Genetic determinants of common epilepsies: a meta-analysis of genome-wide association studies

International League Against Epilepsy Consortium on Complex Epilepsies

Summary

Background The epilepsies are a clinically heterogeneous group of neurological disorders. Despite strong evidence for heritability, genome-wide association studies have had little success in identification of risk loci associated with epilepsy, probably because of relatively small sample sizes and insufficient power. We aimed to identify risk loci through meta-analyses of genome-wide association studies for all epilepsy and the two largest clinical subtypes (genetic generalised epilepsy and focal epilepsy).

Methods We combined genome-wide association data from 12 cohorts of individuals with epilepsy and controls from population-based datasets. Controls were ethnically matched with cases. We phenotyped individuals with epilepsy into categories of genetic generalised epilepsy, focal epilepsy, or unclassified epilepsy. After standardised filtering for quality control and imputation to account for different genotyping platforms across sites, investigators at each site conducted a linear mixed-model association analysis for each dataset. Combining summary statistics, we conducted fixed-effects meta-analyses of all epilepsy, focal epilepsy, and genetic generalised epilepsy. We set the genome-wide significance threshold at $p<1.66 \times 10^{-8}$.

Findings We included 8696 cases and 26 157 controls in our analysis. Meta-analysis of the all-epilepsy cohort identified loci at 2q24.3 ($p=8.71 \times 10^{-10}$), implicating SCN1A, and at 4p15.1 ($p=5.44 \times 10^{-9}$), harbouring PCDH7, which encodes a protocadherin molecule not previously implicated in epilepsy. For the cohort of genetic generalised epilepsy, we noted a single signal at 2p16.1 ($p=9.99 \times 10^{-9}$), implicating VRK2 or FANCL. No single nucleotide polymorphism achieved genome-wide significance for focal epilepsy.

Interpretation This meta-analysis describes a new locus not previously implicated in epilepsy and provides further evidence about the genetic architecture of these disorders, with the ultimate aim of assisting in disease classification and prognosis. The data suggest that specific loci can act pleiotropically raising risk for epilepsy broadly, or can have effects limited to a specific epilepsy subtype. Future genetic analyses might benefit from both lumping (ie, grouping of epilepsy types together) or splitting (ie, analysis of specific clinical subtypes).

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Introduction

Epilepsy is a common disorder, affecting up to 4% of people at some time in life. The disorder includes a group of heterogeneous syndromes defined by clinical, electroencephalographic (EEG), and brain imaging criteria. Broadly, the epilepsies are divided clinically into generalised and focal forms. Genetic factors contribute to both, as shown by findings from familial aggregation and twin studies. Causative mutations in many genes, including some genes coding for ion channel subunits and others involved in synaptic function or brain development, have been reported. Most of these findings were reported in patients with fairly rare familial epilepsies segregating in a Mendelian way or epilepsies arising from de-novo mutations (particularly in patients with severe infantile epilepsies). The genetic determinants underlying the common epilepsies, for which clinical genetic data suggest complex inheritance, remain largely unknown. Some evidence suggests a role for rare sequence and copy number variants, whereas the contribution of common polymorphisms is still unclear, partly as a result of the relatively small sample sizes analysed to date.

Findings from the largest genome-wide association study (GWAS) in epilepsy so far, including 3445 patients with focal epilepsy, showed no variants of genome-wide significance. More recently, findings from a study of 1018 patients with mesial temporal lobe epilepsy with hippocampal sclerosis (a subtype of focal epilepsy) implicated the 2q24.3 region around the gene encoding the sodium channel SCN1A, and findings from an independent study of Han Chinese patients with known or suspected lesional focal epilepsy showed evidence for a risk allele at 1q32 on the basis of a discovery sample of 504 cases.

For generalised epilepsy, a GWAS included 1527 European patients with genetic generalised...
epilepsies in the discovery analysis and 1493 patients in the replication cohort; investigators reported evidence for common risk alleles at 2p16.1 and 17q21.32, and suggestive evidence at the SCN1A locus.\(^\text{16}\) Additionally, associations were reported for the juvenile myoclonic subtype of genetic generalised epilepsy at 1q43 and for absence epilepsy at 2q22.3.\(^\text{16}\)

In a large multicentre collaboration, we undertook a meta-analysis to detect variants that could increase risk for common epilepsies. In view of clinical evidence that some genetic factors might increase risk for epilepsy broadly and in a syndrome-specific manner,\(^\text{17–19}\) we prespecified three analyses as part of the study. Variants were sought that affected risk for all epilepsies, genetic generalised epilepsy (previously known as idiopathic generalised epilepsy),\(^\text{2,20}\) or focal epilepsy.

## Methods

### Study design and participants

We did a meta-analysis of data from 12 previously published or unpublished genetic cohort studies from EPICURE,\(^\text{16}\) EPIGEN,\(^\text{13}\) Philadelphia (PA, USA), the Imperial-Liverpool-Melbourne Collaboration,\(^\text{21}\) GenEpa,\(^\text{13}\) and Hong Kong (China)\(^\text{15}\) (appendix). We identified these studies from the scientific literature (through searches of PubMed in December, 2011, with the terms “epilepsy”, “seizures”, and “association studies”), through publicity via Chapters of the International League Against Epilepsy, and during international conferences. All participants in these 12 case cohorts (and their associated controls) were of European, Asian, or African ancestry (table 1, appendix).

### Criteria for genetic generalised epilepsy

We assigned patients to one of three phenotypic categories: genetic generalised epilepsy, focal epilepsy, or unclassified epilepsy.

### Statistical analysis

We used prespecified criteria for quality control to filter cases and controls from the 12 cohorts (appendix).

## Results

The genetic cohort studies used a combination of population-based datasets as controls. These control cohorts were either screened or unscreened by questionnaire for neurological disorders (table 1, appendix).

All study participants provided written informed consent for DNA analysis. Local institutional review boards reviewed and approved study protocols at each site.

### Procedures

We classified seizures and epilepsy syndromes according to the International League Against Epilepsy terminology.\(^\text{2,20}\) For all cases, epilepsy specialists assessed phenotype at the source centre. Patients with epilepsy were assigned to one of three phenotypic categories: genetic generalised epilepsy, focal epilepsy, or unclassified epilepsy.

In the phenotypic category of focal epilepsy, we included patients with a confirmed diagnosis of focal epilepsy, including cases with focal structural brain lesions. These cases were predominantly adults, and as such, cases of benign epilepsy of childhood with centro-temporal spikes were not specifically included.

Unclassified epilepsy consisted of patients in whom there was neither electroclinical evidence for generalised epilepsy nor evidence for a focal seizure onset. Additionally, cases with evidence for both generalised and focal epilepsy were included here.

The phenotyping committee curated patient phenotypes into a single database. Details relating to individual case cohorts are provided in the appendix. Analyses were done for three phenotypic groups: genetic generalised epilepsy, focal epilepsy, and all epilepsy (consisting of all patients with a confirmed diagnosis of epilepsy, including genetic generalised epilepsy, focal epilepsy, and unclassified epilepsy).

## Table 1: Cases and controls, by index GWAS

<table>
<thead>
<tr>
<th>Ethnic origin</th>
<th>All epilepsy (n=8696)</th>
<th>Genetic generalised epilepsy (n=2666)</th>
<th>Focal epilepsy (n=3110)</th>
<th>Population controls (n=26 157)</th>
</tr>
</thead>
<tbody>
<tr>
<td>EPIGEN-Dublin</td>
<td>Irish</td>
<td>638</td>
<td>520</td>
<td>2232</td>
</tr>
<tr>
<td>EPIGEN-Brussels</td>
<td>Belgian</td>
<td>505</td>
<td>406</td>
<td>1675</td>
</tr>
<tr>
<td>EPIGEN-Duke†</td>
<td>African-American and European-American</td>
<td>760</td>
<td>551</td>
<td>504</td>
</tr>
<tr>
<td>EPIGEN-London</td>
<td>British and other</td>
<td>1007</td>
<td>773</td>
<td>2494</td>
</tr>
<tr>
<td>ILM Collaboration</td>
<td>European descent</td>
<td>3703</td>
<td>2126</td>
<td>2699</td>
</tr>
<tr>
<td>GenEpa</td>
<td>Finnish</td>
<td>422</td>
<td>422</td>
<td>1963</td>
</tr>
<tr>
<td>EPICURE</td>
<td>Northwest European</td>
<td>1440</td>
<td>222</td>
<td>2454</td>
</tr>
<tr>
<td>Philadelphia_S50_AA</td>
<td>African-American</td>
<td>324</td>
<td>378</td>
<td>5736</td>
</tr>
<tr>
<td>Philadelphia_S50_CAU</td>
<td>European-American</td>
<td>819</td>
<td>106</td>
<td>97</td>
</tr>
<tr>
<td>Philadelphia_Omni_AA</td>
<td>African-American</td>
<td>106</td>
<td>106</td>
<td>97</td>
</tr>
<tr>
<td>Philadelphia_Omni_CAU</td>
<td>European-American</td>
<td>485</td>
<td>288</td>
<td>682</td>
</tr>
<tr>
<td>Hong Kong</td>
<td>Asian-Han</td>
<td>487</td>
<td>487</td>
<td>2875</td>
</tr>
</tbody>
</table>

Numbers of cases and controls are after quality control filtering. GWAS=genome-wide association study. ILM=Imperial-Liverpool-Melbourne. *Broad ethnic origin of the cohort. Other indicates people of mixed ethnic origin, as would be expected in a cosmopolitan population. European descent refers to white European. †EPIGEN-Duke individuals of African-American ancestry were merged with participants in the Philadelphia_S50_AA cohort. ‡See appendix for further details about control cohorts. §Small sample size prohibited epilepsy subtype analysis in this cohort.
according to a standardised protocol. This protocol used IMPUTE2 to infer and impute haplotypes, with the 1000 Genomes Phase 1 (interim) June, 2011, reference panel (appendix).

Investigators at each site did a linear mixed-model association analysis for each of their datasets with FaSTLMM (version 1.09).22 This analysis uses linear regression, including a polygenic term designed to account for the contributions of population stratification and causal variants aside from the one being tested. Although we were assessing a binary trait, we used linear regression (rather than logistic regression) because we expected effect sizes to be small. We did this analysis separately for each of the preselected phenotypic categories of epilepsy (all epilepsy, genetic generalised epilepsy, and focal epilepsy). Sex was included as a covariate.

We did a fixed-effects meta-analysis with METAL (version generic-metal-2011-03-25).23 Because almost all epilepsy cases were of European descent (table 1), we chose a fixed-effects model to optimise power. Single nucleotide polymorphisms showing significant amounts of heterogeneity (p<0.05) were removed before application of the fixed-effects analysis. We applied genomic correction to the association analysis results for each dataset before combining for meta-analysis. These steps were done separately for each of the three phenotypic tests.

We set our genome-wide threshold for statistical significance at 1.66×10⁻⁸, representing an empirical genome-wide significance threshold for three tests. We regarded signals with p values between 1.66×10⁻⁸ and 5×10⁻⁷ as suggestive evidence of association.

We calculated the proportion of phenotypic variance a variant must explain (heritability) for the detection power to be at least 80%. We used variance explained on the liability scale,24 for which we assumed a point prevalence of 0.5% for all epilepsy, 0.2% for genetic generalised epilepsy, and 0.3% for focal epilepsy.25 The required heritability was 0.07% or greater for all epilepsy, 0.17% or greater for genetic generalised epilepsy, and 0.10% or greater for focal epilepsy (appendix).

In addition to the main association analysis, we did logistic regression for variants in a 1 megabase window centred on each variant that showed suggestive evidence of association (p<5×10⁻⁷) from any of the three meta-analyses (all epilepsy, genetic generalised epilepsy, or focal epilepsy). The purpose of this analysis was technical validation and to submit for publication. The strategy committee (appendix) of the Consortium takes final responsibility for the decision to submit for publication.

Role of the funding source
The funders had no role in the study design, data collection, data analysis, data interpretation, or writing of the report. The members of the strategy and analysis committees of the International League Against Epilepsy Consortium on Complex Epilepsies had full access to all data in the study. The strategy committee (appendix) of the Consortium takes final responsibility for the decision to submit for publication.

Results
40789 participants, comprising 10064 people with epilepsy from 12 cohorts and 30725 controls, were studied. After application of our quality control criteria (appendix), we included a total of 34853 individuals (8696 with epilepsy and 26157 controls) in the meta-analysis for all epilepsies (table 1).

Principal component analysis suggested that the cohorts clustered in three broad ethnic origins (European, Asian, and admixed African-American), as expected (appendix). We noted an inflation factor of 1.031, suggesting adequate control for possible cryptic stratification (appendix).

In the all-epilepsy analysis, we identified two loci with genome-wide significance (p<1.66×10⁻⁸; figure 1). The
first signal was located at 2q24.3 (figure 2). This signal was
centred on the voltage-gated sodium channel gene SCN1A,
which is a known gene associated with some monogenic
epilepsies.\textsuperscript{7,28,29} The most strongly associated variant in this
interval was rs6732655 (\(p=8.71 \times 10^{-10}\), OR 0.89, 95% CI
0.86–0.93; table 2, appendix), located in intron 16 of
SCN1A. Seventy other variants in this region satisfied the
threshold for genome-wide significance. Logistic regres-
sion validated the association with 2q24.3 (appendix). The
direction of effect was consistent across most cohorts, and
there was no evidence of substantial heterogeneity.

In view of the extent of linkage disequilibrium between
the variants associated with all epilepsy in the 2q24.3 region
(figure 2), we did logistic regression conditioned on the
most significant variant identified from the univariate
analysis (rs6732655). Our results suggested a tentative
independent signal, coming from rs13406236, in an intronic
variant in SCN9A (\(p=1.39 \times 10^{-4}\) on conditioning; appendix).
We did not identify any further significant signals.

A second signal for the all-epilepsy phenotype was
located at 4p15.1 and included the 3’ end of the
protocadherin gene, PCDH7 (figure 3). The most strongly
associated variant in this region was rs28498976
(\(p=5.44 \times 10^{-9}\), OR 0.90, 95% CI 0.87–0.94; table 2),
located 2.5 kilobases from the 3’ end of PCDH7. Logistic
regression across PCDH7 supported the association with

\begin{figure}

\centering

\includegraphics[width=\textwidth]{manhattan_plots}

\caption{Manhattan plots for meta-analyses of all epilepsy (A), genetic generalised epilepsy (B), and focal epilepsy (C)}

The red line shows our threshold of significance set at \(p=1.66 \times 10^{-8}\), and the green line shows the suggestive threshold of \(p=5 \times 10^{-7}\). Y axis is broken in all graphs.

\end{figure}
We noted no additional significant signals from 4p15.1 on conditioning for rs28498976 (appendix). The direction of effect was consistent across all cohorts and we noted no evidence of heterogeneity. Although achieving genome-wide significance only for the all-epilepsy phenotype, the PCDH7 signal seemed stronger in genetic generalised epilepsy than in focal epilepsy (appendix).

PCDH7 encodes a calcium-dependent adhesion protein, not previously associated with epilepsy. It is a member of the cadherin gene family. The gene is expressed in the CNS, specifically in thalamocortical circuits and the hippocampus,27,28 and expression of PCDH7 is controlled by MECP2,32 mutations in which cause Rett syndrome. The cytoplasmic domain of the PCDH7 protein binds to protein phosphatase 1α (PPP1CA), which is enriched in dendritic spines and is important in learning and memory,33 and to template activation factor 1 (TAF1), which along with PCDH7 is involved in neurite extension.34,35

Figure 2: Genomic context of 2q24.3 signal from all-epilepsy analysis
Plot created with LocusZoom (version 1.1). Linkage disequilibrium data taken from the 1000 Genomes Project, HG19, March, 2012.

Table 2: Genome-wide associated loci at p<5.0 × 10⁻⁷

<table>
<thead>
<tr>
<th>Cytogenetic band</th>
<th>Base pair position</th>
<th>Allele 1, allele 2</th>
<th>Minor allele frequency</th>
<th>Candidate gene</th>
<th>Annotation</th>
<th>Phenotype</th>
<th>OR (95% CI)</th>
<th>ps</th>
<th>pcond</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs6732655</td>
<td>2q24.3</td>
<td>16689066</td>
<td>T*, A</td>
<td>SCN1A</td>
<td>Intronic</td>
<td>All epilepsy</td>
<td>0.89 (0.86–0.93)</td>
<td>8.71 × 10⁻⁷</td>
<td>4.95 × 10⁻⁷</td>
</tr>
<tr>
<td>rs28498976</td>
<td>4p15.1</td>
<td>31151327</td>
<td>A, G*</td>
<td>PCDH7</td>
<td>Intergenic</td>
<td>All epilepsy</td>
<td>0.90 (0.87–0.94)</td>
<td>5.44 × 10⁻⁷</td>
<td>2.29 × 10⁻⁴</td>
</tr>
<tr>
<td>rs111577701</td>
<td>3q26.2</td>
<td>167861408</td>
<td>T, C*</td>
<td>GOLM4</td>
<td>Intergenic</td>
<td>All epilepsy</td>
<td>1.16 (1.09–1.24)</td>
<td>4.42 × 10⁻⁷</td>
<td></td>
</tr>
<tr>
<td>rs553066</td>
<td>4p12</td>
<td>46240287</td>
<td>T, G*</td>
<td>GABRA2</td>
<td>Intergenic</td>
<td>All epilepsy</td>
<td>1.10 (1.05–1.16)</td>
<td>7.11 × 10⁻⁴</td>
<td></td>
</tr>
<tr>
<td>rs2947349</td>
<td>2p16.1</td>
<td>58059803</td>
<td>A*, C</td>
<td>VRK2/FANKL</td>
<td>Intergenic</td>
<td>GGE</td>
<td>1.23 (1.16–1.31)</td>
<td>9.99 × 10⁻⁴</td>
<td>1.0 × 10⁻⁴</td>
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<tr>
<td>rs1939012</td>
<td>11q22.2</td>
<td>102595135</td>
<td>C, T*</td>
<td>MMP8</td>
<td>Intronic</td>
<td>GGE</td>
<td>1.12 (1.07–1.17)</td>
<td>2.37 × 10⁻⁴</td>
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<tr>
<td>rs404352</td>
<td>11q22.1</td>
<td>31147874</td>
<td>T, G</td>
<td>PCDH7</td>
<td>Synonymous</td>
<td>GGE</td>
<td>0.88 (0.82–0.93)</td>
<td>1.87 × 10⁻⁷</td>
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<tr>
<td>rs55670112</td>
<td>5q23.3</td>
<td>114268470</td>
<td>A*, C</td>
<td>None</td>
<td>Intergenic</td>
<td>GGE</td>
<td>1.18 (1.1–1.26)</td>
<td>6.34 × 10⁻⁴</td>
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<tr>
<td>rs1298787</td>
<td>2q24.3</td>
<td>166858391</td>
<td>C, T*</td>
<td>SON1A</td>
<td>Intronic</td>
<td>Focal epilepsy</td>
<td>1.12 (1.01–1.14)</td>
<td>1.45 × 10⁻⁴</td>
<td></td>
</tr>
</tbody>
</table>

Base pair position refers to build 37 (hg19). Minor allele frequency is from all populations from the 1000 Genomes Project. Candidate gene refers to the most plausible candidate gene attributable to the signal. OR corresponds to allele 2, computed from logistic regression. Annotation refers to type of SNP. ps refers to p value from linear mixed-model meta-analysis. pcond refers to p value when conditioning on this specific SNP to determine independent signals from same locus. OR=odds ratio. GGE=genetic generalised epilepsy. SNP=single nucleotide polymorphism. *Ancestral or chimpanzee allele.
Suggestive signals of note (p<5×10^−7) for the all-epilepsy phenotype were detected at 3q26.2 (p=4·42×10^−7) and 4p12 (p=1·71×10^−7; table 2). The 3q26.2 region contained the 5′ end of GOLIM4 (appendix). This gene encodes Golgi internal membrane protein 4, which is degraded when manganese increases above normal concentrations, suggesting a role for this protein in manganese homoeostasis.36 Almost all brain manganese is bound to glutamine synthetase, an enzyme playing a key part in production or degradation of the neurotransmitters glutamate, glutamine, and GABA. Decreased brain glutamine synthetase and manganese concentrations have been reported in epilepsy.37,38 The 4p12 region contained the 3′ end of the GABA receptor, α2-subunit gene (GABRA2). Mutations in other GABA receptors have been reported to cause epilepsy.39

After quality control, we included 21 596 individuals (2606 cases and 18 990 controls) across eight cohorts in the meta-analysis of genetic generalised epilepsy (table 1), a subset of those included in the all-epilepsy analysis. Results from the genetic generalised epilepsy meta-analysis suggested an inflation factor of 1·05 (appendix). A single signal achieved the threshold of genome-wide significance (figure 1). Located at 2p16.1, the interval contained genes encoding vaccinia-related kinase 2 (VRK2) and Fanconi anaemia, complementation group L (FANCL; figure 4). The most strongly associated variant in this region was the intergenic variant rs2947349 (p=9·99×10^−9, OR 1·23, 95% CI 1·16–1·31; table 2). Logistic regression analysis supported the association with 2p16.1 (appendix). We noted no additional significant signals from 2p16.1 on conditioning for rs2947349 (appendix). The direction of effect was consistent across all cohorts, and the association seemed to be specific to genetic generalised epilepsy (appendix).

VRK2 is a serine-threonine protein kinase involved in signal transduction and apoptosis.40,41 Variation in VRK2 has previously been suggested as a risk factor for epilepsy42 and schizophrenia.43–44 Indeed, the schizophrenia-associated risk variant (rs2312147)43 shows also a strong signal for genetic generalised epilepsy (p=2·3×10^−6, OR 1·22, 95% CI 1·14–1·30) and is in high linkage disequilibrium with the strongest variant for genetic generalised epilepsy (r²=0·82), although the direction of the effect is opposite (ie, the protective variant for epilepsy raises risk for schizophrenia). The EPICURE cohort, in which 2p16.1 was originally proposed as a risk factor for genetic generalised epilepsy, was included in our meta-analysis. After exclusion of the EPICURE cohort, the top single nucleotide polymorphism from their study (rs13026414)44 remained nominally significant at p=7×10^−3 here. These results provide further support to the...
suggestion that VRK2 is a risk locus for both epilepsy and schizophrenia. The other gene in the region, FANCL, codes for a RING-type E3 ubiquitin ligase of the Fanconi anaemia pathway. FANCL mono-ubiquitinates FANCD2 and FANCI, proteins involved in DNA repair and homologous recombination. FANCL has not been previously implicated in epilepsy or any seizure-related phenotype.

We detected suggestive evidence for association with genetic generalised epilepsy at 4p15.1 (p=1·87×10⁻⁷), 5q22.3 (p=6·34×10⁻⁸), and 11q22.2 (p=2·37×10⁻⁸; table 2). The 4p15.1 PCDH7 signal was the same as that with genome-wide significance for the all-epilepsy phenotype (figure 3, appendix). The 5q22.3 signal was intergenic (appendix). The 11q22.2 signal contained the 5’ end of the matrix metallopeptidase gene MMP8 (appendix). The direction of effect was consistent across all cohorts and seemed specific to genetic generalised epilepsy (appendix). With a p value of 2·37×10⁻⁸, the 11q22.2 signal reached the conventional threshold for genome-wide significance (p<5×10⁻⁸), but not our more stringent value (p<1·66×10⁻⁸). Matrix metallopeptidases are zinc-dependent endopeptidases involved in the breakdown of the extracellular matrix in physiological processes and in blood–brain inflammation. Increased expression of MMPs has been recorded in various neurological disease states, and epileptogenesis is decreased in MMP9 knockout mice but increased in transgenic rats overexpressing MMP9.

After quality control, we included 28916 individuals (5310 cases and 23606 controls) from ten cohorts in our meta-analysis of focal epilepsy. No signal achieved genome-wide significance. Results from the focal meta-analysis suggested an inflation factor of 1·014 (appendix). We observed one notable subthreshold signal (rs12987787, p=1·45×10⁻⁷) from 2q24.3, the region containing SCN1A (appendix).

Targeted genotyping of the three GWAS-significant signals supported the accuracy of imputation, with a minimum correlation of 0·98 noted between experimentally determined and imputed genotypes (appendix). Assessment of enrichment of gene ontology terms for regions containing variants with nominally significant p values (p<1×10⁻⁵) for each of the three phenotypes showed enrichment in several signalling pathways (appendix). Although none of these variants remained significant after correction for multiple testing, our results suggest pathways with biological plausibility.

Finally, we investigated whether any of the four susceptibility loci at nominal genome-wide significance (p<5×10⁻⁸) were associated with outcome of newly treated epilepsy with use of data from Speed and colleagues. We used both the index single nucleotide polymorphism (table 2) and single nucleotide polymorphisms within a 20 kilobase window around each of the five genes (SCN1A, PCDH7, VRK2/FANCL, and MMP8;
The minimum p value of association with outcome of newly treated epilepsy for any susceptibility locus was 8.14 x 10^{-4} (MMP8). We noted no evidence for an association between SCN1A (the gene that codes for the target of sodium-channel-blocking class antiepileptic drugs) and epilepsy outcome.

Discussion
In this genome-wide association meta-analysis of epilepsy and its most common subtypes, we identified three loci with genome-wide significance, and our findings suggest that some loci might be specifically associated with an epilepsy type.

In the whole cohort consisting of all epilepsy, the region of the sodium channel subunit gene SCN1A was clearly associated with the disease. This gene is a well-established cause of genetic epilepsy with febrile seizures plus (GEFS+), a generally mild, familial form of epilepsy, and with Dravet syndrome, a severe epileptic encephalopathy usually arising from de-novo mutations.

SCN1A was associated with mesial temporal lobe epilepsy and hippocampal sclerosis with febrile seizures in a recent GWAS and in a meta-analysis of SCN1A rs3812718. SCN1A mutations have also been reported in a range of paroxysmal neurological disorders including familial hemiplegic migraine and, more rarely, in some focal epilepsies. Whether this robust association with all epilepsy is a true common variant association or a synthetic association due to tagged rare variants in cases with GEFS+ is therefore not clear. Although the cohorts might have included individuals from monogenic GEFS+ families with SCN1A mutations of large effect, review of the phenotyping data suggested that inclusion of more than a few such cases was unlikely; moreover, SCN1A variants have been reported only in about 10% of large GEFS+ families.

Our all-epilepsy analysis identified a second locus (4p15.1) that satisfied our threshold for genome-wide significance. This locus is newly associated with epilepsy and implicates the gene PCDH7. This protocadherin gene is a plausible candidate for common forms of epilepsy, as mutations in another protocadherin gene, PCDH19, cause epilepsy and mental retardation in female patients.

For the specific category of genetic generalised epilepsy, we noted the association at 2p16.1 that was previously reported in the EPICURE cohort; this cohort provided about half of our sample for the meta-analysis of this subtype (table 1). The association maintained nominal significance after removal of EPICURE cases for this locus, where the genes VRK2 and FANCL are within close proximity. With our additional samples, we did not note significance for the 17q21 locus reported by EPICURE investigators for genetic generalised epilepsy (appendix).

For the subcategory of focal epilepsy, we did not note any locus with genome-wide significance, consistent with negative findings from the EPIGEN study of focal epilepsy (samples from which were included in our analysis). However, a signal at 2q24.3 (containing SCN1A) in focal epilepsy approached but did not achieve significance (appendix). This signal in focal epilepsy was in high linkage disequilibrium with that noted for all epilepsy (r^2=0.85). Importantly, the 2q24.3 signal for focal epilepsy that we recorded differed to that reported in a recent study of the narrow focal epilepsy phenotype of mesial temporal lobe epilepsy and hippocampal sclerosis with febrile seizures. rs7587026 (the previously reported variant) was not significant in our analysis of a broader focal epilepsy phenotype consisting of all focal epilepsies (p=0.01; appendix). We also did not note the association at 1q32.1 (implicating CAMSAPIL) that was previously reported in the Hong Kong cohort, which was included in our sample (appendix). Most patients in this cohort had focal epilepsy due to known lesions.

Consistent with experience of GWAS in other neuropsychiatric disorders, and common disorders in general, this study reinforces the value of large sample sizes. In the epilepsies, electroclinical and imaging data allow the identification of clinical syndromes that share common clinical features. Our study findings suggest that an experimental design that includes fractionation of samples into clinical subtypes can reveal syndrome-specific risk alleles, but the identification of these alleles will be assisted by the collection and genotyping of larger sample sizes. Although this lumping versus splitting debate in genetic analyses is not unique to the epilepsies, there has been longstanding controversy about it in clinical epileptology, which genetics will help to inform.

Limitations of our study include sample size; although ours is large, even larger samples have yielded more findings in other disorders. Larger samples would enable further analysis of epilepsy subtypes, and the International League Against Epilepsy Consortium on Complex Epilepsies now provides a useful vehicle for future efforts. Second, our meta-analysis relied on genotypes generated separately on various platforms, an issue common to most meta-analyses. Third, extension of the phenotyping data to include treatment outcome would be ideal, but in a cross-sectional cohort this approach has methodological difficulties. Finally, we did not have an independent replication sample. However, stringent criteria for statistical significance were set a priori, and for loci achieving our threshold of genome-wide significance the direction of effects were largely consistent across the cohorts, and extended over multiple variants in high linkage disequilibrium.

Taken together, these data show that, with sufficient sample size, susceptibility loci for common epilepsies can be identified through the analysis of common variation. The role of rare variants of large effect is also well established, particularly in rarer Mendelian epilepsies. The role of rare variants in the common...
epilepsies is at present under exploration by deep-
sequencing approaches.12,28,39 A dual approach of 
identification of both rare and common variation 
will result in improved understanding of the genetic 
architecture for the overall population of people with 
epilepsy, necessary for precision medicine. Although 
our findings will not be of immediate clinical usefulness, 
they are an important first step to understand the genetic 
arquitectures of the epilepsies, which could lead to 
clinically relevant markers of prognosis and outcome.

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