**Title:**

Genomic and epidemiologic investigation of *Mycobacterium abscessus* isolates in a cystic fibrosis center to determine potential routes of transmission

**Lay Title**:

Tracking the spread of *Mycobacterium abscessus* in a CF center: What bacterial genetics and patient data reveal and why it matters

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**What was your research question?**

Can analysis of patient records and bacterial genetic fingerprints identify if people are acquiring *M. abscessus* infections from the clinic or from each other?

**Why is this important?**

People with CF are vulnerable to infections with nontuberculous mycobacteria (NTM) and in particular *M.* abscessus of which there are multiple subspecies, and which are very difficult to treat. It is important to know if *M. abscessus* is spreading through the clinic or between patients so that precautions can be taken to prevent its spread. The Healthcare-Associated Links in Transmission (HALT) toolkit provides a step-by-step guide to researchers and CF care teams on how to investigate NTM infections arising from or spreading through healthcare centers.

**What did you do?**

With the Dell Children’s/Ascension Pediatric and Adult program CF care team, we used the HALT toolkit to:

* Collect all *M. abscessus* isolates grown from sputum of people receiving care in the CF center
* Gather information about patient’s infection timelines
* Sample the healthcare environment for the presence of NTM isolates
* Look at origins of water sources infected patients had from their home environment.

We used M. abscessus genetic fingerprinting to determine if any *M. abscessus* isolates had spread from either the healthcare environment to patients or between patients.

**What did you find?**

We found four groups of isolates that were similar within the *M*. *abscessus* family-two groups contained the subspecies *abscessus* and two groups contained the subspecies *massiliense*. One person had infection with both subspecies. Looking at the infection timelines, we found that people in each group had chances to be exposed to M. abscessus during care at the clinic. Cross-infection of M. abscessus between two siblings may have happened at home. We found one patient whose M. *abscessus* infection matched an M. *abscessus* isolate recovered from the clinic environment, although the patient had never visited that specific location. Overall, we found the rate of transmission of M. *abscessus* from person-to-person was very low.

**What does this mean and reasons for caution?**

These results help doctors, infection control teams, and CF care teams understand the risk for NTM infection transmission and acquisition in the healthcare system and to take specific steps to reduce their spread, protect our patients, and make the CF healthcare system a safer space. These findings also show how important it is to regularly test for NTM infections in people with CF, to routinely test the healthcare environment for NTM, and to use instruments like the HALT toolkit to assess for healthcare-associated infections and guide decisions to prevent the infection from spreading.

**What’s next?**

The Prospective HALT of NTM study is collecting and analyzing all respiratory NTM from people with CF with comparison to infections recovered in the healthcare environment over a four-year period. This will improve our understanding of healthcare-associated sources of NTM infections and reduce risk for future infections.

**Original manuscript citations in PubMed**

<https://pubmed.ncbi.nlm.nih.gov/40783340/>