INVESTIGATION OF SEVEN INTERLEUKIN POLYMORPHISMS IN MULTIPLE SCLEROSIS

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BACKGROUND: Following the disruption of the blood-brain barrier, cell adhesion molecules, cytokines and interleukins play important role in the migration of the white blood cells into the central nervous system, but the exact mechanisms are still to be revealed. Therefore, different interleukin (IL) polymorphisms have been investigated in the pathomechanism of multiple sclerosis (MS) however; the impact of the different single nucleotide polymorphisms (SNPs) on the age at onset or the first attack interval is poorly investigated.
OBJECTIVE: To investigate the potential roles of SNPs of interleukin genes in MS.
METHODS: We involved 578 MS patients and 540 age- and gender-matched healthy controls to investigate the possible effects of different SNPs of interleukin genes. Fluorescently labeled Taqman probes were used for allele discrimination.
SPSS software version 20 was utilized for statistical analysis.
RESULTS: The IL2RA SNP was statistically associated with MS (p=0.019). The C allele of the SNP was more common in the patient group (p=0.005, odds ratio: 1.404 CC+CT vs TT) and the observed genotype frequencies were in accordance with the Hardy-Weinberg equilibrium in both groups. None of the investigated IL SNP had impact on the age at onset, but one of the SNP of the IL7 gene had impact on the first attack interval (p=0.023).
CONCLUSIONS: The IL2RA SNP showed association with MS, with the C allele showing risk affect.
This is the first study in which the impact of the different alleles on the first attack interval and the age of onset were studied together in MS.