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Cystic Fibrosis Research News

Title:

Total bacterial load, inflammation, and structural lung disease in paediatric cystic fibrosis

Authors:

Steven L. Taylor[1,2], Lex E.X. Leong[3], Kerry L. Ivey[2,4,5], Steve Wesselingh[2], Keith Grimwood[6], Claire E. Wainwright[7,8], Geraint B. Rogers[1,2], On behalf of the Australasian Cystic Fibrosis Bronchoalveolar Lavage (ACFBAL) study group

Affiliations:

[1]SAHMRI Microbiome Research Laboratory, Flinders University College of Medicine and Public Health, Adelaide, SA, Australia
[2]Microbiome and Host Health, South Australia Health and Medical Research Institute, North Terrace, Adelaide, SA, Australia
[3]Microbiology and Infectious Diseases, SA Pathology, South Australia, Australia
[4]Department of Nutrition, Harvard T. H. Chan School of Public Health, Boston, MA, USA
[5]Department of Nutrition and Dietetics, College of Nursing and Health Sciences Flinders University, Adelaide, SA
[6]School of Medicine and Menzies Health Institute Queensland, Griffith University Gold Coast Campus and Departments of Infectious Diseases and Paediatrics, Gold Coast Health, Gold Coast, Queensland, Australia
[7]Respiratory and Sleep Medicine, Queensland Children's Hospital, South Brisbane, Queensland, Australia
[8]Child Health Research Centre, The University of Queensland, Brisbane, Queensland, Australia

What was your research question?

With detection of pathogens currently being our most useful microbial measure to assess and predict lung disease in children with CF, we asked, how informative would it be to use molecular/genetic methods to measure the total amount of all bacteria in the lungs, regardless of what the bacterial species are?

Why is this important?

There are decades of research describing associations between specific pathogens, such as the bacterial species *Pseudomonas aeruginosa* or *Staphylococcus aureus*, and lung disease. Because of this, we relate the type of pathogen detected to how a child's disease is likely to progress, and which treatments are likely to be most helpful. However, in the same way that

different measures of lung function tell us different aspects of lung health, it is important that we assess how different measures of lung bacteria relate to disease. Our current method cultures or grows known pathogens; however, another method is to simply count all the bacteria in the lungs.

What did you do?

Lung disease was measured in 78 5-year-old children with CF, based on lung (CT) scans. We also collected lung samples and performed bacterial culture to detect common CF-associated pathogens (*Pseudomonas aeruginosa, Staphylococcus aureus, Haemophilus influenzae,* and *Stenotrophomonas maltophilia*), which is the standard practise. Further, we applied a molecular/genetic method to lung samples, called quantitative polymerase chain reaction (qPCR), which measures 1) total bacterial levels and 2) specific levels of the four cultured bacteria (*Pseudomonas, Staphylococcus, Haemophilus,* and *Stenotrophomonas*). We then assessed which bacterial measure was most strongly associated with lung disease.

What did you find?

Supporting previous findings, we saw a relationship between *P. aeruginosa* levels and airway wall thickening and *S. maltophilia* levels and air trapping, both common signs of CF disease. These associations were similar irrespective of the method used (both culture and qPCR showed these associations). However, our most important finding was that total bacterial levels (measured by qPCR) was strongly associated with four measures of lung disease (bronchiectasis, airway wall thickening, mucus plugging, and parenchymal disease) and that its ability to predict the cumulative lung disease score was stronger than any other bacterial measure.

What does this mean and reasons for caution?

These findings suggest that the total amount of bacteria that are in the lungs may provide a useful additional indicator of airway disease. Our observations also highlight that the relationship between bacteria and disease in the lungs of young children is likely to work in two directions. As well as bacteria driving inflammation and damage, airway inflammation and reduced clearance of mucus is likely to contribute to bacterial accumulation. This is supported by our finding that the number of bacteria was strongly associated with disease, regardless of what types of bacteria these were.

What's next?

We now need to investigate further whether measuring total bacterial load is useful to predict long-term outcomes in children with CF.

Original manuscript citation in PubMed

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