Readme

Human gut microbiota and its metabolites were assessed in a healthy control group (n=11) (HC) unexposed to SARS-CoV-2 and an LCOVID group (n=11) in Hainan, China, using Shotgun metagenomics and liquid chromatography-mass spectrometry (LC-MS) of feces. The causal role of the microbiota in LCOVID was further validated by transplanting feces from the subjects into ABx mice using Histopathology and 16S rRNA sequencing. Fecal microbial diversity was lower in patients with LCOVID than that in HC. Pro-inflammatory bacteria such as Streptococcussalivarius and Streptococcusparasanguinis increased, whereas anti-inflammatory bacteria such as FaecalibacteriumSGB15346 and Alistipesonderdonkii decreased. Fecal metabolites from LCOVID were impaired in carbohydrate degradation, indole production, SCFA production, and fatty acid degradation. Transplantation of feces from patients with LCOVID into mice results in lung inflammation, intestinal inflammation, and anxiety. In addition, transplanted mice showed worse outcomes during Klebsiella pneumoniae infections. Transplanted mice and the key bacteria Streptococcussalivarius had the same worse outcomes in the D-IBS model by limb binding.