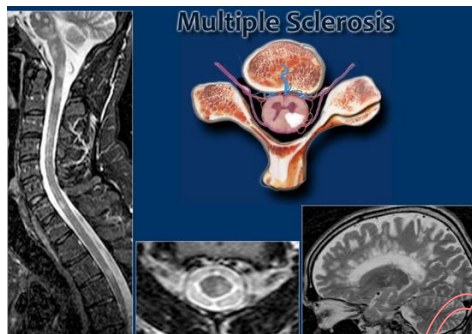# Genetic Science Spotlight

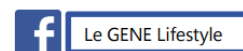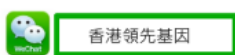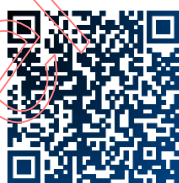## Updated Review of Multiple Sclerosis Genetics – UCSF

Multiple sclerosis (MS) is the most common chronic neurological disease which affects more than 2.3 million people worldwide, predominantly young people between the ages of 30 and 40 years old. MS is a complex disease with multiple causes, which are largely unclear to researchers. However, a series of genomic studies have confirmed the central role of genetic risk factors in MS susceptibility. The two best known genetic factors are HLA-DRB1 and IL7R, both are involved in the human immune system and alterations of which can lead to autoimmune responses that damage the myelin sheath and nerve cells and lead to the signs and symptoms of MS. With the advancement of technology in whole genome sequencing (WGS), over 50 MS risk loci with MS significance have been identified. Furthermore, copy number variations (CNV) studies, expression studies and post-transcriptional studies have also shed light on the pathogenesis of the disease. Taking into account the complexity of MS, a gene panel for sequencing related risk loci as well as microarrays for CNV and other epigenetic factors, and even a WGS for patients and families may worth considering and be crucial in clarifying the picture. Contact LeGENE professionals for WGS/Microarray tests.

https://www.ncbi.nlm.nih.gov/pubmed/22725956

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3760455/

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