

## Analysis of the Lung Microbiome in Cystic Fibrosis Patients Using 16S Sequencing

**Authors :** Manasvi Pinnaka, Brianna Chrisman

**Abstract :** Cystic fibrosis patients often develop lung infections that range anywhere in severity from mild to life-threatening due to the presence of thick and sticky mucus that fills their airways. Since many of these infections are chronic, they not only affect a patient's ability to breathe but also increase the chances of mortality by respiratory failure. With a publicly available dataset of DNA sequences from bacterial species in the lung microbiome of cystic fibrosis patients, the correlations between different microbial species in the lung and the extent of deterioration of lung function were investigated. 16S sequencing technologies were used to determine the microbiome composition of the samples in the dataset. For the statistical analyses, referencing helped distinguish between taxonomies, and the proportions of certain taxa relative to another were determined. It was found that the *Fusobacterium*, *Actinomyces*, and *Leptotrichia* microbial types all had a positive correlation with the FEV1 score, indicating the potential displacement of these species by pathogens as the disease progresses. However, the dominant pathogens themselves, including *Pseudomonas aeruginosa* and *Staphylococcus aureus*, did not have statistically significant negative correlations with the FEV1 score as described by past literature. Examining the lung microbiology of cystic fibrosis patients can help with the prediction of the current condition of lung function, with the potential to guide doctors when designing personalized treatment plans for patients.

**Keywords :** bacterial infections, cystic fibrosis, lung microbiome, 16S sequencing

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