Title: LSC 2013 abstract - Defining the bacterial microbiota of adult non-CF bronchiectasis

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Body: Background: Despite its prevalence and contribution to morbidity, the microbiology of non-CF bronchiectasis is poorly defined. We present an in depth, cross-sectional, analysis of the bacteria present in the lower airways in this condition. Methods: Paired induced sputum and bronchoalveolar lavage samples were obtained from 42 adult non-CF bronchiectasis patients and 16 healthy individuals. The bacterial species in these samples were detailed by 16S rRNA gene pyrosequencing, with meta-analysis use to distinguish 'core' and 'satellite' populations. Results: Over 140 bacterial species were identified, including those associated with respiratory tract and opportunistic infections. Detected species included many that would be unlikely to be reported through standard diagnostic surveillance, such as those requiring anaerobic conditions for growth. Substantial species overlap was observed for paired samples. A core group of species, detected frequently and in high abundance, was defined. Within this group, Haemophilus influenzae made the greatest contribution to non-CF bronchiectasis sample similarity, though a range of respiratory pathogens and oral cavity species were also detected. A relatively small group of rare and low abundance satellite species were identified. The comparative contribution of core and satellite groups suggests a low level of random species acquisition. Conclusions: This study has shown a complex and defined bacterial microbiota is present in non-CF bronchiectasis that is distinct from other respiratory contexts, and provides a basis for further investigations into the potential contribution of these bacteria to disease.