Commentary

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Metagenomic Analysis reveals Patients with COVID-19

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COVID-19 remains a significant emerging global ill health, and tiny is understood about the role of oropharynx commensal microbes in infection susceptibility and severity. Here, we present the oropharyngeal microbiota characteristics identified by shotgun meta-genomic sequencing analyses of oropharynx swab specimens from 31 COVID-19 patients, 29 influenza B patients, and 28 healthy controls. Our results revealed a definite oropharyngeal microbiota composition within the COVID-19 patients, characterized by enrichment of opportunistic pathogens like *Veillonella* and *Megasphaera* and depletion of *Pseudopropionibacterium, Rothia*, and *Streptococcus* supported the relative abundance of the oropharyngeal microbiome, we built a microbial classifier to differentiate COVID-19 patients from flu patients and healthy controls with an AUC of 0.889, during which *Veillonella* was identified because the most prominent biomarker for COVID-19 group. Several members of the genus *Veillonella*, especially *Veillonella parvula* which was highly enriched within the oropharynx of our COVID-19 patients, were also overrepresented within the BALF of COVID-19 patients, indicating that the mouth acts as a natural reservoir for pathogens to induce co-infections within the lungs of COVID-19 patients.

We also found the increased ratios of *Klebsiella* sp., *Acinetobacter* sp, and *Serratia* sp. were correlated with both disease severity and elevated systemic inflammation markers (neutrophil–lymphocyte ratio, NLR), suggesting that these oropharynx microbiota alterations may impact COVID-19 severity by influencing the inflammatory response. Moreover, the oropharyngeal microbiome of COVID-19 patients exhibited a big enrichment in aminoalkanoic acid metabolism and xenobiotic biodegradation and metabolism. Additionally, all 26 drug classes of antimicrobial resistance genes were detected within the COVID-19 group, and were significantly enriched in critical cases. Last we found that oropharyngeal microbiota alterations and functional differences were related to COVID-19 severity.

The outbreak of coronavirus disease 2019 (COVID-19), caused by severe acute respiratory coronavirus 2 (SARS-CoV-2), has become an ongoing global pandemic. The disease ranges from mild to critical, and most infected people have mild or moderate disease and eventually get over COVID-19. However, ~5% of patients develop severe to critical disease. Several risk factors, like genetics, comorbidities, age, and gender are reported to influence the relative severity of COVID-19 complications. The most complications of severe COVID-19, like pneumonia and acute respiratory distress syndrome, are suspected to be caused by bacterial superinfections; moreover, 50% of patients with severe COVID-19 who died presented with a secondary bacterial infection. Antibiotics play a clearly influential role within the treatment outcome of COVID-19. Bacterial superinfections and required antibiotics illustrate the potential importance of bacteria in COVID-19 complications.

A few current studies have explored the function of the microbiome within the development of COVID-19, suggesting possible relationships between the gut, pulmonary, nasopharyngeal, or oral microbiome and COVID-19. Several bacterial taxa in oral or intestinal microbiomes are found to be related to disease severity and may be wont to predict the clinical outcomes of COVID-19.9 because the major portal of entry for SARS-CoV-2, the human upper tract contains an airway microbiome representing its microenvironment and serving as an important component of the airway epithelial barrier. The epithelial barrier plays a crucial role during virus infection. Bacteria of the airway microbiome can directly impact influenza viral infection 3 or act indirectly though the host system.

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