

Genome study reveals human-to-human spread of multidrug resistant mycobacterial infection

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Using DNA tracking of an outbreak among cystic fibrosis patients at a treatment centre in the UK, the scientists identified frequent patient-to-patient transmission despite stringent infection control measures.

The authors warn that the findings, published Online First in *The Lancet*, will have major implications for how patients with [cystic fibrosis](#) are cared for in hospitals and raise critical questions about the adequacy of current infection control measures and the potential for cross-infection in other [patient groups](#).

Estimates suggest between 3% and 10% of individuals with cystic fibrosis in the USA and Europe are currently infected with multi-drug resistant *M abscessus* and numbers are rising. The organism causes progressive lung damage and is extremely difficult to treat.

Andres Floto from the University of Cambridge, Julian Parkhill from the Sanger Institute, and colleagues used whole genome sequencing and antimicrobial susceptibility testing to compare the [genetic relatedness](#) of individual *M abscessus* isolates from 31 infected [cystic fibrosis patients](#) attending the Cambridge Centre for [Lung Infection](#) at Papworth Hospital between 2007 and 2011.

They also used social network analysis to compare opportunities for cross infection between patients carrying genetically clustered and

unclustered cases, and environmental testing to exclude obvious potential sources of infection such as bronchoscopes and [tap water](#).

Findings showed that two clustered outbreaks were caused by genetically identical or near-identical strains of *M abscessus* subspecies *massiliense* (from 11 patients), that differed by less than ten [base pairs](#).

"Isolates from these 11 patients were often more closely related to each other than to other samples from the same individual, strongly suggesting that cross-infection has occurred widely between patients", explains Floto.

What is more, he adds, "this group of patients had numerous opportunities for within-hospital transmission from other individuals, while widespread environmental sampling failed to detect any specific source of exposure to NTM infection."

The team further cemented their theory of cross-infection by demonstrating that the clusters of *M abscessus* subspecies *massiliense* had evidence of transmission of mutations acquired during infection of an individual to other patients, and isolated bacteria with resistance to amikacin and clarithromycin from several patients with no history of long-term use of these antibiotics.

"The increased resolution provided by [whole genome sequencing](#) over previous typing techniques allowed us to clearly identify the existence, and in some cases the direction, of patient-to-patient transmission, something that would not previously have been possible"* , says Parkhill.

According to Floto, "Despite our evidence of transmission of *M abscessus* subspecies *massiliense* between patients, the exact mechanism of cross-infection remains to be established. Because of strict infection control policies, we believe that transmission probably occurred

indirectly, for example via fomite (eg, hair, clothing, and bedding) contamination or aerosol generating procedures such as lung function testing."

More information: Josephine M. Bryant, Dorothy M. Grogono, Daniel Greaves, Juliet Foweraker, Iain Roddick, Thomas Inns, Mark Reacher, Charles S. Haworth, Martin D. Curran, Simon R. Harris¹, Sharon J. Peacock, Julian Parkhill¹ and R. Andres Floto. (2013) 'Evidence for transmission of *Mycobacterium abscessus* between Cystic Fibrosis patients from whole-genome sequencing. Published in the *Lancet* online 29 March 2013. [doi: 10.1016/S0140-6736\(13\)60632-7](https://doi.org/10.1016/S0140-6736(13)60632-7) [www.thelancet.com/journals/lan ... \(13\)60632-7/abstract](http://www.thelancet.com/journals/lan... (13)60632-7/abstract)

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