Resistomics of sputum from COPD and healthy subjects reveals bacterial load-related prevalence of antimicrobial-resistance-encoding genes.

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Background: Antibiotic resistance is a major global threat. The bacterial community in the lower respiratory tract might be a reservoir of antibiotic-resistant genes in health and chronic obstructive pulmonary disease (COPD).

Methods: We undertook high-throughput quantitative PCR targeting 279 specific Antibiotic resistance genes (ARGs) in DNA extracts from (a) sputum samples obtained from COPD subjects with High Gammaproteobacteria (HG) (n=20) or High Firmicutes (HF) (n=35), at stable, exacerbation and recovery visits (COPD-BEAT study), or healthy controls with (n=7) or without (n=22) exposure to antibiotics in the last 12 months (EXCEED study); and (b) bronchial brush samples from subjects with COPD (n=8) and healthy controls (n=7) (EvA study).

Results: ARGs were highly prevalent in BEAT sputum samples. Broadly similar patterns appeared to be maintained by individuals across all three stages and there were no obvious differences between the HG and HF groups. A higher prevalence of ARGs was observed in sputum samples from COPD compared with healthy controls and bronchial brush samples; this was related to the higher bacterial load in COPD. The ARG prevalence was not related to COPD symptoms or lung function. The prevalence of beta-lactamase family genes decreased significantly in exacerbation and recovery compared with stable state, however this effect was independent of which antibiotic the COPD subject had received for their exacerbation.

Conclusion: ARGs are common in the airway, their prevalence is associated with bacterial load and their pattern is similar in health and disease and unrelated to COPD severity.