

Import and Transmission of *Mycobacterium Orygis* and *Mycobacterium Africanum*, Norway

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Abstract

Background : The aim of the current study was to improve our understanding of the origins and transmission of *Mycobacterium africanum* (MAF) in Norway.

Methods : Whole-genome sequences (WGS) were generated for all (n=29) available clinical isolates identified as in Norway in the period 2010 – 2020. Phylogenetic analyses were performed.

Results : The analyses indicated multiple imports of MAF lineage 6 from both East and West African countries, whereas MAF lineage 5 was restricted to patients with West African connections. We also find evidence for transmission of MAF in Norway. Finally, our analyses revealed that a group of isolates from patients originating in South Asia, identified as MAF by means of a commercial line-probe assay, in fact belonged to *Mycobacterium orygis*.

Conclusions : Most MAF cases in Norway are the result of import, but transmission is occurring in immigrant communities.

Full Text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the latest manuscript can be downloaded and [accessed as a PDF](#).

Figures

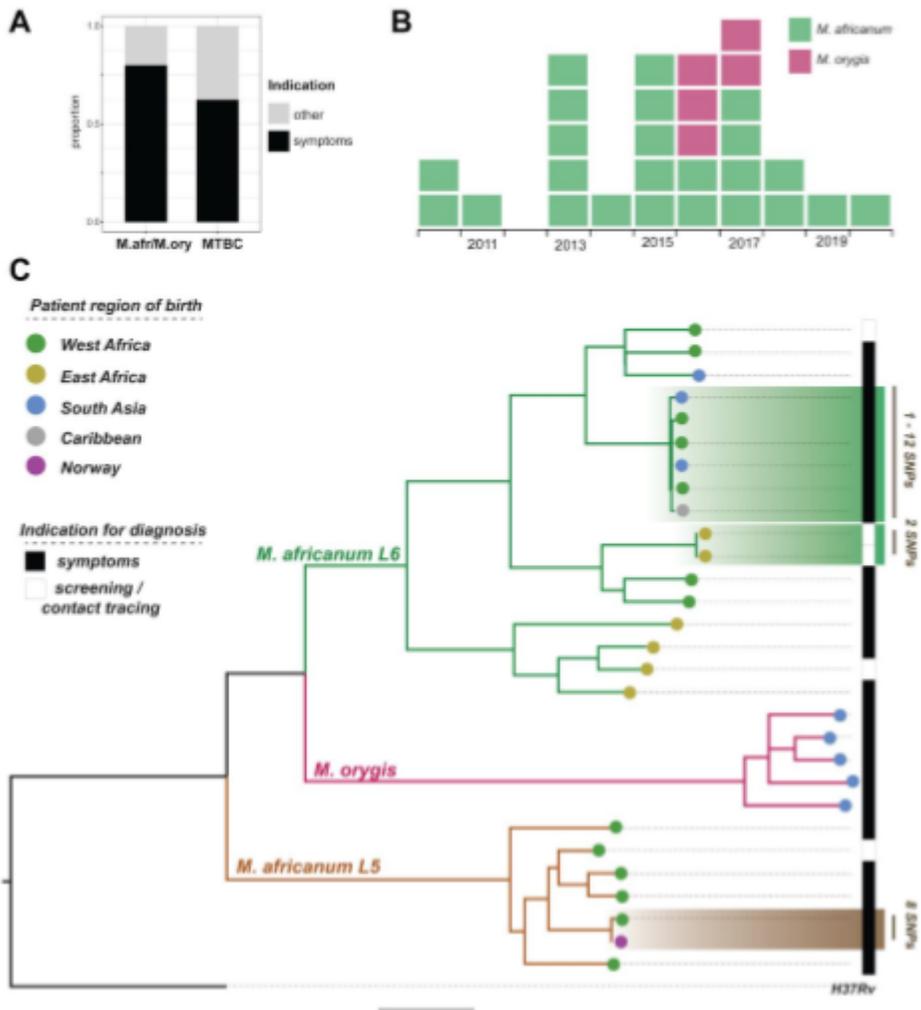


Figure 1

Overview of samples originally identified as *M. africanum* in Norway 2010-2020. (A) Fraction of isolates diagnosed on the basis of symptoms vs all other indications. *M.afr/M.ory* correspond to the 29 *M. africanum* and *M. orygis* isolates study isolates, whereas MTBC includes all MTBC isolates identified in Norway in the period 2011-2020. (B) Epi-curve illustrating the temporal distribution of the cases. (C) Maximum likelihood phylogeny of the 29 presumed MAF isolates. Clusters compatible with recent transmission are highlighted with boxes colored according to the lineage they belong to.