FIND and tuberculosis sequencing

The use of next-generation sequencing technologies for the detection of mutations associated with drug resistance in *Mycobacterium tuberculosis* complex: technical guide

Technical report on critical concentrations for drug susceptibility testing of medicines used in the treatment of drug-resistant tuberculosis

Includes target product profile: detection of resistance associated mutations in MTBC utilizing next generation sequencing (Appendix 3)

The use of next-generation sequencing technologies for the detection of mutations associated with drug resistance in *Mycobacterium tuberculosis* complex: technical guide

Built by the TB community to serve the TB community

Cloud-based portal to rapidly predict phenotypic antimicrobial resistance from Mtb sequences

Hosted by WHO from 2019

www.reseqtb.org  @reseqtb

Key publications

**Integrating standardized whole genome sequence analysis with a global *Mycobacterium tuberculosis* antibiotic resistance knowledgebase**

Ezuwodo et al (2018)

A validated, standardized bioinformatics pipeline in ReSeqTB for automated detection of clinically relevant drug resistance mutations from raw sequencing data.

**Prediction of susceptibility to first-line tuberculosis drugs by DNA sequencing**

CRyPTIC Consortium and the 100,000 Genomes Project (2018)

A comprehensive evaluation of sequencing for predicting phenotypic resistance to all first-line TB drugs in a globally representative sampling of clinical MTBC strains demonstrating high sensitivity and specificity.

**A standardised method for interpreting the association between mutations and phenotypic drug resistance in *Mycobacterium tuberculosis***

Miotto et al (2017)

A systematic review establishing the first confidence-graded list of important mutations for predicting clinically relevant phenotypic resistance to first- and second-line anti-TB drugs.

**TB sequencing webinar series launching early 2019**

Jointly coordinated by FIND, WHO, New Diagnostics Working Group and partners.

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