NEW SEROVARS AND MULTIDRUG-RESISTANT STRAINS OF *SALMONELLA* IN WILDLIFE: IMPLICATIONS FOR PUBLIC HEALTH POLICIES IN CHILE AND ARGENTINA

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n recent decades, the increasing interaction between humans and wildlife, mainly due to urban expansion and deforestation, has increased the transmission of multi-host pathogens with zoonotic potential, such as Salmonella enterica. Although salmonellosis is mainly recognized as a foodborne illness, about 10% of cases arise from direct contact with infected animals¹. Research conducted on wildlife from South America (Brazil, Chile, Colombia, Argentina), suggested a diversity of serovars present in these animal populations²⁻⁵. This is especially problematic considering the migratory patterns of certain wildlife species, and the natural borders we share across the continent. These animals move freely across these boundaries, creating opportunities for the transmission of pathogens between countries.

Historically, S. Enteritidis and S. Typhimurium serovars have prevailed among clinical cases in our countries^{6,7}, as well as in domestic production, and wild animals. However, recent studies have shown the emergence of less common serovars that may possess specific adaptations for survival in different hosts and environments, potentially enhancing their transmission capacity. This characteristic is particularly concerning when these serovars also exhibit phenotypes of multidrug resistance (MDR), a phenomenon that severely compromises therapeutic options in human infections. Among these, S. Infantis and S. Goldcoast represent emerging serovars in wild animals, with resistance profiles that include beta-lactams, tetracyclines, chloramphenicol, and fluoroquinolones^{5,8}. Salmonella infections with MDR strains not only increases morbidity and mortality but also imposes additional burdens on healthcare systems, requiring prolonged hospitalizations, increasing costs for both the healthcare system and patients, and necessitating the use of critically important antibiotics.

Recently, S. Infatis and S. Goldcoast were identified in wild birds along the central coast of Chile⁵, and it is very probable that they are also present in Argentinian wildlife. S. Infantis is a widely distributed serotype and is the most common cause of human salmonellosis in Europe and United States, mainly associated with poultry meat products. It is currently considered an emerging serotype worldwide, with a marked increase in reported cases since 20119. On the other hand, S. Goldcoast, for which there are no reports in Chile or Argentina from domestic animals or humans, is also considered an emerging serotype on an international scale, associated with animal-derived foods and responsible for foodborne outbreaks in Europe, Asia, and North America⁸. Given the ongoing spread of multidrug-resistant S. Goldcoast strains, it is essential to investigate their global distribution and the underlying mechanisms of antimicrobial resistance. The limited understanding of the impact of these serotypes in our countries makes this a priority topic for microbiological and epidemiological research at the human-animal-environment interface.

Research on salmonellosis suggest that the bacteria detected in humans and domestic ani-

mals are also present in wild reservoirs¹⁰, highlighting the need for a robust epidemiological surveillance that incorporates wildlife into monitoring schemes. These findings should prompt public health policymakers to enhance *Salmonella* surveillance in wild animals, but it is also crucial to develop preventive strategies that address the bidirectional transmission between these reservoirs and humans, considering the environmental impact of human activities that facilitate this interface¹⁰.

Public health policies must not only focus on outbreak containment once they occur; besides adopt a proactive approach that includes research and prevention. Implementing community education programs, regulating human-animal interactions in wild areas, and promoting agricultural and livestock practices that reduce contamination by zoonotic pathogens are just a few examples of the measures needed to address this issue comprehensively. The lack of control over wildlife movement in our shared ecosystems highlights the importance of cross-border collaboration in monitoring and managing zoonotic diseases, as wildlife acts as a reservoir that can spread infections across regions, further complicating containment efforts.

Salmonella infections in wild animals and the emergence of MDR strains represent a significant risk to public health. Integrating the findings from research conducted in Chile and Argentina into public health policies could not only prevent human infections but also mitigate the impact of antimicrobial resistance, a challenge that requires urgent and coordinated multidisciplinary attention at both regional and global levels.

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