

POSTER PRESENTATION

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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<sup>-5</sup> 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<sup>-8</sup>) 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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