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Migraine without aura: genome-wide association analysis identifies several novel susceptibility

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Introduction

Genome-wide association studies (GWAS) are a novel and promising method to study genetic susceptibility factors for common disorders, including migraine.

Objective

Here we performed the first GWAS in migraine without aura (MO), which is the most common form of migraine.

Methods

To identify common genetic variants for this migraine type, we analyzed genome-wide association data of 2,326 clinic-based German and Dutch patients and 4,580 population-matched controls. Loci with two or more SNPs with P-values < 1 x 10-5 were selected for follow-up in 2,508 Dutch, Spanish, Finnish and Norwegian patients and 2,652 controls.

Results

Meta-analysis of the discovery and replication data yielded four genome-wide significant (P < 5 x 10-8) MO susceptibility loci in or nearby MEF2D, PHACTR1, ASTN2 and TGFBR2. In addition, SNPs in two loci (in or near TRPM8 and LRP1) that were previously identified in a GWAS on population-based migraine were significantly replicated in our clinic-based MO cohort.

Conclusion

This study reveals the first susceptibility loci for migraine without aura, thereby expanding our knowledge of this debilitating neurological disorder.

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