

Genome sequence of *Mycobacterium yongonense* RT 955-2015 isolate from a patient misdiagnosed with multi-drug resistant tuberculosis: First clinical detection in Tanzania**Nicholaus Peter Mnyambwa**

School of Life Science and Bioengineering, Tanzania

Background: *Mycobacterium yongonense* is a recently described novel species belonging to *Mycobacterium avium* complex, which is the most prevalent aetiology of non-tuberculous mycobacteria associated with pulmonary infections, and poses tuberculosis diagnostic challenges in high-burden, resource-constrained settings.


Methods: Whole genome shotgun sequencing and comparative microbial genomic analyses were used to characterize the isolate from a patient diagnosed with multidrug-resistant tuberculosis (MDR-TB) after relapse.

Results: The genome sequence of the first case of *M. yongonense* (*M. yongonense* RT 955-2015) in Tanzania is presented. Sequence analysis revealed that the RT 955-2015 strain had a high similarity to *M. yongonense* 05-1390(T) (98.74%) and *Mycobacterium chimaera* DSM 44623(T) (98%). Its 16S

rRNA showed similarity to *Mycobacterium paraintracellulare* KCTC 290849(T) (100%), *Mycobacterium intracellulare* ATCC 13950(T) (100%), *M. chimaera* DSM 44623(T) (99.9%), and *M. yongonense* 05-1390(T) (98%). The strain exhibited a substantially different *rpoB* sequence to that of *M. yongonense* 05-1390 (95.16%), but closely related to that of *M. chimaera* DSM 44623(T) (99.86%), *M. intracellulare* ATCC 13950(T), (99.53%), and *M. paraintracellulare* KCTC 290849(T) (99.53%).

Conclusions: In light of the OrthoANI algorithm and phylogenetic analysis, it was concluded that the isolate was *M. yongonense* Type II genotype, which is an indication that the patient was misdiagnosed with TB/MDR-TB and received inappropriate treatment.

e: lodnicho@gmail.com

 Notes: