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Molecular characterization of mycobacterial species isolated from patients with clinical symptoms suggestive of tuberculosis presenting Ndola

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Background: Tuberculosis is the leading cause of mortality worldwide and kill 3 million people every year. It is caused by members of the *Mycobacterium tuberculosis complex (MTC)*. Zambia is ranked among the world's top 10 high incident countries. Lack of routine mulecular characterization of mycobacteria in patients presenting with pulmonary tuberculosis in the country's health facilities including Ndola Central Hospital has led to non availablity of data on specific species other than *M. tuberculosis* that are in circulation. This information is vital for proper patient management, as different species and strains of mycobacteria have varying sensitivies to drugs, pathogenesis as well as their epidemiology. The study was aimed at characterizing members of the MTC in patients presenting with pulmonary tuberculosis at Ndola Central Hospital in Zambia from February 2012 to August 2012.

Methods & Materials: This was a cross-sectional study targeting symptomatic and clinically suspected pulmonary TB patients attending Ndola Central Hospital. A total of 197 consenting adult patiets were included in the study, from whom a structured questionnaire probing their socio- economic, HIV status and possible source of the disease status. Additionally, 2 sputum samples were collected from where Microscopy, culture, spoligotyping and deletion analysis were carried out.

Results: About 60% of the participants were male. The total positivity rate on culture was 65% (N = 138). Out of seventy-one samples analysed for IS6110 deletion analysis, 41 samples where confirmed to be *M. tuberculosis* since they were positive for RD1, RD4, RD9 and RD12. Four samples were confirmed to be *M. canettii* as characterized by the absence of RD12 amplification. Among the six clusters obtained by spoligotyping, the SAF1 family was largest comprising 43.5% of the isolates. The study also found four orphan strains which did not match with previously identified strains.

Conclusion: Other than M. tuberculosis, *M canetti*i has also been implicated in Tuberculosis infection in Ndola.

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Evaluation of AFB smear, culture, real-time PCR methods for detection of tuberculosis

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Background: Direct microscopy and culture of microorganism are conventional methods for detection of mycobacteria infections. Rapid and accurate laboratory diagnosis is important for global control of tuberculosis. Nucleic acid amplification tests which are recommended by World Health (WHO) become popular methods for rapid detection of Mycobacterium tuberculosis complex.

Methods & Materials: In this study, we assessed the performance of two different real-time PCR methods (Cepheid GeneXpert and Roche Cobas TaqMan MTB) in diagnosis of tuberculosis. 50 AFB (+) and 50 AFB (-) sputum samples were studied.

Results: The sensitivity, specificity, positive predictive value and negative predictive value of Cepheid GeneXpert test were 75%,100%, 100% and 41.7, respectively.

The sensitivity, specificity, positive predictive value and negative predictive value of Roche Cobas TaqMan MTB test were 64.6%, 93.3%, 98.1% and 32.6, respectively.

Conclusion: We conclude that, Cepheid GeneXpert test and Roche Cobas TaqMan MTB tests can allow rapid results useful both for rapid treatment and patient management.