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Titel des Beitrags:
Successful Replication of GWAS Hits for Multiple Sclerosis in 10,000 Germans Using the Exome Array.

Abstract:
Genome-wide association studies (GWAS) successfully identified various chromosomal regions to be associated with multiple sclerosis (MS). The primary aim of this study was to replicate reported associations from GWAS using an exome array in a large German study. German MS cases (n = 4,476) and German controls (n = 5,714) were genotyped using the Illumina HumanExome v1-Chip. Genotype calling was performed with the Illumina Genome Studio(TM) Genotyping Module,
followed by zCall. Single-nucleotide polymorphisms (SNPs) in seven regions outside the human leukocyte antigen (HLA) region showed genome-wide significant associations with MS (P values< $5 \times 10^{-8}$). These associations have been reported previously. In addition, SNPs in three previously reported regions outside the HLA region yielded P values< $10^{-5}$. The effect of nine SNPs in the HLA region remained (P< $10^{-5}$) after adjustment for other significant SNPs in the HLA region. All of these findings have been reported before or are driven by known risk loci. In summary, findings from previous GWAS for MS could be successfully replicated. We conclude that the regions identified in previous GWAS are also associated in the German population. This reassures the need for detailed investigations of the functional mechanisms underlying the replicated associations.