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secretion composition

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Body: Background: The microbiota associated with the adult CF lower airways differs between individuals, but the factors that determine its composition are not known. We hypothesised that high levels of pseudomonal growth could influence airway secretion composition, with differences clinical isolate phenotype reflected in their metabolomes. In this way, the selective growth environment of the lower airways might differ between CF patients due to divergence in P. aeruginosa strain characteristics. Methods: ¹H NMR spectroscopy was used to characterise the impact of P. aeruginosa growth on a synthetic CF medium as part of an in vitro lower airways model system. Metabolomic analysis was performed on 15 CF clinical isolates and the type strain, PA01. Principal component analysis (PCA) and orthogonal projection to latent structures discriminant analysis (OPLS-DA) were used to compare metabolomic strain profiles. Results: Isolates differed in both their amino acid utilisation and their production of large-scale metabolites. PCA identified five distinct strain clusters. These clusters were confirmed by OPLS-DA and cross-validation showed them to have high predictive capacity. Correlation of clinical data with strain clustering revealed a significant relationship between cluster membership and patient lung function (FEV₁) (P = 0.023). Conclusions: Significant metabolomic divergence observed between CF clinical P. aeruginosa isolates suggests that dominant strain characteristics have the potential to play both a selective role in bacterial community composition and to influence pseudomonal behaviour in vivo. These characteristics may have direct prognostic implications.