Quantitative proteome analysis of cystic fibrosis patient bacterial isolates across clinical periods
Chunxiang Zheng, Benjamin J. Staudinger, Pradeep K. Singh, Xia Wu, Colin Manoil, James E. Bruce*
Departments of Genome Sciences, Medicine, and Microbiology, University of Washington, Seattle, WA

Overview
- Pseudomonas aeruginosa isolates collected from patient sputum during well/sick/treatment
- Quantitative proteome analysis performed on dominant isolates from each clinical periods
- Several virulence proteins were observed to be differentially regulated in isolates that dominate during the different clinical periods

Introduction
Cystic fibrosis (CF) is a common and life threatening genetic disease with approximately 30,000 new patients diagnosed every year. CF is caused by a mutations in the cystic fibrosis transmembrane conductance regulator protein (CFTR), resulting in abnormal epithelial ion transport. Chronic lung infections are the most important clinical manifestation of cystic fibrosis; and most patients are infected with Pseudomonas aeruginosa (PA)1. Once infection is established, patients suffer frequent disease flares producing increased lung inflammation, and marked respiratory symptoms. While some flares produce transient illness, one out of four causes permanent lung function decline. Our overall goal is to develop and utilize label free quantification strategies to identify changes in pathogen protein abundance levels that occur during disease flares.

Methods
- 12 dominant isolates from each period, collected individually
- Post the isolates from each period
- LC-MS/MS
- Raw data

Results
- Proteins related to alginate biosynthesis and regulation, small molecular transport, and protein folding were observed to decrease during sick period.
- Hypothetical proteins were observed to increase during sick period.
- Heat shock, type IV pili synthesis and regulation, and antibiotic sensitivity were observed to increase during sick period.

Conclusions
- 1005 proteins were quantified from dominant isolates during well, sick and treatment periods.
- Proteins related to antibiotic sensitivity, hydrogen cyanide production, flagella synthesis regulation, and type IV pili synthesis were observed to increase during sick period.
- Proteins related to alginate biosynthesis and regulation, small molecular transport, and protein folding were observed to decrease during sick period.

References

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