

Perspective

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# Gut microbiota in COVID-19: key microbial changes, potential mechanisms and clinical applications

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## Supplementary information

### **Supplementary Box 1 | Search strategy and study selection criteria.**

We searched the PubMed, Web of Science, Google Scholar, Cochrane Library, MEDLINE, and Embase (between December 31, 2019 and August 28, 2022) by using the keywords 'COVID-19' or 'SARS-CoV-2' or 'Coronavirus' in combination with the terms 'gut microbiota' or 'microbiota' or 'microbes' or 'bacteria' or 'viruses' 'fungi' or 'probiotics' or 'prebiotics' or 'diet' or 'nutrition' 'gastrointestinal tract' or 'intestine' or 'gut' or 'faecal shedding' or 'ACE2' to identify relevant English-language publications. A total of 417 articles were selected, including 75 clinical studies, *in vitro* and *in vivo* studies, systematic reviews, and high-quality narrative reviews. Additionally, we searched [ClinicalTrials.gov](https://clinicaltrials.gov) for unpublished trials.

**Supplementary Table 1 | Clinical studies reporting gut microbiome composition in COVID-19.**

Supplementary Table 1 summarises selected human observational studies reporting gut microbiota composition of patients with acute and post-acute COVID-19. As of August 2022, a total of 46 human studies (38 acute COVID-19; 8 post-acute COVID-19) showed alterations of gut microbiota composition in patients with COVID-19 compared with uninfected controls. The region, sample size of study participants, sequencing method and results of alterations of gut microbiota composition in patients with COVID-19 compared with controls are presented. COVID-19, coronavirus disease 2019; ITS, internal transcribed spacer; PACS, post-acute COVID-19 syndrome; qPCR, quantitative PCR; rRNA, ribosomal RNA; MIS-C, multisystem inflammatory syndrome in children.

Studies	Region	Study participants	Disease phase	Sequencing method	Alterations in Gut Microbiota
Romani, et al. <sup>51</sup> (2022)	Rome, Italy	68 patients with COVID-19; 16 non-COVID-19 control; 4 patients with MIS-C; 95 healthy controls	Acute	16S rRNA gene sequencing	Enriched bacterial taxa in patients with COVID-19: <i>Faecalibacterium</i> , <i>Fusobacterium</i> , and <i>Neisseria</i> Enriched bacterial taxa in healthy controls: <i>Bifidobacterium</i> , <i>Blautia</i> , <i>Ruminococcus</i> , <i>Collinsella</i> , <i>Coprococcus</i> , <i>Eggerthella</i> , and <i>Akkermansia</i>
Mizutani, et al. <sup>52</sup> (2022)	Tokyo, Japan	22 patients with COVID-19(7 mild, 8 moderate, 1 severe); 40 healthy individuals as controls	Acute	16S rRNA gene sequencing	Enriched bacterial taxa in patients with COVID-19: <i>Bifidobacterium</i> , <i>Bacteroides</i> , <i>Parabacteroides</i> and <i>Escherichia-Shigella</i> Enriched bacterial taxa in controls: <i>Faecalibacterium</i> , <i>Subdoligranulum</i> , <i>Dorea</i> and <i>Enterobacter</i>
Rafiqul Islam, et al. <sup>53</sup> (2022)	Chattogram, Bangladesh	22 patients with COVID-19; 15 healthy controls	Acute	16S rRNA gene sequencing	Enriched bacterial taxa in patients with COVID-19: <i>Bacteroides</i> , <i>Escherichia-Shigella</i> , <i>Enterococcus</i> , <i>Bifidobacterium</i> , <i>Megamonas</i> , <i>Streptococcus</i> , <i>Rothia</i> , <i>Klebsiella</i> , and <i>Veillonella</i>
Schult, et al. <sup>54</sup> (2022)	Freiburg, Germany	108 patients with COVID-19; 22 post-COVID-19; 20 with pneumonia as controls; 26 asymptomatic individuals as controls	Acute	16S rRNA gene sequencing	The occurrence of individual complications was correlated with low-risk (e.g. <i>Faecalibacterium prausnitzii</i> ) and high-risk bacteria (e.g. <i>Parabacteroides</i> )
Sun, et al. <sup>55</sup> (2022)	Shanghai, China	63 patients with COVID-19 (39 mild, 24 severe); 8 healthy individuals as controls	Acute	Shotgun metagenomic sequencing	Positive correlation with COVID-19 severity: <i>Burkholderia contaminans</i> , <i>Bacteroides nordii</i> , <i>Bifidobacterium longum</i> , and <i>Blautia sp. CAG 257</i>
Britton, et al. <sup>56</sup> (2021)	New York, USA	44 patients with COVID-19; (6 mild, 22 moderate, 16 severe)	Acute	Shotgun metagenomic and 16S rRNA gene sequencing	Gut microbiome of patients with COVID-19 is unrelated to disease severity or gastrointestinal symptoms
Gaibani, et al. <sup>57</sup> (2021)	Bologna, Italy	69 patients as COVID-19; 69 healthy individuals as controls	Acute	16S rRNA gene sequencing	Enriched bacterial taxa in patients with COVID-19: <i>Lactobacillus</i> , <i>Collinsella</i> , <i>Staphylococcus</i> , <i>Akkermansia</i> , <i>Parabacteroides</i> , <i>Actinomyces</i> , <i>Serratia</i> , <i>Lactococcus</i> , <i>Phascolarctobacterium</i> , <i>ErysipelotrichaceaePSBM3</i> , <i>Odoribacter</i> , <i>Acidaminococcus</i> , <i>Methanobrevibacter</i>  Enriched Bacterial taxa in controls: <i>Prevotella</i> , <i>Bacteroides</i> , <i>Faecalibacterium</i> , <i>Coprococcus</i> , <i>Blautia</i> , <i>Ruminococcus</i> , <i>Erwinia</i> , <i>Roseburia</i> , <i>Oxalobacter</i> , <i>Clostridiaceae</i> , <i>Anaerofustis</i> , <i>Lachnospira</i> , <i>Scardovia</i> , <i>Anaerofilum</i> , <i>Dialister</i> , <i>Oscillospira</i> , <i>Holdemania</i> , <i>Cloacibacillus</i> , <i>Christensenella</i> ,  Reduced diversity in patients with COVID-19
Li, et al. <sup>58</sup> (2021)	Beijing, China Changsha, China	47 patients with COVID-19; (7 mild, 25 moderate, 12 severe)	Acute	Shotgun metagenomic sequencing	Enriched bacterial taxa in patients with COVID-19: <i>Bacteroides stercoris</i> , <i>Bacteroides vulgatus</i> , <i>Bacteroides massiliensis</i> , <i>Bifidobacterium longum</i> , <i>Streptococcus thermophilus</i> , <i>Lachnospiraceae bacterium 5163FAA</i> ,

		severe, 3 critical); 19 healthy individuals as controls			<p><i>Prevotella bivia</i>, <i>Erysipelotrichaceae</i> bacterium 6145, <i>Erysipelotrichaceae</i> bacterium 2244A</p> <p>Enriched bacterial taxa in controls: <i>Clostridium nexile</i>, <i>Streptococcus salivarius</i>, <i>Coprococcus catus</i> <i>Eubacterium hallii</i>, <i>Enterobacter aerogenes</i>, <i>Adlercreutzia equolifaciens</i></p> <p>Negative correlation with COVID-19 severity: <i>Roseburia inulinivorans</i>, <i>Bacteroides faecis</i>, <i>Megasphaera unclassified</i>, <i>Bifidobacterium bifidum</i>, <i>Parabacterioides goldsteinii</i>, <i>Lachnospiraceae</i> bacterium 9143BFAA</p> <p>Positive correlation with COVID-19 severity: <i>Paraprevotella unclassified</i>, <i>Streptococcus thermophilus</i>, <i>Clostridium ramosum</i>, <i>Bifidobacterium animalis</i></p>
Moreira-Rosário, et al. <sup>59</sup> (2021)	Lisbon, Portugal	115 patients with COVID-19; (19 mild, 37 moderate, 59 severe)	Acute	16S rRNA gene sequencing	Compared with patients with mild COVID-19, those with more severe disease had: lower <i>Firmicutes:Bacteroidetes</i> ratio; higher abundance of <i>Proteobacteria</i> ; and lower abundance <i>Roseburia</i> and <i>Lachnospira</i>
Newsome, et al. <sup>510</sup> (2021)	Mississippi, USA	50 patients with COVID-19; 9 individuals recovered from COVID-19; 24 healthy individuals as controls	Acute	16S rRNA gene sequencing	Enriched bacterial taxa in patients with COVID-19: <i>Peptoniphilus</i> , <i>Corynebacterium</i> and <i>Campylobacter</i>
					Enriched bacterial taxa in patients with SARS-CoV-2-positive stool: <i>Klebsiella</i> and <i>Agathobacter</i>
Reinold, et al. <sup>511</sup> (2021)	Essen, Germany	117 patients with COVID-19 (79 non-severe, 26 severe, 12 critical); 95 hospitalised individuals as controls	Acute	16S rRNA gene sequencing	Enriched bacterial taxa in patients with COVID-19: <i>Bacteroides</i> , <i>Enterobacteriaceae</i>
					Enriched bacterial taxa in controls: <i>Bifidobacterium</i> , <i>Streptococcus</i> , <i>Collinsella</i>
					Negative correlation with COVID-19 severity: <i>Faecalibacterium</i> and <i>Roseburia</i>
					Lower bacterial richness in COVID-19
Ren, et al. <sup>512</sup> (2021)	Central China and East China	36 patients with COVID-19; 70 healthy individuals as controls	Acute	16S rRNA gene sequencing	Enriched bacterial taxa in patients with COVID-19: lipopolysaccharide-producing bacteria
					Enriched bacterial taxa in controls: butyrate-producing bacteria
					Reduced diversity in patients with COVID-19
Wu, et al. <sup>513</sup> (2021)	Zhuhai, China	53 patients with COVID-19; 76 healthy individuals as controls	Acute	16S rRNA gene sequencing	Enriched bacterial taxa in patients with COVID-19: <i>Streptococcus</i> , <i>Weissella</i> , <i>Enterococcus</i> , <i>Rothia</i> , <i>Lactobacillus</i> , <i>Actinomyces</i> , <i>Granulicatella</i> , <i>Clostridium citroniae</i> , <i>Bifidobacterium longum</i> , and <i>Rothia mucilaginosa</i>
					Enriched bacterial taxa in controls: <i>Blautia</i> , <i>Coprococcus</i> and <i>Collinsella</i> , <i>Bacteroides caccae</i> , <i>Bacteroides coprophilus</i> , <i>Blautia obeum</i> and <i>Clostridium colinum</i>
Xu, et al. <sup>514</sup> (2021)	Shanghai, China	35 patients with COVID-19 (34 mild, 1 severe); 19 healthy individuals as	Acute	16S rRNA gene sequencing	Reduced diversity in patients with COVID-19

		controls; 10 patients with other diseases (non-COVID)			
Yeoh, et al. <sup>515</sup> (2021)	Hong Kong, China	100 patients with COVID-19 (47 mild, 45 moderate, 5 severe, 3 critical); 78 uninfected individuals as controls	Acute	Shotgun metagenomic sequencing	Enriched bacterial taxa in controls: <i>Faecalibacterium prausnitzii</i> , <i>Eubacterium rectale</i> and <i>Bifidobacteria</i>  Negative correlation with COVID-19 severity: <i>Faecalibacterium prausnitzii</i> and <i>Bifidobacterium bifidum</i>
Zhou, et al. <sup>516</sup> (2021)	Wuhan, China	187 patients with COVID-19 (187 moderate)	Acute	Shotgun metagenomic sequencing	Enriched bacterial taxa in patients with COVID-19 with fever: <i>Enterococcus faecalis</i> and <i>Saccharomyces cerevisiae</i>  Enriched bacterial taxa in patients with COVID-19 with non-fever: <i>Bacteroides fragilis</i> and <i>Eubacterium ramulus</i>
Al Bataineh, et al. <sup>517</sup> (2021)	Abu Dhabi, United Arab Emirates	86 patients with COVID-19; 57 healthy individuals as controls	Acute	16S rRNA gene sequencing	Enriched bacterial taxa in patients with COVID-19: <i>Blautia</i> , <i>Faecalibacterium</i> , and <i>Streptococcus</i> .  Enriched bacterial taxa in controls: <i>Intestinibacter</i> , <i>Enterorhabdus</i> , <i>Anaerostipes</i> , <i>Bifidobacterium</i> , <i>Bacteroides</i> , and <i>Prevotella</i> .
Babszky, et al. <sup>518</sup> (2021)	Budapest, Hungary	20 athletes with COVID-19 (3 mild, 15 moderate, 2 severe); 20 non-athletes with COVID-19 as controls (7 mild, 13 moderate)	Acute	16S rRNA gene sequencing	Statistically significant differences were not found in microbiota of trained and untrained individuals.
Gu, et al. <sup>519</sup> (2020)	Zhejiang, China	30 patients with COVID-19; 24 patients with H1N1; 30 healthy individuals as controls	Acute	16S rRNA gene sequencing	Enriched bacterial taxa in patients with COVID-19: <i>Streptococcus</i> , <i>Rothia</i> , <i>Veillonella</i> , <i>Erysipelatoclostridium</i> , <i>Actinomyces</i>  Enriched bacterial taxa in controls: <i>Romboutsia</i> , <i>Faecalibacterium</i> , <i>Fusicatenibacter</i> , <i>Eubacterium hallii</i> , <i>Agathobacter</i> , <i>Ruminococcus torques</i> , <i>Klebsiella</i> , <i>Dorea</i> , <i>Anaerostipes</i> , <i>Intestinibacter</i> , <i>Clostridium_sensu_stricto_1</i> , <i>Turicibacter</i> .  Reduced diversity in patients with COVID-19
Tang, et al. <sup>520</sup> (2020)	Hangzhou, China	57 patients with COVID-19 (20 general, 19 severe, 18 critical)	Acute	qPCR	Enriched bacterial taxa in patients with COVID-19 (critically ill): <i>Enterococcus</i> , <i>Enterobacteriaceae</i>  Enriched bacterial taxa in controls: <i>Faecalibacterium prausnitzii</i> , <i>Clostridium butyricum</i> , <i>Clostridium leptum</i> , and <i>Eubacterium rectale</i>
Tao, et al. <sup>521</sup> (2020)	Hefei, China	62 patients with COVID-19; 33 patients with seasonal flu; 40 healthy individuals as controls	Acute	16S rRNA gene sequencing	Enriched bacterial taxa in patients with COVID-19: <i>Escherichia</i> , <i>Streptococcus</i> , <i>Clostridium</i> , <i>Veillonella</i> , <i>Lactobacillus</i> , <i>Bifidobacterium</i> , <i>Scardovia</i> , <i>Helicobacter</i> , <i>Actinomyces</i> , <i>Moryella</i> , <i>Proteus</i> , <i>Rothia</i> , <i>Shuttleworthia</i> , <i>Enterococcus</i>  Enriched bacterial taxa in controls: <i>Bacteroidetes</i> , <i>Roseburia</i> , <i>Faecalibacterium</i> , <i>Coprococcus</i> , <i>Ruminococcus</i> , <i>Lachnospira</i> and <i>Parabacteroides</i>

Zuo, et al. <sup>522</sup> (2021)	Hong Kong, China	98 patients with COVID-19 (3 asymptomatic, 53 mild, 34 moderate, 5 severe, 3 critical); 78 healthy individuals as control	Acute	Shotgun metagenomic sequencing	Enriched viral taxa in patients with COVID-19: Environment-derived eukaryotic DNA viruses Enriched viral taxa in controls: Pepper mild mottle virus (RNA virus) and multiple bacteriophage lineages (DNA viruses)
Maeda, et al. <sup>523</sup> (2022)	Osaka, Japan	78 patients with COVID-19 (40 severe patients and 38 mild patients); 30 healthy individuals	Acute	ITS rRNA Sequencing	The prevalence of <i>Candida albicans</i> is higher in severe and mild groups than in healthy control group.
Lv, et al. <sup>524</sup> (2021).	Zhejiang, China	67 patients with COVID-19 (31 non-severe, 36 severe); 35 patients with H1N1; 48 healthy individuals as controls	Acute	ITS rRNA Sequencing	Enriched fungal taxa in controls: <i>Aspergillus</i> and <i>Penicillium</i> Higher fungal burden in patients with COVID-19
Zuo, et al. <sup>525</sup> (2020)	Hong Kong, China	30 patients with COVID-19 (1 asymptomatic, 12 mild, 10 moderate, 5 severe, 2 critical); 9 patients with pneumonia as controls; 30 healthy individuals as controls	Acute	Shotgun metagenomic sequencing	Enriched fungal taxa in patients with COVID-19: <i>Candia albicans</i> Highly heterogeneous mycobiome configuration in patients with COVID-19
Chen, et al. <sup>526</sup> (2022) Post-acute	China	30 patients with COVID-19; 30 uninfected individuals as controls; 6-month follow up	Post-acute	16S rRNA sequencing	Microbiota richness was not restored to normal levels after 6-month recovery. Post-convalescence patients with lower microbial richness had worse pulmonary functions.
Liu, et al. <sup>527</sup> (2022)	Hong Kong, China	106 patients with COVID-19; 68 uninfected individuals as controls; 6-month follow up	Post-acute	Shotgun metagenomic sequencing	Enriched in patients with PACS: <i>Ruminococcus gnavus</i> and <i>Bacteroides vulgatus</i>  Enriched in patients without PACS: <i>Faecalibacterium prausnitzii</i>
Vestad, et al. <sup>528</sup> (2022)	Norway	181 patients with COVID-19; 149 completed the 3-month follow-up	Post-acute	16S rRNA gene sequencing	Long-term respiratory dysfunction was associated with increased relative abundance of genus <i>Veillonella</i> , <i>Flavonifractor</i> and reduced relative abundance of <i>Erysipelotrichaceae</i> UCG-003 and several members of the Lachnospiraceae and Ruminococcaceae family
Cui, et al. <sup>529</sup> (2022)	Zhengzhou, China <sup>95</sup>	35 patients with COVID-19; 160 healthy controls; 1-year follow-up	Post-acute	16S rRNA gene sequencing	The microbial diversity, butyric acid-producing microbes and <i>Bifidobacterium</i> gradually increased, whereas lipopolysaccharide-producing microbes gradually decreased at 1-year follow-up, when compared with at discharge.
Su, et al. <sup>530</sup>	Hong Kong, China	155 patients with COVID-1; 155 patients with COVID-19 ; an average of 14-month (IQR 11–18 months) follow-up	Post-acute	Shotgun metagenomic sequencing	Enriched bacteria taxa in recovery patients: <i>Erysipelatoclostridium ramosum</i> and <i>Ruminococcus gnavus</i> ,  Enriched bacteria taxa in healthy controls: <i>Bifidobacterium adolescentis</i> and <i>Bifidobacterium pseudocatenuatum</i>

## Supplementary Table 2 | Clinical trials using gut microbiota modulation in COVID-19 management.

Table 2 provides an overview of clinical trials using gut microbiota modulation for COVID-19 management, in both acute COVID-19 and post-acute COVID-19 treatment. As of August 2022, a total of 34 studies have been registered on [ClinicalTrials.gov](https://clinicaltrials.gov) to evaluate the efficacy of oral probiotics and FMT in the treatment and prevention of COVID-19. COVID-19, coronavirus disease 2019; FMT, faecal microbiota transplantation.

<i>Acute COVID-19 and post-acute COVID-19 Treatment</i>				
<b>Trial identification</b>	<b>Location</b>	<b>n</b>	<b>Intervention</b>	<b>Study aim</b>
NCT04366089	Italy	152	Probiotics ( <i>Bifidobacterium lactis</i> DSM 32246 + <i>Bifidobacterium lactis</i> DSM 32247 + <i>Lactobacillus acidophilus</i> DSM 32241 + <i>Lactobacillus helveticus</i> DSM 32242 + <i>Lactobacillus paracasei</i> DSM 32243 + <i>Lactobacillus plantarum</i> DSM 32244 + <i>Lactobacillus brevis</i> DSM 27961 + <i>Streptococcus thermophilus</i> DSM322245) + Oxygen-ozone therapy + Azithromycin + Hydroxychloroquine	To evaluate the effects on early control of COVID-19 progression as an adjuvant and modulation of gut microbiota
NCT04390477	Spain	41	Probiotics	To evaluate the effects in hospitalised patients with COVID-19
NCT04420676	Austria	30	Probiotics ( <i>Bifidobacterium bifidum</i> W23 + <i>Bifidobacterium lactis</i> W18 + <i>Bifidobacterium longum</i> W51 + <i>Enterococcus faecium</i> W54 + <i>Lactobacillus acidophilus</i> W55 + <i>Lactobacillus acidophilus</i> W37 + <i>Lactobacillus salivarius</i> W24 + <i>Lactobacillus plantarum</i> W62 + <i>Lactobacillus paracasei</i> W72 + <i>Lactobacillus rhamnosus</i> W71) vs placebo	To evaluate the effects on gastrointestinal symptoms in COVID-19
NCT04507867	Mexico	80	Probiotics ( <i>Saccharomyces boulardii</i> CNCM I-745)	To evaluate the efficacy in reducing complications and co-morbidities in severe COVID-19
NCT04517422	Mexico	300	Probiotics ( <i>Lactobacillus plantarum</i> CECT30292 + <i>Lactobacillus plantarum</i> CECT 7484 + <i>Lactobacillus plantarum</i> CECT 7485 + <i>Pediococcus acidilactici</i> CECT 7483) vs placebo	To evaluate the effects and safety in adults with COVID-19
NCT04581018	Hong Kong, China	50	Synbiotics (SIM01)	To evaluate the efficacy in alleviating symptoms in hospitalised COVID-19 patients
NCT04621071	Canada	17	Probiotics vs placebo	To evaluate the efficacy in reducing duration and symptoms of COVID-19



NCT04666116	Spain	96	Probiotics ( <i>Bifidobacterium longum</i> + <i>Bifidobacterium animalis</i> subsp. <i>Lactis</i> + <i>Lactobacillus rhamnosus</i> ) + Vitamin D + Selenium + Zinc	To evaluate the change in viral load in patients with COVID-19
NCT04730284	Hong Kong, China	20	Synbiotics (SIM01)	To evaluate the efficacy in alleviating symptoms in COVID-19 outpatients
NCT04824222	Poland	366	FMT vs placebo	To evaluate the efficacy in reducing the risk of COVID-19 disease progression with escalating cytokine storm and inflammatory parameters
NCT04877704	UK	60	Probiotics ( <i>Enterococcus faecium</i> + <i>Lactobacillus acidophilus</i> + <i>Lactobacillus plantarum</i> + <i>Lactobacillus rhamnosus</i> ) vs placebo	To evaluate the effects on COVID-19 management as an adjuvant
NCT04907877	Ukraine	300	Probiotics ( <i>Bifidobacteria</i> + <i>Lactobacilli</i> ) vs placebo	To evaluate the effects in symptomatic adult outpatients with COVID-19
NCT04937556	Spain	60	Probiotics ( <i>Lactobacillus salivarius</i> ) + Vitamin D + Zinc vs placebo	To evaluate the effects in immune response in COVID-19
NCT04941703	USA	30	Probiotics + Magnesium citrate	To evaluate the effects on COVID-19 severity
NCT05043376	Pakistan	50	Probiotics ( <i>Streptococcus salivarius</i> K12)	To investigate the treatment benefits for non-ICU hospitalised patients with COVID-19
NCT05175833	Brazil	70	Probiotics ( <i>Streptococcus salivarius</i> K12 + <i>Lactobacillus brevis</i> CD2) vs placebo	To evaluate the effects on secondary bacterial pneumonia in severe COVID-19
NCT05474144	Czech Republic	83	Probiotics ( <i>Bifidobacterium animalis</i> BA77 + <i>Bifidobacterium bifidum</i> BB47 + <i>Bifidobacterium breve</i> BB8 + <i>Bifidobacterium infantis</i> BI211 + <i>Bifidobacterium lactis</i> BI516 + <i>Bifidobacterium lactis</i> BI-04 + <i>Bifidobacterium lactis</i> HN019 + <i>Bifidobacterium lactis</i> subsp. <i>Infantis</i> Bi-07 + <i>Bifidobacterium longum</i> BL88 ONLLY + <i>Lactobacillus acidophilus</i> LA 11 ONLLY + <i>Lactobacillus acidophilus</i> LA14 + <i>Lactobacillus acidophilus</i> NCFM + <i>Lactobacillus casei</i> LC18 + <i>Lactobacillus plantarum</i> LP ONLLY + <i>Lactobacillus reuteri</i> LE16 + <i>Lactobacillus rhamnosus</i> HN001 + <i>Lactobacillus rhamnosus</i> LGG + <i>Lactobacillus rhamnosus</i> LR22 + <i>Streptococcus thermophilus</i> ST6) vs placebo	To evaluate the effects in patients with severe COVID-19

NCT04813718	Austria	20	Probiotics ( <i>Lactobacillus delbrueckii</i> ssp. <i>Bulgaricus</i> LB2 (LMG P-21905) + <i>Lactobacillus rhamnosus</i> SP1 (DSM 21690) + <i>Lactobacillus reuteri</i> DSM 12246 + <i>Lactobacillus rhamnosus</i> CRL1505 (DSM 29673) + <i>Bifidobacterium animalis</i> ssp. <i>Lactis</i> DSM 15954) vs placebo	To evaluate the effects on post-acute COVID-19 syndrome
NCT04950803	Hong Kong, China	280	Synbiotics (SIM01) vs placebo	To evaluate the efficacy in alleviating symptoms of post-acute COVID-19 syndrome
NCT05080244	Canada	618	Probiotics vs placebo	To evaluate the efficacy in reducing occurrence of post-acute COVID-19 syndrome
NCT05227170	USA	80	Probiotics ( <i>Lactobacillus plantarum</i> 299v) vs placebo	To evaluate the effects on vascular function in patients with post-acute COVID-19 syndrome
<b>Prevention of COVID-19 and enhancement of vaccine response</b>				
<b>Trial Identification</b>	<b>Location</b>	<b>Number of Participants</b>	<b>Intervention</b>	<b>Study Aim</b>
NCT04366180	Spain	314	Probiotics vs placebo	To evaluate the effect on COVID-19 prevention in healthcare workers
NCT04399252	USA	182	Probiotics ( <i>Lactobacillus rhamnosus</i> GG) vs placebo	To evaluate the effects on the microbiome in household contacts exposed to COVID-19
NCT04462627	Belgium	500	Probiotics	To evaluate the effects on circulating levels of natural anti-A and anti-B antibodies in healthy individuals
NCT04734886	Sweden	161	Probiotics ( <i>Lactobacillus reuteri</i> DSM 17938) + vitamin D vs placebo + vitamin D	To evaluate the effects on antibody response upon and after COVID-19 in healthy adults
NCT04756466	Spain	201	Probiotics ( <i>Lactobacilli</i> ) vs placebo	To evaluate the effects on COVID-19 incidence in those aged over 60 years
NCT04847349	USA	54	Probiotics vs placebo	To evaluate the efficacy in boosting anti-SARS-CoV-2 immunity
NCT04884776	Hong Kong, China	484	Synbiotics (SIM01) vs placebo	To evaluate the efficacy in enhancing immunity and reducing hospitalisation in patients with diabetes and those

				aged over 65 years during COVID-19 pandemic
NCT04922918	Spain	25	Probiotics ( <i>Ligilactobacillus salivarius</i> MP101)	To evaluate the effects in elderly during COVID-19
NCT04979065	Indonesia	80	Probiotics + Vitamin D vs placebo	To evaluate the efficacy in reducing COVID-19 risk in obese people
NCT04798677	Spain	90	Probiotics ( <i>Saccharomyces cerevisiae</i> ) + Beta-glucan complex + Selenium + Zinc vs placebo	To evaluate the effects and tolerability in COVID-19 or flu vaccinees
NCT05195151	Canada	668	Probiotics vs placebo	To evaluate the efficacy in modulating COVID-19 vaccine response

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