



# Cystic Fibrosis Research News

**Title:**

Diversity of cystic fibrosis chronic rhinosinusitis microbiota correlates with different pathogen dominance

**Lay Title:**

Microbiota diversity in CF chronic sinusitis

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**What was your research question?**

Chronic infection of the nose and its cavities is called rhinosinusitis (CRS) and it affects nearly all people with cystic fibrosis (CF). How is the composition of different bacterial communities in the sinuses related to disease severity?

**Why is this important?**

*Pseudomonas aeruginosa* and *Staphylococcus aureus* have long been recognized as bacteria that are involved in CRS, but more recent techniques called sequencing have revealed that the upper airways contain more complex bacterial communities than previously thought. There is growing appreciation that interactions between bacterial species affect the power of bacteria to cause symptoms (virulence), antibiotic resistance, and disease progression, but the mechanisms of these interactions are poorly understood.

**What did you do?**

To gain a greater insight into bacterial composition in the CRS sinuses of people with CF, we used a technique called genomic sequencing to generate a profile of bacteria found within mucus removed from people undergoing sinus surgery. We paired these data with patient clinical characteristics to identify relationships between bacterial composition and CRS disease states.

**What did you find?**

Using sequencing, we demonstrate that the CF sinuses contain bacteria not captured by

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standard laboratory culture methods. Culture data generally identified the most dominant bacteria as determined by sequencing, though rare bacteria are not always detectable. We also found that sinus mucus bacterial communities that were dominated by *Staphylococcus aureus* were more diverse compared to late-stage disease communities typified by *Pseudomonas*. These trends mirror bacterial community dynamics in the lungs of people with CF, suggesting that sinus cavity microbiology may predict CF lung disease progression.

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

The “unified airway” model is now widely appreciated to be a significant determinant of CF lung disease. In this model, the sinuses serve as a reservoir of bacteria that may seed the lower airways. Yet, little is known about the bacteria of the sinuses and how they shape chronic CF lung disease. By showing that the upper airways mirror bacterial community dynamics of the lung, we provide evidence that sinus bacteria may reflect, or even predict, the trajectory of subsequent CF lung infection. Yet, we also acknowledge limitations of the study – we sampled a small number of people, our sequence data do not provide specific strain information, and that details about how bacteria move from the upper to lower airways are still not well understood.

## **What’s next?**

Further investigations of interbacterial interactions will be critical to identify the contributions of sinus bacterial communities to the mechanisms of CF-associated sinus disease.

## **Original manuscript citation in PubMed**

<https://pubmed.ncbi.nlm.nih.gov/33931358/>