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Title: Severity-related microbiome changes in COPD

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Body: BACKGROUND<INS dateTime=2013-02-25T12:23 cite="mailto:Marian"></INS>. Bronchial secretion cultures have shown that bronchial colonization is a common finding in COPD, but have the disadvantage that depend on the recovery of bacteria in selective cultures. Culture-independent techniques allow the examination of the whole range of the bronchial flora. OBJECTIVE: Analysis and comparison of the bronchial microbiome in moderate and severe COPD patients, in order to identify changes in the COPD microbiome related to disease progression. METHODS DNA sputum samples were obtained from 4 stable moderate and 9 severe COPD patients. Microbiome diversity was determined by 454 pyrosequencing of PCR-amplified 16S rDNA. Sequences were filtered and analysed using QIIME software. RESULTS Moderate COPD patients showed higher microbial diversity than severe COPD subjects (Shannon Index, p=0.02; Simpson inverse Index, p=0.005) and the PCA analysis revealed one cluster of bacterial community composed by the severe COPD patients. The vast majority of the sequences were assigned to 5 bacterial phyla (Firmicutes, Proteobacteria, Bacteroidetes, Actinobacteria, and Fusobacteria, representing the 99%). The relative abundance of commensal phyla was significantly lower in severe COPD patients (Bacteroidetes [p=0.005], Fusobacteria [p=0.005] and SR1 [p=0.02]). Moderate COPD patients showed higher relative abundance of 19 genera representing 48% and 2% of relative abundance. CONCLUSIONS: In COPD severe disease is associated with a significant decrease in microbiome diversity with a loss of commensal flora, without significant change in the potentially pathogenic microbiota. Funded by Fundacio Tauli, SOCAP, FUCAP I Menarini.