

Could *Faecalibacterium prausnitzii* Amount in the Gut Microbiota Be Used to Monitor the COVID-19 Severity?

Mehmet Demirci 

Department of Medical Microbiology, Kirklareli University Faculty of Medicine, Kirklareli, Turkey

Cite this article as: Demirci M. Could *Faecalibacterium prausnitzii* amount in the gut microbiota be used to monitor the COVID-19 severity? *Turk J Gastroenterol.* 2022;33(10):899-900.

Dear Editor,

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic is not over yet. It continues to cause concern worldwide with its emerging new variants. The immunopathogenesis mechanism and relationship with the disease severity in individuals are still not clearly understood. Coronavirus disease 2019 (COVID-19) severity is thought to depend on the host, virus, and environmental factors. Therefore, evidence that will enable us to detect new biomarkers to target COVID-19 severity may be more helpful in this battle. It is known that gut microbiota is associated with disease severity in SARS-CoV-2-positive patients.¹ *Faecalibacterium prausnitzii* is an important bacterium with anti-inflammatory properties capable of producing short-chain fatty acids (SCFAs),

such as butyrate, and is considered a new probiotic in the gut microbiota.²

When searched Pubmed and Pubmed Central on January 25, 2022, with the keywords "*Faecalibacterium*" and "COVID-19," 480 articles were found, but only 4 of them investigated *F. prausnitzii* amounts in the gut microbiota between severe and non-severe COVID-19 patients. In these 4 articles, 215 non-severe and 88 severe (severe/critical) COVID-19 patients were analyzed for *F. prausnitzii* amounts in the gut microbiota.^{1,3-5} Regardless of age differences, *F. prausnitzii* was reported to have decreased in the gut microbiota of severe COVID-19 patients compared to non-severe COVID-19 patients.^{1,3-5} Figure 1 shows a comparison of *F. prausnitzii* in the gut microbiota reported in severe COVID-19 patients with those in

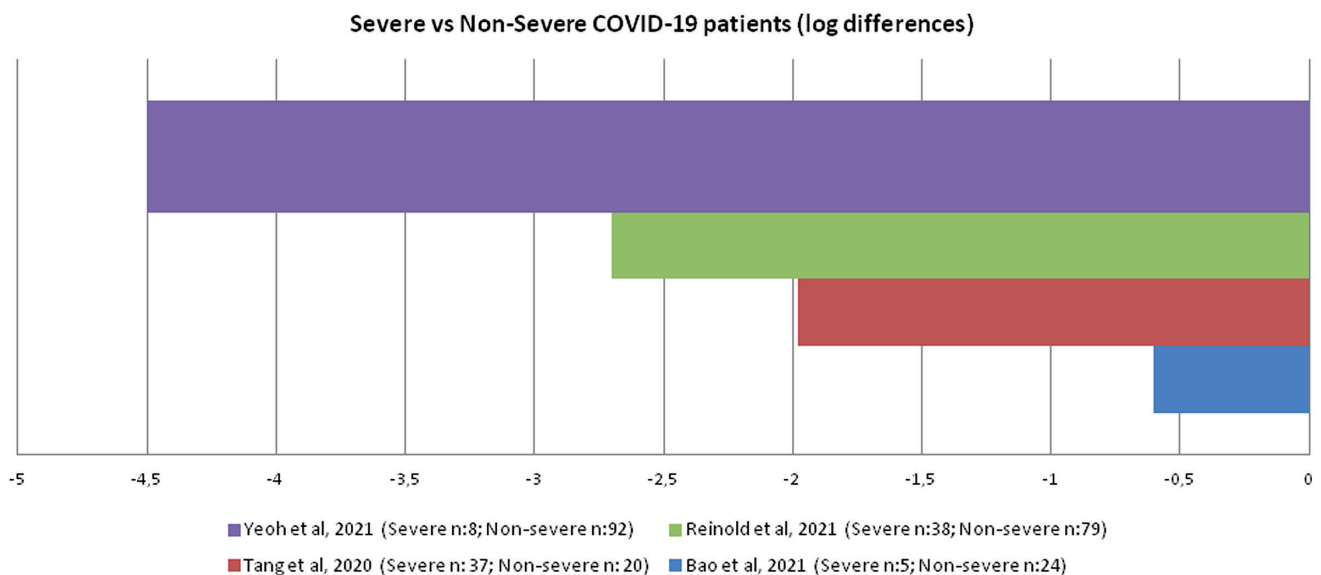


Figure 1. Comparison of *Faecalibacterium prausnitzii* in the gut microbiota reported in severe COVID-19 patients with those in non-severe COVID-19 patients. COVID-19, coronavirus disease 2019.

Corresponding author: Mehmet Demirci, e-mail: demircimehmet@hotmail.com

Received: February 8, 2022 Accepted: May 24, 2022 Publication Date: October 10, 2022

DOI: 10.5152/tjg.2022.22100



non-severe COVID-19 patients. Reinold et al³ reported that proinflammatory cytokines such as interleukin-6 were high and the anti-inflammatory response was suppressed in severe COVID-19 patients compared to non-severe COVID-19 patients. This was correlated with a decrease in *F. prausnitzii* amounts in the gut microbiota. The "lung-gut axis" indicates bidirectional communication, and it appears that SCFAs-producing bacteria in the gut microbiota play an important role in the inflammatory response in the lungs. We obtained data supporting the lung-gut axis effect of *F. prausnitzii* in the gut microbiota of children with asthma²

To conclude, *F. prausnitzii* might be declining in the gut microbiota of severe and critical COVID-19 patients. The monitoring of the *F. prausnitzii* amount in the gut microbiota using the quantitative polymerase chain reaction method can be evaluated to follow-up disease severity. In addition, the follow-up of this bacterium in donor stools and the standardized use of this bacterium in fecal microbiota transplantation could be considered in the treatment of severe and critical COVID-19 patients. On the other hand, due to both limited studies and difficulties in comparing results, definite conclusions cannot be drawn. The decline of *F. prausnitzii* abundance in the gut microbiota may be innocent. Prospective follow-up

is required. In addition, some clinical trials investigating the safety of *F. prausnitzii* in case of therapeutic use are ongoing; it should be approached carefully until its safety is confirmed.

Peer-review: Externally peer-reviewed.

Declaration of Interests: The author declare that he has no competing interest.

REFERENCES

1. Yeoh YK, Zuo T, Lui GC, et al. Gut microbiota composition reflects disease severity and dysfunctional immune responses in patients with COVID-19. *Gut*. 2021;70(4):698-706. [\[CrossRef\]](#)
2. Demirci M, Tokman HB, Uysal HK, et al. Reduced *Akkermansia muciniphila* and *Faecalibacterium prausnitzii* levels in the gut microbiota of children with allergic asthma. *Allergol Immunopathol (Madr)*. 2019;47(4):365-371. [\[CrossRef\]](#)
3. Reinold J, Farahpour F, Fehring C, et al. A pro-inflammatory gut microbiome characterizes SARS-CoV-2 infected patients and a reduction in the connectivity of an anti-inflammatory bacterial network associates With severe COVID-19. *Front Cell Infect Microbiol*. 2021;11:747816. [\[CrossRef\]](#)
4. Bao L, Zhang C, Lyu J, et al. Beware of pharyngeal *Fusobacterium nucleatum* in COVID-19. *BMC Microbiol*. 2021;21(1):277. [\[CrossRef\]](#)
5. Tang L, Gu S, Gong Y, et al. Clinical significance of the correlation between changes in the major intestinal bacteria species and COVID-19 severity. *Engineering (Beijing)*. 2020;6(10):1178-1184. [\[CrossRef\]](#)