



Mycobacterium avium complex genomics and transmission in a London hospital

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Transmission of *Mycobacterium avium* complex (MAC) species is indirect and may involve environmental intermediates or asymptomatic carriage in the wider population <https://bit.ly/3FQWqnF>

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Abstract

Background Non-tuberculous mycobacteria (NTM) are environmental microorganisms and opportunistic pathogens in individuals with pre-existing lung conditions such as cystic fibrosis (CF) and non-CF bronchiectasis. While recent studies of *Mycobacterium abscessus* have identified transmission within single CF centres as well as nationally and globally, transmission of other NTM species is less well studied.

Methods To investigate the potential for transmission of the *Mycobacterium avium* complex (MAC) we sequenced 996 isolates from 354 CF and non-CF patients at the Royal Brompton Hospital (London, UK; collected 2013–2016) and analysed them in a global context. Epidemiological links were identified from patient records. Previously published genomes were used to characterise global population structures.

Results We identified putative transmission clusters in three MAC species, although few epidemiological links could be identified. For *M. avium*, lineages were largely limited to single countries, while for *Mycobacterium chimaera*, global transmission clusters previously associated with heater-cooler units (HCUs) were found. However, the immediate ancestor of the lineage causing the major HCU-associated outbreak was a lineage already circulating in patients.

Conclusions CF and non-CF patients shared transmission chains, although the lack of epidemiological links suggested that most transmission is indirect and may involve environmental intermediates or asymptomatic carriage in the wider population.

