TRANSCRIPTIONAL ANALYSIS OF T CELL REGULATORY CYTOKINES IN MULTIPLE SCLEROSIS PATIENTS

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Introduction: Multiple Sclerosis (MS) is considered a classical T cell–mediated autoimmune disease with a complex genetic background. The characterization of the relationship between MS and cytokines associated with T lymphocyte differentiation should provide a better understanding of the mechanisms that generate and sustain the pathogenic immune responses in this disease. Here we analyzed the transcriptional profile of cytokines involved in T cells regulatory mechanisms in MS patients and healthy donors.
Methods: IL-12p35, IL-12/23p40, IL-23p19, IL-17, IL-22, IL-10, IL-4 and INF-gamma expressions have been evaluated by Real Time PCR (RT-PCR) in peripheral blood mononuclear cells (PBMC) from clinically definite relapsing-remitting MS (RR-MS) patients, with a Kurtzke's EDSS score ≤5.5 and from healthy donors, matched for gender and age. All the real time data were analyzed with Biogazelle qbasePLUS software.
Results and conclusions: RT-PCR analysis showed that in RR-MS patients INF-gamma, IL-17, IL-12/23p40, IL-23p19 and IL-22 transcripts were increased, while IL-10 was reduced and IL-12p35 unchanged in comparison to healthy individuals. Overall, our results highlight the complex cytokines network involved in the demyelinization process and suggest that the cytokine profile as well as individual cytokine alterations might be useful as markers both at the time of diagnosis and for MS patients' management.