Identification of low level proteins through proteomic approaches in the CSF and serum samples of clinically different multiple sclerosis subtypes

Timucin Avsar1, Melih Tütüncü2, N. Onat Demirci2, Sabahattin Saip1, Aksel Siva1 and Eda Tahir Turanlı1

1Dr. Orhan Öcalgiray Molecular Biology-Biotechnology and Genetics Research Center, Istanbul Technical University, Turkey
2Department of Neurology, Cerrahpasa School of Medicine, Istanbul University, Turkey

Complex pathogenesis and different prognosis of MS requires reliable biomarkers in order to help both in diagnosis and prognosis of disease. The aim of this study is to identify new biomarkers in the CSF and serum pool samples of clinically different MS subtypes. To this aim, randomly selected each of 11 CIS, RRMS, PPMS and control samples were used to mix pool samples. For both serum and CSF pools same patients were used. For CSF protein mix 500µg protein of each samples, and for serum samples 1000µg protein of each samples were used. 2D-PAGE analysis were done by using pool samples. Clinically different MS-subtypes and control samples were compared. Following the 2D-PAGE analysis, at least 4 times differently expressed protein spots were selected and removed from the gel for mass spectrometry analysis (MALDI-TOF-MS). 192 of 179 spots were analyzed with MALDI-TOF-MS. 179 spots indicated 73 different proteins. When RRMS-control samples were compared 46 spots indicated 30 different proteins were identified, CIS-control groups were compared 46 spots indicating 27 different proteins and PPMS-control group were compared 58 spots indicating 30 proteins and RRMS-CIS subgroups were compared 29 spots indicating 20 different proteins were identified. Proteomic investigation in CSF and serum samples of clinically different MS patients and controls revealed that, there are number of proteins belonging to albumin, immunoglobulin, interferons, kinases, ligases lipoproteins, MAP, serpin, SSP, transferrin and transmembrane protein families differs between the different MS subtypes and control groups. These proteins are identified and listed (List-1).

Biography

Timucin Avsar is a Ph.D candidate at the age of 28 years from Istanbul Technical University Molecular Biology and Genetics Department. He has published 3 papers in reputed journals related to his research are about proteomics of neurodegenerative diseases.