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Cystic Fibrosis Research News

Title:

Relationship between airway dysbiosis, inflammation and lung function in adults with cystic fibrosis

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What was your research question?

Is there a relationship between the lung microbiome (bacteria that inhabit people's lungs), levels of inflammation in the lung and the overall lung function?

Why is this important?

There is still no cure for CF, but for most of the patients the disease is detected early in life, which critically allows physicians to treat the patients from very early on in the disease. In

patients suffering from CF, changes in the type of bacteria that inhabit the lung also starts early in life. Moreover, inflammation is an important disease driver in this early phase of disease. A complete picture of how these alterations relate to changes in lung function and clinical outcome is missing. By putting together, the relationship between the lung microbiome, lung inflammation and course of CF disease, we may be better informed at how to treat patients more efficiently, thereby improving quality of life.

What did you do?

We collected and analysed sputum of more than 100 patients of various ages and treatment programs to establish a basic understanding of the average CF patients' lung microenvironment. The samples were analysed for the bacterial composition and inflammatory molecules, as well as, the lung function of the patients assessed. The individual parameters were compared with each other by statistical methods. In the second step, the patients were grouped based on the bacteria types living in their microbiome. The inflammatory parameters and lung function of the subgroups were compared to each other.

What did you find?

We found a link between bacterial subtypes to inflammatory markers and impaired lung function. The overall composition of the types of bacteria present in the microbiome correlated strongly to levels of inflammation. Patients with a more diverse microbiome, that is many different types of bacteria, showed lower levels of inflammatory markers and a better lung function. In contrast, microbiomes dominated by a single pathogen showed higher inflammation and worsening of lung function in patients.

What does this mean and reasons for caution?

It is not sufficient to only take the prevalence of key bacteria such as *Pseudomonas aeruginosa,* which is already well known to be associated with CF disease severity. Our study highlights attention must also be paid to the complete bacterial profile living in the lung of people with CF. The results have to be interpreted with a certain caution however, as the method we applied cannot identify any specific details about all the bacteria types and it also cannot provide any data on how the bacteria are behaving. In our study, some of the experimental groups examined did only feature a small number of individuals, which limits how confident we can be in our findings.

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What's next?

The results of this cross-sectional study help us to understand how the microbiome, inflammation and lung function are linked and change during disease progression. Assessing the microbiome structure as a diagnostic measure might be a way of measuring CF disease severity. Next, a longitudinal study is important to check on an individual patient level, which factors are the key drivers of the worsening of the disease.

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