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Gut Microbial Dysbiosis and Correlation with Long COVID and ME/CFS among Patients in New York

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Research Question: Do alterations of gut microbiome in patients with Long COVID and ME/CFS suggest similar pathogenesis?

BACKGROUND

Patients of Long COVID have commonly shown symptoms similar to that of myalgic encephalomyelitis/ chronic fatigue syndrome (ME/CFS), a neurocognitive condition characterized by prolonged fatigue, cognitive dysfunction, and dysautonomia.[1,2] Gut microbial dysbiosis has also been observed among Long COVID patients, marked by decreased diversity and variations in species prevalence.[3]

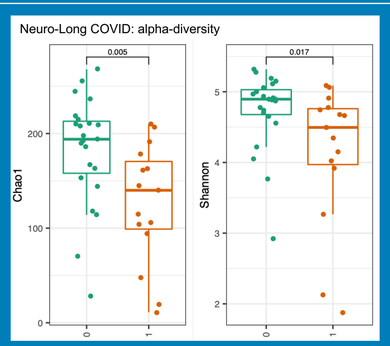
Overlapping symptoms of Long COVID and ME/CFS have suggested links in pathogenesis.[4] Notably, gut dysbiosis in ME/CFS patients has involved short-chain fatty acid producing species, specifically reduction in butyrate-producing microbes (*Faecalibacterium prausnitzii* and *Eubacterium rectale)* and propionate-producing microbes (*Akkermansia muciniphila)*.[5] Decrease in species prevalence with increased severity of ME/CFS has suggested microbial pathogenesis of ME/CFS[5] and has further proposed associations with Long COVID.

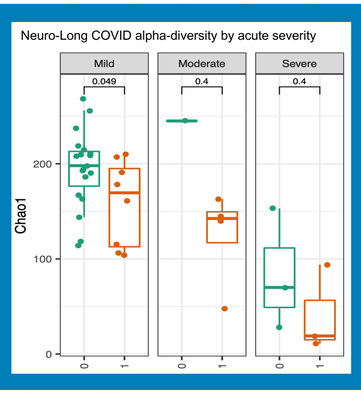
METHODS

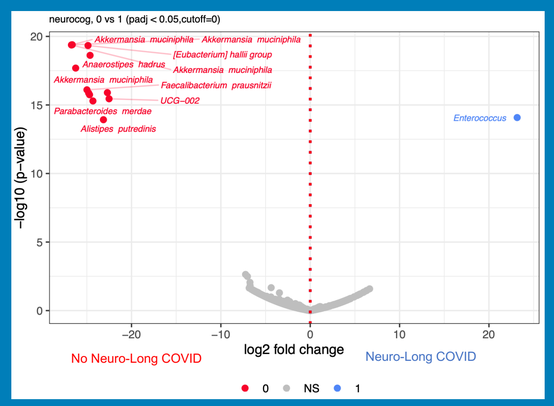
Participants were recruited under the CPIC study and microbiome testing was performed on the first 42 patients with available samples. Participant data were analyzed based on demographics, antibiotic use, acute COVID severity, and presence of self-reported neurocognitive symptoms. Patients classified under ”Neuro” had symptoms such as headache, peripheral neuropathy, sleeping difficulties chronic fatigue, brain fog, and dysautonomia.

Rectal swabs from patients diagnosed with Long COVID and different severities of acute symptoms were collected. Microbial DNA extraction was performed through Zymo MagBead DNA/RNA kit and was sequenced through Illumina MiSeq 16S.

RESULTS







RESULTS

Decreased alpha diversity (Chao1 and Shannon) was associated in participants with neurocognitive symptoms. As the severity of acute COVID symptoms increased from mild to severe, the alpha diversity of participants under “neuro” decreased further.

Multiple differing species abundance was seen through the volcano plot. In the assessment of differential abundance, short-chain fatty acid producing species were reduced. Butyrate-producing species (*F. prausnitzii* and *E. halii*) and propionate-producing species (*A. municiphilla*) were significantly reduced.

Patients with neurocognitive symptoms had decreased alpha diversity and reduced abundance of butyrate and propionate-producing species.

DISCUSSION

Decrease in short-chain fatty acid producing species suggests similar microbial pathogenesis of Long COVID and neurocognitive conditions, as deficiency in butyrate and propionate-producing species has been found to correlate with the symptoms of ME/CFS. Reduction of *F. prausnitzii*, *E. halii,* and *A. municiphilla* may indicate a species-level link with the ME/CFS symptoms frequently observed in patients with Long COVID. Bigger sample is needed for statistical power.

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