Potential of TH cell profiling in personalized multiple sclerosis treatment planning.

The increasing lifespan of people in developed countries makes neurodegenerative diseases, in addition to cardiological and oncological diseases, a serious challenge for medical science. Multiple Sclerosis (MS), a chronic demyelinating disease, is the most common neurological disorder of young people and reduces the ability to work and activity. Although the mechanisms underlying MS etiology have been partly recognized and there are several options for treatment, the unpredictability of MS due to individual variation remains a challenge and the pathogenesis of MS remains elusive.
In some cases of relapsing-remitting multiple sclerosis (RRMS) treatment does not produce the desired improvement which causes patients to discontinue treatment. It is necessary to develop new treatment strategies, which is a long-term process, therefore there is a need to develop a new approach to the currently used treatment with immunomodulatory drugs (IMDs). For this reason, research on the patients treated with approved disease modifying treatments and clinical response, can indicate immune mechanisms in MS pathogenesis and identify immune targets.

Our previous multidisciplinary study indicated four major molecular phenotypes of T cells in RRMS that determine the response to in vitro stimulation. Based on these results and progress made in understanding the molecular basis of the pathogenesis of multiple sclerosis, we propose a continuation of this research with the use of single-cell RNA sequencing (scRNA-seq) technology to identify the molecular phenotype of T cells that determine the response to the currently used IMDs. scRNA-seq is the most advanced technique and the best way to identify previously detected and undetected expressed genes. It is the most comprehensive transcript typing procedure available.

Results of the project will improve our understanding of TH cell heterogenity in RRMS and allow the development of an algorithm to model the response to currently used immunomodulatory drugs. The identification of biomarkers which determine the response to the therapy is of great importance, because it opens the possibility of new therapeutic targets and helps to identify non-responding patients who need personalized therapy.