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Title: Changes in the lower airway bacterial community of from adult non-CF bronchiectasis population are significantly associated with exacerbations and the presence of *Haemophilus influenzae*

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Body: Background: The aim was to investigate the polymicrobial communities in sputum samples derived from an adult non cystic fibrosis bronchiectasis (nCFBr) population using culture independent methods. The cohort consisted of 70 individuals with HRCT proven nCFBr. Twenty patients presented at the clinic for sputum collection with symptoms consistent with exacerbations, the remainder were clinically stable. Methods: DNA was extracted from sputum samples of all patients (n=70). Universal primers were used to amplify the 16S and 28S rDNA, the resulting fragments were analysed by denaturing gradient gel electrophoresis. Demographic and culture data were used in constrained ordination analyses to identify any significant associations between these data and changes in the sputum microbiota. Results: The presence of *P. aeruginosa* was significantly correlated with a reduced lung function. Bacterial profiles indicated a significantly different community was present in exacerbating patients compared to those that were clinically stable (P = 0.002). *H. influenzae* carriage also produced significant changes (P = 0.004) in community structure. Moreover, *H. influenzae* was never found in samples that harboured *P. aeruginosa*. Bacterial communities appeared to be randomly assembled. Fungal taxa were scarce. Conclusions: Bacterial communities from adult non-CF bronchiectasis patients have distinct differences between exacerbating and clinically stable episodes. Persistent colonisation by *P. aeruginosa* is significantly associated with reduced lung function, and is negatively correlated with *H. influenzae* carriage.