Diagnosis and Prognosis of Multiple Sclerosis by Gene Expression Analysis

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<th>Diagnostics, Biomarkers, Neurology, Autoimmunity, DNA microarrays</th>
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<td>Tested in over 100 clinical specimens</td>
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<td>Market</td>
<td>With over 2.5 million patients worldwide, the MS global market surpassed the 9 billion U$, having grown over 15% in the last 5 years.</td>
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Background

Multiple sclerosis (MS) is the most common central nervous system disease affecting young adults. Four subtypes of the disease have been described: Relapsing remitting (RRMS), primary progressive (PPMS), secondary progressive (SPMS), and progressive relapsing (PRMS). Further classifications include: Definite MS, which is diagnosed only after the occurrence of a second neurological relapse; probable MS, which is diagnosed to patients between relapses in the first year; and Benign MS (BMS), a preferable clinical variant of RRMS in which the patient remains fully functional in all neurologic systems years after disease onset.

MS sub-classifications are important for prognosis as well as for therapeutic decisions. However, MS prognosis is difficult to predict; depending on the subtype of the disease, the individual patient's disease characteristics, the initial symptoms and the degree of disability the person experiences as time advances. To date, there are no biological molecular markers to follow the progression of the disease and its responsiveness to treatment.

The Invention

An extensive research brought innovative molecular methods allowing diagnosis, disease assessment and prognosis, prediction outcome in relapsing–remitting multiple sclerosis, definite MS determination, and drug personalization. The diagnosis is based on classification by gene expression pattern analysis of readily-available peripheral blood cells.

Characteristic groups of genes were identified that allow accurate assessment of different aspects of the pathology.
Development Stage

Several sets of unique expressed genes were identified and correlated with MS diagnosis, disease assessment and prognosis, prediction outcome in relapsing–remitting multiple sclerosis and drug personalization. Several studies and validation analyses were performed in over 100 clinical specimens, reaching over 80% classification accuracy. Differentially regulated genes may serve as novel drug development targets, as well as for drug discovery platforms.

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