

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

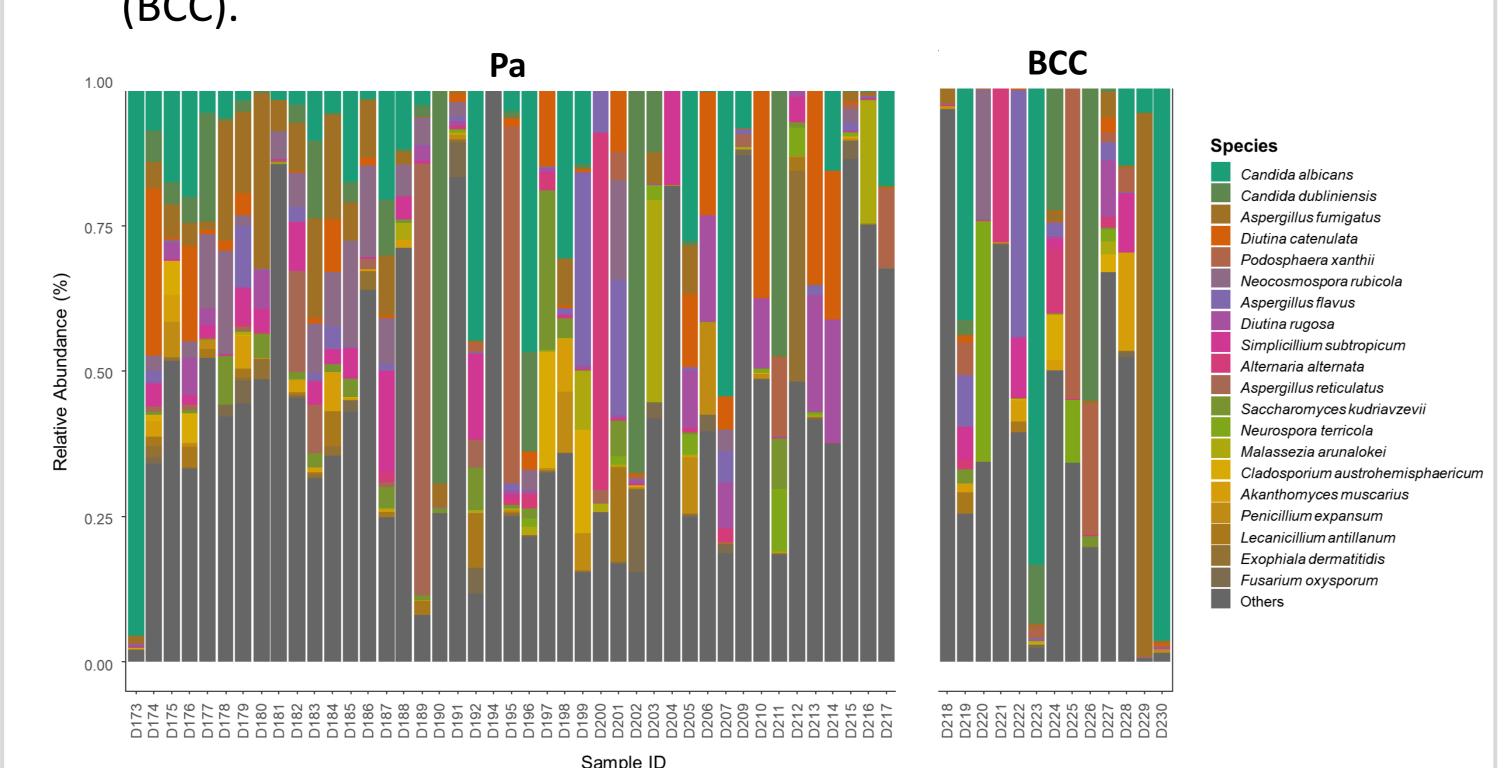
## Mycobiome diversity analysis in adult cystic fibrosis (CF) patients: analysis of samples from the OligoG phase 2b clinical trials

#### **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.

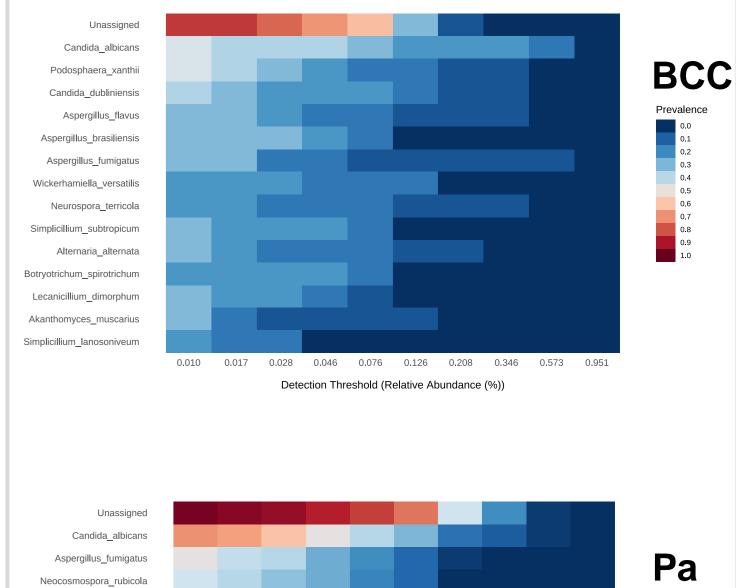
#### **Key findings:**

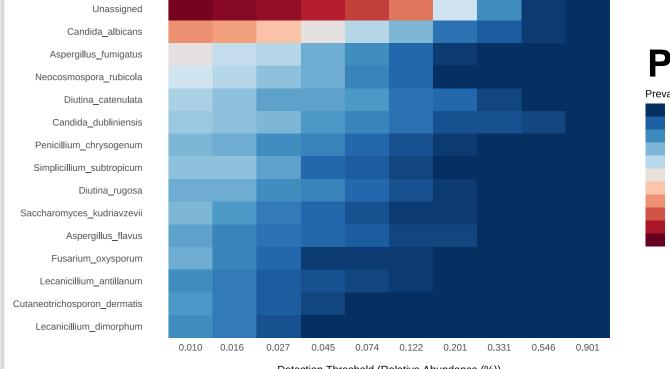
The relative abundance (%) of fungal community in the sputum of adult CF patients who had either a dominant infection of Pseudomonas aeruginosa (Pa) or Burkholderia cepacia complex (BCC).



**Additional results:** 

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

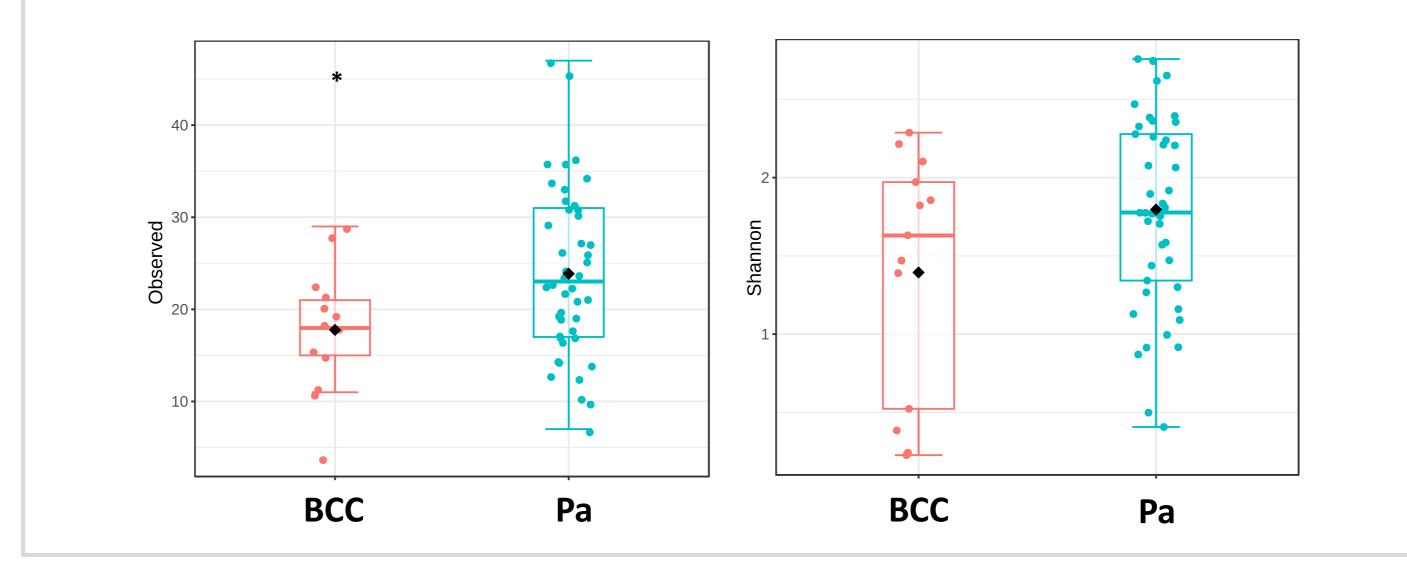




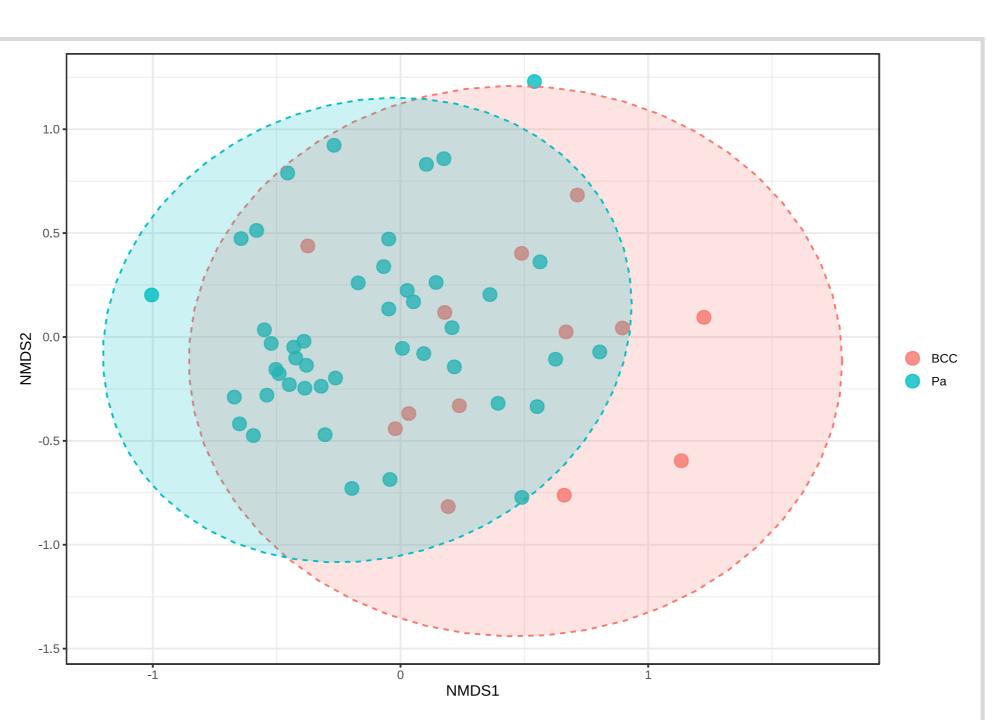
### **Methods:**

- 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) webbased 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.

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.



#### **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.



