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Cystic Fibrosis Research News

Title:

INTESTINAL FUNCTION AND TRANSIT ASSOCIATE WITH GUT MICROBIOTA DYSBIOSIS IN CYSTIC FIBROSIS

Lay Title:

Bacterial communities relate to gut function and transit in the cystic fibrosis gut

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What was your research question?

We wanted to investigate how altered gut function in cystic fibrosis (CF), alongside other elements of disease like antibiotic usage, disrupts the community of bacteria living in the gut. We combined magnetic resonance imaging (MRI) results with bacterial community data for both people with CF (pwCF) and without CF.

Why is this important?

Disruption to the bacterial community (dysbiosis) is evident in CF, with links between gut dysbiosis, intestinal inflammation and tissue damage. In older pwCF this remains understudied, despite the CF community ranking “how can we relieve gut symptoms such as stomach pain, bloating and nausea?” as a priority research question. Given the recent success of non-invasive MRI to investigate gut function problems in CF, we can utilise this data alongside other patient characteristics to better understand what parts of CF associate with bacterial community changes in the gut.

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What did you do?

We analysed the bacterial communities present in stool samples collected from pwCF and without CF (12-36 years) using DNA sequencing. After looking for differences between the groups, statistical tests were used to determine which bacteria were responsible for driving these differences. We then combined bacterial community data with the MRI and clinical data to see how CF disease, antibiotics, gut function, and other factors influenced the overall bacterial community, the common bacteria, and rarer bacteria. We also looked at how these factors influenced the specific bacteria we identified earlier as driving the differences between the pwCF and healthy controls.

What did you find?

We found a reduction in the number of different species (diversity) in pwCF compared to without CF. The bacterial community composition was also significantly different between the two groups. Twenty bacteria were responsible for over 50% of the differences between the two groups, with *E. coli* contributing to the dissimilarity most, alongside bacteria that are deemed beneficial to the gut. The common bacteria were more affected by the presence of CF disease itself, whilst the rarer bacteria (includes *E. coli*) were more affected by antibiotic usage but also gut function, such as increased food transit time in the gut.

What does this mean and reasons for caution?

Alterations in gut function and transit due to CF disease are associated with changes to the gut bacterial community, specifically the rarer bacteria including *E. coli*. Delayed transit in the small intestine will allow more growth and division of the resident bacteria in this area. Their increased numbers may impact the community of bacteria further along the intestinal tract, such as those residing in the colon that have been identified as beneficial to host health through the substances they produce. We could investigate this further with more participants, especially since MRI is non-invasive and well tolerated by pwCF.

What's next?

We will similarly investigate how new CF treatments impact gut function and the bacterial communities present, considering links with patient symptoms. We also want to determine if alternate bacteria can fulfill the roles of the beneficial bacteria that are typically reduced in abundance within the CF gut.

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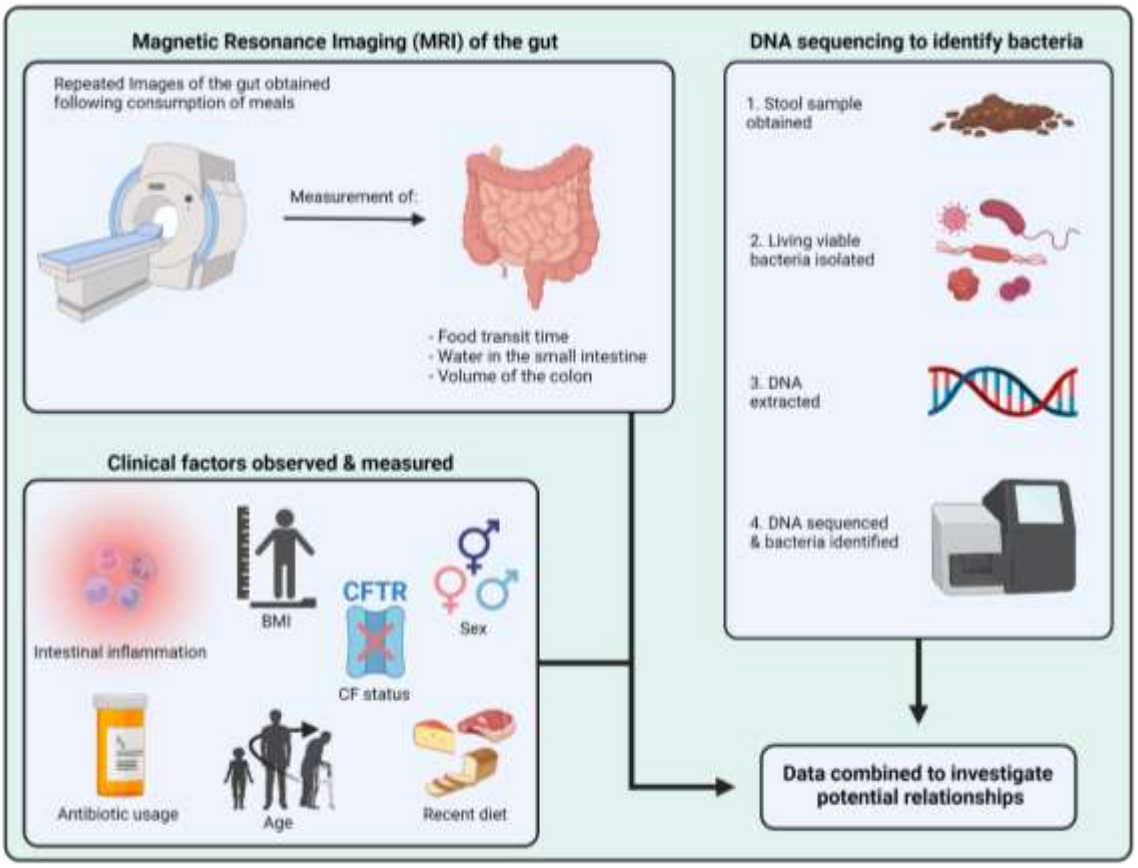

Figure 1. *Overview of the study design. Created with BioRender.com.*

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