P014

Genetics of MS in Saudi Arabia

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Pathogenesis of multiple sclerosis (MS) is poorly under- stood, evidence suggests that genetic and environmental factors may play substantial roles in disease development. The role of genetics is evident by many reports showing familial aggregation of the disease, high concordance rate among twins, association with MHC and the increased risk among relatives of MS patients. Genome-wide association studies (GWAS) showed an association between subset of single- nucleotide polymorphism (SNPs) and multiple sclerosis.

The Saudi community is a very young population where 54% are below the age of 18 years. It is characterized by large family size and prevalent consanguineous marriages. The incidence and prevalence of multiple sclerosis have been increasing in the last few years regionally in Saudi Arabia and it is expected from demographics point view to further increase. In our local registry we have found that 21% of our patients reported having at least one relative affected. It is not clear if parental consanguinity has any role in non-genetic diseases, especially those with an expected genetic predis- position such as MS.

We have reported that parental consanguinity might be a risk factor for familial multiple sclerosis. WE have studied and reported the common association of single-nucleotide poly- morphism (SNPs) and multiple sclerosis by Genome-wide association studies (GWAS). We found that SNPs rs6498169 and 10984447 are the two most significant multiple sclerosis linked SNP in our Saudi MS population outside the MHC region. Our results suggest that it is possible to use a more homogenous genetic pool to identify the most significant MS-linked SNPs in the Saudi population, even with a very small sample size. Our finding is in agreement with many other studies that used much larger sample sizes and were performed in many ethnic groups. These data has encouraged us to further study the genetic basis of MS in the Saudi MS patients. Our ongoing investigations included using whole genome, high-resolution array compara- tive genomic hybridization (array CGH) of variations in genomic dosage compared to the normal reference dosage within FMS cases as well as Hall exon sequencing and studying the MHC region by junior sequencing of the HAL region. We will present the initial data from two large families.