Leveraging surveillance data to map sources and spread of *Salmonella Enteritidis* in four European countries

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The trend for Salmonella infections in the EU has been increasing since 2020. The most common serovar causing human infections is *Salmonella* Enteritidis (*S*. Enteritidis), which accounted for over 50% of recorded infections in 2024, according to the European Union One Health 2024 Zoonoses Report. The primary source of these infections is poultry. The focus of this project is therefore bacterial isolates from this sector. Multi-country outbreaks of *S*. Enteritidis ST11 occur frequently and it is difficult to resolve these outbreaks because the genetic variation detected using cgMLST is low. This project aims to improve the available methods by enhancing genomic resolution and advancing source tracing. The goal is to better understand the spread of *S*. Enteritidis throughout the EU and identify opportunities for intervention. This will be achieved using existing data from the surveillance systems in both food, animal, and human sector in Belgium, Denmark, Sweden, and the Netherlands. These surveillance data have been supplemented with additional sequences from the last 10 years, accompanied by epidemiological information linking them to the poultry industry. A preliminary SNP analysis has already been conducted. This confirmed that strains found across Europe are highly similar, with phylogenetic clusters containing isolates from different countries as well as spanning multiple years. Further analysis will investigate the presence of plasmids, resistance and virulence genes of interest to determine whether these provide additional discriminatory power. In addition, novel bioinformatics approaches, such as analysis of the flanking regions of genes of interest, will be performed. We expect these methods to improve our understanding of evolutionary mechanisms and help identify transmission routes. Ultimately, we aim to perform phylodynamic analysis to trace the spread of *S*. Enteritidis in the region over the past 10 years, reconstructing transmission pathways and identifying potential introduction events. We hope that our findings will contribute to the development of effective intervention strategies and support the resolution of international foodborne outbreaks.

References:

1. EFSA and ECDC (2025). The European Union One Health 2024 Zoonoses Report. EFSA Journal, 23(12). https://doi.org/10.2903/j.efsa.2025.9759