[5].12:i:-, *S.* Veneziana and *S.* Newport were the most prevalent serotypes identified in humans, environmental samples and wild boar, respectively. The degree of antimicrobial resistance varied according to different sources, with 80.4% of *Salmonella* isolates from humans, 50.0% of those obtained from environment and 7.7% from wild boars displaying resistance for at least one molecule. We uncovered highest levels of resistance against to the combinations of sulfadiazine + sulfamerazine + sulfamethazine, in human (93.3%; 95% CI=87.0–97.0) and environmental strains (74.2%; 95% CI=62.0–84.2) and trimethoprim + sulfamethoxazole (human strains: 66.7%; 95% CI=43.0–85.4), (environmental strains: 58.3%; 95% CI= 36.6–77.9), while only one resistance pattern was observed against to trimethoprim + sulfamethoxazole in wild boar isolates. Multiple resistant patterns (≥ 2 molecules) were observed in both environmental and human isolates, which concurrently displayed resistant behaviour to up to 5 and 8 antibiotics, respectively. Notwithstanding, multiple resistant patterns often occurred among human serotypes (58.9%; 95% CI=51.5–66.1) compared with environmental isolates (16.4%; 95% CI=8.8–27.0). Fortunately, apart a high resistance observed against azithromycin in environmental strains, the resistances against high critically important molecules observed were generally low. Considering the public health safety, this is an important observation, being these molecules essential for specific treatments in humans.

[1] EFSA and ECDC. The European Union One Health 2020 Zoonoses Report. *EFSA Journal*, 19: 6971, 2021

[2] Florez-Cuadrado D. et al. Chapter Five - Antimicrobial Resistance in the Food Chain in the European Union, in Advances in Food and Nutrition Research, Academic Press, 86: 115-136, 2018

[3] Takur S. et al. The mandate for a global "One health" approach to antimicrobial resistance surveillance. American Journal of Tropical Medicine Hygene 100: 227-228, 2019.

[4] Joint report by ECDC, EFSA, EMA, and OECD on antimicrobial resistance in the EU/EEA and a One Health response, 2022.