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Characterizing Nasal Microbiota in COVID-19 Patients: Insights from Nanopore Technology and Comparative Analysis

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Abstract : The COVID-19 pandemic has left an indelible mark on global health, leading to a pressing need for understanding the intricate interactions between the virus and the human microbiome. This study focuses on characterizing the nasal microbiota of patients affected by COVID-19, with a specific emphasis on the comparison with unaffected individuals, to shed light on the crucial role of the microbiome in the development of this viral disease. To achieve this objective, Nanopore technology was employed to analyze the bacterial 16s rRNA full-length gene present in nasal swabs collected in Malta between January 2021 and August 2022. A comprehensive dataset consisting of 268 samples (126 SARS-negative samples and 142 SARS-positive samples) was subjected to a comparative analysis using an in-house, custom pipeline. The findings from this study revealed that individuals affected by COVID-19 possess a nasal microbiota that is significantly less diverse, as evidenced by lower α diversity, and is characterized by distinct microbial communities compared to unaffected individuals. The beta diversity analyses were carried out at different taxonomic resolutions. At the phylum level, Bacteroidota was found to be more prevalent in SARS-negative samples, suggesting a potential decrease during the course of viral infection. At the species level, the identification of several specific biomarkers further underscores the critical role of the nasal microbiota in COVID-19 pathogenesis. Notably, species such as Finegoldia magna, Moraxella catarrhalis, and others exhibited relative abundance in SARS-positive samples, potentially serving as significant indicators of the disease. This study presents valuable insights into the relationship between COVID-19 and the nasal microbiota. The identification of distinct microbial communities and potential biomarkers associated with the disease offers promising avenues for further research and therapeutic interventions aimed at enhancing public health outcomes in the context of COVID-19.

Keywords : COVID-19, nasal microbiota, nanopore technology, 16s rRNA gene, biomarkers
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