European Cystic Fibrosis Society

Journal of Cystic Fibrosis
The Official Journal of the European Cystic Fibrosis Society

# Cystic Fibrosis Research News

**Title:**
Covid-19 in cystic fibrosis patients compared to the general population: severity and virus-host cell interactions

**Lay Title:**
Analysis of cell mechanisms influencing Covid-19 disease in cystic fibrosis patients and in the general population

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## What was your research question?

We asked whether the severity of Covid-19 was different compared to the general population and investigated the reasons for this possible difference.

## Why is this important?

In general, the respiratory condition of cystic fibrosis patients may be worsened by viral infections. Therefore, it was important to understand if this was also the case for Covid-19.

## What did you do?

Individuals with/without Covid-19 symptoms from the general population and from cystic fibrosis patients were enrolled to collect clinical data and to perform nasopharyngeal swabs. On the material collected with the swabs, two tests were done. First, the presence of the virus was assessed with a polymerase chain reaction. Second, the expression of genes in the nasal epithelial cells was quantified with a technique named RNA sequencing.

## What did you find?

We found that Covid-19 in cystic fibrosis patients, unlike other types of viral infections, is not more severe compared to individuals from the general population. This observation suggests that cystic fibrosis patients have a protective factor. Actually, our analysis of gene expression by RNA sequencing revealed that nasal epithelial cells from cystic fibrosis patients show some significant differences compared to those of the general population. This different gene expression may create in cystic fibrosis cells an environment unfavourable for viral growth.

## What does this mean and reasons for caution?

Our results reveal that epithelial cells from cystic fibrosis patients have a particular pattern of gene expression that is probably connected to the basic genetic defect. The importance of this finding goes beyond its role in Covid-19 disease since it may reveal unsuspected cellular mechanisms that are disrupted by the loss of the cystic fibrosis gene (CFTR). However, gene expression analysis needs to be carried out in other parts of the respiratory system to confirm the difference between cystic fibrosis patients and the general population.

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**What's next?**

It will be important now to investigate the molecular basis of the differences in gene expression that we have found in our study. This type of analysis could reveal novel mechanisms that are disrupted in cystic fibrosis.

**Original manuscript citation in PubMed**

https://pubmed.ncbi.nlm.nih.gov/38508950/