

PA-060 **EMERGENCE OF NONTUBERCULOUS MYCOBACTERIUM  
PULMONARY INFECTIONS, ANALYSIS OF ISOLATES  
FROM PREVIOUSLY TREATED TB CASES**

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**Background** The main objective of this study was to characterise supposed non-tuberculous mycobacteria (NTM) found in previously treated tuberculosis (TB) cases to inform policy on inclusion of NTM diagnosis and management as a differential in TB care. In addition, the objective was to test the sensitivity or otherwise of the identification algorithm used in Ghana to declare an isolate an NTM.

**Methods** Thirty-one supposed NTM isolates from previously treated TB patients were collected. The NTM identification was based on culture positivity by BD MGIT 960TM, smear positivity for acid fast bacilli and finally by BD MGIT TB-cIDTM test kit. DNA was extracted using the Hain Lifescience GMBH GenolyseTM kit. The specimens were further subjected to sequencing.

**Results** Five (16%) of the previously treated cases were *Mycobacterium tuberculosis complex (MTBC)*; two (6.5%) were *M. abscessus/cholerae*; 1 case (3.2%) for *M. fortuitum* and *M. goodii* each. One (3.2%) was an unknown mycobacterium and 4 (12.9%) were other bacteria. Streptomyces and Brevibacteria were 8 (25.8%) and 6 (19.4%), respectively. There were three incidences of mixture with other bacteria; 2 MTBCs (6.5%) and 1 NTM (3.2%).

**Conclusions** There is some evidence to suggest the prevalence of NTM colonisation and disease in previously treated TB patients. There is the possibility of some smear positive new cases being NTM lung diseases but may be put on TB treatment. Emphasis on differentiation of AFB positive smears before treatment especially for retreatment cases must be made. The rapid deployment of new molecular methods has the potential of bridging the gap. There is the need for a definite diagnostic algorithm that can detect both NTMs and MTBCs. Further studies are encouraged to determinate whether the other organisms identified are relevant possible pathogens or contaminants.