## LETTER TO THE EDITOR



# Gut dysbiosis and long COVID-19: Feeling gutted

To the Editor,

COVID-19 is primarily a respiratory illness, however, there is compelling evidence proposing a lung-gut axis involved in the disease. We explored emerging evidence suggesting a possible link between dysbiosis of the gut microbiota and long-term complications from COVID-19.

Emerging evidence has suggested that the pathology of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) may in part be explained by microbial species,<sup>1</sup> contributing to the inflammatory phenotype commonly seen in patients with coronavirus disease (COVID-19).<sup>2,3</sup> Indeed, dysbiosis of the gut microbiota has been associated with poor clinical outcomes in mechanically ventilated COVID-19 patients. Specifically, Wu et al. observed elevated Granulicatella and Rothia mucilaginosa in the gut microbiome of COVID-19 hospitalized patients when compared to healthy individuals.<sup>4</sup> Additionally, increased Burkholderia cepacia complex, Staphylococcus epidermidis, Mycoplasma hominis, and Mycroplasma orale species have been observed in severely ill COVID-19 patients as opposed to mildly affected ones.<sup>5</sup> These findings hint at a possible yet prominent link between gut microbiota and SARS-CoV-2 repercussions, which may also be related to the imminent occurrence of long-term COVID-19 complications.

Contemporary research has revealed a disruption of the gut microbiota in stool samples of SARS-CoV-2 patients that may explain the well-described cytokine storm-induced ramifications post-infection.<sup>6</sup> Interestingly, fecal transplantation may regenerate gut microbiota diversity, bolstering the respiratory system of patients suffering from COVID-19.<sup>7</sup> Considering that long-term complications following recovery from SARS-CoV-2 persistently exhibit a damaged microbial microenvironment compared to uninfected controls,<sup>8</sup> these changes may hint at alterations in the patients' microbiome. We describe recently published data on the relationship of the long COVID-19 phenomenon with gut microbiota dysbiosis, providing a mechanistic insight. Our aim is to raise awareness of the impact SARS-CoV-2 imposes on public health that in part may be explained through a gut-lung axis cascade.

The depletion of immunomodulatory microbiota from severe SARS-CoV-2 infection may prolong physiological repercussions (i.e., lung injury) during long COVID-19, induced by systemic inflammation.<sup>9</sup> The recent study by Chen *et al.* showed significant reductions of microbial diversity in patients with COVID-19 during a 6-month follow-up, as opposed to the aseptic group.<sup>10</sup> Particularly, following acute (30 days) and prolonged (3 months)

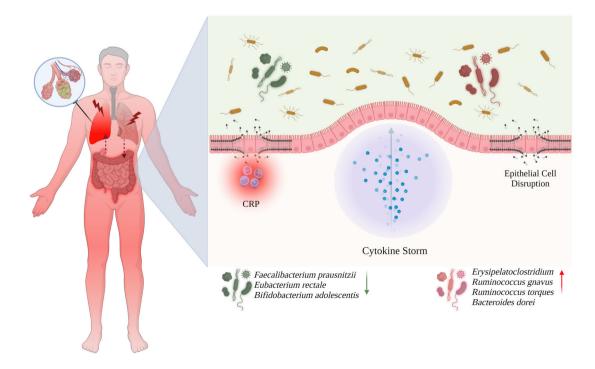


FIGURE 1 Lung-gut axis microbial dysbiosis in long SARS-CoV-2. CRP, C-reactive protein

EY-MEDICAL VIROLOGY

SARS-CoV-2 recovery, suppression of anti-inflammatory bacteria such as *Faecalibacterium prausnitzii*, *Eubacterium rectale*, and *Bifidobacterium adolescentis*, and enrichment of pathogens, including *Rothia*, *Erysipelatoclostridium*, *Ruminococcus gnavus*, *Ruminococcus torques*, and *Bacteroides dorei* have been observed.<sup>8,11</sup> These changes may underlie the association between lower gut microbiota diversity and higher C-reactive protein levels in long COVID-19 patients (Figure 1).

The substantial increase of pathogenic bacteria concomitantly with decreased anti-inflammatory microbiota, advocates for a prominent link between sustained intestinal inflammation during COVID-19 infection. Therefore, these alterations may subsequently lead to prolonged SARS-CoV-2 recovery, campaigning for the importance of a favorable gut microenvironment. Clinical trials experimenting with supplementation of anti-inflammatory bacterial species and/or fecal transplantation may be imperative to accelerate gut microbiota restoration and long COVID-19 rehabilitation.

#### AUTHOR CONTRIBUTIONS

Panagiotis Giannos made an investigation plan and drafted the manuscript. Konstantinos Prokopidis conceived the idea and revised the manuscript critically for important intellectual content.

### CONFLICTS OF INTEREST

The authors declare the absence of any commercial or financial relationships that could be construed as a potential conflicts of interest.

Panagiotis Giannos<sup>1</sup> 🝺

Konstantinos Prokopidis<sup>2</sup> (D)

<sup>1</sup>Department of Life Sciences, Faculty of Natural Sciences, Imperial College London, London, UK <sup>2</sup>Department of Musculoskeletal Biology, Institute of Life Course and

Medical Sciences,

University of Liverpool, Liverpool, UK

#### Correspondence

Konstantinos Prokopidis, Department of Musculoskeletal Biology, Institute of Life Course and Medical Sciences, University of Liverpool, Liverpool L7 3FA,UK. Email: k.prokopidis@liverpool.ac.uk

### ORCID

Panagiotis Giannos D http://orcid.org/0000-0003-1037-1983 Konstantinos Prokopidis D http://orcid.org/0000-0002-6264-9388

#### REFERENCES

- Xu R, Lu R, Zhang T, et al. Temporal association between human upper respiratory and gut bacterial microbiomes during the course of COVID-19 in adults. *Commun Biol.* 2021;4:1-11.
- Lloréns-Rico V, Gregory AC, Van Weyenbergh J, et al. Clinical practices underlie COVID-19 patient respiratory microbiome composition and its interactions with the host. *Nat Commun.* 2021;12:1-12.
- Hoque MN, Sarkar M, Rahman MS, et al. SARS-CoV-2 infection reduces human nasopharyngeal commensal microbiome with inclusion of pathobionts. *Sci Rep* 2021;11:24042.
- Wu Y, Cheng X, Jiang G, et al. Altered oral and gut microbiota and its association with SARS-CoV-2 viral load in COVID-19 patients during hospitalization. NPJ Biofilms Microbiomes. 2021;7:1-9.
- Zhong H, Wang Y, Shi Z, et al. Characterization of respiratory microbial dysbiosis in hospitalized COVID-19 patients. *Cell Discov*. 2021;7:1-14.
- Zuo T, Liu Q, Zhang F, et al. Depicting SARS-CoV-2 faecal viral activity in association with gut microbiota composition in patients with COVID-19. *Gut.* 2021;70:276-284.
- Biliński J, Winter K, Jasiński M, et al. Rapid resolution of COVID-19 after faecal microbiota transplantation. *Gut.* 2022;71: 230-232.
- Yeoh YK, Zuo T, Lui GCY, et al. Gut microbiota composition reflects disease severity and dysfunctional immune responses in patients with COVID-19. *Gut*. 2021;70:698-706.
- Zhang Q, Ran X, He Y, Ai Q, Shi Y. Acetate downregulates the activation of NLRP3 inflammasomes and attenuates lung injury in neonatal mice with bronchopulmonary dysplasia. *Front Pediatr.* 2021;8:985.
- 10. Chen Y, Gu S, Chen Y, et al. Six-month follow-up of gut microbiota richness in patients with COVID-19. *Gut*. 2022;71:222-225.
- 11. Tian Y, Sun KY, Meng TQ, et al. Gut microbiota may not be fully restored in recovered COVID-19 patients after 3-month recovery. *Front Nutr.* 2021;8:182.