Dysregulation of the microbial 'gut-lung' axis in bronchiectasis

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Introduction: Emerging work supports the existence of a microbial 'gut-lung' axis which remains unexplored in bronchiectasis. Methods: Prospective and concurrent sampling of sputum (lung) and stool (gut) in a bronchiectasis cohort (n=57) was performed and subjected to bacteriome (16S rRNA) and mycobiome (18S ITS) assessment. Shotgun metagenomics was performed in a subset (n=15). Data from lung and gut compartments were integrated by weighted similarity network fusion (wSNF) followed by spectral clustering and co-occurrence analysis to assess clinically relevant 'gut-lung' networks. Results: We report the first description of a 'gut-lung' axis in bronchiectasis. Microbial communities demonstrate greater fungal overlap but reduced bacterial diversity between the lung and gut, respectively. Multi-biome integration followed by clustering reveals a 'high-risk' patient group characterised by severe clinical and radiological bronchiectasis including increased exacerbations. These patients exhibit enhanced 'gut-lung' microbial interactions and significant increases in airway *Pseudomonas* accompanied by gastrointestinal *Bacteroides* and *Saccharomyces*. Profiles of the 'low-risk' group were characterized by oral commensals.

Conclusion: A dysregulated 'gut-lung' axis associates with poorer clinical outcome in bronchiectasis. Immunomodulation of the 'gut-lung' axis in bronchiectasis warrants further assessment. Funding: Singapore Ministry of Health's National Medical Research Council under its Clinician-Scientist Individual Research Grant (MOH-000141) (S.H.C) and Clinician Scientist Award (MOH-000710) (S.H.C).

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