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Cystic Fibrosis Research News

Title:

Mycobacterium abscessus smooth and rough colony variants in cystic fibrosis patients

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What was your research question?

During the follow-up of two cystic fibrosis patients, we isolated from sputum cultures of both patients isolates of the germ Mycobacterium abscessus that featured an unusual(?) mixed morphologic appearance, both smooth and rough. We investigated whether this morphotype change was related to the germ's antibiotic susceptibility, the treatment outcome and on the overall patient management.

Why is this important?

It is important to understand if this morphotype change has an impact on the evolution of the disease in a patient chronically colonized with *M. abscessus*. If they have different antibiotic susceptibilities, it is important for laboratories to know how to identify the colonies.
Finally, from a scientific point of view, it is interesting to understand the genetic factors that lead to the modification of the morphology of the colonies.

What did you do?

We have characterized the genetic (DNA) and phenotypic differences (physical bacterial differences) of these two types of colonies. We sequenced the whole genome of the rough and smooth colonies of both patients. We studied mutations in genes involved in antibiotic resistance as well as in genes previously described to be involved in this smooth-to rough transition. We then compared these results to the phenotypes (bacterial cells) observed *in vitro* (under microscope).

What did you find?

We identified two situations. In the first case, the patient was colonized by an isolate that have mutated, leading to a smooth-to-rough transition. This patient had been previously treated with tobramycin (antibiotic) which may have promoted this transition. The rough clone was associated with higher virulence and recurrent infection. The second patient was colonized by two different isolates of *M. abscessus*. The smooth isolate was susceptible to the antibiotic clarithromycin while the rough isolate was resistant. Laboratories need to careful they don't make a false susceptibility rating for antibiotics, in the case they identify only the smooth colony, and must consider that the antibiotic resistant rough isolate could also be present.

What does this mean and reasons for caution?

We suggest a closer follow-up of the patient infected with a rough colony, in order to properly identify an unfavourable evolution of the infection. The isolation of two colonies with different antibiotic susceptibility profile must be taken into account to adapt the antibiotic therapy. Finally, it is important to remind CF patients of the possibility of recolonization with several strains of the same difficult-to-treat bacteria.

What's next?

We propose systematic whole genome (DNA) sequencing to guarantee the identification of different *M. abscessus* isolates and their antibiotic susceptibility profile, to guide the most appropriate treatment in CF patients.

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