

## Harnessing Metabolomics for Microbial Identification in Complex Samples

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Cystic fibrosis (CF) is autosomal recessive disorder that critically affects the lungs. Caused by mutations within the CF transmembrane conductance regulator (CFTR), CF patients have abnormal ion transport across the epithelium leading to production of thick, sticky and viscous bronchial mucus. This moist, warm and nutrient rich environment allows microbes to colonize and infect CF patients. While the lungs of a CF patient harbor a diverse microbial community, as individuals with CF age, specific microbial pathogens become chronic infections leading to progressive decline of lung function and ultimately, premature death.

Current methods are adept at quickly identify the microbial pathogens affecting these patients, however, the detection is limited to identification of the genus and species. It is well understood that microbes produce a wide variety of molecules to interact with each other and the host. These metabolites function as toxins, antibiotics, redox active molecules and nutrient scavenging entities. Using newly developed bioinformatics tools, we can begin to evaluate whether specific specialized metabolites are detectable in clinical samples and if those metabolites can provide insight into patient status. Here, we describe the application of MS/MS based molecular networking to identify *Pseudomonas aeruginosa* metabolites in sputum samples from CF patients.