

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

B. cepacia complex infected CF patientsharbour a different fungal diversity toP. aeruginosa positive individuals.

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

Itroduction:

Methods:

- 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.

Total sputum DNA from individuals

Pseudomonas aeruginosa (Pa; n=45)

and Burkholderia cepacia complex

(BCC; n= 13) was analysed by ITS2

region sequencing to identify their

ITS2 sequences were processed using

EasyAmplicon (v1.18.1) pipeline and

downstream analysis was conducted

on MicrobiomeAnalyst (2.0) web-

A total of 948 different Amplicon

identified and indicated the presence

Filtering to the minimum library size

of 4600 sequence reads resulted in 2

were present across the remaining 56

samples being excluded; 76 ASVs

Sequence Variants (ASVs) were

of multiple fungal taxa.

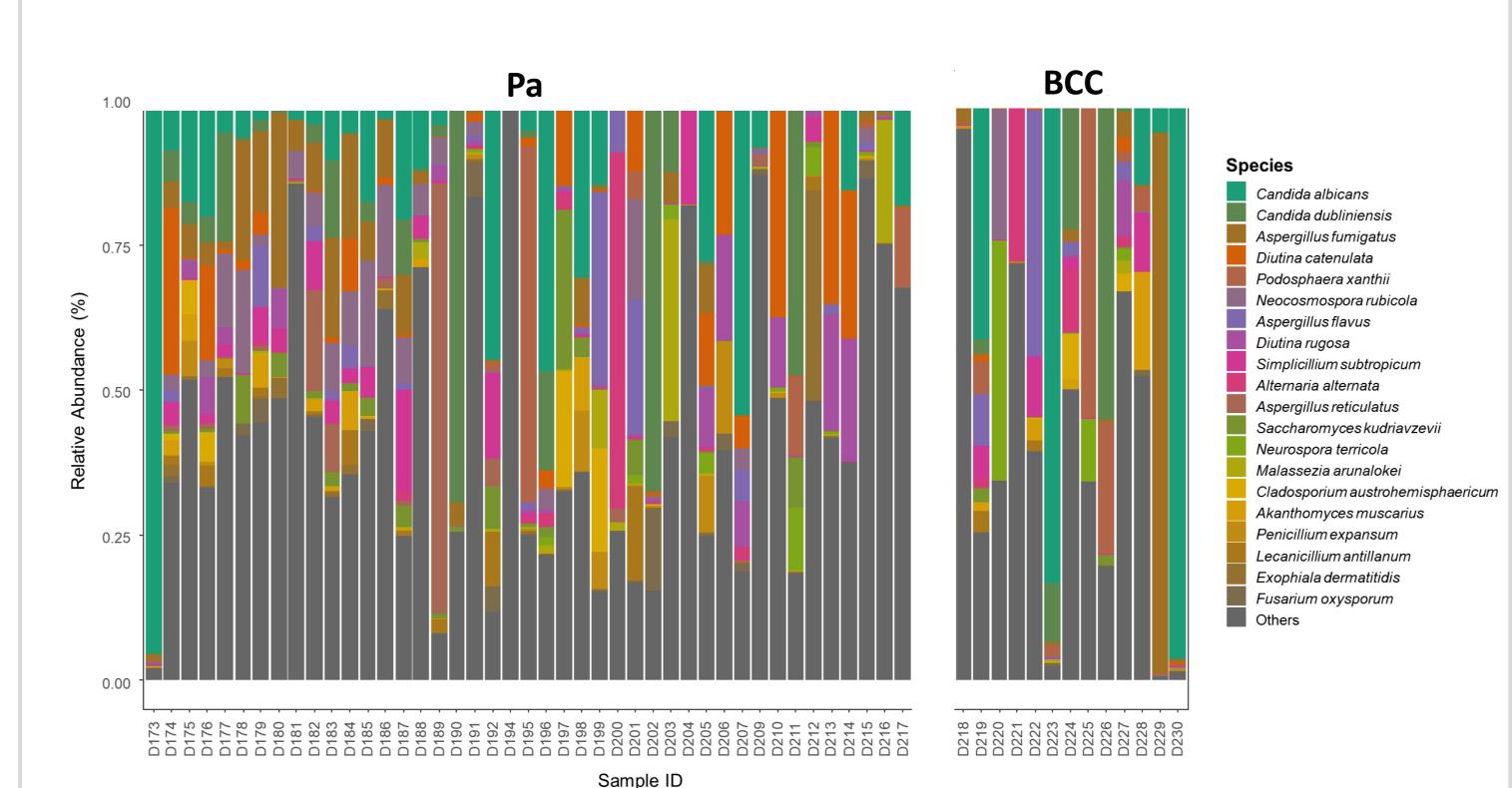
infected with the bacteria

fungal diversity.

based platform.

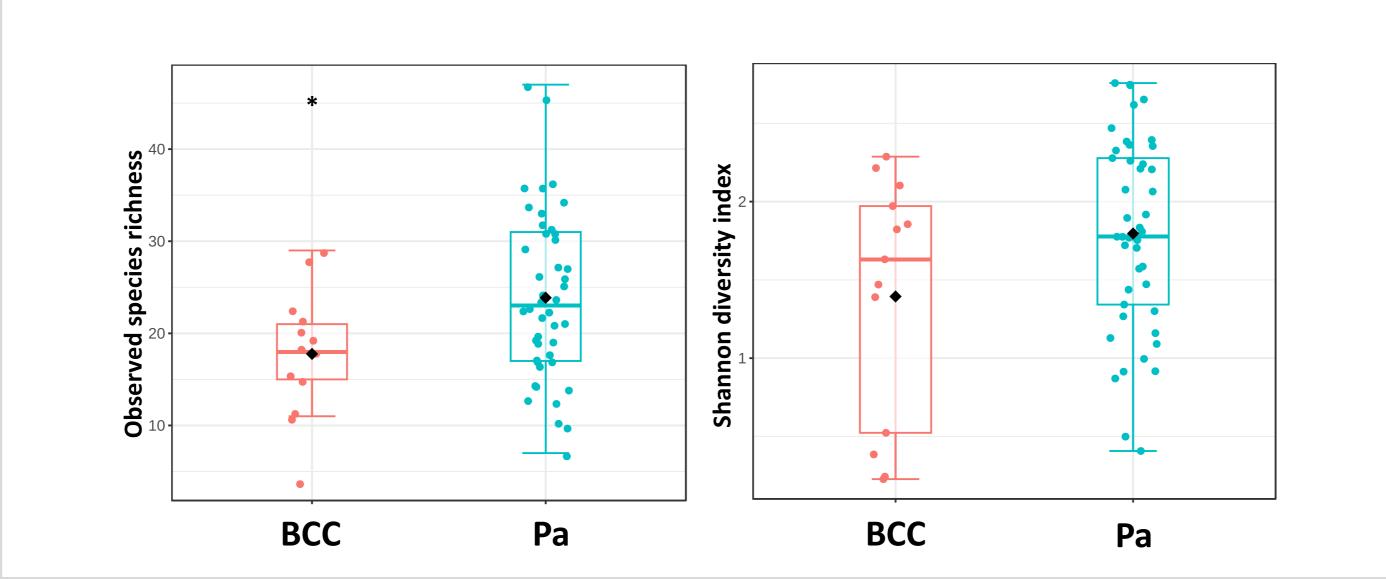
Key findings:

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).



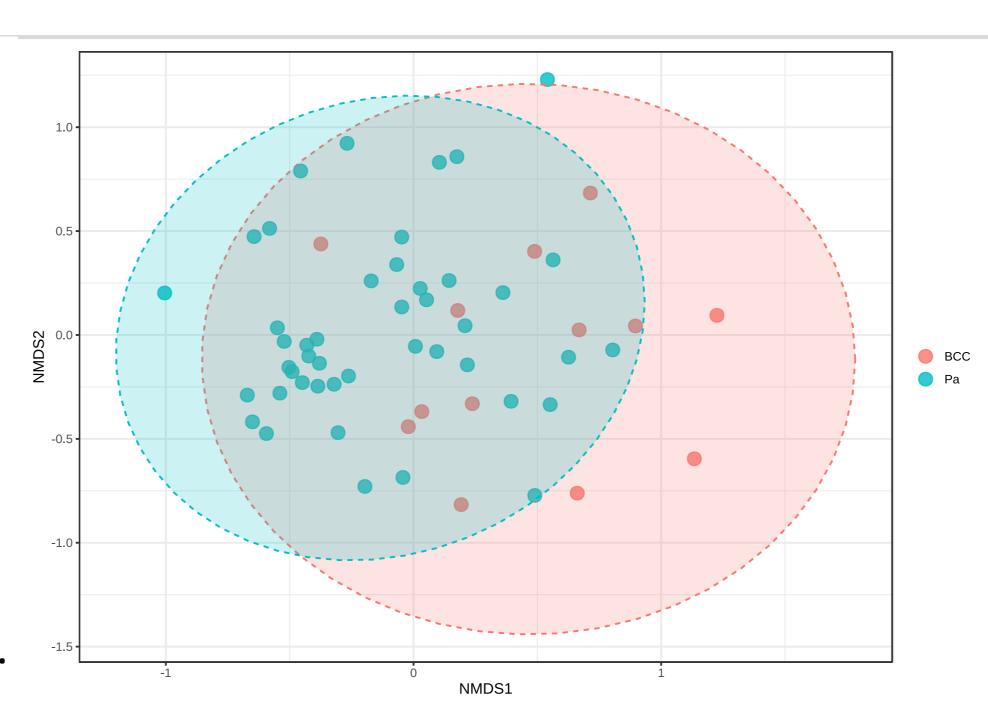
2. The alpha diversity comparison between the Pa and BCC samples

showed less fungal diversity observed in patients with BCC infections.



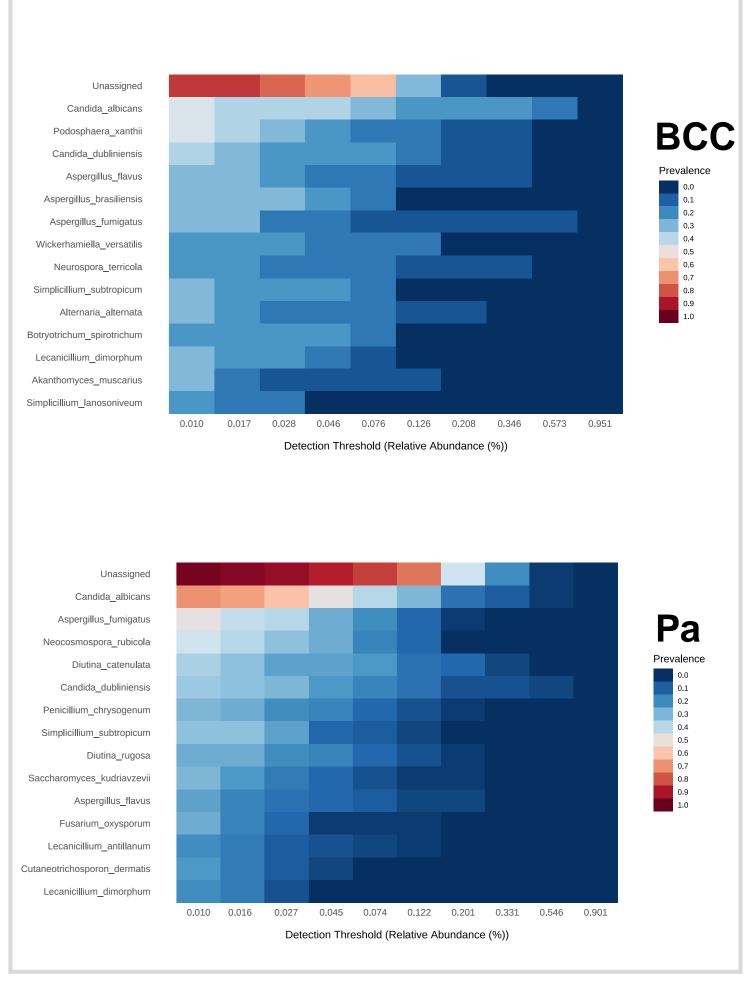
significant difference in the fungal community composition between the two groups (*p* = 0.016); suggesting the grouping variable (Pa vs BCC infection) is associated with a difference in fungal community composition.

³AlgiPharma AS, Industriveien 33, N-1337 Sandvika, Norway



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.



