

*Mycobacterium malmesburyense* sp. nov., a non-tuberculous species of the genus *Mycobacterium* revealed by multiple gene sequence characterization

Gcebe N  
Rutten V  
Gey van Pittius N  
Naicker B  
Michel A

**ABSTRACT:**

Non-tuberculous mycobacteria (NTM) are ubiquitous in the environment, and an increasing number of NTM species have been isolated and characterized from both humans and animals, highlighting the zoonotic potential of these bacteria. Host exposure to NTM may impact on cross-reactive immune responsiveness, which may affect diagnosis of bovine tuberculosis and may also play a role in the variability of the efficacy of *Mycobacterium bovis* BCG vaccination against tuberculosis. In this study we characterized 10 NTM isolates originating from water, soil, nasal swabs of cattle and African buffalo as well as bovine tissue samples. These isolates were previously identified during an NTM survey and were all found, using 16S rRNA gene sequence analysis to be closely related to *Mycobacterium moriokaense*. A polyphasic approach that included phenotypic characterization, antibiotic susceptibility profiling, mycolic acid profiling and phylogenetic analysis of four gene loci, 16S rRNA, hsp65, sodA and rpoB, was employed to characterize these isolates. Sequence data analysis of the four gene loci revealed that these isolates belong to a unique species of the genus *Mycobacterium*. This evidence was further supported by several differences in phenotypic characteristics between the isolates and the closely related species. We propose the name *Mycobacterium malmesburyense* sp. nov. for this novel species. The type strain is WCM 7299T (=ATCC BAA-2759T=CIP 110822T).