PhD defence Mebrat Ejo Kitata

Molecular epidemiology and population structure of Mycobacterium tuberculosis complex strains in tuberculosis patients: Implications for diagnostic approaches

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Institute of Tropical Medicine - Antwerpen

Dit is de omschrijving

Attendance

This is a hybrid PhD defence. Follow the public PhD defence via Zoom here.

Supervisors

- Prof. dr. Leen Rigouts (University of Antwerp/ITM)
- Prof. dr. Bouke de Jong (ITM)
- Dr. Gabriela Torrea (ITM)
- Dr. Ermias Diro (University of Gondar, Ethiopia)
- Dr. Florian Gehre (East African Community Secretariat (EAC), Arusha, Tanzania)

Abstract

Tuberculosis (TB) is a disease caused by tubercle bacteria belonging to the *Mycobacterium tuberculosis* complex (MTBc), comprising nine distinct lineages (L1 to L9) with sublineages or families. The bacteria mostly affect the lungs, resulting in pulmonary TB, but can also affect lymph nodes and other parts of the body, named extrapulmonary TB. The potential impact of various lineages and genotypes on disease control efforts remains unclear. Our study mainly focused on the genetic characterization of MTBc bacilli under the supervision of Prof. dr. Bouke de Jong and Prof. dr. Leen Rigouts at the Department of Biomedical Sciences of the Antwerp University and Institute of Tropical Medicine, Antwerp, Belgium. We analyzed the genotypes from TB patient's clinical samples and the respective MTBc isolates in Ethiopia and Niger, two countries in East and West Africa that carry a high burden of TB. We observed the expected lineage distribution and resistance-causing mutations in both countries. The genotypes were similarly distributed between pulmonary and lymph node TB, and the diagnostic tools (culture and rapid identification test) performed equally across the genotypes. On the other hand, we revealed that the delay in treatment response of TB patients is associated with the type of infecting strain. Finally, the rapid molecular tests that were used in our test settings, could rule out patients with resistance to specific drugs, prior to the initiation of the treatment. Therefore, these findings provided information to clinicians and public health scientists for knowing the lineages and resistance profiles of circulating MTBc strains, and added to the evidence that treatment response varied by MTBc lineage.