

Molecular Epidemiology of Drug-Resistant *Mycobacterium tuberculosis* Isolates from the Republic of Korea, 2021–2025

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ABSTRACT

Background: Drug-resistant tuberculosis (DR-TB) remains a major public health concern. Molecular epidemiological approaches help clarify transmission and genetic diversity, supporting effective TB control.

Methods: A total of 304 DR-TB isolates were collected in the Republic of Korea and analyzed using spoligotyping and cgMLST.

Results: Most isolates (89.8%) belonged to the East Asian lineage, and cgMLST identified 293 unique genotypes and 9 clusters.

Conclusion: DR-TB cases appeared predominantly sporadic, with no evidence of large-scale transmission. Continuous molecular surveillance remains essential for national TB control.

MATERIALS AND METHODS

Strain collection and DNA extraction

A total of 304 DR-TB isolates (excluding isoniazid-resistant) were collected from clinical cases in Republic of Korea. gDNA was extracted using commercial kits (Zymo Research, USA).

Spoligotyping

Spoligotyping was performed using a spoligotyping kit (Ocimum Biosolutions, India). Resulting patterns were analyzed using SITVIT2 and TB-Insight databases.

INTRODUCTION

- DR-TB remains a critical global health issue due to prolonged treatment, reduced efficacy, increased toxicity, and lower cure rates compared with drug-susceptible TB. These challenges contribute to higher mortality and ongoing transmission of resistant strains.
- Molecular epidemiological approaches provide valuable insights into transmission dynamics and genetic diversity, thereby enhancing TB control efforts.
- This study aimed to characterize the molecular epidemiology and genetic diversity of DR-TB isolates collected in the Republic of Korea (2021–2025) to inform national TB control and prevention policies.

Whole-genome sequencing (WGS)

DNA libraries were prepared and sequenced using the Ion GeneStudio S5 platform (Thermo Fisher Scientific, USA). Reads were mapped to the *M. tuberculosis* H37Rv reference genome (NC_000962.3).

cgMLST analysis

cgMLST analysis was performed using the Ridom SeqSphere+ (Ridom GmbH, Germany) based on 2,891 loci. A minimum spanning tree (MST) was generated to assess genetic relationships among isolates.

RESULTS

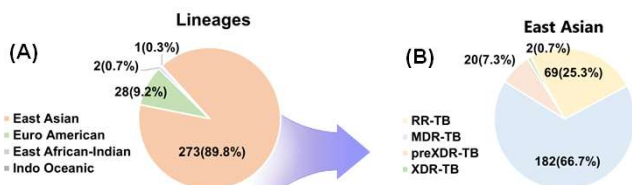


Figure 1. Lineage distribution and drug-resistant profiles of DR-TB isolates

(A) Proportion of lineages in all isolates.

(B) Drug-resistant categories within East Asian lineage.

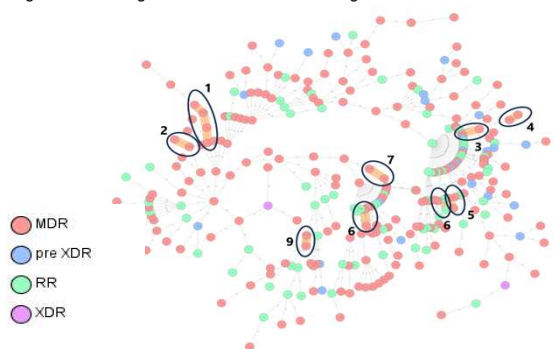


Figure 2. Minimum spanning tree (MST) of 304 DR-TB isolates based on cgMLST

* Black circles represent isolates within genetic clusters

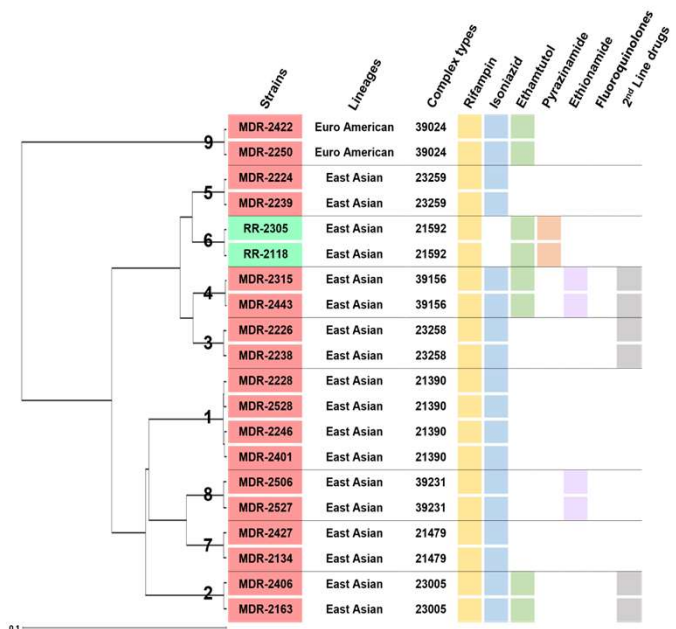


Figure 3. Phylogenetic analysis and drug-Resistant profiles of genomic clusters among DR-TB isolates

CONCLUSIONS

- The East Asian lineage predominated among DR-TB isolates in Republic of Korea.
- cgMLST analysis revealed 293 unique genotypes and 9 clusters with consistent resistant profiles.
- These findings highlight high genetic diversity and indicate sporadic, rather than widespread, recent transmission events.
- Continuous molecular surveillance is essential for monitoring genetic diversity and elucidating transmission dynamics.

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