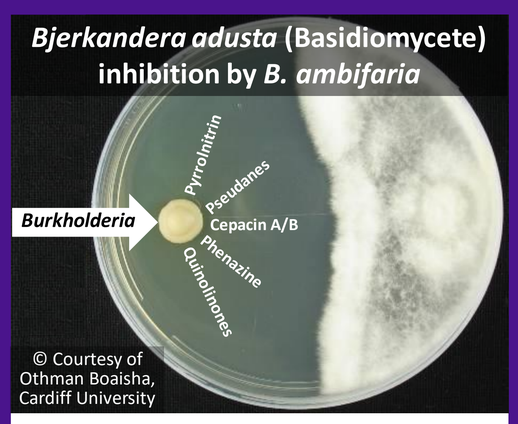


Does the production of antifungals by *Burkholderia* alter the fungal community in the CF lung?

B. cepacia complex infected CF patients **harbour a different** fungal diversity to ***P. aeruginosa*** positive individuals.

Mycobiome diversity analysis in adult cystic fibrosis (CF) patients: analysis of samples from the OligoG phase 2b clinical trials

Introduction:

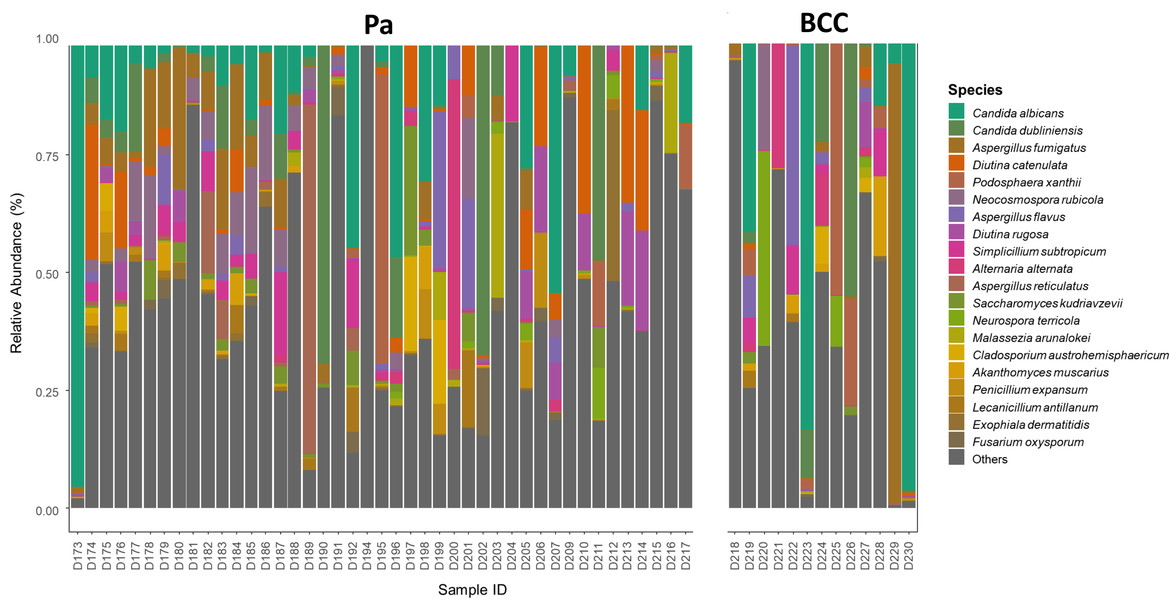
- CF lung infections are polymicrobial in nature.
- Traditional diagnosis of CF infection identifies priority microbial pathogens by growth and does not capture the full diversity of microorganisms present.
- We used culture-independent approaches to explore fungal community composition in adults with cystic fibrosis who participated in the OligoG phase 2b clinical trials.

Methods:

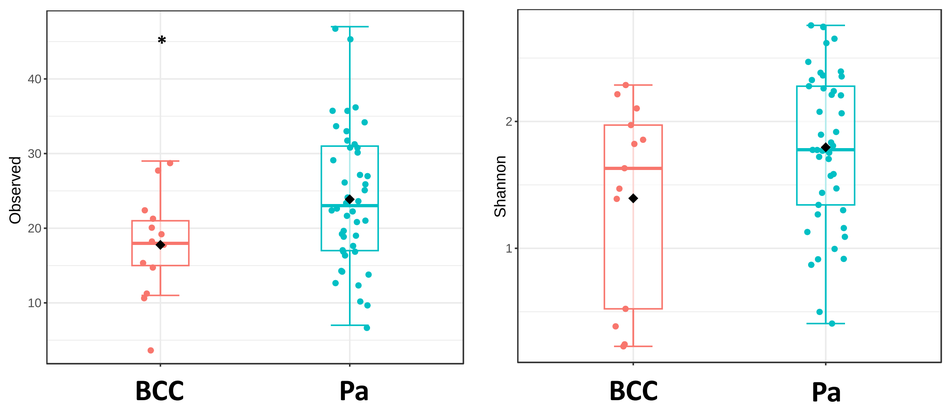
- Total sputum DNA from individuals infected with the bacteria *Pseudomonas aeruginosa* (Pa; n=45) and *Burkholderia cepacia* complex (BCC; n= 13) was analysed by ITS2 region sequencing to identify their fungal diversity.
- ITS2 sequences were processed using EasyAmplicon (v1.18.1) pipeline and downstream analysis was conducted on MicrobiomeAnalyst (2.0) web-based platform.
- A total of 948 different Amplicon Sequence Variants (ASVs) were identified and indicated the presence of multiple fungal taxa.
- Filtering to the minimum library size of 4600 sequence reads resulted in 2 samples being excluded; 76 ASVs were present across the remaining 56 samples.

Key findings:

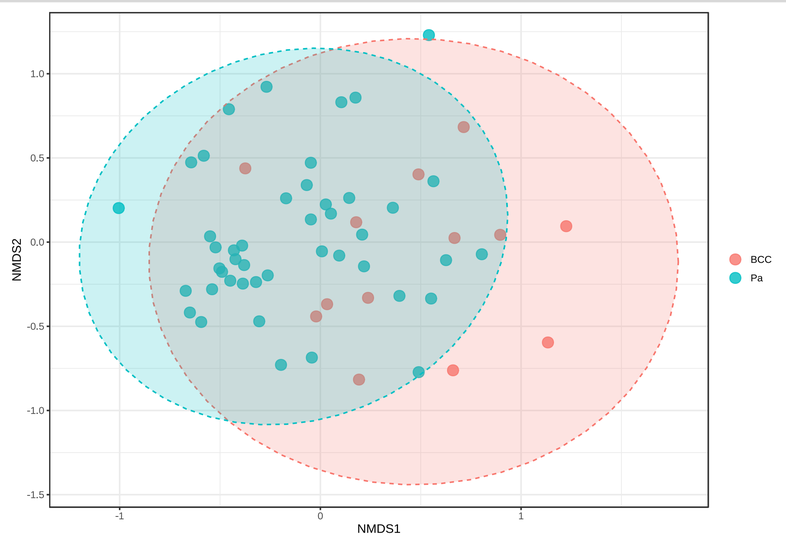
1. The relative abundance (%) of fungal community in the sputum of adult CF patients who had either a dominant infection of *Pseudomonas aeruginosa* (Pa) or *Burkholderia cepacia* complex (BCC).



2. The alpha diversity comparison between the Pa and BCC samples showed less fungal diversity observed in patients with BCC infections.

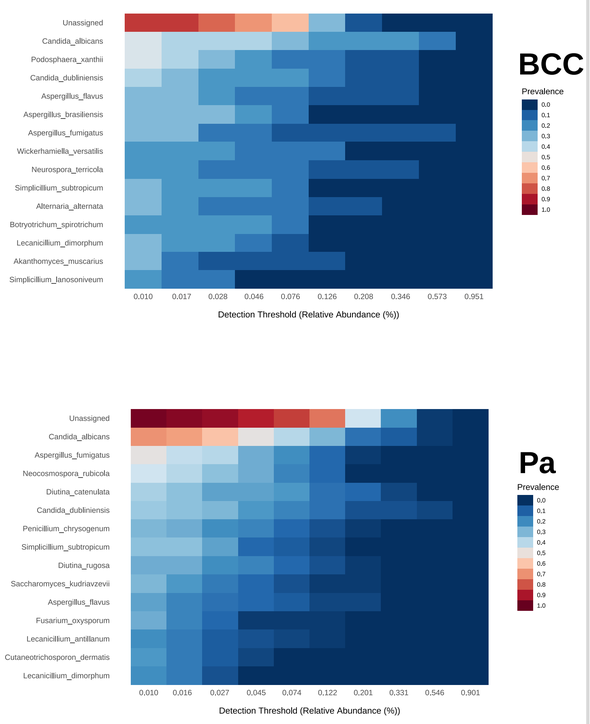


3. There was a significant difference in the fungal community composition between the two groups (p = 0.016); suggesting the grouping variable (Pa vs BCC infection) is associated with a difference in fungal community composition.



Additional results:

4. Core features composition presents in sample groups (Pa or BCC) based on relative abundance.



Conclusions:

Initial mycobiome analysis of lung infections in CF individuals who participated in the OligoG clinical trial shows that *B. cepacia complex* infected CF patients harbour a different fungal diversity to *P. aeruginosa* positive individuals.

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