P12 & FP - **Metagenomic analysis of gut microbiota in Myasthenia Gravis and Multiple Sclerosis patients**

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Background: Growing evidences support the role of gut microbiota in immune-mediated diseases, by influencing the immune system activation and controlling the pro- and anti-inflammatory balance. These aspects may play a role in autoimmune diseases, where predisposing genetic factors and environmental components could trigger pathogenic mechanisms, and an altered microbiota could contribute to disease progression (1). Data coming from animal models of autoimmune diseases and from patients demonstrated an alteration of intestinal microbial composition (2).

Objective: Aim of the present study was the characterization of the gut microbiota composition in myasthenia gravis (MG) and multiple sclerosis (MS) patients and in and healthy donors - HD.

Methodology: The study was done on 49 MG, 31 MS patients, and 14 HD subjects, on voluntary bases. Bacterial DNA was isolated by combining classical lysis method and mechanical dissociation. To evaluate gut eubiosis, the ratio of Firmicutes and Bacteroidetes phyla was calculated by real-time qPCR. Metagenomic analysis was performed in 20 MG, 22 MS and in 7 HD subjects on hypervariable regions of bacterial 16S rRNA with the Ion Torrent PGM System platform.

Results: Firmicutes/Bacteroidetes ratio > 60, indicative of dysbiosis, was observed in 11/49 (22.4%) MG, in 5/31 (16.1%) MS patients, and in 4/14 (28.6%) HD subjects, without statistical significance (chi-square 0.97, p ns). 16S rRNA was performed; taxonomic analysis at the phylum level showed a decrease of Firmicutes proportion (MG 52.7%; MS 58.5%) compared with HD (72.6%; $p<0.01$) and increase of Bacteroidetes proportion (MG 29.3%; MS 26.5%) compared with HD (9.1%; $p<0.01$). Moreover, Actinobacteria slightly decreased in MG patients (3.5%) compared to healthy subjects (14.4%).

Conclusions: Our study shows differences in bacterial components of the gut microbiota in MG and MS patients compared with HD. Modifications of relative abundancies among microbiota may underly dysregulatory mechanisms affecting immune-inflammatory pathways that deserve further investigations. These studies may allow the identification of bacterial strains with immunoregulatory profile that could be tested in preclinical research.

References

1) de Oliveira GLV, et al. Immunology 2017; 152:1-12.

2) Rinaldi E, et al. Ann N Y Acad Sci. 2018. 1413(1):49-58