Detection of drug resistance in *Mycobacterium tuberculosis* using next generation sequencing

Unarine Matodzi[1,2]; Awelani Mutshembele[2]; Ndivhuho. A Makhado[3]; Halima. M Said[4]; Oleg Reva[1]

[1.] Centre for bioinformatics and Computational Biology; Department of Biochemistry, Genetics and Microbiology, University of Pretoria.

[2.] Tuberculosis Platform Unit, South African Medical Research Council, Pretoria.

[3.] Department of Microbiological Pathology, Sefako Makgatho Health Science University, Pretoria, South Africa.

[4.] Centre for Tuberculosis, National TB Reference Laboratory, National Institute for Communicable Diseases, National Health Laboratory Service, Johannesburg, South Africa.

PHASA 2023
TRANSFORMING RESEARCH TRANSLATION-
REIMAGINING
PUBLIC HEALTH EVIDENCE, POLICIES, AND PRACTICE

transform
translate

PHASA
Public Health Association of South Africa

BACKGROUND

The emergence of drug-resistant tuberculosis (TB) is presenting a notable obstacle to the global success of TB treatment and control measures.

Unfortunately, the potency and efficacy of currently used anti-TB drugs are slowly diminishing as a result of mutations taking place within the *Mycobacterium tuberculosis* (MTB) genome.

Rapid detection of MTB and drug susceptibility testing (DST) is crucial for creating effective treatment plans, curbing transmission, and minimizing the development of resistance.

Whole genome sequencing (WGS) has the potential to expedite the detection of drug resistance surpassing the time taken by phenotypic DST methods.

The drawback of WGS is associated with limited technical experience and clinical interpretation of data.

This study aims to develop a user-friendly Bioinformatics tool that rapidly analyse WGS data without the needs of expertise.

OBJECTIVES

This study determines mutations in MTB complete genome that will be used to develop a free online Bioinformatics analysis tool that detects drug resistance and lineages from raw sequence data.

To create a catalogue of genetic determinants of resistance to anti-TB drugs for each phylogenetic clade.

METHODOLOGY

Fig.1. Methodology

RESULTS

The study is ongoing, with further analysis planned to identify mutations that will be utilized to develop bioinformatics tool.

Mutations associated with drug resistance were identified and recorded in the mutation catalogue.

Figures below show the preliminary results of this study

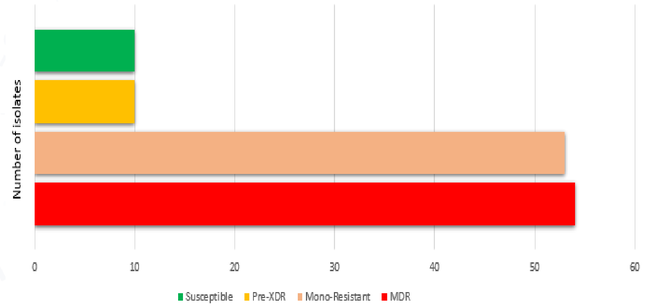

Fig.2. Drug resistance profile of isolates

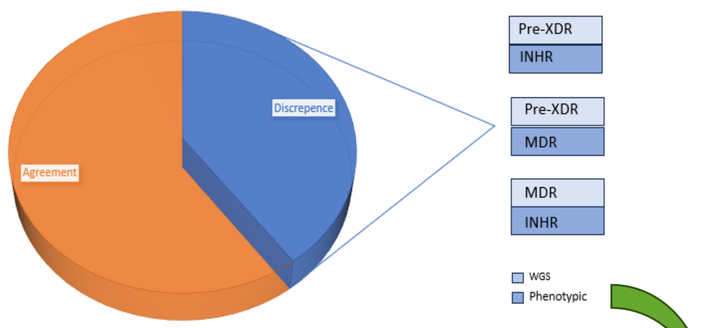

Fig.3. Comparison between WGS and phenotypic DST

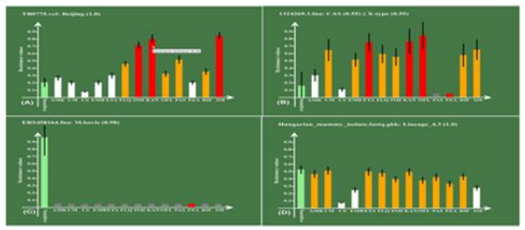

Fig.4. Drug resistance analysis using this study's bioinformatics tool

CONCLUSIONS

This study anticipates that WGS has the potential to significantly accelerate the detection of drug resistance profiles compared to phenotypic DST methods.

Our end goal is to have a significant impact on the global TB diagnosis and treatment.

ADVOCACY MESSAGE

This study aims to develop a bioinformatics tool will have an impact in TB treatment and vaccine development. Our target audiences are researchers, pharmacist and any public or health care workers.

ACKNOWLEDGEMENTS

The work reported herein was made possible through funding by the South African Medical Research Council through its Division of Research Capacity Development under the Bongani Mayosi National Health Scholars Programme from funding received from the Public Health Enhancement Fund / South African National Department of Health. The content hereof is the sole responsibility of the authors and does not necessarily represent the official views of the SAMRC

saMRC advancinglife

UNIVERSITEIT VAN PRETORIA
UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA
Denkleiers • Leading Minds • Dikgopolo tša Dihlalefi

NATIONAL HEALTH LABORATORY SERVICE

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES
Division of the National Health Laboratory Service

KNOWLEDGE
SEFAKO MAKGATHO HEALTH SCIENCES UNIVERSITY
FOR QUALITY HEALTH SERVICES