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Title: The impact of bacterial colonisation on airway inflammation in stable COPD

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Body: Culture-independent approaches are increasingly used for diagnostic microbiology. Quantitative PCR (qPCR) enables accurate assessment of bacterial load in sputum. We hypothesised that the degree of airway inflammation relates to bacterial load in colonised stable COPD patients and may increase over time. Sputa prospectively collected from stable patients in the London COPD Cohort were analysed using qPCR, to detect H. influenzae, M. catarrhalis and S. pneumoniae, and ELISAs for sputum IL-1β and IL-8. 18 patients with bacterial colonisation (detection in two successive stable samples) were included. Mean age was 71.1 years (SD 8.0), FEV_1 1.3L (0.5), FEV_1 predicted 51.0% (17.5). The mean interval between samples was 217 days (142). Airway inflammation was higher with increasing sputum bacterial load (IL-1β: r=0.448, p=0.006; IL-8: r=0.513, p=0.001, figure 1).

There was no change in bacterial load or airway inflammation over time (table 1).

Changes in bacterial load and airway inflammation over time

	Stable visit 1	Stable visit 2	p-value
Total bacterial load (Log_{10}copies/ml)	7.4 (1.5)	7.5 (1.3)	0.76
IL-1β (pg/ml)	4843 (5659)	3979 (4421)	0.26
IL-8 (pg/ml)	2876 (3461)	2919 (3166)	0.95

Bacterial load and airway inflammation are stable over time in successive samples. Increasing bacterial load, identified by qPCR, is associated with airway inflammation in stable COPD, suggesting the importance of airway infection in COPD pathogenesis.