

Cystic Fibrosis Research News

Title:

16S rRNA GENE SEQUENCING REVEALS SITE-SPECIFIC SIGNATURES OF THE UPPER AND LOWER AIRWAYS OF CYSTIC FIBROSIS PATIENTS

Authors:

Sarah K. Lucas^a, Robert Yang^b, Jordan M. Dunitz^c, Holly C. Boyer^b, Ryan C. Hunter^a

Affiliations:

^aDepartment of Microbiology & Immunology, University of Minnesota, USA

^bDepartment of Otolaryngology, Head and Neck Surgery, University of Minnesota, USA

^cDivision of Pulmonary, Allergy, Critical Care & Sleep Medicine, University of Minnesota, USA

What was your research question?

Most people with cystic fibrosis (CF) will develop chronic inflammation in the sinuses which is often due to bacterial infections. Many will receive the same antibiotics for their sinus and lung infections, however it is unknown how bacteria in the sinus and lungs compare within and between individuals.

Why is this important?

Understanding how bacteria colonise the human body and cause infection is important to improve medical treatment of people with CF. We aimed to compare the bacteria of the sinuses and lungs with the overall goal to improve the diagnosis and treatment of sinus infections. Also, we wanted to better understand the bacterial communities in chronic infections of the sinus, as they may contribute to the development of lung infections that often lead to an individual's decline in health. DNA sequencing allows us to identify microorganisms that cannot grow in a laboratory, allowing a more detailed understanding of these microbial habitats.

What did you do?

To characterise the microorganisms of the sinuses, sputum (a mixture of saliva and mucus coughed up from the lungs) was collected from people with CF prior to sinus surgery for the treatment of chronic sinus infections and inflammation. A paired sinus mucus sample was collected during this surgery. DNA was extracted from these samples, and a unique gene (16S rRNA) found in all bacteria, was sequenced. DNA analysis allowed us to identify all the

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different types of bacteria in both sample types. We then compared the number of different bacteria and the types of bacteria found in the sinuses and sputum samples.

What did you find?

We found that sample pairs were very similar to each other. The sinuses and the lungs of individuals with CF contained similar bacterial community compositions. However, sinus samples always had a bacterium that was dominant, while the lung samples displayed evenly distributed types of bacteria. Notably, some individuals had bacterial pathogens (that cause disease) that were present in the sinus sample but not in the sputum sample, and vice versa, which may be important in deciding how to treat sinus and lung infections.

What does this mean and reasons for caution?

There are similar bacteria shared between the lungs and sinuses of people with CF, but these body sites remain distinct in their microbiology. Simple culture techniques such as sinus swabs may be useful for diagnosis of lung infections. However, using sputum respiratory cultures for the treatment of chronic sinus infections may not be as effective, as the bacteria are different in the sinuses and lungs.

What's next?

This research has presented us with many new ideas. We are currently investigating the presence of anaerobic (living in the absence of air) bacteria observed in sputum, as well as their role in CF bacterial infections. The contribution of these bacteria in CF infections has not been studied very well.

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