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Relationship between mir‑155 and mir‑146a polymorphisms and susceptibility to multiple sclerosis in an Egyptian cohort

By
MARWA A. ALI[1], OLFAT G. SHAKER[2], HANAA M. EID[3], E. E. MAHMOUD[4], EMAN M. EZZAT[5] and **SYLVANA N. GABER[3]**

1Department of Medical Biochemistry and Molecular Biology, Faculty of Medicine, Fayoum University, Fayoum 2Department of Medical Biochemistry and Molecular Biology, Faculty of Medicine, Cairo University, Cairo; 3Department of Medical Microbiology and Immunology; Faculty of Medicine, Fayoum University, Fayoum
4Department of Clinical and Chemical Pathology; Faculty of Medicine, Fayoum University, Fayoum
5Department of Internal Medicine, Faculty of Medicine, Fayoum University, Fayoum, Egypt

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Abstract

Multiple sclerosis (MS) is an autoimmune disorder of the central nervous system. It was previously demonstrated that miR‑155 and miR‑146a served a vital role in the pathophysiology of MS, and single nucleotide polymorphisms in miR‑155 and miR‑146a were found to be associated with the susceptibility to different autoimmune diseases, such as systemic lupus erythematosus, rheumatoid arthritis and type I diabetes. The aim of the present study was to analyze the association between susceptibility to MS and two genetic polymorphisms (miR‑155 rs767649 A>T and miR‑146a rs57095329 A>G) in a cohort of Egyptian patients. The presence of the two polymorphisms were analyzed in 114 patients with MS and 152 healthy controls using quantitative PCR. The present study demonstrated for the first time that: The TT genotype and T allele in miR‑155 (rs767649 A>T) polymorphism were associated with an increased risk of MS; the miR‑146a (rs57095329 A>G) mutated G allele conferred protection against the development of MS in all genetic models; miR‑155 rs767649 A>T was a risk associated polymorphism of MS in females, but not in males; and miR‑155 rs767649 AT/TT and miR‑146a rs57095329 GG genotypes showed significantly higher distributions among patients with higher Expanded Disability Status Scale scores and secondary progressive MS subgroups. Therefore, miR‑155 rs767649 polymorphism may confer susceptibility to MS, whereas miR‑146a rs57095329 may be protective against MS in an Egyptian cohort.