The Journal of Headache and Pain
a SpringerOpen Journal

POSTER PRESENTATION Open Access

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

Boukje de Vries[1*†], Tobias Freilinger[2,3†], Verneri Anttila[4,5†], Rainer Malik[1], Mikko Kallela[6], Gisela M Terwindt[7], Patricia Pozo-Rosich[8,9], Bendik Winsvold[10,4], Dale R Nyholt[11], Willebrordus PJ van Oosterhout[7], Ville Artto[6], Unda Todt[12], Eija Hämäläinen[4,5], Jèssica Fernández-Morales[4,9], Mark A Louter[7,13], Mari A Kaunisto[5,14], Jean Schoenen[15], Olli Raitakari[16], Terho Lehtimäki[17], Marta Vila-Pueyo[18], Hartmut Göbel[19], Erich Wichmann[20], Cèlia Sintas[21,22], Andre G Uitterlinden[23], Albert Hofman[24], Fernando Rivadeneira[23,24], Axel Heinze[19], Erling Tronvik[25], Cornelia M van Duijn[24], Jaakko Kaprio[5,26,27], Bru Cormand[21,22,28], Maija Wessman[5,14], Rune R Frants[1], Thomas Meitinger[29,30], Bertram Müller-Myhsok[31], John-Anker Zwart[10], Markus Färkkilä[6], Alfons Macaya[18], Michel D Ferrari[7], Christian Kubisch[12], Aarno Palotie[4,5,32,33,34†], Martin Dichgans[2†], Arn MJM van den Maagdenberg[1,7†], International Headache Genetics Consortium[1]

From The European Headache and Migraine Trust International Congress
London, UK. 20-23 September 2012

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.

† Contributed equally
[1]Department of Human Genetics, Leiden University Medical Centre, Leiden, The Netherlands
Full list of author information is available at the end of the article

Author details
[1]Department of Human Genetics, Leiden University Medical Centre, Leiden, The Netherlands. [2]Institute for Stroke and Dementia Research, Klinikum der Universität München, Munich, Germany. [3]Department of Neurology, Klinikum der Universität München, Munich, Germany. [4]Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Cambridge, UK. [5]Institute for Molecular Medicine Finland (FIMM), University of Helsinki, Helsinki, Finland. [6]Department of Neurology, Helsinki University Central Hospital, Helsinki, Finland. [7]Department of Neurology, Leiden University Medical Centre, Leiden, The Netherlands. [8]Department of Neurology, Vall d'Hebron University Hospital, Universitat Autònoma de Barcelona, Barcelona, Spain. [9]Headache Research Group, Vall d'Hebron Research Institute, Universitat Autonoma de Barcelona, Barcelona, Spain. [10]Department of Neurology, Oslo University Hospital and University of Oslo, Oslo, Norway. [11]Neurogenetics Laboratory, Queensland Institute of Medical Research, Brisbane, Australia. [12]Institute of Human Genetics, University of Ulm, Ulm, Germany. [13]Department of Psychiatry, Leiden University Medical Centre, Leiden, The Netherlands. [14]Folkhälsan Research Center, Helsinki, Finland. [15]Headache Research Unit, Department of Neurology and Groupe Interdisciplinaire de Génoprotéomique Appliquée (GIGA)-Neurosciences, Liège University, Liège, Belgium. [16]Department of Clinical Physiology, University of Turku and Turku University Central Hospital, Turku, Finland. [17]Department of Clinical Chemistry, Tampere University Hospital and University of Tampere, Tampere, Finland. [18]Pediatric Neurology Research Group, Vall d'Hebron Research Institute, Barcelona, Spain. [19]Kiel Pain and Headache Center, Kiel, Germany. [20]Institute of Epidemiology, Helmholtz Center Munich, Neuherberg,

Germany. [21]Department of Genetics, University of Barcelona, Barcelona, Spain. [22]Biomedical Network Research Centre on Rare Diseases (CIBERER), Barcelona, Spain. [23]Department of Internal Medicine, Erasmus Medical Center, Rotterdam, The Netherlands. [24]Department of Epidemiology, Erasmus University Medical Center, Rotterdam, The Netherlands. [25]Department of Neuroscience, Norwegian University of Science and Technology, Trondheim, Norway. [26]Department of Public Health, University of Helsinki, Helsinki, Finland. [27]Department of Mental Health and Alcohol Research, National Institute for Health and Welfare, Helsinki, Finland. [28]Institut de Biomedicina de la Universitat de Barcelona (IBUB), Barcelona, Spain. [29]Institute of Human Genetics, Helmholtz Zentrum München, Neuherberg, Germany. [30]Institute of Human Genetics, Klinikum rechts der Isar, Technische Universität München, Munich, Germany. [31]Max Planck Institute of Psychiatry, Munich, Germany. [32]The Broad Institute of MIT and Harvard, Boston, Massachusetts, USA. [33]Department of Medical Genetics, University of Helsinki, Helsinki, Finland. [34]Department of Medical Genetics, Helsinki University Central Hospital, Helsinki, Finland.

Published: 21 February 2013

doi:10.1186/1129-2377-14-S1-P18
Cite this article as: de Vries *et al.*: Migraine without aura: genome-wide association analysis identifies several novel susceptibility. *The Journal of Headache and Pain* 2013 **14**(Suppl 1):P18.