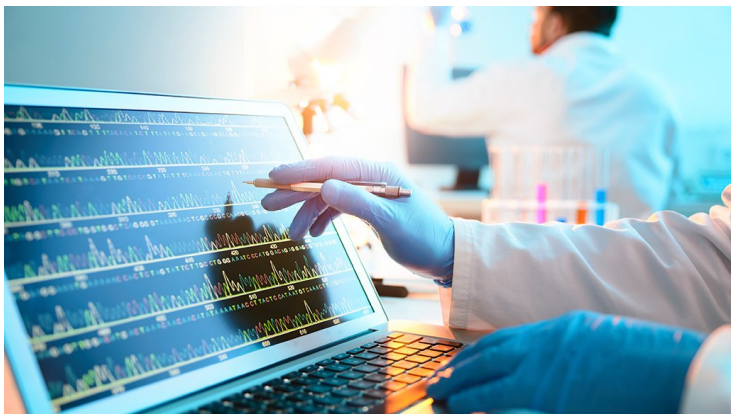
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Global Health Partners adopt bioinformatics platform for TB diagnosis

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The platform will serve as a resource for the development of global policies on new TB diagnostics and will ultimately support clinical management of DR-TB.



The World Health Organization (WHO), the Foundation for Innovative New Diagnostics (FIND) and the Critical Path Institute (C-Path), recently announced that the Relational Sequencing for Tuberculosis (ReSeqTB) Platform, a global TB knowledgebase for predicting TB drug resistance, will be adopted as the WHO bioinformatics platform for surveillance of drug-resistant TB (DR-TB).

The development of ReSeqTB has been supported by the Bill & Melinda Gates Foundation, and renewed funding has been applied for to support integration into the WHO Sequencing-based TB Drug Resistance Surveillance Programme. The platform will also serve as a resource for the development of global policies on new TB diagnostics and will ultimately support clinical management of DR-TB.

ReSeqTB serves a diverse TB community to rapidly evaluate phenotypic antimicrobial resistance from raw sequence data from *Mycobacterium tuberculosis* (Mtb) in clinical samples – enabling large-scale, culture-free surveillance of TB drug resistance and informing development of new diagnostics and treatment regimens. It is designed to capture, analyse and report in-country data on mutations associated with TB drug resistance based on an expert-graded mutations list.

In this new project phase, the ReSeqTB platform will support surveillance and global policy development for sequencing-based clinical diagnosis of DR-TB. It could also serve as a model for the broader goals of establishing global antimicrobial resistance surveillance and clinical diagnosis networks for WHO high-priority pathogens.