Poster

Study of technical validation of molecular biomarkers for the development of a diagnostic tool for Fibromyalgia.

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ABSTRACT

Fibromyalgia (FM) is a disease characterized by widespread pain and both physical and psychological symptoms. These influence the normal course of daily life on a personal and professional level, generating a considerable deterioration in the quality of life of patients. The prevalence of FM is estimated to be between 2% and 8% of the world population, with women being the most affected. A large proportion of patients with FM are currently not properly diagnosed and face sub-optimal treatment, whose efficacy is variable among patients. While the molecular pathomechanism of FM remains unclear, several factors that could be behind its pathogenesis have been suggested in recent years, including oxidative stress, inflammation, mitochondrial dysfunction and disturbances in the gut microbiome. Therefore, the aim of this study is to validate the use of various biomarkers for the molecular diagnosis of FM through the determination of mitochondrial metabolism balance, total antioxidant capacity and the presence of intestinal dysbiosis in patients with FM in order to develop a diagnostic tool.

Methods: Peripheral blood and fecal samples were collected from patients diagnosed with FM and healthy controls. An isolation of peripheral blood mononuclear cells (PBMCs) and protein extraction was performed to measure the levels of certain proteins described to be altered in FM patients by Western blot. The plasma serum has also been isolated to evaluate several biomarkers that are related to intestinal permeability status. In addition, we have isolated the DNA from fecal samples for its subsequent sequencing. We are currently in the process of validating the total antioxidant capacity by spectrophotometry and intestinal dysbiosis by enzymeimmunoassay.

Results: We have observed significative differences in the expression levels of VDAC and LC3B, which are proteins involved in autophagy and mitochondrial mass.

Conclusions: The results obtained so far confirm the validity of using molecular biomarkers related to mitochondrial metabolism balance levels to differentiate between FM patients and healthy people. Further studies will be performed to verify these results by a proteomic approach and sequencing of FM patients for the determination of the proteome and intestinal dysbiosis. A complete characterization of these biomarkers will contribute for a more accurate diagnosis of the disease, leading to a better course and allowing the monitorization of the treatment outcome.

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