SputOMICs identifies common and distinct markers in cystic fibrosis and chronic obstructive pulmonary disease

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Authors

Sebastien Boutin Dario Frey Barbara Helm Matteo Guerra Matthias Hagner Junyan Lu Susanne Dittrich Sabine Wege Ralf Eberhardt Felix Herth Olaf Sommerburg Carsten Schultz Alexander Dalpke **Ursula Klingmueller** Marcus Mall

Abstract

Cystic fibrosis (CF) and chronic obstructive pulmonary disease (COPD) are muco-obstructive lung diseases. Knowledge of molecular processes has much improved therapeutic options in CF, whereas much less is known for COPD, a disease affecting an increasing number of patients. Here, we report a multilayer workflow integrating microbiome, inflammation and proteome profiling with clinical data to identify disease specific characteristics in sputum. Our proof-of-concept study shows that CF sputum is dominated by Pseudomonas and Staphylococcus, exhibits heightened neutrophilic inflammation, and a severe protease-antiprotease imbalance. In contrast, COPD displays heterogeneous microbiome composition, eosinophilic inflammation, and altered extracellular matrix remodeling. Proteome-based cellular deconvolution identifies disease-specific immune cell signatures, underscoring the complexity, especially in COPD. Multi-omics factor analysis establishes matrisome, and nucleotide metabolism changes as key disease discriminators. These findings highlight the potential of our integrated approach to uncover sputum biomarkers as tools for patient stratification and personalized therapeutic strategies in CF and COPD.