Salmonella in Chile: an urgent need for timely data and WGS implementation

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Salmonella is a major foodborne pathogen, producing significant health and economic burdens worldwide, a problem aggravated by the emergence and dissemination of antibiotic-resistant lineages that challenge the treatment of severe infections in people at higher risk.[1] In Chile, *Salmonella* is the main foodborne pathogen, accounting for more than 45% of all foodborne infections with known etiology from 2018 to 2020, and rising to 82.4% in 2021.[2]

In recent years, Chile has made important advances strengthening its regulatory framework for *Salmonella* surveillance and antimicrobial resistance (AMR) monitoring. The last update of the Regulation on Mandatory Notification and Surveillance of Communicable Diseases, enacted in March 2019, incorporated a One Health approach for the surveillance of *Salmonella* and other pathogens. It also mandates that all isolates collected from clinical and environmental sources—including food, water, pharmaceutical products, and medical supplies—have to be submitted to the Instituto de Salud Pública de Chile (ISP) for phenotypic serotype identification and antimicrobial susceptibility testing.[3] Additionally, the second version of the National Action Plan on Antimicrobial Resistance (2021–2025) expanded the pilot study of the Integrated AMR Surveillance Project —originally focused on *Salmonella* in chicken meat— to include samples from farms and slaughterhouses, aiming to provide the basis for implementing an integrated approach for pathogen surveillance across different food chains.[4] Nevertheless, despite these policy advances, significant gaps persist in our understanding of the *Salmonella* population dynamics and resistance trends in the country. This problem is exacerbated by a lack of timely public data and the limited use of whole genome sequencing (WGS).

The most recent official *Salmonella* surveillance report was published in 2019 and covered data from 2014 to 2018.[5] Therefore, there is currently a six-year gap of public epidemiological data. The 2019 report documented a significant increase in the prevalence of antibiotic-resistant *Salmonella* Infantis from clinical origin, data that suggested the spread of a multidrug-resistant lineage in Chile. However, it was not until 2024 when application of WGS in a large-scale genomic study confirmed the dissemination of the globally emergent *Salmonella* Infantis lineage in the country.[6] Further serovar trends, obtained via Chile's Transparency Law (N° 20.285), show continued shifts in serovar prevalence among human infections. While Enteritidis, Typhimurium, and Infantis remain as the predominant serovars, there has been a reduction in *Salmonella* Stanley isolations, a sustained increase in *Salmonella* Newport from 2019 to 2022, and a marked rise in *Salmonella* Agona from 2022 to 2024 (Fig. 1). Since this information is not publicly available without a formal request, the implications of these prevalence changes and their potential drivers have not been explored, potentially hiding the introduction of high-risk lineages and the dissemination of antimicrobial resistance genes, as was observed for *Salmonella* Infantis.[6]

Although not yet part of the routine surveillance, WGS have already proven highly valuable for obtaining and contextualizing the yet scarce *Salmonella* genomic data currently available from Chile. Genomic studies have uncovered widespread dissemination of different *Salmonella* lineages in surface waters from central Chile (prevalence: 20.0–43.4%), wild birds (including gulls, owls, and penguins), and chicken meat production facilities, along with the presence of mobile genetic elements driving the spread of antimicrobial resistance genes.[6–9] Nevertheless, the available studies provide mostly isolated, time-limited data, and without a systematic follow-up, their relevance may soon become outdated due to the changing serovar dynamics.

Implementing a national genomic surveillance system with a One Health approach is a major undertaking that requires strong partnerships, open collaboration,

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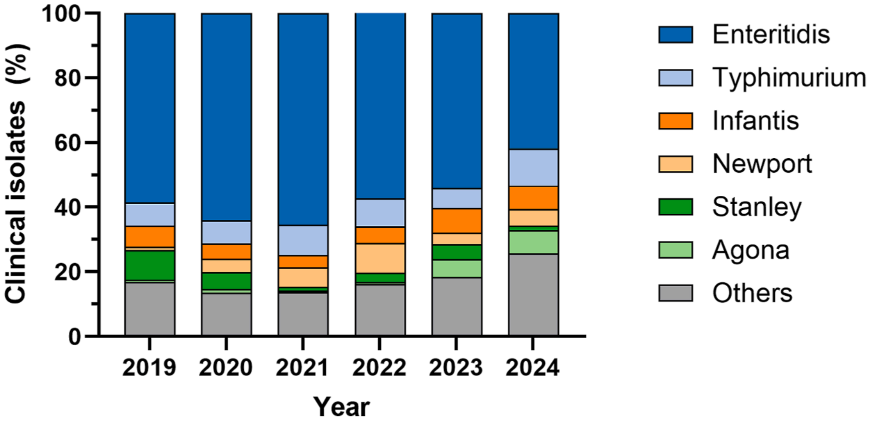

***Fig. 1:* Top 6 *Salmonella* serovars causing human infections in Chile.** Percentage of *Salmonella* serovar isolates of clinical origin submitted to the ISP by laboratories across all 16 administrative Regions of Chile during the period 2019–2024.

and timely, transparent communication between public health agencies, academia, and laboratories in both public and private sectors. This effort must also address key challenges related to infrastructure, qualified personnel, data management, timely reporting, and sustained political and financial commitment.[10] Therefore, incorporating WGS into foodborne outbreak investigations may offer a cost-effective entry point for Chile, as it is less resource-intensive yet provides critical data for epidemiological interpretation, source traceback, and hypothesis generation, while can also help to assess the feasibility of a nationwide routine WGS surveillance program.[10] We strongly emphasize that the upcoming National Action Plan on Antimicrobial Resistance for 2026–2030, the recently updated Official Program for the Control and Reduction of *Salmonella* spp. in the Poultry Production Chain (promulgated in December 2024; https://www.bcn.cl/leychile/navegar?idNorma=1209778), the third version of the National Food Safety and Quality Policy for 2025–2035 (recently under public consultation until June 30th; https://www.achipia.gob.cl/politica-de-inocuidad-y-calidad-de-los-alimentos/) and future updates to *Salmonella* surveillance and control strategies should prioritize WGS implementation, as it is critical for enabling effective, data-driven responses to foodborne disease threats.

Contributors

API conceived the study and prepared the original draft. All authors revised, edited, and approved the final version of this Comment.

Data sharing statement

The raw data used for Fig. 1 can be requested from the Instituto de Salud Pública using the form at the following link: https://www.portaltransparencia.cl/PortalPdT/ingreso-sai-v2?idOrg=1052.

Declaration of interests

All authors declare no competing interests related to this work.

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