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## Title

Microbial Community Profiling of Peripheral Blood in Myalgic Encephalomyelitis/Chronic Fatigue Syndrome

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## Abstract

Myalgic encephalomyelitis/chronic fatigue syndrome (ME/CFS) is estimated to afflict hundreds of thousands, if not millions, of Americans with vastly more impacted individuals worldwide; however, the etiology of this disease has not been well established. Based on the features of ME/CFS, we hypothesized an unrecognized vascular infection may be involved. To evaluate this possibility, we performed a blinded pilot study of 30 ME/CFS patients meeting the Fukuda criteria and 48 normal controls. A community-wide analysis using next-generation DNA sequencing methods detected prokaryotic and eukaryotic populations in the peripheral blood of both ME/CFS patients and normal controls. Analysis of the prokaryotic portion of the samples revealed that organisms belonging to the *Pseudomonas asplenii* species, *Pseudomonadaceae* family, *Pseudomonadales* order, and  $\gamma$ -*proteobacteria* class are inversely correlated with RAND-36 scores, a quality of life metric that is reduced in ME/CFS patients. In addition, analysis of the detected eukaryotic species suggests that the *Perkinsus* genus is also inversely associated with RAND-36 scores. The most frequently observed eukaryotic DNA was for *Funneliformis*

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