Accession ID:	XXXXXXX
Sample Type:	Sputum
Patient's Name:	XXXXXXX
Gender/Age	XXXXXXX

CliSeq

TB NGS Panel

Data Uploaded On:	XXXXXXX	**Report Generated On:**	XXXXXXX

Clinical History:

1. Species Identification and Developmental Lineage

Oraganism	Reads	Identity(%)
Mycobacterium_tuberculosis_complex	108944	99.52
Mycobacterium_tuberculosis_H37Rv	71931	65.71
Mycobacterium_canettii_CIPT_140010059	37013	33.81

Phylogenetic Lineage Based on SNPs Lineage 2.2.1.1

2. Drug Resistance Profile

Fig.1. Antibiotic resistance gene prediction in MTBC

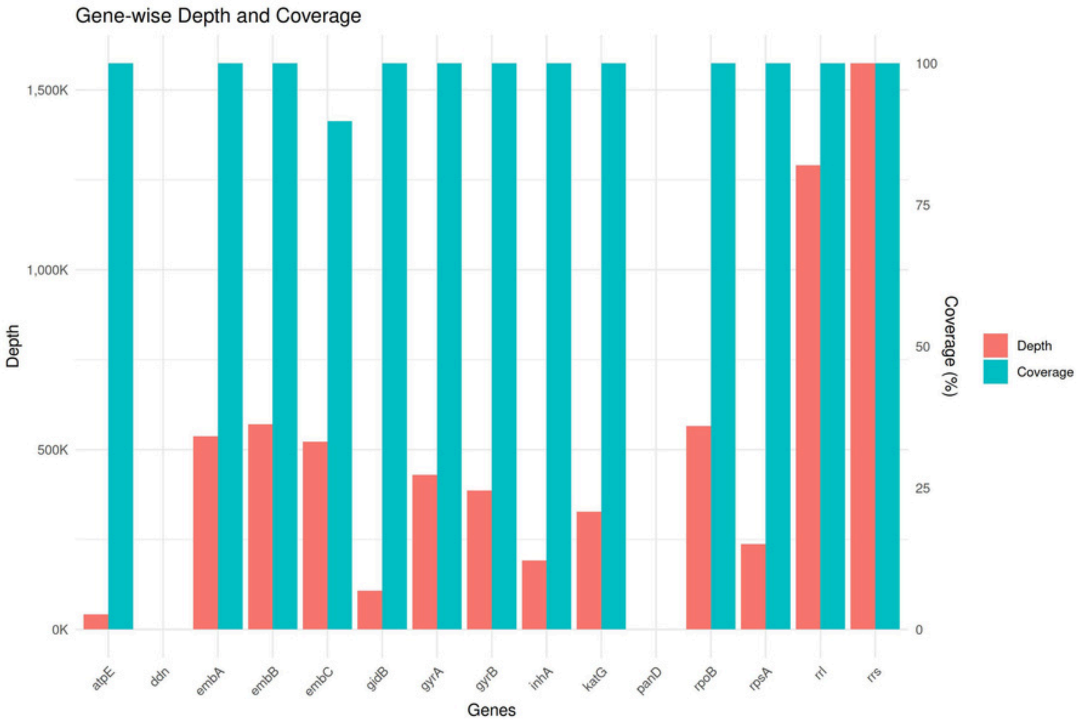
The circular map is divided into three rings. The outer rings displays the resistant anitbiotics. The middle ring display the genes responsible for resistance in antibiotics, while the inner ring shows the mutations involved in drug resistance.

3. Sample Quality Control

The proportion of human reads

The proportion of human origin reads
0.5%

The coverage of drug-resistance gene



Coverage Depth of Major Drug Resistance Genes

Note:

- Coverage： Data coverage in the target region.
- Average depth ： The average depth in the target region.

4. Detected Mutation Results

Resistance-Related Mutations

Gene Name	Genome position	Depth	Change	Drug
gyrA	7563	19785	Gly88Cys	MXF

5. Appendix

Common Drugs and Resistance Genes of Mycobacterium tuberculosis

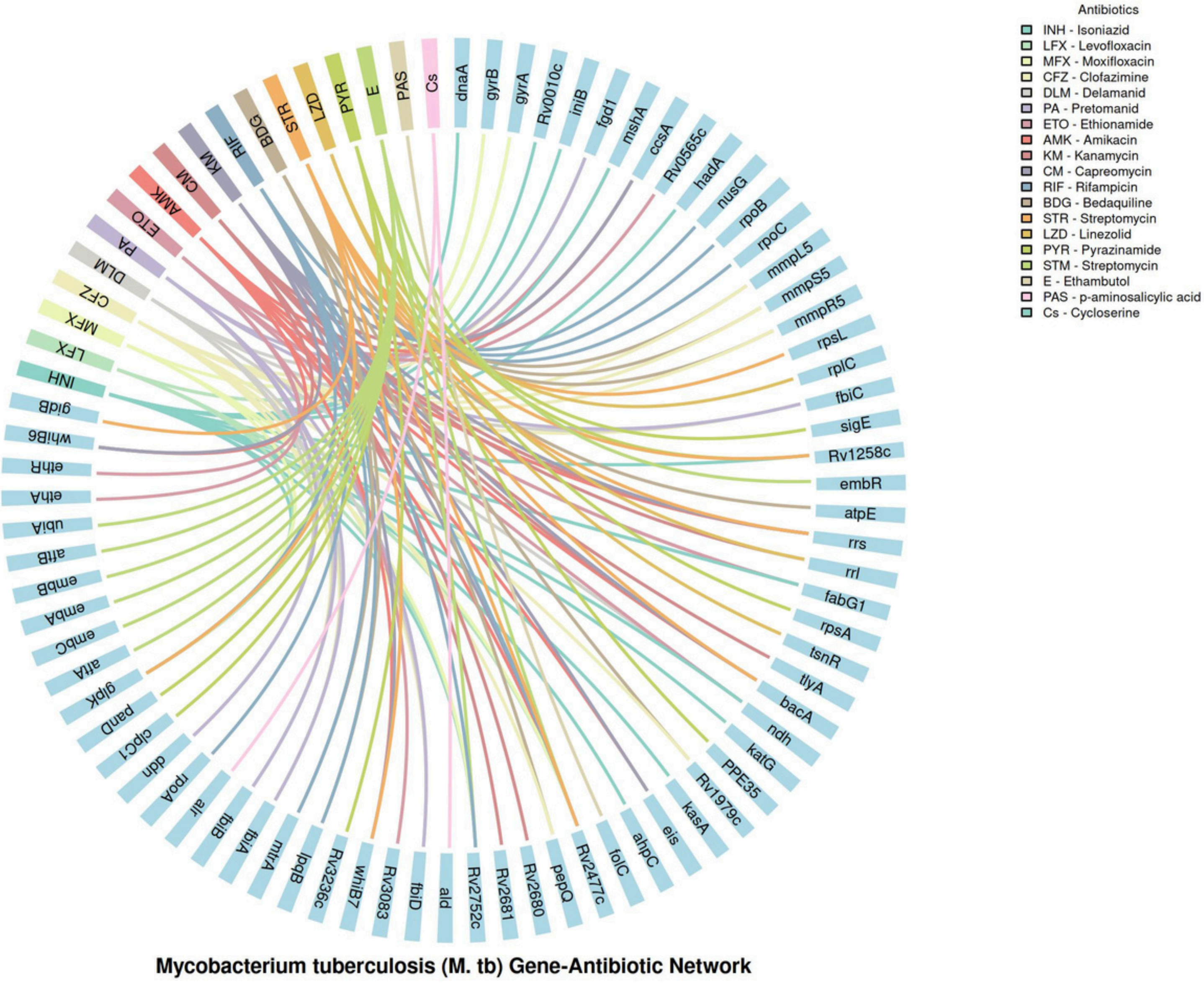


Fig.2. Visual Representation of Gene - Antibiotics Resistance in M.tb

6. Limitations of Test Results:

This report only includes mutations of interest related to drug resistance within the targeted range. A negative result does not exclude the possibility of other drug-resistant mutations.

Low-frequency mutations below the sequencing detection limit may affect the

typing results. The provided interpretation is based on the current understanding of genotype-phenotype relationships. All results are referenced according to the Mycobacterium tuberculosis mutation numbering system, which differs from the Escherichia coli numbering system.

Drug resistance-related mutations are referenced from the 'Mycobacterium tuberculosis Drug Resistance-Related Gene Mutation Catalog and Clinical Application Guidelines' (WHO 2023). The resistance rules for the tlyA and rv0678 genes are not restricted by WHO guidelines. All in-frame deletions, frameshift mutations, and large deletions in the tlyA and rv0678 genes are considered functionally inactivating and associated with drug resistance.

7. Disclaimer:

The test was developed, and its performance characteristics were determined by Genes2me Private Limited. The test results are dependent on factors like time and quality of the specimen collected and the antibiotics administered.

Genes2Me clarify that the generated report(s) doesn’t provide any kind of diagnosis or opinion or recommendation for any disease and its cure in any manner. It is therefore recommended that the patient and/or the guardian(s) of the patient must take the consultation of the clinician or a certified physician or doctor for further course of action.

If the provided material quality and/or quantity not up to the desired level so, in that case, test(s) result(s) may be misleading or even wrong. Therefore, Genes2Me hereby disclaims all liability arising in this connection with the test(s) and report(s).

The analysis pipeline is developed in-house and the performance characteristics of this analysis are determined by Genes2Me only.

This test result should be used as a reference by the healthcare provider for diagnosis and development of treatment plan.

8. References:

1.Li Y, Jiao M, Liu Y, et al. Application of Metagenomic Next-Generation Sequencing in Mycobacterium tuberculosis Infection. Front Med (Lausanne). 2022 Apr 1;9:802719

2.Management of Tuberculosis: Practical Review for Implementation in Pathogens.2023Jul26;12(8):978. 4.Gröschel, M.I., Owens, M., Freschi, L. et al. GenTB: A user-friendly genome-based predictor for tuberculosis resistance powered by machine learning. Genome Med 13, 138 (2021)

3.Phelan JE, O'Sullivan DM, Machado D, et al. Integrating informatics tools and portable sequencing technology for rapid detection of resistance to anti-tuberculous drugs. Genome Med. 2019 Jun 24;11(1):41

4.Coll F, McNerney R, Guerra-Assunção J A, et al. A robust SNP barcode for typing Mycobacterium tuberculosis complex strains[J]. Nature communications, 2014, 5(1): 4812. 2.https://www.who.int/publications/i/item/9789240082410

5.Beviere M, Reissier S, Penven M, et al. The Role of Next-Generation Sequencing (NGS) in the Management of Tuberculosis: Practical Review for Implementation in Routine. Pathogens. 2023 Jul 26;12(8):978.