# THE PULMONARY MICROBIOME IN NON-CYSTIC FIBROSIS BRONCHIECTASIS


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## AIMS

Pulmonary microbiome composition can predict future exacerbations in bronchiectasis [1]. To date, most data in this field is derived from European populations and focuses primarily on the bacterial component of the microbiome (the bacteriome). Consequently little data is available in Asian cohorts, and the fungal component of the microbiome (the mycobiome) is infrequently reported [2].

We recruited patients with stable bronchiectasis at three separate clinical sites across Singapore. To determine the bacteriome and mycobiome in patient sputum, we performed shotgun sequencing of 16S rRNA and 18S ITS amplicons respectively [3].

**The objective of the study was to determine the bacteriome and mycobiome in Asian bronchiectasis patients in Singapore**

## METHODS

### Our Singapore Non-CF Bronchiectasis Platform

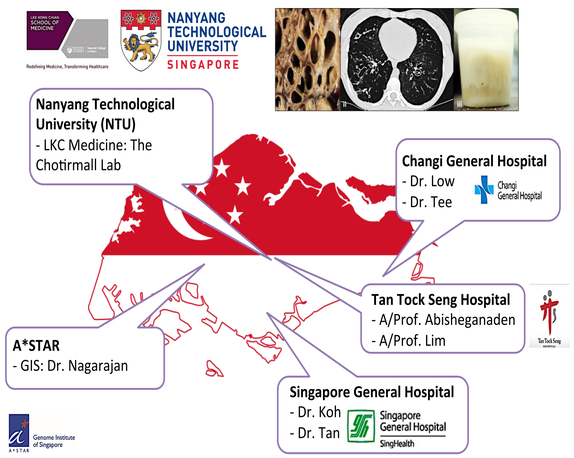
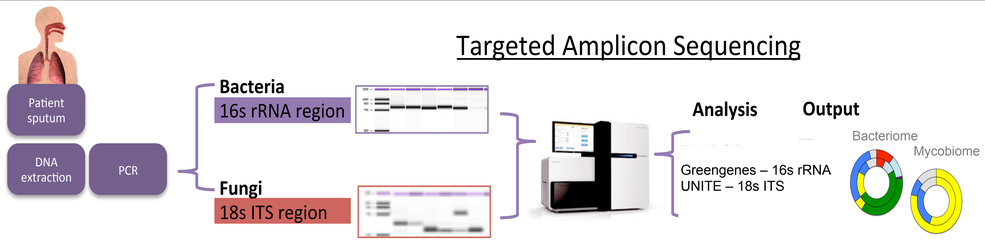



**Figure 1**. We have established a research network for the study of bronchiectasis involving key clinical collaborators form several institutions across Singapore and our partners at the Genome Institute of Singapore.

**Figure 2.** (below) Our sequencing and analysis workflow for bacteria and fungi present in patient sputum. Target amplicons for bacteria (16s rRNA) and Fungi (18s ITS) are amplified and sequenced using a shotgun amplicon sequencing approach [3].

### Our Sequencing and Analysis Workflow




## RESULTS

### Phylum level

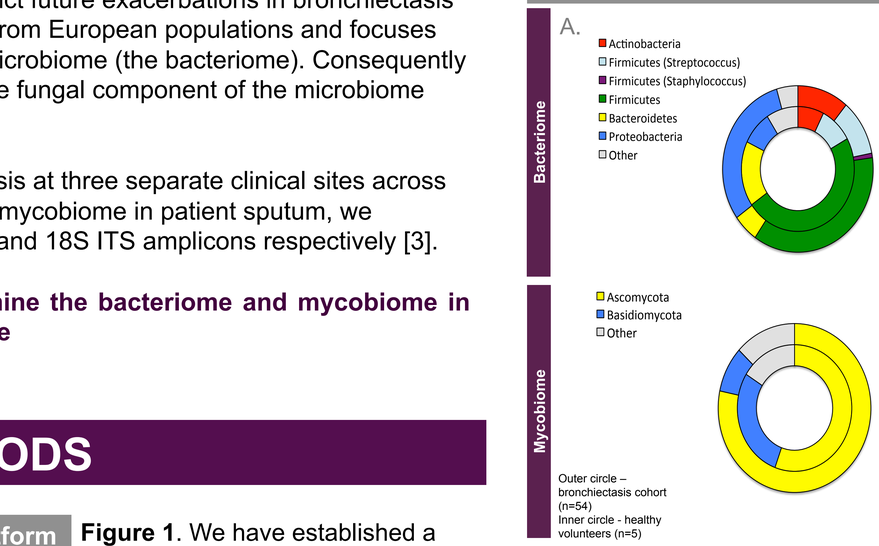



**Figure 3A.** Bronchiectasis patients exhibit increased abundance of Proteobacteria (bacteria – top) and Ascmycota (fungi - bottom).

### Genus level

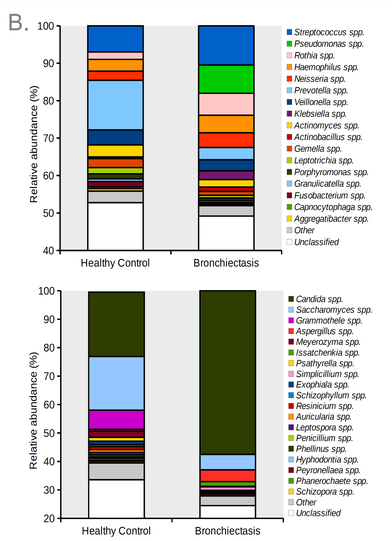



**Figure 3B.** Higher relative abundance of *Pseudomonas* and *Klebsiella spp.* (bacteria – top) and *Candida* and *Aspergillus spp.* (fungi – bottom) are observed in bronchietasis patients at the genus level.

### Prevalence

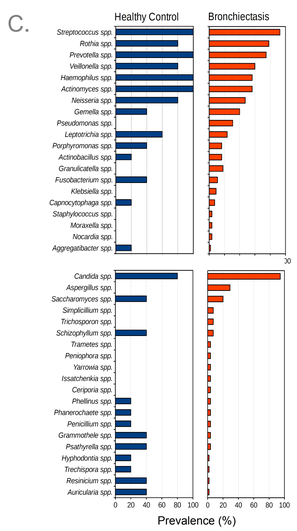



**Figure 3C.** Higher frequencies of *Pseudomonas, Granulicatella and Klebsiella spp.* (bacteria – top) as well as *Aspergillus, Simplicillium and Trichosporon spp.* (fungi – bottom) are observed in bronchiectasis patients.

### Patient stratification

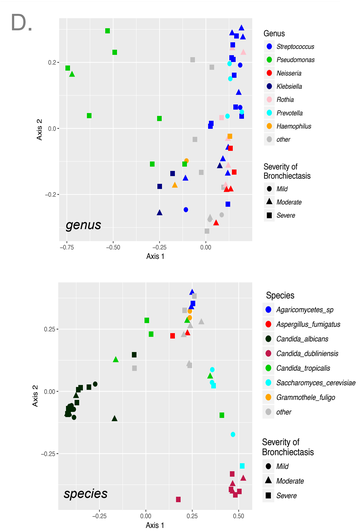



**Figure 3D.** Principal coordinate analysis (PCoA) using a Bray-Curtis dissimilarity matrix of taxonomic relative abundances. Dominant taxa and disease severity of each patient indicated by colouring and shape respectively.

### Dominant taxa associated with disease severity

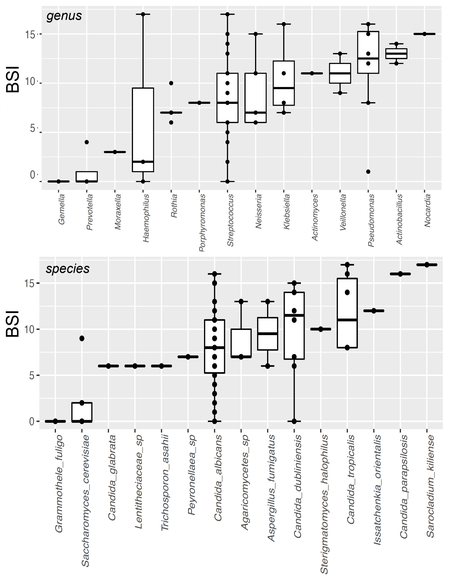



**Figure 4.** Identified taxa of high relative abundance (bacteria – top, fungi – bottom) ranked by average by disease severity - bronchiectasis severity index (BSI). Bacteria associated with higher BSI included *Neisseria Klebsiella* and *Pseudomonas spp.,* while dominance of *A. fumigatus* and specific *Candida* species was seen in patients with more severe disease.

## CONCLUSIONS

Our findings represent the first characterisation of the Asian pulmonary microbiome in bronchiectasis, including analysis of the bacterial and fungal microbiota. Notable observations included the enrichment of *Pseudomonas and Aspergillus spp.* (predominantly *A. fumigatus*) and *Candida spp.* in Singaporean bronchiectasis patients.
The direct and mechanistic implications of these findings on clinical disease, in comparison to European cohorts, require further investigation.

## REFERENCES


[1] Rogers GB *et al.* A novel microbiota stratification system predicts future exacerbations in bronchiectasis. Ann Am Thorac Soc. 2014 May;11(4):496-503.
[2] Chotirmall SH *et al.* Microbiomes in respiratory health and disease: An Asia-Pacific perspective. Respirology. 2017 Feb;22(2):240-250.
[3] Ong SH *et al.* Species identification and profiling of complex microbial communities using shotgun Illumina sequencing of 16S rRNA amplicon sequences. PLoS One. 2013 Apr 8;8(4):e60811.


## ETHICS AND FUNDING

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