

Quantitative proteome analysis of cystic fibrosis patient bacterial isolates across clinical periods

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Overview

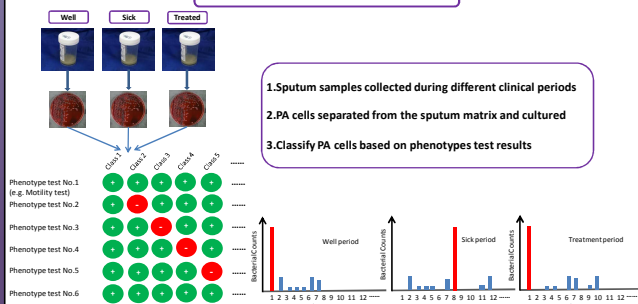
- ◀ *Pseudomonas aeruginosa* isolates collected from patient sputum during well/sick/treatment
- ◀ Quantitative proteome analysis performed on dominant isolates from each clinical periods
- ◀ Several virulence proteins were observed to be differentially regulated in isolates that dominate during the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

Introduction

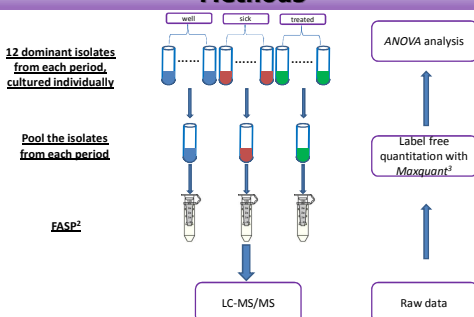
Cystic fibrosis (CF) is a common and life threatening genetic diseases with approximately 30,000 new patients diagnosed every year. CF is caused by a mutations in the cystic fibrosis transmembrane conductance regulator protein (CFTR), resulting in abnormal epithelial ion transport. Chronic lung infections 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

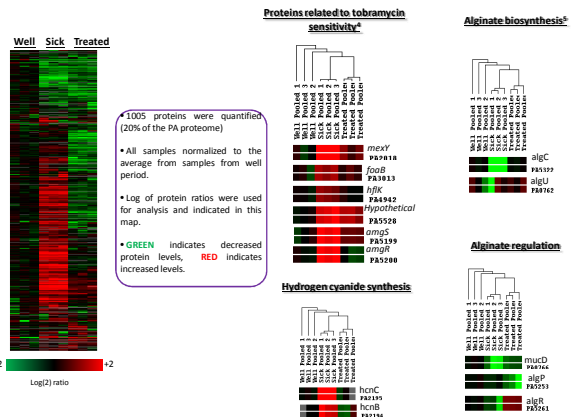
Bacterial cell collection and classification



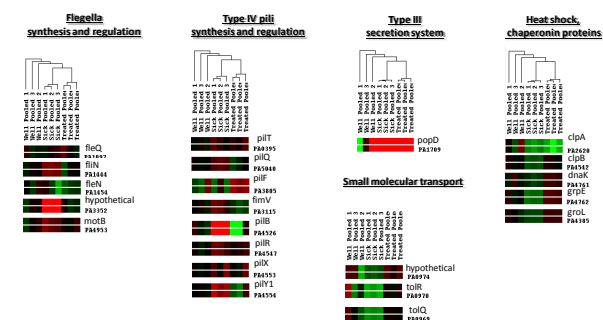
Methods



Results



Results



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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