2017 Internship Project & Abstract - Calin Dumitrescu

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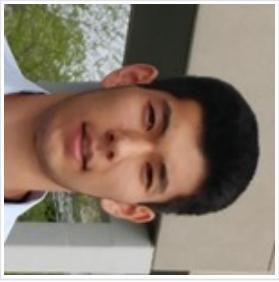
Investigation of Changes in Gut and Blood Microbiota After Maximal Exercise in Myalgic Encephalomyelitis/ Chronic Fatigue Syndrome



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Research area: Genetics

Background: Myalgic encephalomyelitis/chronic fatigue syndrome (ME/CFS) is a heterogeneous disease of unknown etiology characterized by persistent fatigue for at least six months, post-exertional malaise (PEM), sleeping disturbances, cognitive impairment, systemic inflammation, and both gastrointestinal (GI) and neurological disturbances. Due to the presence of GI disturbances in ME/CFS, a new interest has emerged in investigating whether the dysbiosis in the gut microbiota of ME/CFS patients is associated with the disease. This study aimed to identify the existence of dysbiosis in the gut microbiota and bacterial translocation into the blood after a maximal exercise test in ME/CFS.

Methods: Blood and stool samples were collected from 13 clinically characterized ME/CFS patients and 12 age and gender matched healthy controls at 0 min (pre-exercise), and 24 and 72 hours post-exercise (as well as 15 minutes post-exercise for blood). The microbiotas of the samples were determined by amplifying and sequencing the V4 hypervariable region of the 16S rRNA gene. Quantitative Insights Into Microbial Ecology, Linear discriminant analysis Effect Size and Phylogenetic Investigation of Communities by Reconstruction of Unobserved States were used to analyze the sequencing data.

Results: As expected, phylogenetic diversity, chao1 index, and observed operational taxonomic units were higher in stool, representing a higher overall alpha diversity. The mean phylogenetic diversity in the blood after maximal exercise was significantly different in ME/CFS patients than in controls, and this difference was not present at baseline. Principal Coordinate Analysis of weighted UniFrac distance matrices illustrated a slight difference in beta diversities between pre- and post-exercise blood groups among ME/CFS patients.

Conclusions: An altered gut and/or blood microbiome could be responsible for the PEM experienced by some ME/CFS patients. However, further studies with larger sample sizes are needed to demonstrate the role of the microbiome in the symptomatology of ME/CFS.