

# Cystic Fibrosis Research News

**Title:** Assessment of stability and fluctuations of cultured lower airway bacterial communities in people with cystic fibrosis

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## What was your research question?

We wanted to see if (1) the amount and the number of different types of bacteria found in sputum (i.e. the bacterial airway community) change over time both in people with stable disease and in people who need treating for an exacerbation (flare up of symptoms) and (2) if the bacterial airway community can predict if a person is likely to experience an exacerbation in the future.

## Why is this important?

A large variety of bacteria are found in sputum; however, hospital microbiological laboratories normally look at the growth of bacteria that are known to cause disease (e.g. *Pseudomonas aeruginosa*). This information is used by doctors to guide clinical decisions.

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Research suggests that looking at all bacteria in the airway community will give us a better understanding of how lung disease progresses. Most of these studies are based on bacterial DNA taken from sputum rather than bacteria grown in the laboratory. In this approach, the amount of different types of bacteria cannot be precisely determined and dead bacteria may be included in the analyses. To overcome these limitations, a variety of growth conditions can be used in the laboratory to work out the amounts of bacteria that are alive ('viable') more accurately. It is unclear whether this type of sputum analyses could be useful for doctors to inform clinical decisions.

## What did you do?

We recruited 80 people with CF and asked participants to provide sputum on up to four successive occasions, which included during outpatient appointments and when admitted to hospital for treatment of an exacerbation. All sputum samples were transferred to the research laboratory and bacteria were grown under different conditions, e.g. different kinds of growth media and atmospheric conditions. The amount of each type of bacterium in each sample was then worked out to provide information on the viable bacterial airway community.

## What did you find?

Multiple bacteria were grown from 199 sputum samples. Twenty-five participants provided at least 3 successive sputum samples during the study: 18 had stable disease; 7 were being treated for an exacerbation. These participants had their own individual bacterial airway community. However, the bacterial communities in people with stable disease were more similar over time compared to those who had an exacerbation. Variation in the exacerbation group was found during treatment for exacerbation. Furthermore, the bacterial airway community of 52 participants at the start of the study did not predict if they were likely to experience a future exacerbation.

## What does this mean and reasons for caution?

This type of sputum analysis provides a detailed picture of the viable bacterial airway community. Since researchers could not use the bacterial airway community to predict future exacerbations, its predictive value to clinical practice might be restricted. Limitations of this study are the small number of people included and that most participants were adults and chronically infected with CF bugs; therefore, results may be different for people without chronic infection or younger people. Furthermore, the laboratory conditions used might not have allowed all types of bacteria to grow.



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## What's next?

Further studies could determine if this type of sputum analysis can be used to track disease progression or guide selection of antibiotics.

## Original manuscript citation in PubMed

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