# **Global Salmonella Concord Genomics**

# *Zaynab, FAIZAN, Yousra.W, Mariam, Richie, Sopuruchi, Ayo, Chris*

**Introduction**

*Salmonella* is a gram-negative bacteria, encompassing thousands of serovars, belonging to the Enterobacteriaceae family [1]. The family causes a range of human infections worldwide. The development of antimicrobial resistance (AMR) by bacterial strains is a growing global concern [2]. *Salmonella enterica* Concord (*S*.Concord), which causes gastritis and infections of the bloodstream, is an emerging concern as a potential worldwide threat of AMR [3]. In this study, we observed the genomic variety and AMR profiles of 50 isolates of *S*.Concord.We also carried out a phylogenetic analysis to understand how these samples are evolutionarily linked to each other. This information coupled with the AMR genes (ARGs) profiles help us understand the patterns of AMR traits dissemination in *S*.Concord, hence is crucial in developing surveillance and treatment options for illnesses associated with the pathogen.

**Methods**

Raw sequencing data were downloaded using SRAtools v3.1.0, via accession numbers in the [supplementary data](https://docs.google.com/spreadsheets/d/1qkvpdnnuBQkD0cPKuKsgM5xbc0PfBKxy5S9-hYYLd74/edit?usp=sharing). Quality assessment was performed using FastQC v0.12.1, followed by trimming of adapters and low-quality sequences using fastp v0.23.4. The reads were assembled into contigs using SPAdes v3.15.5. Insilico serotyping was conducted with SeqSero2 v1.3.1, and ARGs were identified using AMRFinderPlus v2.1.6. Replicon genes were detected through Abricate employing the PlasmidFinder database v2.1. All outputs were consolidated into a single CSV file and visualized using ComplexHeatmap v2.8.0 and ggplot in R. Core genome SNPs were extracted by aligning the trimmed reads against the reference genome using Snippy v4.6.0, and integrated into a unified file with Snippy-core. Phylogenetic analysis was performed using RAxML-NG v1.2.1 under the GTR+G model to construct a tree, visualised with ggtree v2.2.4 in R.

**Results**

Serotyping revealed the antigenic profile of the isolates is “7:1,v:1,2”. We observed a heterogeneous distribution of ARGs among the samples with sul1, sul2 and blaTEM-1 being the most prevalent. Analysis of plasmid genes revealed a variable presence of replicon genes but the frequent co-occurrence of IncA/C2\_1 and IncHI2\_1 were notable. The samples had varied ARGs and plasmid gene profiles with few showing no observable genes while others such as ERR9516192, ERR9516269, and ERR9516279 exhibited multiple ARGs and replicon genes.

**Discussion**

This study provides important insights into the phylogenetic relationship and AMR profiles of the bacteria. The prevalence of sul1, sul2 and blaTEM-1 as ARGs indicates the diversity in resistance mechanisms, most likely influenced by selective pressures in an environment rich in sulfonamides and beta-lactams. As observed in previous studies, the variable exhibition of plasmid genes and co-occurrence of the plasmids IncA/C2\_1 and IncHI2\_1 suggest the spread of ARGs via plasmid-linked mechanisms. For instance, Inch12\_1 was responsible for the invasive *S. enterica* serovar Typhimurium epidemic in South Africa [4, 5]. While the exhibition of multiple ARGs and plasmid genes seen in ERR9516192, ERR9516269, and ERR9516279 indicates significant antibiotic pressures leading to multidrug resistance, the absence of ARGs implies low exposure to antibiotics or effective treatment strategies adopted in these environments. This corroborates the report of Alam, et. al., 2021 [6]. This study thus emphasises the need for surveillance and proper treatment strategies to combat further dissemination of AMR.

**References**

1. Grimont, P. A., & Weill, F. X. (2007). Antigenic formulae of the Salmonella serovars. WHO collaborating centre for reference and research on Salmonella, 9, 1-166.

2. Beyene, G., Nair, S., Asrat, D., Mengistu, Y., Engers, H., & Wain, J. (2011). Multidrug resistant Salmonella Concord is a major cause of salmonellosis in children in Ethiopia. *The Journal of Infection in Developing Countries*, *5*(01), 023-033.

3. Hendriksen, R. S., Mikoleit, M., Kornschober, C., Rickert, R. L., Van Duyne, S., Kjelsø, C., ... & Aarestrup, F. M. (2009). Emergence of multidrug-resistant Salmonella Concord infections in Europe and the United States in children adopted from Ethiopia, 2003–2007. The Pediatric Infectious Disease Journal, 28(9), 814-818.

4. Feasey, N. A., Cain, A. K., Msefula, C. L., Pickard, D., Alaerts, M., Aslett, M., Everett, D. B., Allain, T. J., Dougan, G., Gordon, M. A., Heyderman, R. S., & Kingsley, R. A. (2014). Drug resistance in Salmonella enterica ser. Typhimurium bloodstream infection, Malawi. Emerging infectious diseases, 20(11), 1957–1959.

5. Van Puyvelde, S., Pickard, D., Vandelannoote, K., Heinz, E., Barbé, B., de Block, T., Clare, S., Coomber, E. L., Harcourt, K., Sridhar, S., Lees, E. A., Wheeler, N. E., Klemm, E. J., Kuijpers, L., Mbuyi Kalonji, L., Phoba, M. F., Falay, D., Ngbonda, D., Lunguya, O., Jacobs, J., … Deborggraeve, S. (2019). An African Salmonella Typhimurium ST313 sublineage with extensive drug-resistance and signatures of host adaptation. Nature communications, 10(1), 4280.

6. Alam, M. U., Ferdous, S., Ercumen, A., Lin, A., Kamal, A., Luies, S. K., Sharior, F., Khan, R., Rahman, M. Z., Parvez, S. M., Amin, N., Tadesse, B. T., Moushomi, N. A., Hasan, R., Taneja, N., Islam, M. A., & Rahman, M. (2021). Effective Treatment Strategies for the Removal of Antibiotic-Resistant Bacteria, Antibiotic-Resistance Genes, and Antibiotic Residues in the Effluent From Wastewater Treatment Plants Receiving Municipal, Hospital, and Domestic Wastewater: Protocol for a Systematic Review. JMIR research protocols, 10(11), e33365.