Assessing MIC distributions associated with genetic resistance mutations to identify possible treatment options for MDR/XDR tuberculosis

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Acquired drug resistance in *M. tuberculosis* is exclusively due to chromosomal alterations, such as mutations or deletions. Compared to all the genetic insight that has accumulated during the past years, little has changed in the laboratory procedures which define drug resistance for clinical *M. tuberculosis* isolates on the basis of critical concentration testing. Evidence is accumulating that drug resistance in *M. tuberculosis* is quite heterogeneous and composed of low-, moderate-, and high-level drug resistance. Systematic genotype – phenotype studies have revealed that different SNPs are associated with distinct resistance levels. These findings indicate that established procedures for diagnostic drug susceptibility testing based on critical concentration testing have limitations and need to be complemented by quantitative measures of drug susceptibility, with the view to optimize treatment in particular for MDR/XDR tuberculosis.

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