Deciphering role of gut microbiome in the pathogenesis of multiple sclerosis: studies using 16S rRNA gene sequencing

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Human gut contains trillions of bacteria (microbiome), which play an important role in maintaining healthy state of the host. Alteration of gut microbiome can perturb this homeostasis leading to negative consequences that might result in intestinal and systemic disorders such as multiple sclerosis (MS). We employed 16S rRNA based metagenomic sequencing of fecal samples to investigate whether patients have gut microbial dysbiosis.

Our data indicate that patients with MS had decreased bacterial diversity and distinct microbial community profile compared to healthy controls. We are using animal model to test significance of gut bacteria negatively or positively associated with MS.

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