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Association of variants in *HTRA1* and *NOTCH3* with MRI-defined extremes of cerebral small vessel disease in older subjects

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We report a composite extreme phenotype design using distribution of white matter hyperintensities and brain infarcts in a population-based cohort of older persons for gene-mapping of cerebral small vessel disease. We demonstrate its application in the 3C-Dijon whole exome sequencing (WES) study ($n = 1924$, $n_{WESextremes} = 512$), with both single variant and gene-based association tests. We used other population-based cohort studies participating in the CHARGE consortium for replication, using whole exome sequencing ($n_{WES} = 2{,}868$, $n_{WESextremes} = 956$) and genome-wide genotypes ($n_{GW} = 9924$, $n_{GWextremes} = 3308$). We restricted our study to candidate genes known to harbour mutations for Mendelian small vessel disease: *NOTCH3*, *HTRA1*, *COL4A1*, *COL4A2* and *TREX1*. We identified significant associations of a common intronic variant in *HTRA1*, rs2293871 using single variant association testing ($P_{discovery} = 8.21 \times 10^{-5}$, $P_{replication} = 5.25 \times 10^{-3}$, $P_{combined} = 4.72 \times 10^{-5}$) and of *NOTCH3* using gene-based tests ($P_{discovery} = 1.61 \times 10^{-2}$, $P_{replication} = 3.99 \times 10^{-2}$, $P_{combined} = 5.31 \times 10^{-3}$). Follow-up analysis identified significant association of rs2293871 with small vessel ischaemic stroke, and two blood expression quantitative trait loci of *HTRA1* in linkage disequilibrium. Additionally, we identified two participants in the 3C-Dijon cohort (0.4%) carrying heterozygote genotypes at known pathogenic variants for familial small vessel disease within *NOTCH3* and *HTRA1*. In conclusion, our proof-of-concept study provides strong evidence that using a novel composite MRI-derived phenotype for extremes of small vessel disease can facilitate the identification of genetic variants underlying small vessel disease, both common variants and those with rare and low frequency. The findings demonstrate shared mechanisms and a continuum between genes underlying Mendelian small vessel disease and those contributing to the common, multifactorial form of the disease.

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Abbreviations: CADISIL = cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy; CARASIL = cerebral autosomal recessive arteriopathy with subcortical infarcts and leukoencephalopathy; GWAS = genome-wide association studies; SVD = small vessel disease; WES = whole-exome sequencing; WMH = white matter hyperintensity

Introduction

Cerebral small vessel disease (SVD) encompasses a group of pathological processes affecting small arteries, arterioles, capillaries and small veins in the brain. It is associated with cognitive impairment, mood disorders, dysfunction of gait and balance, and with increased risk of stroke, dementia and death (Pantoni, 2010). Specific mechanistic treatments for SVD are yet to be identified. Identifying genes underlying SVD may provide important insight on pathways driving this disease and accelerate the discovery of novel drug targets. SVD is driven by a complex mix of environmental and genetic risk factors (Longstreth, 2005) and both familial and sporadic conditions of the disease have been reported. Mutations in the *NOTCH3*, *HTRA1*, *COL4A1*, *COL4A2* and *TREX1* genes are known to cause rare familial forms of SVD (Joutel *et al.*, 1997; Richards *et al.*, 2007; Vahedi *et al.*, 2007; Hara *et al.*, 2009; Gunda *et al.*, 2014) but endeavours to detect genetic risk factors for the common multifactorial form of SVD are still at a preliminary stage. Studies on multiple complex disorders including a few reports on SVD have suggested that genes harbouring mutations leading to the Mendelian form of the disease may also harbour polymorphisms leading to the sporadic condition (Schmidt *et al.*, 2011; Rannikmae *et al.*, 2015; Stitziel *et al.*, 2015; Fuchsberger *et al.*, 2016).

MRI markers of vascular brain injury, including burden of white matter hyperintensities (WMH) and small subcortical infarcts, namely lacunes of presumed vascular origin (hereafter referred to as lacunes), have been shown to reflect primarily SVD and are commonly used for its diagnosis and assessment of severity (Wardlaw *et al.*, 2013). These MRI markers are heritable with reported heritability estimates ranging between 49% and 80% for WMH burden, and ~29% for lacunes (Turner *et al.*, 2004; DeStefano *et al.*,

2009; Sachdev *et al.*, 2013). To date, genome-wide association studies (GWAS) reported five WMH burden risk loci that explain only a small proportion of its heritable component (Fornage *et al.*, 2011; Verhaaren *et al.*, 2015), whereas no robust genetic association with lacunes has been described. The extreme-phenotype design was shown to be a more powerful strategy to identify rare risk alleles underlying complex traits (Peloso *et al.*, 2016). Moreover, using a composite extreme phenotype derived from two key MRI markers of SVD may increase the phenotype specificity and reduce misclassification bias that may arise when studying individual MRI-markers, as a 'control' without lacunes may for instance well have extensive WMH burden reflecting underlying SVD (Traylor *et al.*, 2015).

Whole exome sequencing (WES) allows a comprehensive survey of both rare and common variants in coding regions and has been helpful in deciphering the genetic architecture of complex diseases (Cruchaga *et al.*, 2014; Lange *et al.*, 2014). Here, we report the first WES study on MRI markers of SVD using a composite extreme phenotype study design, and focus our exploration on genes harbouring mutations causing Mendelian forms of SVD.

Materials and methods

Study population

The Three City Dijon (3C-Dijon) study is a population-based cohort of 4931 French non-institutionalized individuals aged 65 years and older (3C Study Group, 2003). A total of 2763 individuals aged $\leqslant$80 years were invited to undergo a brain MRI between June 1999 and September 2000. Participation rate was high (83%, $n = 2285$) but because of financial restrictions, only 1924 MRI scans were performed. Among the 1924 participants with MRI data, 1683 had also undergone genome-wide genotyping. After exclusion of individuals with brain tumours ($n = 8$), stroke ($n = 71$), or dementia ($n = 7$) at baseline, the remaining sample comprised 1497 participants with automated WMH volume measurement.

The Ethical Committee of the University Hospital of Kremlin-Bicêtre approved the study protocol. All participants signed an informed consent to participate in the study.

Brain MRI

MRI acquisition was performed with a 1.5 T Magnetom scanner (Siemens,) using T_1-weighted, T_2-weighted, and proton density-weighted sequences, according to the same protocol at both baseline and follow-up (Kaffashian *et al.*, 2014). Fully automated image processing software was developed to detect and localize WMH and to measure WMH volume (Maillard *et al.*, 2008). Infarcts were rated on T_1-, T_2- and proton density-weighted images by the same examiner (Y.-C.Z.), using a standardized assessment grid, to visually review all brain scans. Lacunes were defined as infarcts 3–15 mm in diameter having the same signal characteristics as cerebrospinal fluid on all sequences, located in basal ganglia, brainstem or cerebral white matter. Characteristics of lesions were visualized simultaneously in axial, coronal, and sagittal planes to discriminate them from dilated perivascular spaces. Lesions with a typical vascular shape and following the orientation of perforating vessels were regarded as dilated perivascular spaces (Zhu *et al.*, 2010). The nomenclature of MRI markers of SVD in our study is consistent with the recently proposed neuroimaging standards for research into SVD (STRIVE) (Wardlaw *et al.*, 2013; Kaffashian *et al.*, 2014).

Definition of extreme cerebral small vessel disease

The composite extreme phenotype was defined based on the distribution of WMH volume and presence or absence of lacunes in the 3C-Dijon study using 1497 participants from the 3C-Dijon study who had both MRI scan and GWAS data. The objective was to define a group with extensive SVD severity (individuals in the upper quartile of WMH distribution and having one or more brain infarcts) and a group with minimal SVD severity (lower quartile of WMH distribution and without any brain infarcts). We log-transformed WMH volume (natural log of [WMH volume in $cm^3 + 1$]) and extracted residuals adjusted for age, gender, and white matter mask volume, hereafter referred to as WMH-burden residuals. The first and fourth quartiles of these residuals were taken to represent small and large WMH volume, respectively. The 261 participants with extensive SVD were defined from 374 participants within the fourth quartile of WMH-burden residuals distribution by including all participants who also had at least one lacune ($n = 58$) and by selecting additionally 203 participants with the highest WMH-burden residuals within the fourth quartile. Similarly, the 253 participants with minimal SVD were defined from 374 participants within the first quartile of WMH-burden residuals distribution by the absence of MRI-defined brain infarcts and having WMH burden residuals at the bottom tail of the WMH burden residual distribution. The design used for defining extreme SVD is summarized in Fig. 1.

Covariates and clinical events

At baseline, socio-demographics, medical history, and drug use data were collected at home during an interview by trained psychologists. Centralized measurements of fasting plasma glucose, serum total cholesterol, high density lipoprotein cholesterol, and triglycerides were performed using enzymatic methods by the Biochemistry Laboratory of the University Hospital of Dijon. Low density lipoprotein (LDL) cholesterol was calculated with the Friedewald formula (Friedewald *et al.*, 1972). Body mass index (BMI) was defined as the ratio of weight (kg) to the square of height (m). Smoking status was categorized as never, former, and current. Diabetes mellitus was defined as intake of antidiabetic drugs or fasting blood glucose $\geqslant$ 7 mmol/l. Hypertension was defined by systolic blood pressure (BP) $\geqslant$140 mm Hg, or diastolic BP $\geqslant$90 mm Hg, or antihypertensive drug intake. History of cardiovascular disease was defined by history of myocardial infarction, bypass cardiac surgery, angioplasty, or peripheral vascular disease. Hypercholesterolaemia was defined as fasting total cholesterol $\geqslant$6.2 mmol/l or use of any lipid-lowering drug. Information concerning stroke occurrence over time was collected at each follow-up. Incident stroke was defined as a new focal

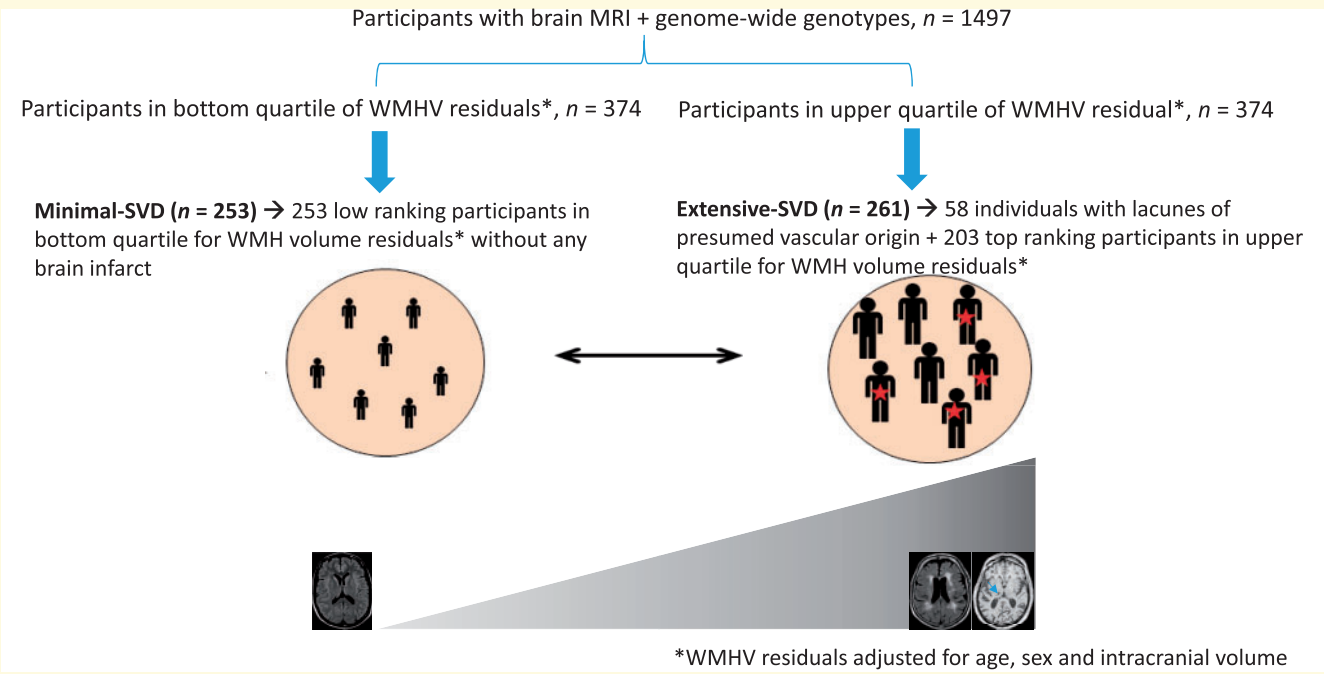

Figure 1 Schematic representation of the extreme SVD design in the 3C-Dijon study.

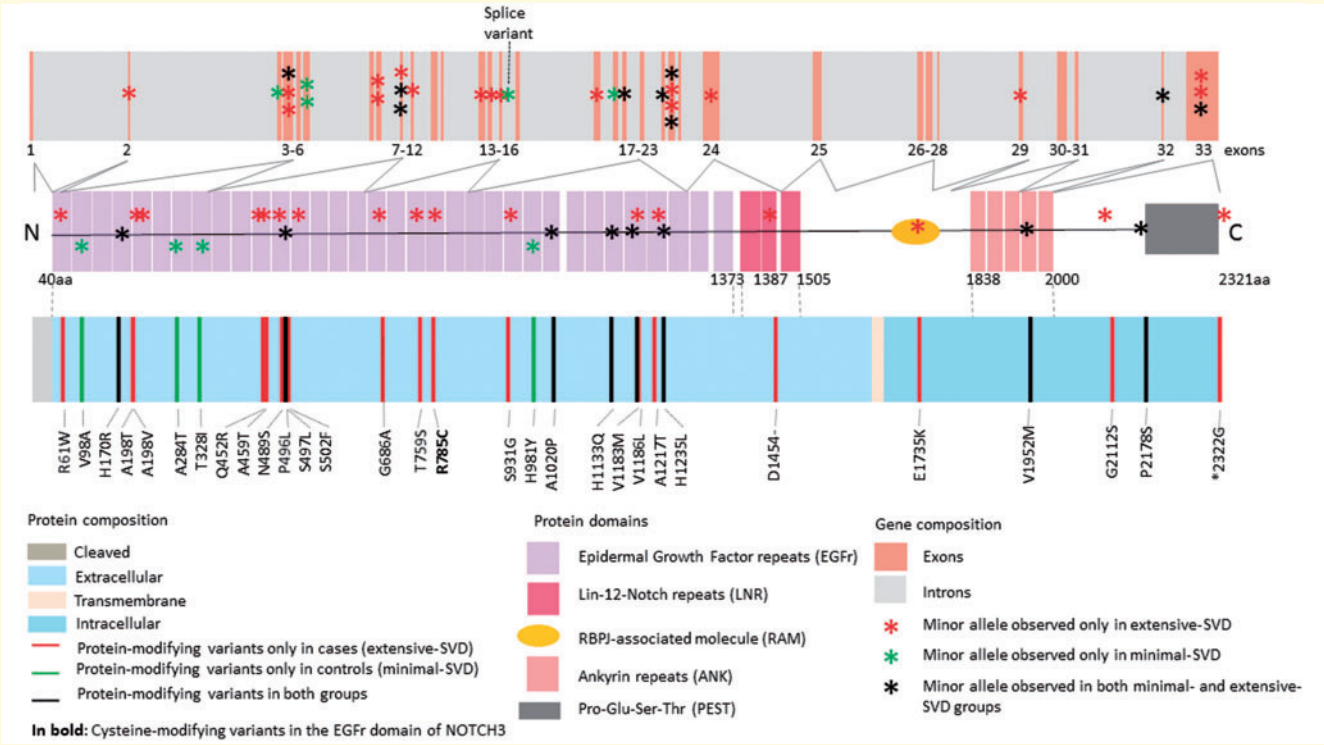

Figure 2 NOTCH3 protein modifying rare and low frequency variants in the 3C-Dijon extreme SVD cohort.

neurological deficit of sudden or rapid onset, of presumed vascular origin, that persisted for >24 h, or leading to death. An expert panel of neurologists adjudicated diagnosis of stroke based on criteria of the WHO (1988). Dementia status was evaluated prospectively by an expert panel using a three-step procedure (Schilling *et al.*, 2017): (i) participants underwent neuropsychological evaluations carried out by trained psychologists; (ii) an examination by a neurologist for those who screened positive at step 1 based on the MMSE and the Isaacs' Set Test; and (iii) an independent committee of neurologists

and geriatricians reviewed all suspected prevalent and incident dementia cases to reach consensus on the diagnosis and aetiology according to the DSM-IV criteria, using all available information (e.g. cognitive functioning, severity of cognitive disorders, hospitalization records when possible, computed tomography scans, MRI, functional assessments).

Exome sequencing and quality control

The DNA samples of 514 participants (261 with extensive SVD and 253 with minimal SVD) with the extremes of SVD severity underwent high depth WES. The majority of samples ($n = 508$) were sequenced at the McGill Genome Center, Montreal, Canada, and remaining six participants were sequenced at the Centre National de Génotypage, Paris, France. The Agilent SureSelect Human All Exome V5 exome capture kit was used for exome capture except for five samples for which the Agilent SureSelect Human All Exome V4 or V5 + UTR exome capture kits were used. The Illumina HiSeq2000 instrument was used to perform paired-end sequencing (2×100 bp). The reads were aligned to the GRCh37 human reference genome sequence using the software Burrows-Wheeler Aligner and duplicate reads were tagged with Picard MarkDuplicates (Li and Durbin, 2009). The Genome Analysis Toolkit (GATK) software was used to perform realignment around InDels and base quality score recalibration (BQSR) (McKenna *et al.*, 2010). Single-sample calling was performed using HaplotypeCaller from GATK 3.3 in GVCF mode with base-pair resolution, except 15 samples, whose calling was generated with default band definition as part of the Alzheimer Disease Exome Sequencing-France (ADSP-FR) project (Bellenguez *et al.*, 2017). Calling was done on the target intervals of each exome kit using a padding of 100 bp. Multi-sample calling was performed with the GenotypeGVCFs tool implemented in GATK 3.4, together with other samples from the ADES-FR project. Our whole exome sequence data covered 17 649 RefSeq genes with an average depth of coverage of $\sim 80\times$ (Supplementary Fig. 1). We filtered out samples with missingness $> 20\%$, and individuals with > 6 standard deviations (SD) for number of singletons, heterozygote to homozygote ratio, mean depth, and transition to transversion (Ti/Tv) ratio. This protocol resulted in filtering out two participants with extensive SVD because of high number of singletons and low mean depth coverage. We filtered out genotypes with Phred-scaled confidence for genotype call < 20 or average depth of coverage $< 8\times$. In our study, we included only biallelic variants [(single nucleotide polymorphism (SNPs) and insertions/deletions (Indels)]. Additionally, we filtered out variants with mean depth higher than 500-fold, missingness $> 20\%$, and Hardy Weinberg equilibrium P-value $< 5 \times 10^{-6}$. Overall, we achieved high quality WES data for 259 extensive SVD and 253 minimal SVD participants ($n = 512$).

Description of the study sample

Baseline characteristics of participants with extensive SVD and participants with minimal SVD were compared using analysis of covariance for continuous variables and chi-square test for categorical variables. After verifying the proportional hazard assumption through Schoenfeld residuals, we examined the association of extreme SVD and 12-year incident dementia using Cox proportional regression with age as the time scale, adjusted for sex and education status. For incident stroke, we used the Cox model with age as a timescale and adjusted for sex, BMI, smoking status, diabetes mellitus, hypertension, history of cardiovascular disease, and hypercholesterolaemia.

Genetic association tests

We performed single-variant and gene-based tests using the R package SeqMeta (https://cran.r-project.org/web/packages/seqMeta/index.html). The primary association models were adjusted for age, sex and the first four principal components of population stratification. In secondary analyses, we additionally adjusted for hypertension status.

Single variant association tests

We performed single variant association tests considering common and low frequency variants [minor allele frequency (MAF) > 0.01] located within 100 kb of the 5′ and 3′ UTR of five candidate genes: *NOTCH3*, *HTRA1*, *COL4A1*, *COL4A2* and *TREX1*. The 100 kb arbitrary boundary was considered to capture cis regulatory variants that might be localized within neighbouring genes. We used a permutation approach to derive the significance threshold correcting for multiple association tests for 389 common and low frequency variants that might be in linkage disequilibrium (Supplementary material, part A). Additionally we performed the top-SNP association tests implemented in the VEGAS2 software (Mishra and Macgregor, 2015) to account for number of variants and linkage disequilibrium structure in the locus.

Gene-based analysis

To increase power for association testing of rare and low frequency variants (MAF < 0.05), we also performed gene-based association tests focusing on five candidate genes: *NOTCH3*, *HTRA1*, *COL4A1*, *COL4A2* and *TREX1*. We used the variant effect predictor (v90) software (McLaren *et al.*, 2016) to annotate functional consequences of genetic variants localized within five candidate genes considering the default 'GRCh37' ensemble annotation database. We used 'filter_vep' module to extract variants with the following functional consequences: splice acceptor variant, splice donor variant, start lost, stop lost, stop gained, frameshift variant, inframe insertion, inframe deletion, and missense variant, to perform gene-based association tests on protein-modifying variants only. We used the SKAT-O approach (Lee *et al.*, 2012) for gene-based analyses of protein-modifying rare and low frequency variants. We considered genes with a cumulative MAF of rare or low frequency protein-modifying variants higher than 1%. We performed power calculations for SKAT-O test using the R package SKAT (Wu *et al.*, 2011).

Replication of significant associations

We sought replication of non-exonic significant findings in genome-wide genotyped subsets imputed to the Haplotype Reference Consortium (HRC) panel and of exonic variants in WES subsets of the Atherosclerosis Risk in Communities (ARIC) study, the Cardiovascular Health study (CHS), the Framingham Heart study (FHS) and the Rotterdam study, all participating in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. The ARIC

study and the CHS analysed European and African ancestry samples separately; the FHS and the Rotterdam study analysed only European ancestry samples. The MRI measurements of WMH burden and lacunes in these cohorts are described in the Supplementary material, part B, which also provides details on quality control of genotyped and WES datasets of these studies. The extreme SVD phenotype in the replication cohorts was defined using the same strategy as described above for the 3C-Dijon cohort. We defined one-third of the total sample with phenotype and genotype information as having extreme-SVD (extensive SVD for one-sixth of the sample, with extensive WMH burden with or without lacunes, and minimal SVD for another sixth of the sample with minimal WMH burden and no brain infarcts). In the FHS and Rotterdam study, WMH burden residuals were computed using automated quantitative WMH volume measures adjusting for age, gender, and intracranial volume, whereas in the ARIC study and CHS WMH burden residuals were derived from visual semi-quantitative WMH burden measures adjusting for age and gender, as intracranial volume was accounted for in WMH burden assessment. In the FHS, WMH burden residuals were additionally adjusted for family structure. We separately defined extreme SVD in genotyped and WES subsets of individual studies (see Supplementary Tables 2 and 3, respectively, for population characteristics of extreme SVD cohorts of genotyped and WES subsets of the ARIC, CHS, FHS and Rotterdam studies). Of those participants with MRI SVD phenotype data, the total sample size with genome-wide genotypes was 9924 for European ancestry participants, of whom 3308 had extreme SVD ($n = 1654$ with extensive SVD and $n = 1654$ with minimal SVD) and 1170 for African ancestry participants, of whom 390 had extreme SVD ($n = 195$ with extensive SVD and $n = 195$ with minimal SVD). The total sample size with WES was 2877 for European ancestry participants, of whom 956 had extreme SVD ($n = 480$ with extensive SVD and $n = 477$ with minimal SVD) and 726 for African ancestry participants, of whom 242 had extreme SVD ($n = 121$ with extensive SVD and $n = 121$ with minimal SVD).

In the ARIC, CHS and Rotterdam studies, the single variant association tests were performed with an additive model in R using logistic regression, whereas in the FHS, a generalized estimation equation was used to account for family structure. Analyses were adjusted for age, sex and the first four principal components of population stratification. We used METAL software (Willer *et al.*, 2010) to perform an inverse variance weighted meta-analysis of association statistics across replication cohorts, and with the discovery study.

We used seqMeta software to perform the SKAT-O gene-based analysis across all replication cohorts. We then meta-analysed the SKAT-O *P*-values from discovery and replication cohorts using Stouffer's method for sample size weighted combination of p-values.

Association of extreme small vessel disease risk variants with related phenotypes

We also tested for association of extreme SVD associated common variants with stroke and continuous measures of WMH, in previously reported GWASs of small vessel ischaemic stroke [NINDS Stroke Genetics Network (SiGN) and International Stroke Genetics Consortium (ISGC), 2016] [defined using the Causative Classification of Stroke (CCS) system] by the National Institute of Neurological Disorders and Stroke and the Stroke Genetics Network (NINDS-SiGN) and of WMH burden (Verhaaren *et al.*, 2015). The GWAS summary statistics on small vessel ischaemic stroke by the NINDS-SiGN consortium were accessed using the Cerebrovascular Disease Knowledge Portal (Crawford *et al.*, 2018).

We additionally performed SKAT-O gene-based analysis of protein-modifying rare and low frequency variants observed within a *NOTCH3* targeted Sanger sequenced subsample of the Austrian Stroke Prevention Study (ASPS) ($n = 277$) cohort. Of these 24 participants were filtered out due to missing information on principal components of population stratification, leaving 171 participants with either coalescent white matter lesions or lacunes and 82 randomly selected participants with no focal changes on magnetic resonance images (Schmidt *et al.*, 2011) for the follow-up analysis. The SKAT-O gene-based analysis was adjusted for age, sex and the first four principal components of population stratification.

In silico functional exploration of non-exonic variants

We used the HaploReg (Ward and Kellis, 2012) (version 4.1) software to perform functional annotation of non-exonic variants that are in linkage disequilibrium ($r^2 > 0.6$ in the 1000 Genomes European panel) with the lead SNP associated with extreme SVD. We also manually explored expression quantitative trait locus (eQTL) databases: the GTeX database (Mele *et al.*, 2015) and the blood eQTL resource (Westra *et al.*, 2013).

NOTCH3 glycosylation site prediction

NOTCH3 functions are regulated by different types of *O*-glycosylation of the EGF repeat (EGFr) domain including *O*-fucose (Moloney *et al.*, 2000), *O*-glucose (Moloney *et al.*, 2000), *O*-GlcNAc (*N*-acetylglucosamine) (Matsuura *et al.*, 2008), *O*-xylose (Takeuchi *et al.*, 2011) and mucin-type O-GalNAc (Boskovski *et al.*, 2013). *O*-fucosylation is mediated by proteins O-fucosyltransferase 1 and Fringe. Cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL)-causing mutations were reported to affect carbohydrate chain elongation of NOTCH3 by Fringe proteins (Arboleda-Velasquez *et al.*, 2005). We investigated whether rare and low frequency missense variants in the *NOTCH3* EGFr domain observed in the 3C-Dijon cohort localized at these computationally predicted mucin-type O-GalNAc glycosylation sites, using the publicly available software for mucin-type O-GalNAc sites prediction (Steentoft *et al.*, 2013).

Survey of pathogenic variants

We manually surveyed the ClinVar database (Landrum *et al.*, 2016) (accessed on 27 February 2017, Supplementary Table 7) to identify participants in the 3C-Dijon cohort carrying a rare allele at SVD causing pathogenic or likely pathogenic

Table 1 Baseline characteristics of 3C-Dijon participants with extreme cerebral SVD

Characteristics	Extensive SVD	Minimal SVD	*P*-value*
Participants, *n*	259	253	NA
WMH volume, ml, mean ± SD	13.18 ± 7.07	2.05 ± 0.63	<0.0001
Presence of lacunes, *n* (%)	58 (22.4)	0	NA
Age at MRI, years, mean ± SD	73.5 ± 4.01	73.19 ± 4.45	0.4
Female, *n* (%)	150 (58.1)	155 (61)	0.51
Hypertension, *n* (%)[a]	223 (86.4)	184 (72.4)	<0.0001
Systolic BP, mmHg, mean ± SD	152.05 ± 22.51	147.07 ± 21.85	0.011
Antihypertensive drug intake, *n* (%)	146 (56.6)	93 (36.6)	<0.0001
Fasting plasma glucose, mmol/l, mean ± SD	5.18 ± 1.51	4.95 ± 0.67	0.026
Diabetes mellitus, *n* (%)[b]	25 (9.7)	14 (5.5)	0.07
HDL cholesterol, mmol/l, mean ± SD	1.64 ± 0.39	1.68 ± 0.41	0.23
LDL cholesterol, mmol/l, mean ± SD	3.53 ± 0.89	3.68 ± 0.84	0.046
TG, mmol/l, mean ± SD	1.26 ± 0.56	1.15 ± 0.52	0.031
Lipid lowering drug, *n* (%)	96 (37.2)	71 (28)	0.026
BMI, kg/m^2, mean ± SD	25.84 ± 3.92	24.86 ± 3.71	0.004
Current smoker, *n* (%)	22 (8.5)	8 (3.1)	0.012
History of CVD at MRI, *n* (%)[c]	15 (5.8)	5 (2)	0.025
Hypercholesterolaemia, *n* (%)[d]	142 (55)	140 (55.3)	0.95

*Significant differences across SVD status obtained from analysis of covariance (continuous variables) or chi-square tests (categorical variables). Models with WMH volume as the dependent variable are adjusted for intracranial volume.
[a]Systolic blood pressure ⩾140 mmHg, or diastolic blood pressure ⩾90 mmHg, or use of antihypertensive drugs.
[b]Fasting blood glucose ⩾7 mmol/l or antidiabetic drug intake.
[c]History of myocardial infarction, bypass cardiac surgery, angioplasty, or peripheral artery disease.
[d]Hypercholesterolaemia was defined as fasting total cholesterol ⩾6.2 mmol/l or use of any lipid-lowering drug (fibrates, statins or bile acid sequestrant).
BMI = body mass index; BP = blood pressure; CVD = cardiovascular diseases; HDL = high-density lipoprotein; LDL = low-density lipoprotein; TG = triglycerides.

mutations in the following genes: *NOTCH3* (Joutel *et al.*, 1997) [causing CADASIL (OMIM:125310)], *HTRA1* (Hara *et al.*, 2009) [causing cerebral autosomal recessive arteriopathy with subcortical infarcts and leukoencephalopathy (CARASIL, OMIM:600142)], *COL4A1* (Vahedi *et al.*, 2007) [causing COL4A1-related familial vascular leukoencephalopathy (OMIM:607595); and pontine autosomal dominant microangiopathy with leukoencephalopathy (PADMAL), porencephaly-1 (OMIM:175780)], *COL4A2* (Gunda *et al.*, 2014) [causing porencephaly-2 (OMIM: 614483)], and *TREX1* (Richards *et al.*, 2007) [causing retinal vasculopathy and cerebral leukodystrophy (RVCL, OMIM:192315)].

In addition to the pathogenic and likely pathogenic variants classified in the ClinVar database, we systematically searched for NOTCH3 EGFr domain cysteine-modifying missense variants, the typical type of mutation causing CADASIL (Rutten *et al.*, 2016*b*), and for variants recently reported to cause *HTRA1* autosomal dominant forms of SVD (Verdura *et al.*, 2015).

Data availability

The data that support the findings of this study are available from the corresponding author, upon reasonable request.

Results

The approach for defining the composite extreme phenotype of SVD (extreme SVD) is schematically presented in Fig. 1. From a total sample of 1497 participants with MRI and genome-wide genotype information within the 3C-Dijon study, 514 participants (261 with extensive SVD and 253 with minimal SVD) were identified. Characteristics of 3C-Dijon participants with extreme SVD are described in Table 1. Participants with extensive and minimal SVD had similar age and gender distributions. Participants with extensive SVD had more vascular risk factors than those with minimal SVD, the most significant association being observed for hypertension. Compared to participants with minimal SVD, those with extensive SVD were more often current smokers, and had more frequently a history of cardiovascular disease, as well as higher fasting plasma glucose, triglycerides, and BMI, but lower LDL-cholesterol (Table 1). Over the mean follow-up period of 9.2 ± 2.7 years, 40 participants were diagnosed with dementia, and 20 with stroke. Compared to participants with minimal SVD, those with extensive SVD showed a significantly increased risk of developing incident dementia [hazard ratio (HR) (95% confidence interval, CI) = 1.94 (1.01–3.73), $P = 0.05$] and a trend towards an increased risk of incident stroke [HR (95%CI) = 2.54 (0.95–6.74), $P = 0.06$]. Characteristics of replication studies with extreme-SVD are described in Supplementary Tables 1 and 2.

Single variant association analyses identified a significant association of an intronic variant in *HTRA1* (rs2293871-T, frequency = 0.19) with extreme SVD (Table 2). This association was significant after correcting for multiple testing

Table 2 Top common or low frequency variant at individual candidate locus

Gene	Top variant (rsID)	Hg19_chr:bp	RA/OA	RA Freq.	3C-Dijon (Discovery, n = 512)			Top-SNP P-value***	ARIC, CHS, FHS and RS1–3 (Replication, n = 3308)		Joint analysis (n = 3802)	
					OR (CI 95%)	P-value*	Variants, n		OR (95% CI)	P-value	OR (95% CI)	P-value
HTRA1#	rs2293871	10:124273671	T/C	0.19	1.92 (1.39–2.65)	8.21×10^{-5}	49	1.77×10^{-3}	1.21 (1.06–1.38)	5.25×10^{-3}	1.29 (1.14–1.46)	4.72×10^{-5}
COL4A1	rs2275842	13:110813523	T/C	0.17	1.52 (1.09–2.11)	0.01	89	0.38	NA	NA	NA	NA
COL4A2	rs2275842	13:110813523	T/C	0.17	1.52 (1.09–2.11)	0.01	154	0.55	NA	NA	NA	NA
NOTCH3	rs1043997	19:15300136	G/A	0.05	1.69 (0.96–2.96)	0.07	60	0.65	NA	NA	NA	NA
TREX1	rs78159609	3:48419898	A/G	0.06	0.62 (0.36–1.08)	0.09	29	0.59	NA	NA	NA	NA

*Significance threshold for discovery is P-value $< 2.89 \times 10^{-4}$ correcting for 389 common and low frequency variants tested.
***Significance threshold for VEGAS2 top-SNP test is P-value < 0.01 correcting for five loci tested.
#After adjustment for hypertension status the association of rs2293871 with extreme SVD was OR = 1.85 (95%CI: 1.33- 2.58), $P = 2.39 \times 10^{-4}$ in the 3C-Dijon Study.
ARIC = Atherosclerosis Risk In Communities; CHS = Cardiovascular Health Study; FHS = Framingham Heart Study; OA = other allele; RA = risk allele; RS1–3 = Rotterdam Studies 1, 2 and 3.

(permutation derived 95% empirical significance threshold $P < 2.89 \times 10^{-4}$, Supplementary material, part A) and remained significant after additionally adjusting for hypertension status (Table 2). Moreover the top-SNP locus-based test implemented in the VEGAS2 software (Mishra and Macgregor, 2015) confirmed that the association of rs2293871 with extreme SVD is independent of the regional properties of the *HTRA1* locus: the linkage disequilibrium structure or number of variants in the region (Table 2). The effect estimates of rs2293871-T appeared larger when comparing the 58 extensive SVD participants with lacunes to minimal SVD participants [OR (95%CI) = 3.04 (1.67–5.50), $P = 2.56 \times 10^{-4}$] than when comparing the 203 participants with extensive SVD without lacunes to minimal SVD participants [OR (95%CI) = 1.80 (1.27–2.56), $P = 9.60 \times 10^{-4}$]. We replicated the association of rs2293871 in independent cohorts of European ancestry (n extreme SVD = 3308) using genome-wide genotype data for this common intronic variant (Table 2). The association of rs2293871 was not significant in the only African ancestry sample (rs2293871-T frequency = 0.14, Supplementary Table 3). The inverse variance weighted meta-analysis of discovery and replication cohorts of European ancestry showed an association of rs2293871-T with extensive SVD at an OR (95%CI) of 1.29 (1.14–1.46), $P = 4.72 \times 10^{-5}$ (Table 2). The same allele at rs2293871 was also associated with increased risk of small vessel ischaemic stroke defined using the CCS system in 16 851 cases and 31 259 controls in the NINDS-SiGN study [NINDS Stroke Genetics Network (SiGN) and International Stroke Genetics Consortium (ISGC), 2016]: OR (95%CI) = 1.12 (1.03–1.22), $P = 6.14 \times 10^{-3}$ for causative CCS and OR (95%CI) = 1.12 (1.04–1.22), $P = 4.68 \times 10^{-3}$ for phenotypic CCS. The rs2293871 variant showed nominal association with continuous WMH burden (n = 17 936, P-value = 0.03) in a previously reported GWAS meta-analysis (Verhaaren *et al.*, 2015). Functional explorations using HaploReg (Ward and Kellis, 2012) suggest that rs2293871 lies in the H3K9ac promoter and H3K4me1, H3K4me3 and H3K27ac enhancer histone marks (Supplementary Table 4). Two proxies of rs2293871 (rs876790 and rs2736928, $r^2 = 0.75$ with rs2293871) are eQTL for *HTRA1* in blood (Westra *et al.*, 2013), with C alleles at rs876790 and rs2736928 (in phase with rs2293871-T) showing significant association with lower *HTRA1* transcript levels (false discovery rate-corrected P-value = 0.03 and 0.04, respectively).

We analysed the association of protein-modifying (splice acceptor variant, splice donor variant, start lost, stop lost, stop gained, frameshift variant, inframe insertion, inframe deletion, and missense variants only) rare and low frequency variants (MAF < 0.05) in candidate genes using the SKAT-O approach (Lee *et al.*, 2012). Only three genes *NOTCH3*, *COL4A1*, and *COL4A2*, satisfied the criteria of cumulative MAF of protein-modifying rare or low frequency variants of >1% (Supplementary Table 5), thus qualifying for gene-based analyses. The SKAT-O gene-based analysis identified a significant association of protein-modifying rare and low frequency variants in the *NOTCH3* gene with extreme SVD (SKAT-O

Table 3 Gene-based association of rare and low frequency protein-modifying variants in *NOTCH3*, *COL4A1*, and *COL4A2* genes with extreme cerebral SVD

Gene[a] (Transcript)	3C-Dijon (Discovery, $n = 512$)				ARIC, CHS, FHS and RSI (Replication, $n = 956$)				Combined ($n = 1467$)
	Variants, *n*	Cumulative MAF	*P* (SKAT-O)*	*P* (SKAT-O) additional adjusted for HT status	Variants, *n*	Cumulative MAF	*P* (SKAT-O)	*P* (SKAT-O) additional adjusted of HT status	*P* (SKAT-O)
NOTCH3 (ENST00000263388)	31	0.10	1.61×10^{-2}	1.58×10^{-2}	36	0.11	3.99×10^{-2}	4.60×10^{-2}	5.31×10^{-3}
COL4A2 (ENST00000360467)	29	0.09	0.23	0.19	NA	NA	NA	NA	NA
COL4A1 (ENST00000375820)	13	0.02	0.40	0.48	NA	NA	NA	NA	NA

[a]Sorted by SKAT-O *P*-value in discovery cohort.
*Significance threshold for discovery is SKAT-O *P*-value $< 1.67 \times 10^{-2}$ correcting for three tested genes.
ARIC = Atherosclerosis Risk In Communities; CHS = Cardiovascular Health Study; FHS = Framingham Heart Study; HT = hypertension; MAF = minor allele frequency; RSI = Rotterdam Study I.

$P = 1.61 \times 10^{-2}$, *n* extreme SVD = 512, Table 3), which remain associated after additionally adjusting for hypertension status (SKAT-O $P = 1.58 \times 10^{-2}$, Table 3). We successfully replicated the gene-based association of protein-modifying rare and low-frequency variants in *NOTCH3* with extreme SVD in four independent cohorts of European ancestry (*n* extreme SVD = 956): SKAT-O $P = 3.99 \times 10^{-2}$ for the replication set and SKAT-O $P = 5.31 \times 10^{-3}$ for the combined discovery and replication samples (Table 3). The *NOTCH3* association was not significant in the African ancestry sample of 242 extreme-SVD participants (SKAT-O $P = 0.78$). Follow-up in a previously described Sanger sequencing subset of the ASPS (Schmidt *et al.*, 2011) did not show any significant association in a cohort of 171 participants with either coalescent white matter lesions or lacunes compared with 82 randomly selected participants with no focal changes on magnetic resonance images (SKAT-O $P = 0.53$), possibly due to limited sample size.

Further exploratory protein-domain specific SKAT-O analyses showed significant association of extreme SVD with the EGFr domain determining region of the *NOTCH3* gene, which is known to preferentially harbour mutations causing CADASIL (SKAT-O $P = 2.14 \times 10^{-2}$ for 3C-Dijon, SKAT-O $P = 3.30 \times 10^{-2}$ for the replication samples, and SKAT-O $P = 4.98 \times 10^{-3}$ for the combined discovery and replication). We also observed, in the 3C-Dijon extreme SVD sample, that five of the missense variants in the EGFr determining region (T328I, S497L, S502F, T759S, and S931G) were predicted mucin type GalNAc *O*-glycosylation sites with predication scores ranging between 0.18 and 0.82 (Supplementary Table 6). The S502F, T759S and S931G variants were observed exclusively in the 3C-Dijon extensive-SVD sample (Fig. 2).

Screening of 3C-Dijon extreme SVD participants for rare alleles at pathogenic or likely pathogenic variants in five candidate genes harbouring mutations causing monogenic SVD, identified two such alleles in the *NOTCH3* and *HTRA1* genes. One extensive SVD participant carried a heterozygote genotype at a *NOTCH3* EGFr domain cysteine altering variant: NM_000435.2 (NOTCH3):c.C2353T:p.R785C (Fig. 2) (participant level depth coverage = 33× and Phred scaled genotype quality = 99, note: Phred score vary from 0 to 99 and 99 represents the highest Phred scaled confidence for genotype quality). This variant leads to addition of a seventh cysteine residue in EGF repeat 20 of the NOTCH3 N-terminus, typical of CADASIL, and was previously described in one Italian CADASIL family with an autosomal dominant inheritance pattern (Mosca *et al.*, 2014). Another extensive SVD participant carried a heterozygote genotype at the CARASIL-causing variant: NM_002775.4 (HTRA1):c.1108C > T (p.Arg370Ter), a nonsense variant resulting in a stop codon at amino acid position 370 (participant level depth coverage = 96× and Phred scaled genotype quality = 99). Only the homozygous TT genotype at this variant has been reported to cause CARASIL in the

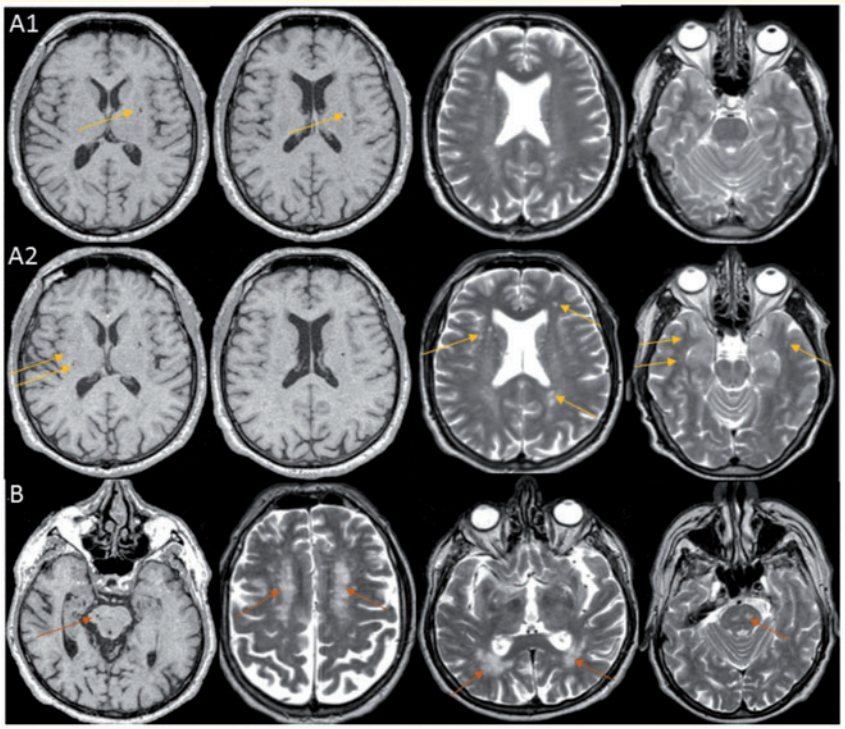

Figure 3 MRI images of participants carrying heterozygote genotypes at CADASIL and CARASIL causing mutations. (**A**) Baseline (**1**) and 4-year follow-up (**2**) MRI scans of a 65-year old female participant with extensive SVD, in whom a NOTCH3 EGFr domain cysteine-modifying mutation was found: NM_000435.2 (NOTCH3):c.C2353T:p.R785C. Images show lacunar infarcts and dilated perivascular spaces in basal ganglia and white matter, and WMH in the periventricular region and deep white matter; on the follow-up MRI scan WMH and dilated perivascular spaces burden had increased and WMH became visible in the anterior temporal lobes (yellow arrows), a typical location for CADASIL. This participant remained free of stroke and dementia until the end of her follow-up at age 77. Her MMSE score was 28 at baseline and 26 at 12 years follow-up (secondary school education but no high school). (**B**) Baseline MRI scan of a 74-year-old female participant with extensive SVD, in whom a heterozygous CARASIL causing mutation was found: NM_002775.4 (HTRA1):c.1108C > T (p.Arg370Ter). Images show WMH and lacunes in the pons and extensive WMH in the deep white matter and periventricular region (magenta arrows). This participant was free of stroke and dementia at baseline but was lost to follow-up. Her baseline MMSE score was 27 (primary school education).

literature, in Asian populations (Hara *et al.*, 2009). This variant was not included in the list of variants reported to cause a dominant *HTRA1*-related SVD phenotype in Europeans (Verdura *et al.*, 2015). Brain imaging characteristics of both participants are shown in Fig. 3. Neither of them had typical imaging features of CADASIL or CARASIL at baseline, but the participant with a NOTCH3 EGFr domain cysteine altering genotype developed WMH in the anterior temporal lobe, a location typical for CADASIL, on a 4-year follow-up MRI scan. Both participants were free of stroke and dementia.

We also observed two minimal-SVD participants carrying a heterozygote genotype at one glycine residue altering missense variant in *COL4A1* [NM_001845.4 (COL4A1): c.3158G > A (p.Gly1053Asp), participant level depth coverage = 125× and Phred scaled genotype quality = 99], and one nonsense (stop gained) variant in *COL4A2* [NM_001846.2 (COL4A2) c.3766C > T (p.Arg1256Ter), participant level depth coverage = 77× and Phred scaled genotype quality = 99]. Heterozygous glycine residue changes and nonsense mutations in *COL4A1* and *COL4A2* are typically described in SVD families with cerebral bleedings, although, to our knowledge, these specific variants have not been described previously in any SVD family. All protein-modifying variants observed in 3C-Dijon participants with extreme-SVD within the five candidate genes are displayed in Fig. 2 (*NOTCH3*) and Supplementary Fig. 2–5 (*HTRA1*, *COL4A1*, *COL4A2* and *TREX1*).

Discussion

We report a novel gene-mapping strategy for SVD in population-based cohorts of older person with MRI-defined extremes of SVD severity. We explored the association with extreme SVD in the general population of common and rare variants in five genes known to harbour mutations causing Mendelian SVD, with a discovery sample of 512 participants and a follow-up sample of 3698 participants for common variants and $n = 1198$ for rare and low frequency variants. We report significant association of a

common intronic variant in the *HTRA1* gene with extreme SVD, with evidence suggesting that the risk allele is lowering *HTRA1* expression. We also found a significant association with extreme SVD of rare and low frequency *NOTCH3* protein-modifying variants using a gene-based approach. Finally, in 512 participants from the 3C-Dijon discovery population-based sample, we also screened for pathogenic variants causing Mendelian SVD and identified two participants with extensive SVD harbouring heterozygote genotypes for such variants in *NOTCH3* (CADASIL-causing missense variant modifying a cysteine-residue of the EGFR domain) and in *HTRA1* (heterozygous carrier of a CARASIL causing mutation).

Our novel approach complements the gene-mapping strategies traditionally being used to identify SVD risk loci in population-based cohorts, consisting of studying each MRI-marker of SVD individually: presence or absence of brain infarct (Debette *et al.*, 2010) and, quantitative measure of WMH burden (Verhaaren *et al.*, 2015), and of efforts to reveal genetic determinants of the clinically defined small vessel ischaemic stroke subtype [NINDS Stroke Genetics Network (SiGN) and International Stroke Genetics Consortium (ISGC), 2016]. The extreme composite phenotype of SVD presented here is likely to be more specific for underlying SVD pathology and provides a better contrast by excluding participants with either lacunes or moderate to extensive WMH burden from the control group. Extreme phenotype association studies have been reported to be better powered for identifying rare risk variants associated with disease by reducing the phenotypic heterogeneity (Peloso *et al.*, 2016), which we demonstrate through association of rare and low frequency *NOTCH3* protein-modifying variants with extreme-SVD. Notably, we also demonstrate that our study design is more powerful to identify some common SVD risk variants, as the common intronic variant rs2293871 in *HTRA1* has greater significance in relation with extreme SVD compared to associations observed with small vessel ischaemic stroke [NINDS Stroke Genetics Network (SiGN) and International Stroke Genetics Consortium (ISGC), 2016] and continuous WMH burden (Verhaaren *et al.*, 2015), which had comparatively more number of participants than the former study. This observation is in line with simulation studies demonstrating that extreme sample phenotyping might identify additional common risk variants (MAF > 0.05) associated with complex diseases by reducing the impact of phenotype misclassification on observed genetic effect size estimates (van der Sluis *et al.*, 2010; Manchia *et al.*, 2013).

We report and replicate an association of a common intronic variant (rs2293871) in *HTRA1* with extreme-SVD in European ancestry cohorts. *HTRA1* encodes a secretory protein of the serine protease family, which regulates transforming growth factor (TGF) signalling (Beaufort *et al.*, 2014). Disruption in HTRA1 activity causing cell death by modulating TGF signalling has been suggested as a possible causal mechanism underlying CARASIL (Beaufort *et al.*, 2014). We identified two blood eQTLs in linkage disequilibrium ($r^2 = 0.75$) with rs2293871, suggesting that the allele associated with increased risk of extensive SVD is associated with lower *HTRA1* expression in blood. Although limited to blood, and based on proxies in moderate linkage disequilibrium, this observation is in line with suggested mechanisms of reduced *HTRA1* activity in CARASIL (Hara *et al.*, 2009; Beaufort *et al.*, 2014), and also the recent description of heterozygote loss-of-function variants in *HTRA1* causing SVD phenotypes in European populations (Verdura *et al.*, 2015).

Using a gene-based approach we also demonstrate significant association with extreme SVD of *NOTCH3* protein-modifying rare and low frequency variants, which were replicated in independent cohorts. This association is primarily driven by variants located in the EGFr domain, known to preferentially harbour CADASIL causing mutations. CADASIL, the most common of all known Mendelian forms of SVD, is an autosomal dominant disease typically caused by cysteine residue altering variants in *NOTCH3* resulting in an uneven number of cysteines in the EGFr domain of NOTCH3, disrupting disulphide bridge formation, causing misfolding of EGFr, and increasing NOTCH3 multimerization (Monet-Lepretre *et al.*, 2013). Some cysteine-modifying mutational hotspots (R91C, R170C or C213S) were reported to cause aberrant dimerization of NOTCH3 fragments by reducing Fringe-mediated elongation of O-fucose glycosylation (Arboleda-Velasquez *et al.*, 2005). In rare instances, cysteine-sparing variants were also reported to cause CADASIL in some families, but their pathogenicity is still debated. Five missense variants in EGFr determining region observed in the 3C-Dijon extreme SVD sample are predicted mucin type GalNAc O-glycosylation sites, of which three variants were exclusively observed in participants with extensive SVD. Because of the lack of publicly available resources to computationally predict other types of *O*-glycosylation than mucin (*O*-fucose, *O*-glucose, *O*-GlcNAc, and *O*-xylose) we have only partially captured the impact of observed *NOTCH3* missense variants on glycosylation disruption in the EGFr domain. Further functional studies are essential to understand the impact of glycosylation disruption in the EGFr domain of NOTCH3 by genetic variants in complex SVD pathophysiology.

Interestingly, two participants with extensive SVD, representing 0.4% of our discovery population-based sample, and 0.8% of participants with extensive SVD, carried heterozygous mutations in *NOTCH3* or *HTRA1* described previously as pathogenic and causing CADASIL or CARASIL, two Mendelian forms of SVD. Of note, this observation is based on high quality WES data but lacks technical validation using targeted Sanger sequencing. The frequency of known pathogenic variants in our community sample is higher than expected, but in line with a recent analysis of *NOTCH3* likely pathogenic variants described in 0.3% of the 60,706 exomes of the publicly available exome aggregation consortium (ExAC) database (Rutten

et al., 2016*a*). The main shortcoming of the ExAC database is the limited clinical information on participants included in the database and the lack of data on covert, MRI-defined SVD phenotypes. Our study provides further evidence that pathogenic variants known to cause rare Mendelian forms of SVD (CADASIL and CARASIL) are less exceptional than previously suspected in the general population. Although they were observed in persons with extensive SVD on brain imaging, they appeared to have mild clinical expression in this population-based setting. The CADASIL causing variant reported in our cohort modifies the cysteine residue of the EGF repeat 20 of the NOTCH3 N-terminus. Interestingly, cysteine modifying mutations at EGF repeats 7–34 may have a milder CADASIL phenotype than those affecting EGFr domain 1–6 at the C-terminal end, because of lower likelihood of interaction of unpaired cysteine with other proteins (Rutten *et al.*, 2016*a*). Our results further add to the debate around returning results on incidental findings from next generation sequencing considering that the penetrance of likely pathogenic variants may be highly variable (Hehir-Kwa *et al.*, 2015; Hofmann, 2016).

Intriguingly we observed two missense variants in *COL4A1* and *COL4A2* in 3C-Dijon participants with minimal SVD, with typical characteristics of SVD causing mutations, although they have not been described previously in SVD families. This may reflect low penetrance. Indeed, clinical studies have shown that a significant proportion of mutation carriers do not develop intracerebral bleedings (Meuwissen *et al.*, 2015). This may also be explained by the fact that our brain imaging protocol did not include gradient echo images to detect previous microbleeds or intracerebral haemorrhages, as the most common manifestations of *COL4A1/2* related SVD are brain haemorrhages (Lanfranconi and Markus, 2010).

Our proof-of-concept gene-mapping study focused on genetic variants within five candidate genes observed using the WES technique. One notable limitation of this work is that it did not report on association of some common risk variants relevant to SVD pathology that were identified using the GWAS approach, as these were not captured by WES, particularly *COL4A2* intronic variants, respectively, rs9515201, rs9521732, rs9521733, and rs9515199, which were recently reported to be associated with WMH volume (Traylor *et al.*, 2016) and deep intracerebral haemorrhage (Rannikmae *et al.*, 2015). Furthermore, as we focused only on SVD candidate genes, our study did not explore the impact on extreme SVD of rare and common variants in other candidate loci, such as those previously associated with continuous WMH burden (Verhaaren *et al.*, 2015; Traylor *et al.*, 2016), stroke (Malik *et al.*, 2018) or Alzheimer's disease (Lambert *et al.*, 2013). These limitations will need to be addressed through a large multi-cohort gene-mapping study using GWAS and possibly whole genome sequencing approaches.

In summary, our proof-of-concept study provides strong evidence that using a novel composite MRI-derived phenotype for extremes of SVD can facilitate the identification of genetic variants underlying SVD, both common variants and those with rare and low frequency. The findings demonstrate shared mechanisms and a continuum between genes underlying Mendelian SVD and those contributing to the common, multifactorial form of the disease. Future studies exploring rare and common genetic variants associated with this composite extreme SVD phenotype at a genome-wide or whole genome level are warranted. Indeed, SVD is a major contributor to stroke and dementia risk worldwide with no specific therapy available to date, and efforts to decipher underlying biological pathways to accelerate the discovery of novel treatment strategies represent a public health priority.

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Competing interests

The authors report no competing interests.

Supplementary material

Supplementary material is available at *Brain* online.

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