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<https://reachmd.com/programs/Audioabstracts/journal-cystic-fibrosis-microbial-colonization-lung-function-adolescents-cystic-fibrosis/8218/>

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## Journal of Cystic Fibrosis: Microbial Colonization and Lung Function in Adolescents With Cystic Fibrosis

### Interpretation:

Patients with cystic fibrosis suffer from chronic progressive pulmonary disease, driven by cycles of airway infection and inflammation. Chronic cystic fibrosis lung disease is characterized by bacterial and fungal colonizations that change upon disease progression and patient aging.

With intensified antibiotic therapy and longer survival, patients with cystic fibrosis are colonized with a more complex pattern of bacteria and fungi. However, the clinical relevance of these emerging pathogens for lung function remains poorly defined. The aim of this study by Hector et al was to assess the association of bacterial and fungal colonization patterns with lung function in adolescent patients with cystic fibrosis.

Microbial colonization patterns and lung function parameters were assessed in 770 adolescent European cystic fibrosis patients in a retrospective study, with median follow-up time being 10 years.

Colonization with *Pseudomonas aeruginosa* and MRSA were most strongly associated with loss of

lung function, while surprisingly, colonization with *Haemophilus influenzae* was associated with preserved lung function. *Aspergillus fumigatus* was the only species that was associated with an increased risk for infection with *P. aeruginosa*. Microbial interaction analysis revealed three distinct microbial clusters within the longitudinal course of cystic fibrosis lung disease.

The results from this retrospective cystic fibrosis study confirm and extend previous studies demonstrating that infections with *P.aeruginosa* or MRSA are strongly associated with loss of lung function in cystic fibrosis.

Collectively, this study identified potentially protective and harmful microbial colonization patterns in adolescent cystic fibrosis patients. Further studies in different patient cohorts are required to evaluate these microbial patterns and to assess their clinical relevance.