Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Reply. We are extremely grateful for the interest of Prof Ponzetto in our article and would like to take the opportunity to answer his very interesting comments.

The possible association of *Helicobacter pylori* with intestinal ischemic manifestations of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) sounds really intriguing. Unfortunately, because all of the analysis was performed during an important sanitary emergency in Lombardy,[1] none of the patients was tested for possible coinfections.

We would also like to emphasize that the strong tropism of SARS-CoV-2 for the gastrointestinal tract may probably be mediated by the abundance of angiotensin-converting enzyme 2 receptors in the intestinal mucosa.[2] A possible explanation for the virus-induced endothelial damage in the gastrointestinal tract could lie in the lectin pathway, which is speculated to be responsible for SARS-CoV-2–mediated thrombotic microangiopathy in lung tissues.[3] The central role of lectin and mannan-binding lectin-associated serine protease-2 in the gastrointestinal ischemic reperfusion damage has already been described in murine model in the pre–COVID-19 era.[4,5] These findings, if confirmed, could open new interesting therapeutic fields of research for SARS-CoV-2 ischemic manifestations.

In conclusion, we would like to thank Prof Ponzetto for the agreeable contributions, and we are pleased to see that our findings are considered valuable and could open new field of research for the scientific community toward an appropriate definition of, and treatment for, SARS-CoV-2.

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Conflicts of interest
The author discloses no conflicts.

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https://doi.org/10.1053/j.gastro.2021.01.197

The New Foe and Old Friends: Are We Ready for Microbiota-Based Therapeutics in Treating COVID-19 Patients?

Dear Editors:

We read with interest the work by Zuo et al[1] reporting altered gut microbiota in patients with coronavirus disease 2019 (COVID-19) during hospitalization. The authors reported that certain beneficial commensals of the patients are in inverse correlation with fecal load of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and/or clinical severity. Although this pioneer study attempts to highlight the potential value of the gut microbiota as a therapeutic target, we believe that extra mechanistic links merit discussion and functional analysis of the readily available metagenomic data would provide further mechanistic insights.

Based on the finding of negative association between the abundances of 4 *Bacteroides* species and the fecal viral load, the authors anticipated that these bacteria may down-regulate angiotensin-converting enzyme 2 (ACE2), the entry point of SARS-CoV-2 into host cells. This justification was based on a previous report in which mice monocolonized with *Bacteroides* species.[2] Most members of *Bacteroides* are able to produce sphingolipids, which play an important role in host–microbial interactions by elevating exogenous sphingolipid (eg, ceramide) levels, while inhibiting de novo synthesis of sphingolipids in both human cells and mice models.[3,4] The benefits of elevated exogenous sphingolipid levels and consequently inhibited de novo synthesis of sphingolipids would be multifaceted. For one thing, increased exogenous sphingolipid levels could suppress the replication of coronaviruses by enhancing the differentiation of regulatory T cells,[5] and stimulating dendritic cell maturation that promotes T cell responses to viral infections.[6] For another, reduced de novo synthesis of sphingolipids in host enterocytes may suppress ACE2 expression and synthesis of human cell surface gangliosides, in which sphingolipids are an integral part. Given that the spike protein of SARS-CoV-2 is known to use the ACE2 receptor and could also use sialic acids linked to host cell surface gangliosides for entry,[7] reduced de novo synthesis of sphingolipids will consequently minimize viral entry. In addition, due to structural differences from host-derived sphingolipids,[4] *Bacteroides*-derived sphingolipids may lower the binding affinity of SARS-CoV-2 spike protein with ACE2 and human cell surface gangliosides and thus reduce viral entry. Given these potential roles of *Bacteroides*-derived sphingolipids, analysis on functional potentials of the microbiome from the readily available metagenomes in this study could somehow reveal possible mechanistic links between gut microbiota–derived sphingolipids and host defense against SARS-CoV-2, although other omics data and experimental studies are needed for verification. It is worth