# Phenotypic versus genotypic resistance in MTB: Evaluating agreement for isoniazid and rifampicin

**Zaidatul Akmar ME, Mathanamogan R, Nik Jasmin NM, Rohani I, Mahfuzah MA, Parvathy SR, Saadiah AM, Puvaneswary AR, Siti Hazimah S, Dayana I, Zirwatul Adilah A**

National Public Health Laboratory, Selangor, Malaysia

## ABSTRACT

**Introduction:** Isoniazid (INH) and rifampicin (RIF) are essential drugs for tuberculosis (TB) treatment. The emergence of drug-resistant Mycobacterium tuberculosis strains challenges tuberculosis prevention efforts. Phenotypic drug susceptibility testing (DST) takes many weeks or months to produce results, whereas genotypic approaches such as the line probe assay (LPA) provide quick detection of resistance mutations. **Objective:** The aim of this study is to assess the concordance between phenotypic and genotypic resistance profiles for INH and RIF in Mycobacterium tuberculosis isolates. **Materials and Method:** We tested a total of 285 Mycobacterium tuberculosis isolates for phenotypic DST by solid or liquid methods and assessed for genotypic resistance using the GenoType MTBDRplus assay (Hain Lifescience, Germany). We analyzed the concordance between these methods. **Results:** Of the 285 isolates, 257 (90.2%) had high concordance between phenotypic and genotypic DST results for INH and RIF. Out of them, 144 isolates showed susceptibility to both INH and RIF, with no resistance mutations detected. In contrast, the remaining concordant cases (113) identified mutations related to resistance to either INH, RIF, or both drugs. However, 28 isolates (9.8%) displayed phenotypic resistance without corresponding mutations identified by LPA. **Discussion:** These discordant cases suggest potential alternative mechanisms of resistance or limitations in the current genotypic detection methods. Even though there is a high concordance between LPA and phenotypic DST, the presence of discordant cases, where phenotypic resistance is not associated with known genotypic mutations, emphasizes the importance of maintaining phenotypic testing. These findings highlight the importance of comprehensive approaches in TB diagnostics to identify all resistance mechanisms. Further research is necessary to understand these discordant cases and improve genotypic detection accuracy.