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ALTERATIONS IN GUT MICROBIOME COMPOSITION ARE ASSOCIATED WITH THE ONSET AND COURSE OF MULTIPLE SCLEROSIS: AN ITALIAN COHORT STUDY

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Authors: Rachele Rosso¹, Alessandro Maglione², Marinella Clerico¹, Simona Rolla¹; ¹University of Turin,

Department of Clinical and Biological Sciences, Orbassano, Italy, ²university of turin, Clinical and

biological sciences, Orbassano, Italy

Backgrounds and Aims

Which are the triggers that convert self-reactive lymphocytes into an autoaggressive phenotype facilitating the first episode of demyelization in multiple sclerosis (MS) are still poorly understood; actually alterations in the composition of the gut microbiota are suggested as contributors. Here, we investigated whether alteration in the composition of the gut microbiota, in terms of species richness, distribution and functional potential, could be associated with the onset of MS and its immune system alteration in an Italian cohort.

Methods

Stool and blood samples were collected from MS patients and Healthy Volunteers (HV) highly matched for age, sex, diet and lifestyle and prospectively followed up after therapy initiation. DNA isolated from stools were subjected to shotgun metagenomic sequencing strategy in order to correlate gut microbiome composition and functions with fecal metabolites, analyzed with Gas chromatography—mass spectrometry, and with Th17 and Treg cells, analyzed by FACS, in the peripheral blood (PB).

Results

At the onset of MS, gut microbiome structure of patients was clearly different from that of HV and displayed a lower species richness and lower number of taxa: a reduction in abundance of genera belonging to Butyrate-producing bacteria correlated with a lower butyrate amount in the feces and with the decrease of Treg cells producing IL-10 and in the PB of MS patients compared to HV.

Conclusions

Our data indicate that gut microbial dysbiosis exist at the onset of MS and could be associated with the autoimmune response in the periphery, highlighting the importance of gut microbiome in the etiology of MS.

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