No evidence for shared genetic basis of common variants in multiple sclerosis and amyotrophic lateral sclerosis.

Abstract:
Genome-wide association studies have been successful in identifying common variants that influence the susceptibility to complex diseases. From these studies, it has emerged that there is substantial overlap in susceptibility loci between diseases. In line with those findings, we hypothesized that shared genetic pathways may exist between multiple sclerosis (MS) and amyotrophic lateral sclerosis (ALS). While both diseases may have inflammatory and neurodegenerative features, epidemiological studies have indicated an increased co-occurrence within individuals and families. To this purpose, we combined genome-wide data from 4088 MS patients, 3762 ALS patients and 12 030 healthy control individuals in whom 5 440 446 single-nucleotide polymorphisms (SNPs) were successfully genotyped or imputed. We tested these SNPs for the excess association shared between MS and ALS and also explored whether polygenic models of SNPs below genome-wide significance could explain some of the observed trait variance between diseases. Genome-wide association meta-analysis of SNPs as well as polygenic analyses fails to provide evidence in favor of an overlap in genetic susceptibility between MS and ALS. Hence, our findings do not support a shared genetic background of common risk variants in MS and ALS.