Microbiota and COVID-19: Microbial Dysbiosis

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Received: 08 August, 2023; Accepted: 31 August, 2023; Published: 06 September, 2023

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Abstract

SARS-CoV-2 causes an acute respiratory syndrome named COVID-19. This virus spread across the globe rapidly and started a pandemic. Many researchers are pursuing finding the mechanisms involved in the disease course and methods of controlling them. In addition to respiratory symptoms, COVID-19 demonstrates digestive symptoms; These findings suggest that microbiota might play a role in the development of COVID-19. Studies showed that lung and gut microbiota composition could change by SARS-CoV-2, and microbial dysbiosis affects disease development and severity. Based on these findings, manipulation of the microbiota utilizing diet, antibiotics, prebiotics, or probiotics can be beneficial in COVID-19 management and improving vaccine efficiency.

Keywords: COVID 19, microbiota, gut, microbiome, dysbiosis.


Introduction

COVID-19 emerged in the final days of 2019 and became a global health issue soon after that. COVID-19 is an acute respiratory disease that is caused by a novel Coronavirus known as SARS-CoV-2. In addition to respiratory symptoms, digestive symptoms are also prevalent in patients with COVID-19; a meta-analysis reported that 20 percent of COVID-19 patients show digestive symptoms⁴. Moreover, viral RNA has been detected in fecal specimens.⁵ ⁶ An increasing body of evidence suggests microbiota alteration during disease progression in the COVID-19, especially gut microbiota⁷-⁹. Understanding the role of microbiota in SARS-CoV-2 infection mechanisms and its pathogenesis may be beneficial in improving disease management.

Microbiota

Microbiota is described as a microbial community that is consisted of archaea, bacteria, viruses, fungi, and protozoa that colonize the surfaces of a host’s body. The genome of these microorganisms is known as the microbiome. They can influence the host’s health and cause many diseases, such as metabolic diseases, neurodegenerative disorders, non-communicable or infectious diseases. The gut microbiome plays a vital role in overall health; however, our knowledge of the pulmonary microbiome is still low⁸.

Lung and gut axis

The gut microbiome plays a vital role in the function and evolution of the host’s immune response in the digestive system and other organs. this role is fulfilled by producing a
certain number of metabolites such as SCFAs. Recent findings point out a connection between 2 microbial populations in the gut and lung known as the gut-lung axis. Besides, Xu et al. reported that the upper respiratory system bacterial microbiome correlates with a gut microbial population during the COVID-19. Gut microbiome conversion can affect pulmonary immune responses and lung homeostasis that mediates susceptibility to respiratory diseases. In patients struggling with COVID-19, gut microbiome composition changes significantly. A reduction in microbial diversity and also shifts in microbial composition have been observed in patients with dysbiosis. Additionally, microbial composition differs between patients based on their illness severity.

**Microbiota and COVID 19**

**Viral composition**

Checking viromes demonstrates a significant difference between COVID-19 patients and HCs. Members of Herelleviridae and Virgaviridae, bacteriophages, and some unclassified viruses have been recognized in the gut virome of COVID-19 patients. An abundance of some phages from Inviridae and Microviridae families and a member of the Virgaviridae family and unclassified viruses is significantly higher in COVID-19 patients than HCs.

**Bacterial species alteration**

Bacterial genera such as Acinetobacter, Chryseobacterium, Burkholderia, Brevundimonas, Sphingobium, and Enterobacteriaceae are most abundant in the pulmonary microbiome of COVID-19 patients. Contrary to pulmonary microbiome, many studies have evaluated gut microbiome in COVID-19 patient, understanding that some bacterial genera and species including Bifidobacterium spp., Lactobacillus spp., Clostridium spp. such as C. butyricum, C. leptum, Eubacterium spp. such as E. rectale, E. hallii and E. eligens, Alistipes spp. such as A. shahii and, A. indistinctus, Roseburia spp. such as R. intestinalis, Paracoccus spp., and A. niger have decreased in numbers while opportunistic pathogens have increased during COVID-19 disease. Furthermore, Ward et al. found a correlation between gut microbial dysbiosis in COVID-19 patients and disease severity and hematological parameters has been observed. The mentioned dysbiosis causes cytokine storm and increased blood markers like CRP and hepatic enzymes. Cytokine storm might be connected to gut microbiota conversion caused by SARS-CoV2 viral infection, as levels of stool IL-18 have demonstrated correlation with relative abundance of species of Peptostreptococcus, Fusobacterium, and Citrobacter. Death by COVID-19 and severe respiratory symptoms can be predicted by gut and oral microbiome composition with 92 and 84 percent accuracy, respectively. This number reaches 96 percent for gut microbiota after being combined with symptoms and comorbidities.

**Clinical Significance And Therapeutic Approaches**

Correlation between gut microbial dysbiosis in COVID-19 patients and disease severity and hematological parameters has been observed. The mentioned dysbiosis causes cytokine storm and increased blood markers like CRP and hepatic enzymes. Cytokine storm might be connected to gut microbiota conversion caused by SARS-CoV2 viral infection, as levels of stool IL-18 have demonstrated correlation with relative abundance of species of Peptostreptococcus, Fusobacterium, and Citrobacter. Death by COVID-19 and severe respiratory symptoms can be predicted by gut and oral microbiome composition with 92 and 84 percent accuracy, respectively. This number reaches 96 percent for gut microbiota after being combined with symptoms and comorbidities. Tang et al. believe that Enterococcus and Enterobacteriaceae can be used as biomarkers for COVID-19, and the Enterococcus to Enterobacteriaceae ratio can be utilized to predict death in patients with the acute disease. Furthermore, Ward et al. found out that Enterococcus faecalis enrichment in patients can predict the disease severity. Dysbiosis and some microbial species might be beneficial for diagnosis and even managing the disease better.

In animal models, recombinant Lactobacillus plantarum affects coronavirus infection in the gut. Some reports indicate beneficial uses of L. rhamnosus GG in maintaining healthy conditions in the gut and lung. Vaccine response enhancement against influenza virus respiratory infections has been observed while utilizing probiotic bacteria such as Bifidobacterium, L. paracasei, and L. rhamnosus. Prebiotics and probiotics might be helpful in the management and treatment of COVID-19. Nevertheless, more research is needed in this matter.
Conclusion

During the COVID-19 disease, the microbiome that occupies the upper respiratory tract, lung and gut goes through many changes. This dysbiosis correlates with cytokine levels like IL-18 and some inflammatory markers in patients. These findings suggest the microbial dysbiosis’ role in inflammation and immunologic procedures in COVID-19. There is evidence suggesting that imbalance in the microbial composition is related to disease severity.

Since microbiome changes by diet, probiotics, and prebiotics, and even consuming antibiotics, more studies are needed to assess its effect on COVID-19 outcomes and microbiota manipulation approaches that might effectively control the COVID-19 disease.

Conflict of Interest

There is no conflict of interest

References