

# Genetic analysis for a shared biological basis between migraine and coronary artery disease

OPEN

Bendik S. Winsvold, MD\*  
Christopher P. Nelson, PhD\*  
Rainer Malik, PhD  
Padhraig Gormley, PhD  
Verner Anttila, PhD  
Jason Vander Heiden, MSc  
Katherine S. Elliott, PhD  
Line M. Jacobsen, PhD  
Priit Palta, PhD  
Najaf Amin, PhD  
Boukje de Vries, PhD  
Eija Hämäläinen, BS  
Tobias Freilinger, MD  
M. Arfan Ikram, MD  
Thorsten Kessler, MD  
Markku Koiranen, MS  
Lannie Ligthart, PhD  
George McMahon, PhD  
Linda M. Pedersen, PhD  
Christina Willenborg, PhD  
Hong-Hee Won, PhD  
Jes Olesen, PhD  
Ville Artto, MD  
Themistocles L. Assimes, PhD  
Stefan Blankenberg, MD  
Dorret I. Boomsma, PhD  
Lynn Cherkas, PhD  
George Davey Smith, DSc  
Stephen E. Epstein, MD  
Jeanette Erdmann, PhD  
Michel D. Ferrari, PhD  
Hartmut Göbel, PhD  
Alistair S. Hall, PhD  
Marjo-Riitta Jarvelin, PhD  
Mikko Kallela, PhD  
Jaakko Kaprio, PhD

## ABSTRACT

**Objective:** To apply genetic analysis of genome-wide association data to study the extent and nature of a shared biological basis between migraine and coronary artery disease (CAD).

**Methods:** Four separate methods for cross-phenotype genetic analysis were applied on data from 2 large-scale genome-wide association studies of migraine (19,981 cases, 56,667 controls) and CAD (21,076 cases, 63,014 controls). The first 2 methods quantified the extent of overlapping risk variants and assessed the load of CAD risk loci in migraineurs. Genomic regions of shared risk were then identified by analysis of covariance patterns between the 2 phenotypes and by querying known genome-wide significant loci.

**Results:** We found a significant overlap of genetic risk loci for migraine and CAD. When stratified by migraine subtype, this was limited to migraine without aura, and the overlap was protective in that patients with migraine had a lower load of CAD risk alleles than controls. Genes indicated by 16 shared risk loci point to mechanisms with potential roles in migraine pathogenesis and CAD, including endothelial dysfunction (*PHACTR1*) and insulin homeostasis (*GIP*).

**Conclusions:** The results suggest that shared biological processes contribute to risk of migraine and CAD, but surprisingly this commonality is restricted to migraine without aura and the impact is in opposite directions. Understanding the mechanisms underlying these processes and their opposite relationship to migraine and CAD may improve our understanding of both disorders. *Neurol Genet* 2015;1:e10; doi: 10.1212/NXG.000000000000010

## GLOSSARY

**CAD** = coronary artery disease; **CARDIoGRAM** = Coronary ARtery Disease Genome-Wide Replication And Meta-Analysis; **CPSM** = Cross-Phenotype Spatial Mapping; **GWAS** = genome-wide association studies; **IHGC** = International Headache Genetics Consortium; **LD** = linkage disequilibrium; **MA** = migraine with aura; **MO** = migraine without aura; **SNP** = single nucleotide polymorphism.

Migraine affects 19% of women and 11% of men worldwide and causes more years lost to disability than any other neurologic disorder.<sup>1,2</sup> In about one-third of patients, headache attacks are preceded by transient neurologic symptoms termed migraine aura, and migraine with and without aura (MA and MO, respectively) are believed to have a partially distinct pathogenic basis.<sup>3</sup> It has long been assumed that the vascular system is involved in migraine pathogenesis, but little is known of the specific biological processes involved, and the relative importance of neuronal and vascular mechanisms remains controversial.<sup>3–6</sup> Supporting a vascular basis, epidemiologic studies have found an increased risk for stroke among patients with migraine, most pronounced for MA.<sup>7</sup> Some recent studies indicate a similar risk increase for coronary artery disease (CAD), the most common vascular disorder, although the association is less certain than for stroke.<sup>8–11</sup> This raises the question of whether migraine and cardiovascular disease have a shared biological basis.

Both migraine and CAD have a strong genetic determination, and recent genome-wide association studies (GWAS) have identified risk variants for each. If migraine and CAD have a shared biological basis, one might anticipate that they will also share genetic variants that affect their risk. In this study, we utilized data from 2 large-scale nonoverlapping GWAS meta-analyses of migraine (the International Headache Genetics Consortium, IHGC)<sup>12</sup> and CAD (Coronary ARtery Disease Genome-Wide Replication And Meta-Analysis, CARDIoGRAM)<sup>13</sup> to quantify shared genetic risk.

**METHODS Study cohorts.** Summary statistics (*p* value and effect size) at single nucleotide polymorphism (SNP) level from 2 recently performed meta-analyses of genome-wide association data on migraine (IHGC)<sup>12</sup> and CAD (CARDIoGRAM)<sup>13</sup> were used in

\*These authors contributed equally to the manuscript.

Author affiliations are provided at the end of the article.

Funding information and disclosures are provided at the end of the article. Go to [Neurology.org/ng](http://Neurology.org/ng) for full disclosure forms. The Article Processing Charge was paid by the authors.

The CARDIoGRAM Consortium and the International Headache Genetics Consortium coinvestigators are listed at [Neurology.org/ng](http://Neurology.org/ng).

This is an open access article distributed under the terms of the Creative Commons Attribution License 4.0 (CC BY), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Author list continued on next page

Sekar Kathiresan, MD  
Terho Lehtimäki, MD  
Ruth McPherson, PhD  
Winfried März, PhD  
Dale R. Nyholt, PhD  
Christopher J. O'Donnell,  
MD  
Lydia Quaye, PhD  
Daniel J. Rader, MD  
Olli Raitakari, PhD  
Robert Roberts, MD  
Heribert Schunkert, MD  
Markus Schürks, MD  
Alexandre F.R. Stewart,  
PhD  
Gisela M. Terwindt, PhD  
Unnur Thorsteinsdottir,  
PhD  
Arn M.J.M. van den  
Maagdenberg, PhD  
Cornelia van Duijn, PhD  
Maija Wessman, PhD  
Tobias Kurth, MD  
Christian Kubisch, MD  
Martin Dichgans, MD  
Daniel I. Chasman, PhD  
Chris Cotsapas, PhD  
John-Anker Zwart, MD  
Nilesh J. Samani, FRCP  
Aarno Palotie, MD  
For the CARDIoGRAM  
Consortium and the  
International Headache  
Genetics Consortium

Correspondence to  
Dr. Palotie:  
aarno@broadinstitute.org

See editorial

Supplemental data  
at [Neurology.org/ng](http://Neurology.org/ng)

the present study. After excluding overlapping samples, the 2 studies consisted of 19,981 cases with migraine vs 56,667 controls, and 21,076 cases with CAD vs 63,014 controls. A proportion of the migraine cases were phenotyped in sufficient detail to allow subclassification into MO (6,413 cases, 32,745 controls) and MA (4,940 cases, 37,557 controls). In addition, individual-level genotype data were available for a proportion of the migraine cohorts (6,350 migraine cases vs 15,069 controls from the German MA and MO cohorts, Dutch LUMINA study, Finnish MA study, and the HUNT Study, Norway). All data sets were imputed by using the HapMap release 21 or 22 as reference. An overview of the study design and the included cohorts is given in figure 1. A detailed description of samples, genotyping, and association analyses is given in e-Methods, tables e-1 and e-2, and figure e-1 at [Neurology.org/ng](http://Neurology.org/ng).

**Standard protocol approvals, registrations, and patient consents.** For all study cohorts, participation was based on informed consent. Each study was approved by local research ethics boards in the country where the study cohort was collected. See original publications of the 2 studies for full details of ethics and consent procedures.<sup>12,13</sup>

**Analytic approach. Evaluating extent of overlapping signals.** To assess whether more association signals were shared between the migraine and CAD studies than would be expected by chance, we used a set of 2,342,101 overlapping SNPs that were directly typed or imputed in both studies. Following the same procedure as described in a previous study,<sup>14</sup> we first sorted the SNPs by association  $p$  value to migraine. Starting from the top of the list, all subsequent SNPs with linkage disequilibrium (LD)  $r^2 > 0.05$  (based on HapMap CEU release 27) were removed. This process was repeated until a set of 92,654 SNPs in approximate linkage equilibrium remained. For each of 5 separate  $p$  value cutoffs ( $1 \times 10^{-2}$ ,  $1 \times 10^{-3}$ ,  $1 \times 10^{-4}$ ,  $1 \times 10^{-5}$ , and  $1 \times 10^{-6}$ ), we counted the number of SNPs above and below the cutoff in each of the 2 studies, resulting in one  $2 \times 2$  table for each  $p$  value cutoff. The Fisher exact test was used to estimate deviation from the expected distribution, and false discovery rate correction was performed on all 6 tests using the  $p$ -adjust function in  $R$ .<sup>15</sup> A corrected Fisher  $p < 0.01$  was taken to indicate an excess of overlapping signals. In order to obtain a more robust estimate of the significance of the observed overlap, this was also assessed through permutations. In each permutation cycle, the relation of  $p$  values to SNPs was randomized within each of the LD-pruned migraine and CAD data sets, and a Fisher  $p$  for overlap was calculated for each  $p$  value cutoff. We generated 100,000 permutations to produce an empirical null distribution of  $p$  values.

In an equivalent manner, secondary analyses were performed for MO (83,373 overlapping SNPs after LD pruning) and MA (88,031 overlapping SNPs after LD pruning).

**Polygenic risk score analysis.** If shared genetic risk variants are in part or fully responsible for comorbidity between migraine and CAD, we would expect an accumulation of CAD risk alleles in migraineurs. To test this hypothesis, we used the 6 migraine cohorts in which individual-level genotype data were available for analysis (6,350 migraineurs vs 15,069 controls; figure 1). For each migraine case or control, we calculated a CAD polygenic risk score based on a previously published method.<sup>16</sup> We first generated 3 sets of CAD risk SNPs by selecting SNPs with strong ( $p < 5 \times 10^{-8}$ ; 149 SNPs), moderate ( $p < 1 \times 10^{-4}$ ; 1,631 SNPs), or weak ( $p < 1 \times 10^{-2}$ ; 36,384 SNPs) association to CAD among the 2,342,101 SNPs with information in both migraine and CAD studies. As suggested in the original description of the method,<sup>16</sup> the analysis was based on non-LD-

pruned SNP sets in order to optimize sensitivity. Using each set of CAD risk SNPs, we calculated a per-individual CAD polygenic risk score by summing the number of CAD risk alleles (or expected allele counts for imputed SNPs), each weighted by the log odds ratio from the CAD study. We subsequently assessed whether CAD polygenic risk score was associated with migraine status by applying a logistic regression model of the effect of CAD polygenic risk score (continuous) on migraine status (case, control), adjusted for sex and dummy-coded covariates representing the 6 individual migraine study cohorts.

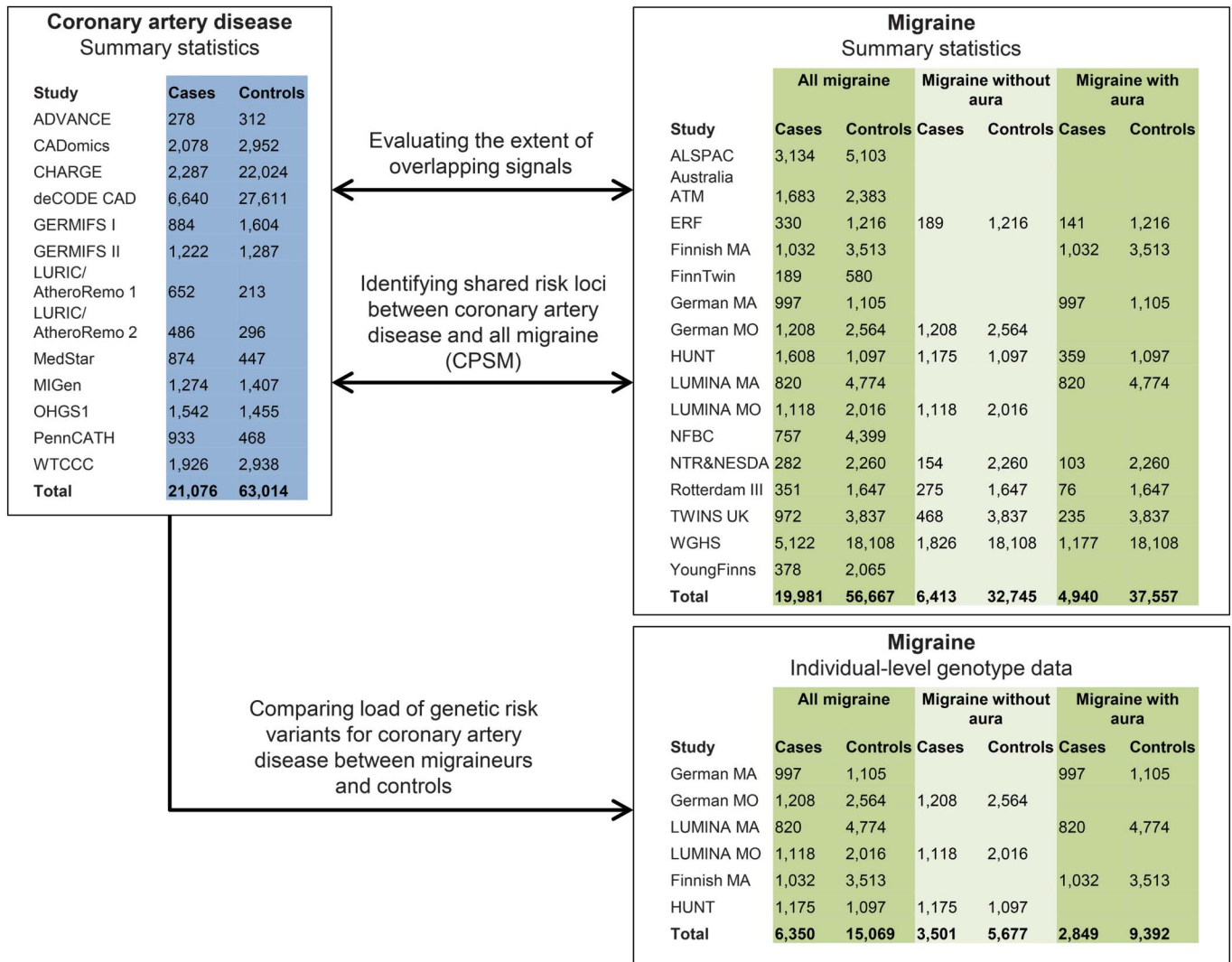
**Identifying shared risk loci.** In order to identify shared risk loci between migraine and CAD, we applied a novel method, Cross-Phenotype Spatial Mapping (CPSM; see e-Methods for an overview). This method compares 2 sets of  $p$  values from GWAS in order to find groups of SNPs at which they are correlated and thus identify shared patterns of association. We applied this method to the 2,342,101 overlapping SNPs from the migraine and CAD studies and selected genomic regions with signal above the 99.95th percentile of 1,000 permutations for further analysis. Potential effects of the shared association loci on regional gene expression (cis effect) were examined using an existing expression quantitative trait locus database from peripheral blood<sup>17</sup> (e-Methods).

Lastly, we analyzed loci with previously reported genome-wide significant association to migraine or CAD (summarized in the original publications).<sup>12,13</sup> The lead SNP at each locus was cross-analyzed for association to the other phenotype, Bonferroni correcting for the number of SNPs tested. All 13 of 13 reported migraine loci and 22 of 25 reported CAD loci were available in our data set and could be tested (excluding CAD risk SNPs rs17465637, rs1746048, and rs12413409).

**RESULTS** Comparing nominally significant SNPs from the migraine and CAD GWAS, we found an overlap of association signals in excess of what would be expected by chance (table 1). An overlap of signals was seen for SNPs with  $p$  values  $\leq 1 \times 10^{-2}$ ,  $1 \times 10^{-4}$ , and  $1 \times 10^{-6}$ . This was supported by permutation testing, which indicated a sharing of association signals at  $p$  value cutoff  $1 \times 10^{-5}$  as well. For reference, the full list of SNPs with association  $p$  value  $\leq 1 \times 10^{-2}$  to both CAD and migraine is given in table e-3. Secondary analyses by migraine subtype revealed an overlap of association signals between MO and CAD at all  $p$  value cutoffs ( $1 \times 10^{-2}$ ,  $1 \times 10^{-3}$ ,  $1 \times 10^{-4}$ ,  $1 \times 10^{-5}$ , and  $1 \times 10^{-6}$ ), while no overlap was seen between MA and CAD at any of the  $p$  value cutoffs. The direction of effect for overlapping association signals did not consistently agree between migraine and CAD, as evidenced by nonsignificant binomial  $p$  values for concordance (table 1).

To examine this further, the second analysis compared the load of genetic risk variants for CAD between migraineurs and controls, using individual-level data. The results indicated that a high CAD polygenic risk score was associated with a reduced risk of migraine (figure 2, further details in table e-4). For migraine overall, this association was seen for only the moderate CAD risk SNP set ( $p = 0.007$ ). Secondary analyses revealed a similar, but more pronounced, association between CAD polygenic risk score and

**Figure 1** Study design and included cohorts



CPSM = Cross-Phenotype Spatial Mapping.

MO ( $p = 1.5 \times 10^{-4}$  and  $5.1 \times 10^{-4}$  for the moderate and strong CAD risk SNP sets, respectively). No association was seen for MA. In the analysis of the weak CAD risk SNP set, there was no association to CAD genetic risk score for either migraine category, indicating that the observed associations were driven by a fairly limited number of loci that are at least moderately associated with CAD. These findings were consistent across men and women (figure e-2) and across individual independent cohorts within the same migraine subtype (figure e-3).

CPSM yielded 16 loci that overlapped between migraine and CAD (table 2; figure e-4). Details of the most significant migraine and CAD SNPs at each locus are given in table e-5. The strongest evidence of shared association was seen at 6p24 (locus no. 1 of table 2), where both CAD and migraine showed genome-wide significant signals within the *PHACTR1* gene (CAD: rs4714955,  $p = 9.8 \times$

$10^{-11}$ ; migraine: rs9349379,  $p = 5.9 \times 10^{-9}$ ). The second strongest overlapping signal was on 17q21 (locus no. 2), where the lead CAD SNP (rs46522,  $p = 2.6 \times 10^{-7}$ ) was intragenic in *UBE2Z*, whereas the lead migraine SNP (rs11079844,  $p = 3.1 \times 10^{-5}$ ) was intergenic between *SNF8* and *GIP*. It is interesting that both lead SNPs are in high LD ( $r^2 > 0.9$ ) with 2 functional variants in *GIP*: Ser103Gly (rs2291725) and a splice site variant (rs2291726) that is predicted to lead to a prematurely truncated transcript<sup>18</sup> (table e-6). The locus was also found to have a potential effect on the expression level of *UBE2Z* (table e-7). Lead SNPs in 5 loci were in high LD ( $r^2 > 0.8$ ) with nonsynonymous or splice site variants in nearby genes (table e-6). Ten of the 16 loci showed opposite direction of effect for migraine and CAD. In the secondary analyses, 12 of the 16 lead migraine SNPs had a lower association  $p$  value in MO than in MA (2-tailed binomial  $p = 0.08$ ), and all 16 SNPs

**Table 1** Analysis of the extent of overlapping signals between migraine and CAD

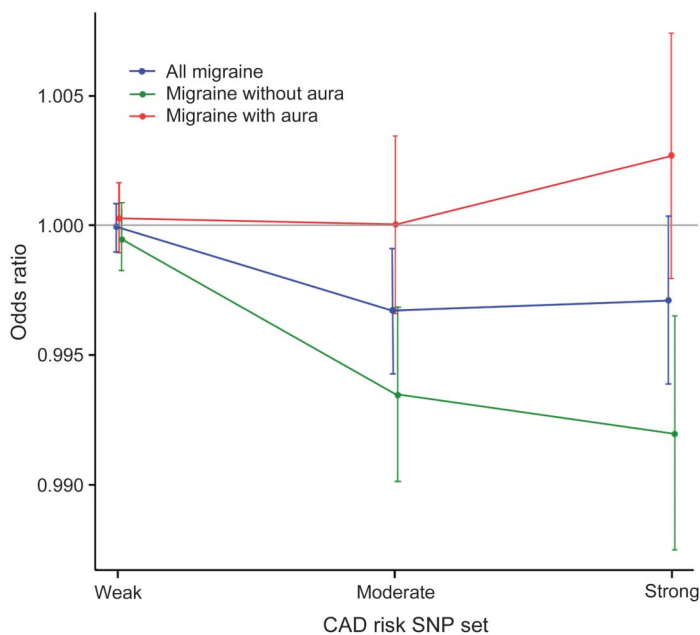
Signal definition (p value cutoff)	Overlapping SNPs	p Value for overlap (Fisher exact test) <sup>a</sup>	p Value for overlap (permutation test) <sup>a</sup>	Concordance of overlapping SNPs <sup>b</sup>	Binomial p value for concordance
<b>All migraine (total no. SNPs: 92,654)</b>					
1E-2	146	1.1E-05 <sup>c</sup>	6.0E-05 <sup>c</sup>	0.534	0.18
1E-3	7	0.099	0.056	0.571	0.23
1E-4	2	9.3E-03 <sup>c</sup>	7.9E-03 <sup>c</sup>	0	0.75
1E-5	1	0.014	2.1E-04 <sup>c</sup>	0	0.50
1E-6	1	5.2E-03 <sup>c</sup>	3.5E-03 <sup>c</sup>	0	0.50
<b>Migraine without aura (total no. SNPs: 83,373)</b>					
1E-2	113	1.6E-04 <sup>c</sup>	1.5E-05 <sup>c</sup>	0.510	0.87
1E-3	8	1.3E-03 <sup>c</sup>	1.1E-04 <sup>c</sup>	0.442	0.86
1E-4	3	2.0E-04 <sup>c</sup>	1.5E-05 <sup>c</sup>	0.250	0.88
1E-5	1	8.5E-03 <sup>c</sup>	1.5E-05 <sup>c</sup>	0	0.50
1E-6	1	3.0E-03 <sup>c</sup>	1.5E-05 <sup>c</sup>	0	0.50
<b>Migraine with aura (total no. SNPs: 88,031)</b>					
1E-2	107	0.13	0.11	0.523	0.28
1E-3	1	1.0	0.64	0.523	0.50
1E-4	0	1.0	1.0	NA	NA
1E-5	0	1.0	1.0	NA	NA
1E-6	0	1.0	1.0	NA	NA

Abbreviations: CAD = coronary artery disease; NA = not applicable; SNP = single nucleotide polymorphism.

<sup>a</sup> False discovery rate corrected p values.

<sup>b</sup> Proportion of overlapping association signals having the same direction of effect in migraine and CAD.

<sup>c</sup>  $p < 0.01$ .

**Figure 2** Association between coronary artery disease polygenic risk score and the presence of migraine

Results are given as odds ratios with 95% confidence intervals. Separate lines are shown for all migraine (blue), migraine without aura (green), and migraine with aura (red). The coronary artery disease (CAD) polygenic risk score was calculated based on single nucleotide polymorphisms (SNPs) with weak ( $p < 1 \times 10^{-2}$ ), moderate ( $p < 1 \times 10^{-4}$ ), or strong ( $p < 5 \times 10^{-8}$ ) association to CAD in the Coronary ARtery Disease Genome-Wide Replication And Meta-Analysis study.

had the same effect direction in each of the 2 migraine subtypes. Local Manhattan plots and covariance plots for the identified loci are given in figure e-4.

When considering previously reported risk loci for migraine and CAD, 3 CAD risk SNPs were associated to migraine at study-wide significance, and 2 migraine risk SNPs were associated to CAD (table 3). These correspond to loci no. 1, 2, 3, 11, and 14 as identified by the CPSM method and corroborate the evidence for shared genetic risk at these loci.

**DISCUSSION** In this study, we used data from 2 recently performed large-scale nonoverlapping GWAS to examine shared genetic risk between migraine and CAD. We found that association signals overlapped in excess of what would be expected by chance. Stratifying by migraine subtype further revealed that MO and MA behaved differently. MO had a genetic overlap with CAD, whereas MA did not. These results are unexpected, given the epidemiologic evidence that comorbidity with CAD is more common in MA than MO. Patients with MA were found to have a 2-fold increased risk for CAD<sup>8,10</sup> and an increased risk for CAD-related mortality,<sup>9,11</sup> although one cross-sectional study failed to find an association between

**Table 2** Overlapping association loci between migraine and CAD as identified by CPSM analysis

Locus no. <sup>a</sup>	Chr band	Position (Mb) <sup>b</sup>		Locus			Genes within locus <sup>c</sup>
		Left margin	Right margin	Size (kb)	Peak SNP	Peak height	
1	6p24	12.929	13.187	257.386	rs7454157	25.2	<i>PHACTR1</i>
2	17q21	44.282	44.512	230.813	rs12601858	13.2	<i>CALCOCO2, ATP5G1, UBE2Z, SNF8, GIP, IGF2BP1</i>
3	6q16	96.917	97.188	271.548	rs12529248	7.8	<i>UFL1, FHL5</i>
4	12q24	110.241	111.064	823.633	rs7962138	7.4	<i>CUX2, FAM109A, SH2B3, ATXN2, BRAP, ACAD10, ALDH2, MAPKAPK5-AS1, MAPKAPK5, ADAM1A, TMEM116, ERP29, NAA25, TRAFD1</i>
5	17p11	17.603	17.992	389.086	rs9890341	6.9	<i>RAI1, SMCR5, SREBF1, MIR33B, TOM1L2, LRRC48, ATPAF2, GID4, DRG2, MYO15A</i>
6	16q23	73.827	74.094	266.738	rs4888396	5.2	<i>BCAR1, CFPD1, TMEM170A, CHST6</i>
7	10q24	104.823	105.178	354.585	rs7067970	5.1	<i>CNNM2, NT5C2, LOC729020, INA, PCGF6, TAF5, USMG5, MIR1307, PDCD11</i>
8	2q33	203.375	203.52	145.53	rs6435169	4.8	<i>ICA1L, WDR12, ALS2CR8</i>
9	10q24	104.569	104.785	216.416	rs1538204	4.1	<i>CYP17A1, C10orf32, C10orf32-AS3MT, AS3MT, CNNM2</i>
10	6q13	72.182	72.403	220.605	rs12207845	3.1	<i>LINC00472</i>
11	8q21	89.53	89.69	160.492	rs1352317	3.1	None
12	19q13	46.543	46.664	120.921	rs3810174	2.9	<i>TGFB1, B9D2, TMEM91, EXOSC5, BCKDHA, B3GNT8, ATP5SL, C19orf69, LOC100505495</i>
13	12q24	109.501	109.714	213.015	rs16940933	2.8	<i>PPTC7, TCTN1, HVCN1, PPP1CC</i>
14	8q21	89.382	89.525	143.754	rs6984041	2.7	<i>MMP16</i>
15	16q24	88.099	88.191	91.257	rs17775174	2.6	<i>SPG7, RPL13, SNORD68, CPNE7</i>
16	9p21	23.429	23.505	75.25	rs10811931	2.5	None

Abbreviations: Chr = chromosome; CAD = coronary artery disease; CPSM = Cross-Phenotype Spatial Mapping; peak height = value of covariance signal at apex of the peak; SNP = single nucleotide polymorphism.

<sup>a</sup>Sorted by decreasing peak height.

<sup>b</sup>Positions refer to build NCBI36/hg18.

<sup>c</sup>RefSeq genes.

CAD and any migraine subtype.<sup>19</sup> Studies not differentiating on migraine subtype have been less conclusive, with some<sup>8,9,20,21</sup> but not others<sup>19,22</sup> indicating an increased risk of CAD related to migraine overall.

For MO, we found a clear overlap of association signals with CAD, whichever *p* value cutoff was used to define signals. Intriguingly, the impact was in the opposite direction, in that patients with MO had a lower load of CAD risk alleles than migraine-free controls. This association seemed to be driven by a limited number of loci. Only a proportion of the included migraine patients were phenotyped in sufficient detail to allow subclassification into MA or MO. When using the considerably larger set of all migraine patients, a similar association was seen as for MO, likely driven by this migraine subtype. While the results suggest that there are shared common risk variants between migraine and CAD, they do not indicate that these variants explain comorbidity between the 2 disorders.

The opposite direction of effect for some of the loci is consistent with a recent GWAS in which the migraine and CAD risk SNP rs9349379 (in

*PHACTR1*) was associated with cervical artery dissection, with effect in the same direction as for migraine but opposite of CAD.<sup>23</sup> Two further migraine SNPs showed evidence of association to cervical artery dissection with the same effect direction as for migraine (rs11172113 in *LRPI* and rs13208321 in *FHL5*, the latter identified as locus 3 in the current study) but opposite direction for CAD.

The significant sharing of risk loci between migraine and CAD may reflect that they involve some of the same biological processes. Experimental studies will be needed to clarify this and whether the shared risk loci can give information on vascular mechanisms involved in migraine pathogenesis.

The lack of overlapping association signals between MA and CAD may indicate that the 2 disorders have separate and nonrelated genetic backgrounds. However, it may also result from insufficient power to detect shared common genetic risk factors for this migraine subtype. This is consistent with the relative failure so far in identifying common risk variants for MA; despite at least as high heritability and comparable study sample sizes, only one genome-wide significant locus has been identified

**Table 3** Cross-analysis of loci previously reported to show genome-wide significant association with migraine or CAD

Lead SNP	Chr band	Reported gene(s)	CAD			Migraine			Migraine without aura			Migraine with aura		
			p Value	Odds ratio (SE)	Dir. <sup>a</sup>	p Value	Odds ratio (SE)	Dir. <sup>a</sup>	p Value	Odds ratio (SE)	Dir. <sup>a</sup>	p Value	Odds ratio (SE)	Dir. <sup>a</sup>
Previously reported loci for migraine in the CAD sample														
rs9349379	6p24	PHACTR1	8.97E-08 <sup>b</sup>	1.1 (0.019)	-	5.88E-09	1.09 (0.015)	-	2.52E-10	1.17 (0.029)	-	0.236	1.03 (0.026)	-
rs10504861	8q21	MMP16	1.96E-03 <sup>b</sup>	1.06 (0.02)	+	1.71E-03	1.05 (0.017)	+	3.36E-08	1.17 (0.032)	+	0.329	1.03 (0.031)	+
rs13208321	6q16	FHL5	2.53E-03 <sup>b</sup>	1.05 (0.018)	-	1.41E-10	1.1 (0.016)	-	1.35E-12	1.19 (0.029)	-	7.40E-04	1.1 (0.03)	-
Previously reported loci for CAD in the migraine sample														
rs12526453	6p24	PHACTR1	9.72E-09	1.09 (0.017)	-	8.18E-06 <sup>b</sup>	0.94 (0.013)	-	7.80E-08 <sup>b</sup>	0.88 (0.02)	-	0.399	0.98 (0.025)	-
rs46522	17q21	UBE2Z, GIP, ATP5G1, SNF8	2.58E-07	0.93 (0.013)	-	1.24E-04 <sup>b</sup>	1.05 (0.013)	-	6.93E-03	1.06 (0.022)	-	0.081	1.04 (0.024)	-

Abbreviations: Chr = chromosome; CAD = coronary artery disease; SNP = single nucleotide polymorphism.

Only SNPs with significant association to the other phenotype after Bonferroni correction are shown ( $p < 0.0038$  for previously reported migraine loci in the CAD sample, and  $p < 0.0023$  for previously reported CAD loci in the migraine sample).  $p$  values may differ from those reported in the original studies since overlapping samples were excluded in the current study.

<sup>a</sup>Direction of effect: SNPs with the same effect direction for association to CAD and migraine are marked as plus (+), opposing effect direction is marked as minus (-).

<sup>b</sup>Significant cross-phenotype  $p$  value.

for MA, compared to 9 for MO.<sup>12,24–27</sup> It is possible that MA is a more heterogeneous disorder or is influenced by rare and low-frequency variants not captured by current imputation panels.<sup>12,28</sup> Larger studies that also interrogate rare variants will be needed to determine the genetic basis of MA and its potential overlap with cardiovascular disease.

Six of the overlapping loci have previously been associated with CAD at genome-wide significant levels (loci 1, 2, 4, 7, 8, and 9 of table 2),<sup>13,29</sup> and 2 with migraine (loci 1 and 3).<sup>12,25</sup> The strongest overlapping region (locus 1) is entirely intragenic in *PHACTR1* (which encodes phosphatase and actin regulator 1 protein). This locus is associated with both migraine and CAD at genome-wide significant levels in the current and previous studies<sup>13,25,30</sup> and has also been associated with coronary artery calcification and stroke.<sup>31,32</sup> *PHACTR1* is highly expressed in the brain, and its transcript is an important regulator of synaptic activity and dendritic morphology through the control of protein phosphatase 1 and actin binding.<sup>33</sup> More recently, *PHACTR1* has been identified as a key regulator of endothelial function, including endothelial cell survival and angiogenesis,<sup>34</sup> and it is associated with altered vasomotor tone.<sup>35</sup> Both endothelial and vasomotor dysfunctions have been implicated in migraine,<sup>36,37</sup> and this locus offers a potential focus for future studies. Alternatively, the pleiotropic effects of this gene on both synaptic and vascular functions may give rise to independent causal pathways for the 2 disorders.

The second strongest overlapping region (locus 2) is a previously identified risk locus for CAD.<sup>13</sup> The lead CAD (*rs46522*) and migraine variants (*rs11079844*) are in strong LD ( $r^2 = 0.94$ ), and both are in strong LD ( $r^2 > 0.90$ ) with 2 potentially functional variants in *GIP* (which encodes gastric inhibitory polypeptide). *GIP* regulates glucose-induced insulin release from pancreatic  $\beta$ -cells and helps resensitize the insulin response.<sup>38</sup> It is also expressed in the brain, where it may be involved in proliferation of neuronal progenitor cells.<sup>39</sup> Whether *GIP* is involved in the observed tendency for insulin resistance and metabolic syndrome in migraineurs should be investigated.<sup>40</sup>

Strengths of this study include the use of large-scale nonoverlapping GWAS of migraine and CAD, stringent quality control measures, and sufficiently rich phenotyping to allow secondary analyses of the 2 migraine subtypes. Nevertheless, some limitations should also be acknowledged. First, only summary statistics and not individual-level genotype data were available for the majority of the samples included in this study. Second, in each included cohort, phenotype information was available on only migraine or CAD, not both. This prevented us from performing

more in-depth analyses, including analysis for potential gene-gene interactions or identification of CAD risk loci specific to migraineurs. Third, considerable effort was devoted to the careful avoidance of shared controls between studies, and stringent quality control measures within each data set were enforced to reduce the risk of spurious effects resulting from biases within the data sets. Nevertheless, we cannot rule out subtle biases that could affect the current results. Two such concerns are the effects of migraine on survival and the possibility that migraineurs may be more likely to seek medical treatment and therefore be under closer surveillance with regards to other disorders. Future efforts should aim to replicate these findings in sufficiently large prospective data sets where both phenotypes are measured in the same individuals.

Our study provides novel insights into the relationship between migraine and CAD. Intriguingly, and unexpectedly, there was no genetic overlap between MA and CAD, for which epidemiologic studies suggest comorbidity, but there was compelling evidence for a genetic overlap between MO and CAD, where the impact of risk variants overall was in opposite direction for the 2 disorders. The results do not demonstrate that shared common genetic risk factors drive comorbidity between the 2 disorders. However, dissecting the mechanisms underlying the shared risk loci may improve our understanding of both disorders.

#### AUTHOR AFFILIATIONS

From the Department of Neurology (B.S.W., J.-A.Z.) and FORMI (B.S.W., L.M.J., L.M.P., J.-A.Z.), Oslo University Hospital, Oslo, Norway; Institute of Clinical Medicine (B.S.W., J.-A.Z.), University of Oslo, Norway; Wellcome Trust Sanger Institute (B.S.W., P.G., V. Anttila, P.P., E.H., A.P.), Wellcome Trust Genome Campus, Cambridge, United Kingdom; Department of Cardiovascular Sciences (C.P.N., N.J.S.), University of Leicester, Clinical Sciences Wing and National Institute for Health Research Leicester Biomedical Research Unit in Cardiovascular Disease (C.P.N., N.J.S.), Glenfield Hospital, Leicester, United Kingdom; Institute for Stroke and Dementia Research (R. Malik, T.F., M.D.), Klinikum der Universität München, Ludwig-Maximilians-Universität, Munich, Germany; Munich Cluster for Systems Neurology (SyNergy) (R. Malik, M.D.), Munich, Germany; Program in Medical and Population Genetics (P.G., V. Anttila, H.-H.W., S.K., C.C., A.P.) and Stanley Center for Psychiatric Research (V. Anttila, A.P.), Broad Institute, Cambridge, MA; Psychiatric & Neurodevelopmental Genetics Unit (P.G., A.P.), Department of Psychiatry, Analytic and Translational Genetics Unit (V. Anttila, A.P.), Department of Medicine, Center for Human Genetic Research (H.-H.W., S.K.), Cardiovascular Research Center (H.-H.W., S.K.), and Department of Neurology (A.P.), Massachusetts General Hospital, Boston, MA; Division of Preventive Medicine (T. Kurth, D.I.C.), Brigham and Women's Hospital and Department of Medicine (V. Anttila, H.-H.W., S.K.), Harvard Medical School, Boston, MA; Department of Genetics (J.V.H., C.C.) and Department of Neurology (C.C.), Yale University School of Medicine, New Haven, CT; Wellcome Trust Centre for Human Genetics (K.S.E.), University of Oxford, United Kingdom; Department of Public Health (J.K.), Hjelt Institute and Institute for Molecular Medicine Finland (P.P., E.H., J.K., M.W., A.P.), University of Helsinki, Finland; Department of Epidemiology (N.A., M.A.I., C.v.D.), Department of Radiology (M.A.I.), and Department of Neurology (M.A.I.), Erasmus University Medical Centre, Rotterdam, the Netherlands; Department of

Human Genetics (B.d.V., A.M.J.M.v.d.M.) and Department of Neurology (M.D.F., G.M.T., A.M.J.M.v.d.M.), Leiden University Medical Centre, Leiden, the Netherlands; Department of Neurology and Epileptology and Hertie-Institute for Clinical Brain Research (T.F.), University of Tübingen, Germany; Deutsches Herzzentrum München (T. Kessler, H.S.), Technische Universität München, Munich, Germany; DZHK (German Centre for Cardiovascular Research) (T. Kessler, H.S.), Partner Site Munich Heart Alliance, Munich, Germany; Institute of Health Sciences (M. Koiranen, M.-R.J.) and Biocenter Oulu (M.-R.J.), University of Oulu, Finland; Department of Biological Psychology (L.L., D.I.B.), VU University and EMGO+ Institute for Health and Care Research (L.L.), VU University Medical Centre, Amsterdam, the Netherlands; Medical Research Council (MRC) Integrative Epidemiology Unit at the University of Bristol (G.M., G.D.S.), United Kingdom; Institut für Integrative und Experimentelle Genomik (C.W., J.E.), Universität zu Lübeck, Lübeck, Germany; DZHK (German Research Centre for Cardiovascular Research) (C.W., J.E.), Partner Site Hamburg/Lübeck/Kiel, Lübeck, Germany; Department of Neurology (J.O.), Glostrup Hospital, University of Copenhagen, Denmark; Department of Neurology (V. Arto, M. Kallela), Helsinki University Central Hospital, Helsinki, Finland; Department of Medicine (T.L.A.), Stanford University School of Medicine, Stanford, CA; Medizinische Klinik und Poliklinik (S.B.), Universitätsmedizin Mainz, Johannes-Gutenberg Universität Mainz, Germany; Department of Twin Research and Genetic Epidemiology (L.C., L.Q.), King's College London, United Kingdom; MedStar Heart Institute (S.E.E.), Washington Hospital Center, Washington, DC; Kiel Pain and Headache Center (H.G.), Kiel, Germany; Division of Cardiovascular and Neuronal Remodelling (A.S. H.), Multidisciplinary Cardiovascular Research Centre, Leeds Institute of Genetics, Health and Therapeutics, University of Leeds, United Kingdom; Department of Children, Young People and Families (M.-R.J.) and Department of Mental Health and Substance Abuse Services (J.K.), National Institute for Health and Welfare, Helsinki, Finland; Department of Epidemiology and Biostatistics (M.-R.J.), School of Public Health, MRC-Health Protection Agency (HPA) Centre for Environment and Health, Faculty of Medicine, Imperial College, London, United Kingdom; Unit of Primary Care (M.-R.J.), Oulu University Hospital, Oulu, Finland; Department of Clinical Chemistry (T.L.), Fimlab Laboratories, Tampere, Finland; University of Tampere School of Medicine (T.L.), Finland; The John and Jennifer Ruddy Canadian Cardiovascular Genetics Centre (R. McPherson, R.R., A.F.R.S.) and Atherogenomics Laboratory (R. McPherson), University of Ottawa Heart Institute, Ontario, Canada; Synlab Center of Laboratory Diagnostics Heidelberg (W.M.), Heidelberg, Germany; Clinical Institute of Medical and Chemical Laboratory Diagnostics (W.M.), Medical University of Graz, Austria; Institute of Public Health (W.M.), Social and Preventive Medicine, Medical Faculty Mannheim, University of Heidelberg, Germany; Institute of Health and Biomedical Innovation (D.R.N.), Queensland University of Technology, Brisbane, Australia; National Heart, Lung, and Blood Institute's Framingham Heart Study (C.J.O.), Framingham, MA; Department of Medicine, Institute for Translational Medicine and Therapeutics, and Cardiovascular Institute (D.J.R.), University of Pennsylvania, Philadelphia, PA; Department of Clinical Physiology and Nuclear Medicine (O.R.), Turku University Hospital, Turku, Finland; Research Centre of Applied and Preventive Cardiovascular Medicine (O.R.), University of Turku, Finland; Department of Neurology (M.S.), University Hospital Essen, Essen, Germany; deCODE genetics (U.T.), Reykjavik, Iceland; Faculty of Medicine (U.T.), University of Iceland, Reykjavik, Iceland; Institute of Genetics (M.W.), Folkhälsan Research Center, Helsinki, Finland; Institut National de la Santé et de la Recherche Médicale (INSERM) Research Center for Epidemiology and Biostatistics (U897) Team-Neuroepidemiology (T. Kurth), Bordeaux, France; University of Bordeaux (T. Kurth), France; and Institute of Human Genetics (C.K.), University Medical Center Hamburg-Eppendorf, Hamburg, Germany.

#### AUTHOR CONTRIBUTIONS

Bendik S. Winsvold and Christopher P. Nelson: performed statistical analysis; conceived and designed the study; analyzed and interpreted the data; contributed data; drafted/ revised the manuscript for content. Rainer Malik: conceived and designed the study; analyzed and interpreted the data; contributed data; drafted/ revised the manuscript for content. Padhraig Gormley, Verner Anttila, Jason Vander Heiden, Katherine S. Elliott, Line M. Jacobsen, and Preet Paltal: analyzed and interpreted the data; contributed data; drafted/ revised the manuscript for content. Najaf

Amin, Boukje de Vries, Eija Hämäläinen, Tobias Freilinger, M. Arfan Ikram, Thorsten Kessler, Markku Koironen, Lannie Ligthart, George McMahon, Linda M. Pedersen, Christina Willenborg, and Hong-Hee Won: contributed data; drafted/revised the manuscript for content. Jes Olesen: analyzed and interpreted the data; contributed data; drafted/revised the manuscript for content. Ville Artto, Themistocles L. Assimes, Stefan Blankenberg, Dorret I. Boomsma, Lynn Cherkas, George Davey Smith, Stephen E. Epstein, Jeanette Erdmann, Michel D. Ferrari, Hartmut Göbel, Alistair S. Hall, Marjo-Riitta Jarvelin, Mikko Kallela, Jaakko Kaprio, Sekar Kathiresan, Terho Lehtimäki, Ruth McPherson, Winfried März, Dale R. Nyholt, Christopher J. O'Donnell, Lydia Quaye, Daniel J. Rader, Olli Raitakari, Robert Roberts, Heribert Schunkert, Markus Schürks, Alexandre F.R. Stewart, Gisela M. Terwindt, Unnur Thorsteinsdottir, Arn M.J.M. van den Maagdenberg, Cornelia van Duijn, and Maija Wessman: contributed data; drafted/revised the manuscript for content. Tobias Kurth and Christian Kubisch: analyzed and interpreted the data; contributed data; drafted/revised the manuscript for content. Martin Dichgans: conceived and designed the study; analyzed and interpreted the data; contributed data; drafted/revised the manuscript for content. Daniel I. Chasman and Chris Cotsapas: analyzed and interpreted the data; contributed data; drafted/revised the manuscript for content. John-Anker Zwart, Nilesh J. Samani, and Aarno Palotie: conceived and designed the study; jointly supervised research; analyzed and interpreted the data; contributed data; drafted/revised the manuscript for content. All authors accept responsibility for conduct of research and will give final approval.

## ACKNOWLEDGMENT

P.P. was supported by the European Commission FP7 project no. 261123 (gEUVADIS). C.K. and H.G. were funded by the German Federal Ministry of Education and Research (BMBF) within the framework of the National Genome Research Network (NGFN-Plus; grants 01GS08120 and 01GS1103 [to C.K.]) and the Deutsche Forschungsgemeinschaft (DFG). The Academy of Finland (grant 139795 to M.W.); the Folkhälsan Research Foundation (to M.W.); the Medicinska Understödsföreningen Liv & Hälsa (to M.W.); the Orion Farnos Research Foundation (to V. Anttila); and the Helsinki University Central Hospital (to M. Koironen and V. Artto). The Women's Genome Health Study (WGHS) is supported by HL043851 and HL080467 from the National Heart, Lung, and Blood Institute and CA047988 from the National Cancer Institute, with collaborative scientific support and funding for genotyping provided by Amgen. Genetic analyses of migraine in WGHS have been supported by NS061836 from the National Institute of Neurological Disorders and Stroke. The Nord-Trøndelag Health Study (The HUNT Study) is a collaboration between HUNT Research Centre (Faculty of Medicine, Norwegian University of Science and Technology, NTNU), Nord-Trøndelag County Council, Central Norway Health Authority, and the Norwegian Institute of Public Institute of Public Health. The Young Finns Study has been financially supported by the Academy of Finland: grants 134309, 126925, 121584, 124282, 129378, 117787, and 41071, the Social Insurance Institution of Finland, Kuopio, Tampere and Turku University Hospital Medical Funds (grant 9N035 for T.L.), Juho Vainio Foundation, Paavo Nurmi Foundation, Finnish Foundation of Cardiovascular Research and Finnish Cultural Foundation, Tampere Tuberculosis Foundation, and Emil Aaltonen Foundation. The authors gratefully acknowledge the expert technical assistance in the statistical analyses by Irina Lisinen and Ville Aalto. TwinsUK: the study was funded by the Wellcome Trust and European Community's Seventh Framework Programme (FP7/2007–2013). The study also receives support from the National Institute for Health Research (NIHR) BioResource Clinical Research Facility and Biomedical Research Centre based at Guy's and St Thomas' NHS Foundation Trust and King's College London. SNP Genotyping was performed by The Wellcome Trust Sanger Institute and National Eye Institute via NIH/CIDR. The authors thank their funders, twin volunteers, and TwinsUK team. The LUMINA study is supported by grants obtained from the Netherlands Organization for the Health Research and Development (ZonMw) no. 90700217 and VIDI (ZonMw) no. 91711319 (to G.M.T.); the Netherlands Organisation for Scientific Research (NWO) VICI (918.56.602) and Spinoza (2009) grants (to M.D.F.); the 7th Framework EU project EUROHEADPAIN (no. 602633); and the Center for Medical Systems Biology (CMSB) established in the Netherlands Genomics

Initiative/Netherlands Organisation for Scientific Research (NGI/NWO), project no. 050-060-409 (to M.D.F. and A.M.J.M.v.d.M.). Phenotype and genotype data collection in the Finnish Twin Cohort has been supported by the Wellcome Trust Sanger Institute, ENGAGE—European Network for Genetic and Genomic Epidemiology, FP7-HEALTH-F4-2007, grant 201413, National Institute of Alcohol Abuse and Alcoholism (grants AA-12502, AA-00145, and AA-09203 to R.J. Rose and AA15416 and K02AA018755 to D.M. Dick), and the Academy of Finland (grants 100499, 205585, 118555, 141054, 265240, 263278, and 264146 to J.K.). Phenotype and genotype data collection in NTR/NESDA was funded by the Netherlands Organization for Scientific Research (NWO: MagW/ZonMW grants 904-61-090, 985-10-002, 904-61-193, 480-04-004, 400-05-717, Addiction-31160008 Middelgroot-911-09-032, Spinozapremie 56-464-14192, Geestkracht program grant 10-000-1002), Centre for Medical Systems Biology (CMSB, NWO Genomics), Biobanking and Biomolecular Resources Research Infrastructure (BBMRI—NL, 184.021.007), the VU University's Institute for Health and Care Research (EMGO+), Neuroscience Campus Amsterdam (NCA), ENGAGE (HEALTH-F4-2007-201413); European Science Council (ERC Advanced, 230374), Rutgers University Cell and DNA Repository (NIMH U24 MH068457-06), the Avera Institute for Human Genetics, Sioux Falls, SD, the National Institutes of Health (NIH, R01D0042157-01A), Genetic Association Information Network (GAIN) of the Foundation for the US National Institutes of Health (NIMH, MH081802), and by the Grand Opportunity grants 1RC2MH089951-01 and 1RC2MH089951-01 from the NIMH. NFBC1966 received financial support from the Academy of Finland (project grants 104781, 120315, 129269, 1114194, 24300796, Center of Excellence in Complex Disease Genetics and SALVE), Oulu University Hospital, Finland, Biocenter, University of Oulu, Finland 75617, 24002054, University of Oulu, Finland (grants 24000692 and 24500283: Well-being and health: Research in the Northern Finland Birth Cohorts 1966 and 1986, Phenotypic and Genomic analyses). NIH/NHLBI NHLBI grant 5R01HL087679-02 through the STAMPEED program (1RL1MH083268-01), NHLBI Consortium for Neuropsychiatric Phenomics Co-ordinating Center (1R01HL087679-01), and NIH/NIMH (5R01MH63706-02), United States. ENGAGE project and grant agreement HEALTH-F4-2007-201413. Medical Research Council (grant G1002319). The DNA extractions, sample quality controls, biobank upkeep, and aliquoting were performed in the National Public Health Institute, Biomedicum Helsinki, Finland and supported financially by the Academy of Finland and Biocentrum Helsinki. The authors thank Ms. Outi Tornwall and Ms. Minttu Jussila (DNA biobanking).

## STUDY FUNDING

This work was supported by Academy of Finland (grant 251704 to A.P.), Sigrid Juselius Foundation (to A.P.), SynSys (to A.P.), the Wellcome Trust (grant 098051 to A.P.), EU FP7-242167 (to A.P.), NIH/RFA-HL-12-007, Genomic and Metabolomic Profiling of Finnish Familial Dyslipidemia Families (to A.P.), the South-Eastern Norway Regional Health Authority (grants 2010075 and 2011083 to B.S.W., L.M.J., and J.-A.Z.), the Research Council of Norway (grant 231187/F20 to B.S.W.), and the NIHR Leicester Cardiovascular Biomedical Research Unit and BHF (to C.P.N.). N.J.S. holds a Chair funded by the British Heart Foundation and is an NIHR Senior Investigator. Funding for study cohorts and remaining authors are listed in the acknowledgment. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

## DISCLOSURE

Bendik S. Winsvold has received research support from the Research Council of Norway, the South-Eastern Norway Regional Health Authority, and Forsberg's and Auli Endowment. Christopher P. Nelson, Rainer Malik, and Padhraig Gormley report no disclosures. Verner Anttila has received research support from Orion Farnos Research Foundation. Jason Vander Heiden has received funding for travel and/or speaker honoraria from New England Biolabs; and has received research support from National Library of Medicine and the United States-Israel Binational Science Foundation. Katherine S. Elliott reports no disclosures. Line M. Jacobsen is employed by AstraZeneca. Priit Palta has received



research support from the Finnish Cultural Foundation. Najaf Amin has received research support from the Netherlands Brain Foundation. Boukje de Vries and Eija Hämmäläinen report no disclosures. Tobias Freilinger has received funding for travel and/or speaker honoraria from Boehringer Ingelheim and Allergan; and has received research support from Deutsche Forschungsgemeinschaft (DFG). M. Arfan Ikram has received funding for travel and/or speaker honoraria from Kaizo, Ltd.; has served on the editorial boards of *Neuroepidemiology*, *PLoS One*, and *Journal of Alzheimer Disease*; and has received research support from Janssen Prevention Center, Netherlands Organization for Health Research and Development, the Netherlands Heart Foundation, Internationaal Parkinson Fonds, Internationale Stichting Alzheimer Onderzoek, and the Alzheimer Association. Thorsten Kessler and Markku Koironen report no disclosures. Lannie Ligthart has received research support from EFIC-Grünenthal. George McMahon, Linda M. Pedersen, Christina Willenborg, and Hong-Hee Won report no disclosures. Jes Olesen has consulted for Janssen Pharmaceutical Products; and has served on speakers' bureaus for Allergan. Ville Artto has received funding for travel and/or speaker honoraria from Boehringer Ingelheim, Orion, Menarini, Migraine Trust, and Bayer; and has received research support from the Finnish Medical Foundation and Helsinki University Central Hospital. Themistocles L. Assimes has served on the editorial board of *Frontiers in Cardiovascular Medicine*; has consulted and received research support from Telomere Diagnostics, Inc.; and has received research support from NHLBI. Stefan Blankenberg, Dorret I. Boomsma, Lynn Cherkas, and George Davey Smith report no disclosures. Stephen E. Epstein has received research support from MedStar Heart and Vascular Institute, MedStar WA Hospital Center; and holds stock/stock options and/or receives Board of Directors Compensation for CardioCell. Jeanette Erdmann reports no disclosures. Michel D. Ferrari has served on the editorial board of *Cephalalgia*; and has received research support from the Netherlands Organization for Scientific Research (NWO), European Community, ZonMW, and the Dutch Heart Foundation. Hartmut Göbel has served on Scientific Advisory Boards for Allergan, Bayer Vital, and St. Jude Medical; has received funding for travel and/or speaker honoraria from Amgen, Allergan, Hormosan, Klosterfrau, MSD, Mundipharma, St. Jude Medical, and Teva; has served on the editorial board of *Der Schmerz, Pain Research and Treatment*; has served on speakers' bureaus for Allergan, Hormosan, Klosterfrau, MSD, Mundipharma, St. Jude Medical, and Teva; and has received research support from St. Jude Medical. Alistair S. Hall and Marjo-Riitta Jarvelin report no disclosures. Mikko Kallela has served on Advisory Boards for MSD and Allergan; has received funding for travel and/or speaker honoraria from MSD, Allergan, TEVA, Novartis, and Genzyme; has received compensation for producing educational material from TEVA and Allergan; has received research support from Helsinki University Central Hospital; and holds stock/stock options and/or has received Board of Directors compensation from Helsinki Headache Center. Jaakko Kaprio has served on an Advisory Board for Copenhagen University; has received funding for travel and/or speaker honoraria; and has consulted for Pfizer Ltd. Sekar Kathiresan has served on scientific advisory boards for Regeneron, Merck, Eli Lilly, Aegerionm, Catabasis, Amarin, and Novartis; and has received research support from Regeneron, Aegerion, Merck, NIH, and Fondation Leducq. Terho Lehtimäki reports no disclosures. Ruth McPherson has served on the editorial board of *Arteriosclerosis, Thrombosis & Vascular Biology*; and has received research support from Canadian Institutes of Health Research and Heart & Stroke Foundation of Canada. Winfried März has served on Scientific Advisory Boards and speakers' bureaus and consulted for Aegerion Pharmaceuticals, AMGEN, Danone Research, Sanofi/Genzyme, Hoffmann LaRoche, MSD, Synageva, Eli Lilly, and BASF; has received funding for travel and/or speaker honoraria from Aegerion Pharmaceuticals, AMGEN, Danone Research, Sanofi/Genzyme, Hoffmann LaRoche, MSD, Synageva, Eli Lilly, and BASF; has served on the editorial boards of *European Heart Journal* and *Journal of Laboratory Medicine*; has been employed by and holds stock/stock options and/or Board of Directors compensation from Synlab Services GmbH; and has received research support from Aegerion Pharmaceuticals, AMGEN, Danone Research, Sanofi/Genzyme, Hoffmann LaRoche, MSD, Synageva, Eli Lilly, BASF, European Union, German Ministry of Research, German Ministry of Commerce, and Wissenschaftsinitiative Oberthhein. Dale R. Nyholt reports no disclosures. Christopher J. O'Donnell

is employed by and has received research support from National Institutes of Health. Lydia Quaye reports no disclosures. Daniel J. Rader has served on the scientific advisory boards of *Arteriosclerosis, Thrombosis & Vascular Biology*; and has received research support from NIH and the Leducq Foundation. Olli Raitakari and Robert Roberts report no disclosures. Heribert Schunkert has served on scientific advisory boards, consulted for, received funding for travel and/or honoraria, and/or received research support from AstraZeneca, AMGEN, MSD SHARP & DOHME, Bayer Vital, Boehringer Ingelheim, Medtronic, Novartis, Pfizer, Sanofi-Aventis, St. Jude, Boston Scientific, and Daiichi Sankyo. Markus Schürks has served on the editorial boards of *The Journal of Headache and Pain*, and *BMC Neurology*; and consults Bayer HealthCare Pharmaceuticals. Alexandre F.R. Stewart has served on the editorial board of *Frontiers in Cardiovascular Medicine—Cardiovascular Genetics*. Gisela M. Terwindt has received research support from the Netherlands Organisation for Scientific Research (NWO). Unnur Thorsteinsdottir is an employee of deCODE genetics/Amgen. Arn M.J.M. van den Maagdenberg and Cornelia van Duijn report no disclosures. Majja Wessman has received research support from Folkhälsan Research Foundation, Academy of Finland, and Medicinska Understödsföreningen Liv och Hälsa. Tobias Kurth has served on editorial boards for *BMJ* and *Cephalalgia*; and has received research support from the French National Research Agency and the University of Bordeaux. Christian Kubisch reports no disclosures. Martin Dichgans has served on editorial boards for *Stroke, the International Journal of Stroke, Cerebrovascular Diseases*, and *Journal of Neurochemistry*; has consulted for Bayer Vital, Boehringer Ingelheim, Bristol-Myers Squibb, and Heel; and has received research support from Wellcome Trust, European Union, and German Federal Ministry of Education and Research. Daniel I. Chasman has served on the editorial board for *Arteriosclerosis, Thrombosis, and Vascular Biology*; and receives publishing royalties for *Protein Structure: Determination, Analysis, and Applications for Drug Discovery* (Marcel Dekker, 2003). Chris Cotsapas has served on the editorial board for *PLoS Genetics*; and has received research support from NINDS, NIAID, and RE Children's Consortium. John-Anker Zwart reports no disclosures. Nilesh J. Samani has served on editorial boards for *Circulation: Cardiovascular Genetics and Heart*; and has received research support from British Heart Foundation and National Institute for Health Research. Aarno Palotie has been a member of the Pfizer Genetics Scientific Advisory Panel; has received travel expenses and/or honoraria for lectures or educational activities not funded by industry; and has received research support from the Finnish Academy, European Union NIH, NINDS, Juselius Foundation, and the Finnish Foundation for Cardiovascular Research. Go to [Neurology.org/ng](http://Neurology.org/ng) for full disclosure forms.

Received April 4, 2015. Accepted in final form May 27, 2015.

## REFERENCES

1. Vos T, Flaxman AD, Naghavi M, et al. Years lived with disability (YLDs) for 1160 sequelae of 289 diseases and injuries 1990–2010: a systematic analysis for the Global Burden of Disease Study 2010. *Lancet* 2012; 380:2163–2196.
2. Headache Classification Committee of the International Headache Society (IHS). The International Classification of Headache Disorders, 3rd edition (beta version). *Cephalalgia* 2013;33:629–808.
3. Charles AC, Baca SM. Cortical spreading depression and migraine. *Nat Rev Neurol* 2013;9:637–644.
4. Charles A. Migraine is not primarily a vascular disorder. *Cephalalgia* 2012;32:431–432.
5. Ashina M. Vascular changes have a primary role in migraine. *Cephalalgia* 2012;32:428–430.
6. Noseda R, Burstein R. Migraine pathophysiology: anatomy of the trigeminovascular pathway and associated neurological symptoms, cortical spreading depression, sensitization, and modulation of pain. *Pain* 2013;154 (suppl 1):S44–S53.

7. Kurth T, Chabriat H, Bousser MG. Migraine and stroke: a complex association with clinical implications. *Lancet Neurol* 2012;11:92–100.
8. Bigal ME, Kurth T, Santanello N, et al. Migraine and cardiovascular disease: a population-based study. *Neurology* 2010;74:628–635.
9. Gudmundsson LS, Scher AI, Aspelund T, et al. Migraine with aura and risk of cardiovascular and all cause mortality in men and women: prospective cohort study. *BMJ* 2010;341:c3966.
10. Kurth T, Schurks M, Logroscino G, Gaziano JM, Buring JE. Migraine, vascular risk, and cardiovascular events in women: prospective cohort study. *BMJ* 2008;337:a636.
11. Liew G, Wang JJ, Mitchell P. Migraine and coronary heart disease mortality: a prospective cohort study. *Cephalalgia* 2007;27:368–371.
12. Anttila V, Winsvold BS, Gormley P, et al. Genome-wide meta-analysis identifies new susceptibility loci for migraine. *Nat Genet* 2013;45:912–917.
13. Schunkert H, König IR, Kathiresan S, et al. Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nat Genet* 2011;43:333–338.
14. Elliott KS, Chapman K, Day-Williams A, et al. Evaluation of the genetic overlap between osteoarthritis with body mass index and height using genome-wide association scan data. *Ann Rheum Dis* 2013;72:935–941.
15. R Core Team. R: A language and environment for statistical computing. R Foundation for Statistical Computing [computer program]. Vienna, Austria; 2013. Available at: <http://www.R-project.org/>. Accessed September 20, 2013.
16. Purcell SM, Wray NR, Stone JL, et al. Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. *Nature* 2009;460:748–752.
17. Wright FA, Sullivan PF, Brooks AI, et al. Heritability and genomics of gene expression in peripheral blood. *Nat Genet* 2014;46:430–437.
18. Nitz I, Fisher E, Weikert C, et al. Association analyses of GIP and GIPR polymorphisms with traits of the metabolic syndrome. *Mol Nutr Food Res* 2007;51:1046–1052.
19. Le H, Tfelt-Hansen P, Russell MB, Skytthe A, Kyvik KO, Olesen J. Co-morbidity of migraine with somatic disease in a large population-based study. *Cephalalgia* 2011;31:43–64.
20. Wang YC, Lin CW, Ho YT, Huang YP, Pan SL. Increased risk of ischemic heart disease in young patients with migraine: a population-based, propensity score-matched, longitudinal follow-up study. *Int J Cardiol* 2014;172:213–216.
21. Sacco S, Ornello R, Ripa P, et al. Migraine and risk of ischaemic heart disease: a systematic review and meta-analysis of observational studies. *Eur J Neurol* 2015;22:1001–1011.
22. Schurks M, Rist PM, Bigal ME, Buring JE, Lipton RB, Kurth T. Migraine and cardiovascular disease: systematic review and meta-analysis. *BMJ* 2009;339:b3914.
23. Debette S, Kamatani Y, Metso TM, et al. Common variation in PHACTR1 is associated with susceptibility to cervical artery dissection. *Nat Genet* 2015;47:78–83.
24. Anttila V, Stefansson H, Kallela M, et al. Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. *Nat Genet* 2010;42:869–873.
25. Freilinger T, Anttila V, de Vries B, et al. Genome-wide association analysis identifies susceptibility loci for migraine without aura. *Nat Genet* 2012;44:777–782.
26. Chasman DI, Schurks M, Anttila V, et al. Genome-wide association study reveals three susceptibility loci for common migraine in the general population. *Nat Genet* 2011;43:695–698.
27. Russell MB, Olesen J. Increased familial risk and evidence of genetic factor in migraine. *BMJ* 1995;311:541–544.
28. Nyholt DR, Anttila V, Winsvold BS, et al. Concordance of genetic risk across migraine subgroups: impact on current and future genetic association studies. *Cephalalgia* 2014;35:489–499.
29. Ozaki K, Sato H, Inoue K, et al. SNPs in BRAP associated with risk of myocardial infarction in Asian populations. *Nat Genet* 2009;41:329–333.
30. Coronary Artery Disease (C4D) Genetics Consortium. A genome-wide association study in Europeans and South Asians identifies five new loci for coronary artery disease. *Nat Genet* 2011;43:339–344.
31. O'Donnell CJ, Kavousi M, Smith AV, et al. Genome-wide association study for coronary artery calcification with follow-up in myocardial infarction. *Circulation* 2011;124:2855–2864.
32. Bevan S, Traylor M, Adib-Samii P, et al. Genetic heritability of ischemic stroke and the contribution of previously reported candidate gene and genomewide associations. *Stroke* 2012;43:3161–3167.
33. Allen PB, Greenfield AT, Svenningsson P, Haspelagh DC, Greengard P. Phactrs 1–4: a family of protein phosphatase 1 and actin regulatory proteins. *Proc Natl Acad Sci U S A* 2004;101:7187–7192.
34. Allain B, Jarray R, Borriello L, et al. Neuropilin-1 regulates a new VEGF-induced gene, Phactr-1, which controls tubulogenesis and modulates lamellipodial dynamics in human endothelial cells. *Cell Signal* 2012;24:214–223.
35. Patel RS, Morris AA, Ahmed Y, et al. A genetic risk variant for myocardial infarction on chromosome 6p24 is associated with impaired central hemodynamic indexes. *Am J Hypertens* 2012;25:797–803.
36. Rodríguez-Osorio X, Sobrino T, Brea D, Martínez F, Castillo J, Leira R. Endothelial progenitor cells: a new key for endothelial dysfunction in migraine. *Neurology* 2012;79:474–479.
37. Tietjen GE. Migraine as a systemic vasculopathy. *Cephalalgia* 2009;29:987–996.
38. Baggio LL, Drucker DJ. Biology of incretins: GLP-1 and GIP. *Gastroenterology* 2007;132:2131–2157.
39. Nyberg J, Anderson MF, Meister B, et al. Glucose-dependent insulinotropic polypeptide is expressed in adult hippocampus and induces progenitor cell proliferation. *J Neurosci* 2005;25:1816–1825.
40. Winsvold BS, Sandven I, Hagen K, Linde M, Midthjell K, Zwart JA. Migraine, headache and development of metabolic syndrome: an 11-year follow-up in the Nord-Trøndelag Health Study (HUNT). *Pain* 2013;154:1305–1311.

# Neurology<sup>®</sup> Genetics

## **Genetic analysis for a shared biological basis between migraine and coronary artery disease**

Bendik S. Winsvold, Christopher P. Nelson, Rainer Malik, et al.

*Neurol Genet* 2015;1;

DOI 10.1212/NXG.0000000000000010

**This information is current as of July 2, 2015**

*Neurol Genet* is an official journal of the American Academy of Neurology. Published since April 2015, it is an open-access, online-only, continuous publication journal. Copyright © 2015 American Academy of Neurology. All rights reserved. Online ISSN: 2376-7839.



<b>Updated Information &amp; Services</b>	including high resolution figures, can be found at: <a href="http://ng.neurology.org/content/1/1/e10.full.html">http://ng.neurology.org/content/1/1/e10.full.html</a>
<b>Supplementary Material</b>	Supplementary material can be found at: <a href="http://ng.neurology.org/content/suppl/2015/07/02/1.1.e10.DC1">http://ng.neurology.org/content/suppl/2015/07/02/1.1.e10.DC1</a> <a href="http://ng.neurology.org/content/suppl/2015/07/02/1.1.e10.DC2">http://ng.neurology.org/content/suppl/2015/07/02/1.1.e10.DC2</a>
<b>References</b>	This article cites 39 articles, 15 of which you can access for free at: <a href="http://ng.neurology.org/content/1/1/e10.full.html##ref-list-1">http://ng.neurology.org/content/1/1/e10.full.html##ref-list-1</a>
<b>Citations</b>	This article has been cited by 5 HighWire-hosted articles: <a href="http://ng.neurology.org/content/1/1/e10.full.html##otherarticles">http://ng.neurology.org/content/1/1/e10.full.html##otherarticles</a>
<b>Subspecialty Collections</b>	This article, along with others on similar topics, appears in the following collection(s): <b>Association studies in genetics</b> <a href="http://ng.neurology.org/cgi/collection/association_studies_in_genetics">http://ng.neurology.org/cgi/collection/association_studies_in_genetics</a> <b>Cardiac; see Cerebrovascular Disease/Cardiac</b> <a href="http://ng.neurology.org/cgi/collection/cardiac_see_cerebrovascular_disease-cardiac">http://ng.neurology.org/cgi/collection/cardiac_see_cerebrovascular_disease-cardiac</a> <b>Migraine</b> <a href="http://ng.neurology.org/cgi/collection/migraine">http://ng.neurology.org/cgi/collection/migraine</a>
<b>Permissions &amp; Licensing</b>	Information about reproducing this article in parts (figures, tables) or in its entirety can be found online at: <a href="http://ng.neurology.org/misc/about.xhtml#permissions">http://ng.neurology.org/misc/about.xhtml#permissions</a>
<b>Reprints</b>	Information about ordering reprints can be found online: <a href="http://ng.neurology.org/misc/addir.xhtml#reprintsus">http://ng.neurology.org/misc/addir.xhtml#reprintsus</a>

*Neurol Genet* is an official journal of the American Academy of Neurology. Published since April 2015, it is an open-access, online-only, continuous publication journal. Copyright © 2015 American Academy of Neurology. All rights reserved. Online ISSN: 2376-7839.

