Background

In this project, we are investigating the microorganism responsible for the public health crisis that occurred in South Africa in 2017. The outbreak was suspected to have originated from the food supply, and neonates were the most affected group. Whole genome sequencing (WGS) was employed to carry out the investigation.
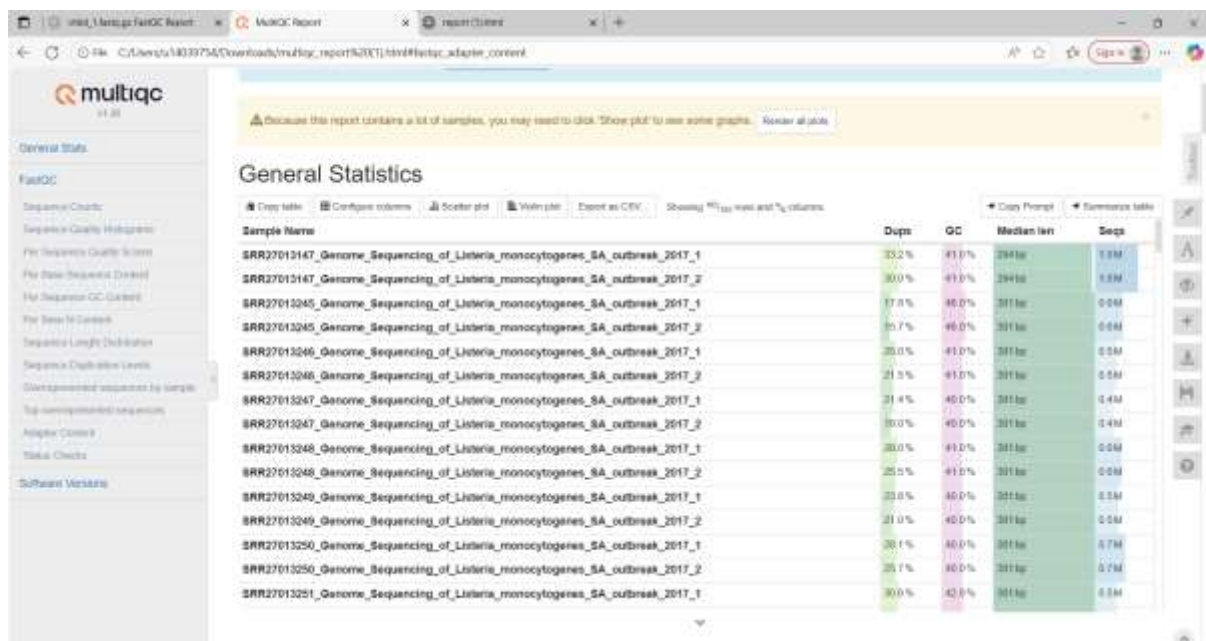
Methods

All analyses were conducted using Bash scripts. Raw data consisting of 100 samples was downloaded from the HackBio-provided link. From this dataset, a subset of 50 paired-end reads was selected for analysis. The first step involved performing quality control of the reads using *FastQC*. A *MultiQC* command was then applied to generate an HTML report summarizing the sequencing run quality.
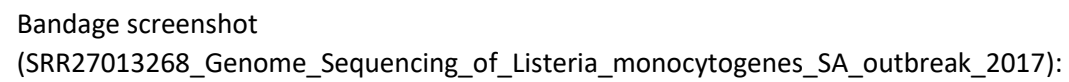
Next, *Fastp* was used to trim adapters and remove sequencing noise. The trimmed reads were subsequently used for **de novo** assembly with *SPAdes*, and the assemblies were assessed using *QUAST*. The assembly_graph.fastg file was downloaded to the local machine and visualized using *Bandage*. Selected nodes from the spaghetti-like graph were extracted and queried in *BLASTn* to confirm the identity of the organism. Finally, *ABRicate* was employed to screen the assemblies for antimicrobial resistance genes.

Results

MultiQC html report:

De-novo assembly html report:

Bandage screenshot
(SRR27013268_Genome_Sequencing_of_Listeria_monocytogenes_SA_outbreak_2017):

NCBI BLASTn

Antimicrobial Resistant genes and toxins

The antimicrobial resistance (AMR) genes identified from the analysis were *lm00919_fam*, which confers resistance to lincomycin, and *fosX*, which confers resistance to fosfomycin. The identification of these AMR genes indicates potential multidrug resistance, which could pose challenges for treatment.

The following toxins were identified:

actA	bsh	clpC	clpE	clpP	fbpA	gtcA	hly	hpt	iap/cwhA	inlA	inlB	inlC	inlF
inlK	lap	lapB	llsA										

Discussion

The pathogen was confirmed as *Listeria monocytogenes*. Genomic analysis revealed antimicrobial resistance genes (e.g., **fosX**, *lm00919*) and multiple virulence/toxin-associated genes (e.g., **hly, actA, internalins, llsA**). These factors are consistent with the ability of *L. monocytogenes* to invade host cells, cross the placental barrier, and cause severe neonatal infections. From a therapeutic perspective, the recommended first-line treatment for invasive listeriosis is **high-dose ampicillin**, often combined with gentamicin for synergistic effect. Alternative therapies, such as trimethoprim-sulfamethoxazole, may be considered in cases of penicillin allergy.

Conclusion

The detection of *L. monocytogenes* in the food supply represents a significant **public health concern**, particularly for vulnerable populations such as pregnant women, neonates, and immunocompromised individuals. Public education is essential: consumers should practice safe food handling and hygiene, avoid prolonged refrigeration of ready-to-eat foods, and ensure that high-risk products such as deli meats are properly cooked or reheated before consumption. Strengthening **food safety regulations, routine surveillance, and screening of food products** is critical to preventing future outbreaks.

References

- Sandra Boatemaa, McKenna Barney, Scott Drimie, Julia Harper, Lise Korsten, Laura Pereira, Awakening from the listeriosis crisis: Food safety challenges, practices and governance in the food retail sector in South Africa, Food Control, Volume 104, 2019, Pages 333-342, ISSN 0956-7135, https://doi.org/10.1016/j.foodcont.2019.05.009.
- https://www.cdc.gov/listeria/about/index.html