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.

Mechanistic studies are also needed to confirm the functions of beneficial gut commensals and to exploit these microorganisms for therapy.

TAO ZUO
YUN KIT YEOH
SIEW C. NG
Center for Gut Microbiota Research
The Chinese University of Hong Kong
Hong Kong, China *and*
Department of Medicine and Therapeutics
LKS Institute of Health Science
The Chinese University of Hong Kong
Hong Kong, China

References

1. Peng Y, et al. Gastroenterology 2021;160:2192–2193.
2. Zuo T, et al. Gastroenterology 2020;159:944–955.e8.
3. Franzosa EA, et al. Nat Methods 2018;15:962–968.
4. Troy EB, et al. Front Biosci 2010;15:25.
5. Ramakrishna C, et al. Nat Commun 2019;10:1–13.
6. Shen Y, et al. Cell Host Microbe 2012;12:509–520.
7. Elhenawy W, et al. mBio 2014;5(2):e00909–e00914.
8. Yeoh YK, et al. Gut 2021;70:698–706.

Conflicts of interest
The authors disclose no conflicts.

https://doi.org/10.1053/j.gastro.2021.01.196

Dysbiosis in SARS-CoV-2–Infected Patients

To the Editors:

Gastrointestinal symptoms are frequently observed in patients with coronavirus disease 2019 (COVID-19), but only limited knowledge is available regarding the ability of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) to influence the host microbiota composition. The entry of SARS-CoV-2 into intestinal cells down-regulates angiotensin-converting 2 receptors and causes microbial dysbiosis.[1,2] An alteration of the microbial composition may impact the pulmonary defense mechanisms through the so-called gut–lung axis.[3] We have read with interest the articles by Zuo et al[4] confirming the impact of COVID-19 on the gastrointestinal tract's microbial community composition. Remarkably, their article represents, to our knowledge, the first publication exploring the complex association between SARS-CoV-2 infection and fungi, a neglected component of the gut microbiota. Gut bacteria inhibit the growth of *Candida albicans* and other gut fungi via the target of rapamycin signaling pathway and through those tryptophan metabolites, which are responsible for an interleukin-22–dependent mucosal response.[5,6] Bacteria and fungi compete for some nutrients and, in this context, bacteria with probiotic properties may control *Candida* overgrowth. In healthy volunteers, a commercially available probiotic product has induced a significant fecal anti-*Candida* activity associated with the augmented production of interferon-alfa in the gastrointestinal tract.[7] Another probiotic formulation administered to patients with COVID-19 has induced a significantly faster remission of gastrointestinal symptoms and other symptoms, such as fever, cough, dyspnea, headache, myalgia, and a decreased risk of evolving respiratory failure compared with nontreated patients.[8] These preliminary data should encourage the scientific community to investigate the possible use of probiotics in patients with COVID-19, keeping in mind that not all probiotic formulations are equivalent for efficacy and safety in these fragile patients.

MASSIMILIANO MARAZZATO
GIANCARLO CECCARELLI
GABRIELLA D'ETTORRE
Department of Public Health and Infectious Diseases
University of Rome
Sapienza, Italy

References

1. Verdecchia P, et al. Eur J Intern Med 2020;76:14–20.
2. Ceccarelli G, et al. Gastroenterol Hepatol 2020;5:721–722.
3. Aktas B, et al. Turk J Biol 2020;44:265–272.
4. Zuo T. Gastroenterology 2020;159:1302–1310.e5.
5. García C, et al. mSphere 2017;2(6). e00555–e00517.
6. Romani L, et al. Eur J Immunol 2014;44:3192–3200.
7. De Angelis M, et al. Microorganisms 2019;7:162.
8. d'Ettorre G, et al. Front Med (Lausanne) 2020;7:389.

Conflict of interest
The authors disclose no conflicts.

https://doi.org/10.1053/j.gastro.2020.12.056

Reply. We are grateful for the interest of Marazzato and colleagues in our article and we would like to take the opportunity to respond to their interesting comments. We agree that intestinal dysbiosis is likely to have a long-reaching impact on the pulmonary immune defense system, and hence might be a risk for respiratory distress or other complications induced by coronavirus disease 2019 (COVID-19).[1] Besides differences in fecal mycobiome composition elucidated in the current article,[2] we have also shown that patients with COVID-19 had altered fecal bacterial microbiome characterized by enrichment of opportunistic pathogens and depletion of beneficial commensals, including short-chain fatty acid producing bacteria.[3] The latter was negatively associated