Understanding the clinical implications of the “non-classical” microbiome in chronic lung disease: a viewpoint

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Descriptive lung microbiome studies are not sufficient to contribute to clinical understanding. Research now requires systematic exploration to identify the contribution of non-classical bacteria to chronic lung disease. https://bit.ly/3UbgVCs


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In the late 1990s, molecular microbial system analytics started to be adapted and applied to chronic lung disease [1, 2]. These approaches revealed microbial diversity in respiratory samples that included many bacterial species more usually associated with the oropharynx (box 1 and figure 1). While contamination of samples by oropharyngeal microbes might account for a portion of these taxa, evidence also emerged that some of these species were proliferating within the lower airways under certain circumstances [3, 4].