The Role of Gut Microbiome in Relapsing Multiple Sclerosis

Background: The etiology of multiple sclerosis (MS) remains unknown; however, both genetic and environmental factors play a role. Increasing evidence from experimental animal models has shown that alteration of the gut microbiota can modulate immune-mediated demyelination, suggesting a role of the microbiome in MS pathogenesis.

Objectives: To study the gut microbiome in patients with relapsing MS versus controls.

Methods: 42 stool samples were obtained from MS patients with relapsing-remitting (RRMS) and secondary progressive MS (SPMS) with relapses. 28 healthy donors (HD) provided control samples. Informed consent was obtained. Demographic and clinical data were obtained from medical record review. DNA was extracted from stool samples using PowerSoil DNA Isolation Kit (MO BIO). Shotgun Whole Genome Sequencing was used with the Illumina HiSeq platform to obtain DNA sequences, which were assembled and clustered to identify operational taxonomic units (OTUs). Samples were grouped according to disease status (MS, HD). Statistical analyses were performed with a pipe-line that included QIIME for comparing OTU representation at the species, genus and family level (Wilcoxon rank-sum test; statistical significance was taken at $p<0.05$), Python and R (The R Project for Statistical Computing).

Results: Ruminococcus torques, Ruminococcus obeum and Lachnospiraces bacterium showed a statistically significant higher abundance in the RRMS population with the strongest p-value ($p<0.01$) compared to HD. This was confirmed at the genus level. Escherichia coli and Oscillibacter showed the second strongest p-value ($p\leq0.02$) confirmed at the genus and family levels. Bacteroides fragilis and Roseburia were more abundant in HD compared to RRMS ($p<0.01$). Haemophilus parainfluenzae and Sutterella wadsworthensis were more present in HD at their species, genus and family levels ($p<0.05$).

Conclusions: There are statistically significant differences in the microbiome composition of MS patients versus HD. Larger studies are necessary to investigate the changes within the gut microbiome and MS, which may lead to potential disease activity biomarkers and therapies.