**Gregor-Mendel: Stage Three Task**

**A global genomic analysis of Salmonella Concord reveals lineages with high antimicrobial resistance in Ethiopia**

**Introduction:** The emergence of antimicrobial resistance (AMR) in S. Concord strains poses a significant public health concern, complicating treatment strategies and potentially leading to more severe clinical outcomes. Molecular surveillance and antimicrobial testing are vital for tracking and controlling Salmonella infections by public health agencies (Park et al., 2021). Comprehending the genomic features of S. Concord strains, especially their phylogenetic relationships and AMR profiles, is essential for efficient surveillance, control, and prevention of infections.

**Aim:** To characterize AMR profiles and understand the phylogenetic relationships among diverse strains from different regions.

**Significance of the Study:** The findings from this study are significant for public health stakeholders in that the analysis of the genetic makeup of S. Concord strains can help design focused strategies to fight antibiotic resistance and lessen the burden of S. Concord infections globally.

**Pipeline:** Data extraction **→**quality control (fastQC v0.11.9 & MultiQC v1.8) **→**Reads trimming (trimmomatics v0.39) **→**Reads alignment to reference genome(Minimap2 v2.17-r941) **→**Filtering clipped alignments (Samclip v0.3.0)**→** processing bam files(Samtools v1.9) **→**taxonomic read classification(Kranken2 v2.0,8) **→**reads assembly(Spades v3.15.5) **→** draft assembly(Quast v5.0.2) **→** reference genomes&draft assemblies annotation(Prokka v1.14.6) **→** typing replicon genes(Abricate v0.9.9) **→**assessing ARG&mutations(AMRFinder v3.10.30) **→** core gene alignments(Roary v3.13.0) **→** phylogenetic tree inference(RAxML-NGv0.90) **→** phylogenetic tree(Ggtree v2.2.4) **→** visualisation/plotting of SNP matrix(ComplexHeatmap v2.8.0)

**Results:**

**Figure 1:** The figure reveals twenty-nine (29) AMR genes, with a total of nine (9) classes. Aminoglycoside and Beta-lactam are highest in abundance, while Macrolide is the least abundant.

**Discussion:**

The variation in the number of subclasses among different types of AMR genes can be attributed to several factors including evolutionary diversity, selective pressure, selective advantage, etc. The high number of Aminoglycoside and Beta-lactam subclasses may have resulted from the extensive use of these antibiotics, thereby driving the evolution and proliferation of resistance mechanisms (Foudraine et al., 2021). The Macrolide AMR gene likely has one subclass due to rare mutations or a broad-spectrum resistance mechanism, leading to fewer subclasses of the AMR gene (Miklasińska-Majdanik, 2021).

**Conclusion**

**References**

Park, C. J., Li, J., Zhang, X., Gao, F., Benton, C. S., & Andam, C. P. (2021). Diverse lineages of multidrug resistant clinical Salmonella enterica and a cryptic outbreak in New Hampshire, USA revealed from a year-long genomic surveillance. *Infect Genet Evol, 87*, 104645. doi:10.1016/j.meegid.2020.104645

Foudraine, D. E., Strepis, N., Stingl, C., Ten Kate, M. T., Verbon, A., Klaassen, C. H. W., Goessens, W. H. F., Luider, T. M., & Dekker, L. J. M. (2021). Exploring antimicrobial resistance to beta-lactams, aminoglycosides and fluoroquinolones in E. coli and K. pneumoniae using proteogenomics. *Scientific Reports*, *11*(1), 12472. https://doi.org/10.1038/s41598-021-91905-w

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