P51 – **Gut microbiome and immune system alteration at the onset of Multiple Sclerosis: a pilot study**

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Background: Which are the triggers that convert self-reactive lymphocytes, normal components of the immune repertoire, into an autoaggressive phenotype facilitating the first episode of demyelization in multiple sclerosis (MS) are still poorly understood. Alterations in the composition of the gut microbiota are now suggested as having a role in the etiology, course and treatment of MS through gut-brain communications that likely involve the immune system.

Objective: 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, namely the first episode of demyelinization, and its immune system alteration in a small Italian cohort.

Methodology: Stool and blood samples were collected from 18 MS patients and 18 Healthy Volunteers (HV) highly matched for age, sex, diet and lifestyle. DNA isolated from stools were subjected to shotgun metagenomic sequencing strategy in order to discover the microbiota composition as well as the microbial function and to correlate it 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 is clearly different from that of HV and displayed a lower species richness and lower number of taxa. It was characterized by a reduction in abundance of genera belonging to short chain fatty acids (SCFA)-producing bacteria that correlated with a lower SCFA 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 / Implications for practice: 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. The identification of the microbial populations and of their functional role within the microbiome will help clinicians to design strategies to modulate the autoimmune response through alteration of gut microbiome.