Sequence similarity between HLA subtypes of Iranian multiple sclerosis

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Back ground: Multiple sclerosis¬(MS) is a chronic inflammatory demyelinating disease of central nervous system(CNS),with unknown etiology in both environmental factors and genetic susceptibility. Recent studies have indicated an association between multiple sclerosis and human leukocyte antigen¬(HLA) in a variety of ethnic groups. Nowadays, there is an increasing interest on exploring of interactions between HLA genes and other genes and environmental risk factors such as viruses and bacterial. Therefore the aim of this study is identification of possible relation between HLA subtypes in MS patient and viral and bacterial peptides. The out come of this research may a possible indicate association a background infection with the incidence of MS.

Materials and methods: Peptide similarity investigation with online software BLAST in NCBI website and then to verify this structural similarity of these peptides by matching method with Gromacs tools.

Results: In this study by employing bioinformatics tools , we have identified a similarity between HLA-A3,HLA-A24,HLA-DQA1*0102 with viral and bacterial peptides. HLAA3 and A24 have 86% identity by [hypothetical protein HMPREF946906078 partial[Clostridiumcitroniae]] and 89%identity with [hypothetical protein GS1911515[Acinetobacter sp.MII]] and HLA-DQA1*0102 has 72% identity with [antigen IA alpha Murid herpes virus]].

Discussion: Our bioinformatics data suggest that there is a possible relationship between gen-environment (specific HLA Loci and viral and bacterial peptides¬)¬with MS.

Key words: Multiple sclerosis,HLA-A3, HLA-A24, HLA DQA1*0102