

Association of common genetic variants with brain microbleeds

A genome-wide association study

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Abstract

Objective

To identify common genetic variants associated with the presence of brain microbleeds (BMBs).

Methods

We performed genome-wide association studies in 11 population-based cohort studies and 3 case-control or case-only stroke cohorts. Genotypes were imputed to the Haplotype Reference

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Glossary

AD = Alzheimer disease; **CHARGE** = Cohorts of Heart and Aging Research in Genomic Epidemiology; **CI** = confidence interval; **CSVD** = cerebral small vessel disease; **BMB** = brain microbleed; **GWAS** = genome-wide association studies; **ICH** = intracerebral hemorrhage; **LD** = linkage disequilibrium; **MAF** = minor allele frequency; **OR** = odds ratio; **SNP** = single nucleotide polymorphism; **SWI** = susceptibility-weighted imaging; **WMH** = white matter hyperintensities.

Consortium or 1000 Genomes reference panel. BMBs were rated on susceptibility-weighted or T2*-weighted gradient echo MRI sequences, and further classified as lobar or mixed (including strictly deep and infratentorial, possibly with lobar BMB). In a subset, we assessed the effects of *APOE* ϵ 2 and ϵ 4 alleles on BMB counts. We also related previously identified cerebral small vessel disease variants to BMBs.

Results

BMBs were detected in 3,556 of the 25,862 participants, of which 2,179 were strictly lobar and 1,293 mixed. One locus in the *APOE* region reached genome-wide significance for its association with BMB (lead *single nucleotide polymorphism* rs769449; odds ratio [OR]_{any BMB} [95% confidence interval (CI)] 1.33 [1.21–1.45]; $p = 2.5 \times 10^{-10}$). *APOE* ϵ 4 alleles were associated with strictly lobar (OR [95% CI] 1.34 [1.19–1.50]; $p = 1.0 \times 10^{-6}$) but not with mixed BMB counts (OR [95% CI] 1.04 [0.86–1.25]; $p = 0.68$). *APOE* ϵ 2 alleles did not show associations with BMB counts. Variants previously related to deep intracerebral hemorrhage and lacunar stroke, and a risk score of cerebral white matter hyperintensity variants, were associated with BMB.

Conclusions

Genetic variants in the *APOE* region are associated with the presence of BMB, most likely due to the *APOE* ϵ 4 allele count related to a higher number of strictly lobar BMBs. Genetic predisposition to small vessel disease confers risk of BMB, indicating genetic overlap with other cerebral small vessel disease markers.

Brain microbleeds (BMBs), also referred to as cerebral microbleeds or cerebral microhemorrhages, correspond to hemosiderin deposits as a result of microscopic hemorrhages that are visible on MRI sequences.¹ The frequency of BMBs increases with age and with certain pathologies, including cerebral small vessel disease (CSVD),² and in prospective studies BMB can predict risk of ischemic stroke and intracerebral hemorrhage (ICH).^{3,4} It has been suggested BMB may represent a marker that can stratify risk, particularly risk of ICH, in patients taking antithrombotic and anticoagulant therapy.⁵

Microbleeds can occur in the cortical area or the cortico-subcortical border (lobar) and the subcortical (deep) structures of the brain. BMBs in lobar regions are often seen in both familial and sporadic cerebral amyloid angiopathy, whereas deep BMBs are more common in sporadic deep perforator arteriopathy.^{6–8} This suggests that different pathophysiologic mechanisms may underlie BMBs in the 2 locations, a situation similar to that of ICH, where the genetic risk factor profiles for lobar and deep hemorrhage have been shown to differ.⁹

BMBs represent one of a spectrum of MRI markers of CSVD, with others including white matter hyperintensities (WMH) and lacunar infarcts.¹ Genome-wide association studies (GWAS) of these other markers, particularly WMH, have provided novel insights into the underlying disease mechanisms.^{10,11} However, much less is known of the genetic basis of BMB.^{12,13} We hypothesized that common genetic variants contribute to interindividual variation in

BMB. Therefore, we performed the largest GWAS on BMB to date to evaluate this. In addition to any BMB, we performed separate GWAS for lobar BMB and mixed BMB.

Methods

Study population

The study included data from 2 large initiatives: the Cohorts of Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium¹⁴ and the UK Biobank (ukbiobank.ac.uk), combined with additional data from the case-control Alzheimer's Disease Neuroimaging Initiative (ADNI) database (adni.loni.usc.edu) and the Massachusetts General Hospital Genes Affecting Stroke Risk and Outcomes Study (MGH-GASROS)¹⁵ and Clinical Relevance of Microbleeds in Stroke due to Atrial Fibrillation (CROMIS-2 AF)⁴ stroke studies. Together this comprised 25,862 individuals from 9 population-based and 2 family-based cohort studies, as well as 1 case-control study and 2 case-only cohorts (table 1).

Standard protocol approvals, registrations, and patient consents

The individual studies have been approved by their local institutional review boards or ethics committees. Written informed consent was obtained from all individuals participating in the study.

Table 1 Population characteristics of contributing studies

| Study | Study design | Ancestry | Total | Any BMBs | Lobar BMBs | Mixed BMBs | Female | Age, y | Age range, y | Dementia | Stroke |
|---------------|--|------------------|--------|----------|------------|------------|--------------|-------------|--------------|----------|--------|
| ADNI | Case-control (AD, MCI, healthy controls) | European | 734 | 149 | 95 | 54 | 330 (45.0) | 73.1 ± 7.5 | 48–94 | 116 | 45 |
| AGES | Population-based | European | 2,894 | 469 | 272 | 197 | 1,679 (58.0) | 76.4 ± 5.5 | 66–95 | 149 | 223 |
| ASPS | Population-based | European | 203 | 34 | NA | 28 | 89 (43.8) | 60.1 ± 6.3 | 46–79 | 0 | 0 |
| ARIC (AA) | Population-based | European | 422 | 118 | 81 | 31 | 281 (66.6) | 75.4 ± 5.1 | 67–89 | 24 | 22 |
| ARIC (EA) | Population-based | African American | 1,174 | 267 | 184 | 74 | 680 (57.9) | 77.0 ± 5.3 | 67–90 | 70 | 34 |
| CROMIS-2 AF | Case-only (stroke cases) | European | 1,238 | 253 | 94 | 158 | 522 (42.2) | 75.1 ± 12.6 | 35–100 | 32 | 1,238 |
| EDIS-SCES | Population-based | Chinese | 130 | 42 | 27 | NA | 69 (53.1) | 70.5 ± 6.1 | 60–85 | 5 | 6 |
| EDIS-SIMES | Population-based | Malay | 204 | 75 | 36 | NA | 107 (52.5) | 70.6 ± 6.6 | 60–85 | 21 | 8 |
| ERF | Family-based | European | 126 | 27 | 15 | 12 | 66 (52.4) | 64.5 ± 4.6 | 55–75 | 0 | 0 |
| FHS | Population-based | European | 3,968 | 257 | 176 | 81 | 2,115 (53.3) | 57.3 ± 13.6 | 25–96 | 25 | 51 |
| LBC1936 | Population-based | European | 626 | 74 | 21 | 53 | 295 (47.1) | 72.7 ± 0.7 | 71–74 | 5 | 43 |
| LLS | Family-based | European | 279 | 39 | 24 | 11 | 147 (52.7) | 65.8 ± 6.9 | 45–84 | 0 | 0 |
| MGH-GASROS | Case-only (stroke cases) | European | 380 | 106 | 51 | 55 | 127 (36.0) | 66.7 ± 15.0 | 18–102 | 0 | 353 |
| PROSPER | RCT/population-based | European | 456 | 104 | 74 | 26 | 197 (43.2) | 75.0 ± 3.2 | 70–83 | 0 | 74 |
| RS1 | Population-based | European | 1,119 | 384 | 234 | 150 | 642 (57.4) | 79.2 ± 5.0 | 68–96 | 30 | 64 |
| RS2 | Population-based | European | 1,206 | 270 | 167 | 103 | 628 (52.1) | 69.7 ± 6.2 | 60–97 | 8 | 23 |
| RS3 | Population-based | European | 2,611 | 318 | 237 | 81 | 1,444 (55.3) | 57.3 ± 6.6 | 45–89 | 0 | 3 |
| UK Biobank | Population-based | European | 8,092 | 570 | 391 | 179 | 4,263 (52.7) | 62.1 ± 7.4 | 44–78 | 3 | 75 |
| Totals | | | 25,862 | 3,556 | 2,179 | 1,293 | | | | | |

Abbreviations: AA = African ancestry; AD = Alzheimer disease; ADNI = Alzheimer's Disease Neuroimaging Initiative; AGES = Age, Gene/Environment Susceptibility-Reykjavik Study; ARIC = Atherosclerosis Risk in Communities; ASPS = Austrian Stroke Prevention Study; BMB = brain microbleed; CROMIS-2 AF = Clinical Relevance of Microbleeds in Stroke due to Atrial Fibrillation; EA = European ancestry; EDIS = Epidemiology of Dementia in Singapore; ERF = Erasmus Rucphen Family; FHS = Framingham Heart Study; LBC1936 = Lothian Birth Cohort 1936; LLS = Leiden Longevity Study; MCI = mild cognitive impairment; MGH-GASROS = Massachusetts General Hospital Genes Affecting Stroke Risk and Outcomes Study; PROSPER = Prospective Study of Pravastatin in the Elderly at Risk; RCT = randomized controlled trial; RS = Rotterdam Study; SCES = Singapore Chinese Eye Study; SIMES = Singapore Malay Eye Study. Values are n (%) or mean ± SD.

Genotyping

Genotyping was performed on commercially available assays from Illumina (San Diego, CA) or Affymetrix (Santa Clara, CA) and were imputed using the Haplotype Reference Consortium or 1000 Genomes reference panels (supplementary table e-1, doi.org/10.5061/dryad.mcvdncjz4). Most cohorts included individuals of European ancestry only, but a subset of individuals with Chinese, Malay, or African American ancestry ($n = 130$, $n = 204$, and $n = 422$, respectively) was also included.

Assessment of brain microbleeds

MRI scans with field strengths of 1T, 1.5T, or 3T and full brain coverage were acquired in each participating study (supplementary table e-2, doi.org/10.5061/dryad.mcvdncjz4). Definitions of BMB have been described previously.¹⁶ Briefly, BMBs can be recognized as small, hypointense lesions on susceptibility-weighted imaging (SWI) sequences or, to a lesser extent, on T2*-weighted gradient echo sequences. Although BMB assessment using SWI sequences is more sensitive than assessment using T2*-weighted sequences,^{17,18} the clinical relevance of this improved sensitivity is debated since it is also less specific.¹⁹ Because previous research has shown differences between risk factors and clinical correlates of BMBs in specific locations of the brain,^{6,8,20} we further differentiated between strictly lobar and deep infratentorial or mixed BMBs. Cases in which there were microbleeds located in cortical gray or subcortical white matter of the brain lobes without any microbleeds in deep or infratentorial regions were classified as lobar BMBs. Microbleeds in the deep gray matter of basal ganglia and thalamus or in brainstem or cerebellum were classified as deep or infratentorial BMBs. Due to the low number of cases of BMB, especially the deep and infratentorial subtypes, we created one group of mixed BMB cases. Mixed BMB was defined as deep or infratentorial BMB, possibly in combination with microbleeds in lobar regions. In a minority of cohorts (table 1), the data on lobar or mixed BMB were not available, and therefore the total number of lobar and mixed BMBs is slightly less than the total number of BMBs. Study-specific methodologies for the identification of BMBs have been described elsewhere.^{1,6,21–30} Because BMB assessment in the UK Biobank has not been described before, additional information regarding the UK Biobank sample, including microbleeds assessment, is provided in the supplementary information (doi.org/10.5061/dryad.mcvdncjz4).

Genome-wide association studies

In each participating study, genome-wide association analyses were performed using logistic regression under an additive model, adjusted for age, sex, and principal components of ancestry to account for population structure (if needed) and family relations (if applicable). For each study, variants were filtered by imputation quality using an INFO or r^2 above 0.5, minor allele frequency (MAF) above 0.005, and $MAF * N_{cases} * \text{imputation quality} > 5$. Within the CHARGE consortium plus additional case-control and case-only studies, only variants available in at least 2 cohorts were analyzed. Then, genetic variants were filtered using $MAF > 0.01$, after which the

CHARGE consortium with additional studies and UK Biobank results were meta-analyzed together. An inverse variance-weighted fixed-effects model was applied in METAL using the standard error analysis scheme.³¹ As a sensitivity analysis, we performed this analysis while excluding individuals with dementia and stroke, to investigate whether the associations were driven by these diseases. To examine whether there was substantial genomic inflation due to population stratification, we inspected the linkage disequilibrium (LD) score regression intercept (supplementary table e-3, doi.org/10.5061/dryad.mcvdncjz4).³² For follow-up analyses, only variants present in more than half of the cases were included. HaploReg v4.1 was used for the functional annotation of the suggestive ($p < 5 \times 10^{-6}$) and genome-wide significant ($p < 5 \times 10^{-8}$) variants, and variants in LD at a threshold of $r^2 > 0.8$.³³

APOE $\epsilon 2$ and $\epsilon 4$ count analysis

In the 2 largest cohorts (i.e., UK Biobank and Rotterdam Study), we investigated the effect of APOE $\epsilon 2$ and $\epsilon 4$ allele counts, directly genotyped using a polymerase chain reaction, inferred from imputed Haplotype Reference Consortium values of rs429358 and rs7412, or a combination of both. Zero-inflated negative binomial regression analysis was performed investigating the association of APOE allele counts with the number of any, lobar, and mixed BMB, adjusted for age, sex, and principal components. For each individual, we counted the number of APOE $\epsilon 2$ alleles ($\epsilon 2\epsilon 2$ coded as 2, $\epsilon 2\epsilon 3$ and $\epsilon 2\epsilon 4$ as 1, and $\epsilon 3\epsilon 3$, $\epsilon 3\epsilon 4$, and $\epsilon 4\epsilon 4$ as 0) and the number of APOE $\epsilon 4$ alleles ($\epsilon 4\epsilon 4$ coded as 2, $\epsilon 2\epsilon 4$ and $\epsilon 3\epsilon 4$ as 1, and $\epsilon 2\epsilon 2$, $\epsilon 2\epsilon 3$, and $\epsilon 3\epsilon 3$ as 0). We repeated these analyses while setting APOE $\epsilon 2\epsilon 4$ values to missing since this combines the protective $\epsilon 2$ and the risk-increasing $\epsilon 4$ allele for Alzheimer disease (AD) and may therefore dilute the effects. For these analyses, counts of more than 100 microbleeds were considered outliers and removed from the analysis ($n = 2$ in the UK Biobank; $n = 2$ in the Rotterdam Study).

Two-sample mendelian randomization

In order to test potential causal effects of cardiovascular risk factors on BMBs, we performed a 2-sample mendelian randomization using an inverse variance-weighted method implemented in the MendelianRandomization R library. Summary statistic data of GWAS were acquired for the following traits: type 2 diabetes mellitus,³⁴ systolic and diastolic blood pressure, pulse pressure,³⁵ body mass index,³⁶ low-density lipoprotein cholesterol, high-density lipoprotein cholesterol, and triglycerides.³⁷

Related phenotypes

For independent ($r^2 \leq 0.8$) variants previously associated at genome-wide significance with other traits that in turn might be related to BMBs, we assessed the association with BMBs as well. First we examined variants associated with other manifestations of CSVD, namely WMH,^{10,11,15} lacunar stroke,^{38,39} and ICH.^{39,40} Second we examined associations with traits that have been shown to be predicted by BMB, namely any stroke, any ischemic stroke,^{41,42} and AD.⁴³ For each related phenotype, we corrected

Table 2 Independent genetic variants significantly ($p < 5 \times 10^{-8}$) or suggestively ($p < 1 \times 10^{-6}$) associated with any or location-specific brain microbleeds (BMBs)

| SNP | Chr | Position | A1 | A2 | EAF | Nearest gene | Outcome | β | SE | OR | Total | Cases | p Value |
|------------|-----|-----------|----|----|------|--------------|------------|---------|-------|------|--------|-------|-----------------------|
| rs769449 | 19 | 45410002 | A | G | 0.13 | APOE | Any BMBs | 0.282 | 0.045 | 1.33 | 20,150 | 2,858 | 2.5×10^{-10} |
| | | | | | | | Lobar BMBs | 0.280 | 0.055 | 1.32 | 18,666 | 1,748 | 4.3×10^{-7} |
| | | | | | | | Mixed BMBs | 0.243 | 0.070 | 1.27 | 18,319 | 1,049 | 5.4×10^{-4} |
| rs6950978 | 7 | 87200467 | A | T | 0.70 | ABCB1 | Any BMBs | -0.154 | 0.030 | 0.86 | 25,528 | 3,439 | 2.7×10^{-7} |
| | | | | | | | Lobar BMBs | -0.153 | 0.037 | 0.86 | 24,101 | 2,101 | 4.1×10^{-5} |
| | | | | | | | Mixed BMBs | -0.179 | 0.046 | 0.84 | 23,033 | 1,239 | 1.0×10^{-4} |
| rs7533718 | 1 | 22281393 | A | G | 0.83 | HSPG2 | Any BMBs | -0.140 | 0.042 | 0.87 | 25,402 | 3,412 | 7.5×10^{-4} |
| | | | | | | | Lobar BMBs | -0.263 | 0.051 | 0.77 | 22,935 | 2,005 | 2.9×10^{-7} |
| | | | | | | | Mixed BMBs | 0.003 | 0.070 | 1.00 | 22,446 | 1,161 | 9.7×10^{-1} |
| rs11025317 | 11 | 3103445 | A | G | 0.12 | OSBPL5 | Any BMBs | 0.172 | 0.049 | 1.19 | 20,330 | 2,918 | 4.3×10^{-4} |
| | | | | | | | Lobar BMBs | 0.305 | 0.060 | 1.36 | 18,666 | 1,748 | 3.0×10^{-7} |
| | | | | | | | Mixed BMBs | -0.027 | 0.082 | 0.97 | 17,714 | 996 | 7.4×10^{-1} |
| rs62522567 | 8 | 103799094 | A | G | 0.92 | GASAL1 | Any BMBs | -0.231 | 0.051 | 0.79 | 24,118 | 3,115 | 6.9×10^{-6} |
| | | | | | | | Lobar BMBs | -0.319 | 0.063 | 0.73 | 22,550 | 1,924 | 4.0×10^{-7} |
| | | | | | | | Mixed BMBs | -0.195 | 0.089 | 0.82 | 17,075 | 942 | 2.8×10^{-2} |
| rs1058285 | 19 | 43680051 | T | C | 0.61 | PSG5 | Any BMBs | 0.082 | 0.030 | 1.08 | 24,794 | 3,290 | 6.0×10^{-3} |
| | | | | | | | Lobar BMBs | 0.188 | 0.038 | 1.21 | 23,535 | 2,021 | 5.3×10^{-7} |
| | | | | | | | Mixed BMBs | -0.051 | 0.045 | 0.95 | 22,729 | 1,216 | 2.6×10^{-1} |
| rs654240 | 11 | 69448373 | T | C | 0.41 | CCND1 | Any BMBs | 0.154 | 0.031 | 1.17 | 25,402 | 3,412 | 7.4×10^{-7} |
| | | | | | | | Lobar BMBs | 0.116 | 0.039 | 1.12 | 23,528 | 2,080 | 2.8×10^{-3} |
| | | | | | | | Mixed BMBs | 0.202 | 0.048 | 1.22 | 23,368 | 1,270 | 3.0×10^{-5} |

Abbreviations: A1 = effect allele; A2 = other allele; Chr = chromosome; EAF = effect allele frequency; OR = odds ratio; SNP = single nucleotide polymorphism. Associations with BMBs with a $p < 1 \times 10^{-6}$. If available, the associations of the same genetic variants in the other analyses are also shown.

the p value for significance, dividing 0.05 by the number of single nucleotide polymorphisms (SNPs) tested. Where we had a sufficient number of variants, we assessed the cumulative association of all variants with BMBs using inverse variance weighting across all SNPs, as implemented in the gtx package in R. For WMH, the effect sizes from the largest GWAS sample were used to estimate an overall effect.¹⁰

Data availability

The summary statistics will be made available upon publication on the CHARGE dbGaP site under the accession number phs000930.v7.p1 and via the Cerebrovascular Disease Knowledge Portal (cerebrovascularportal.org).

Results

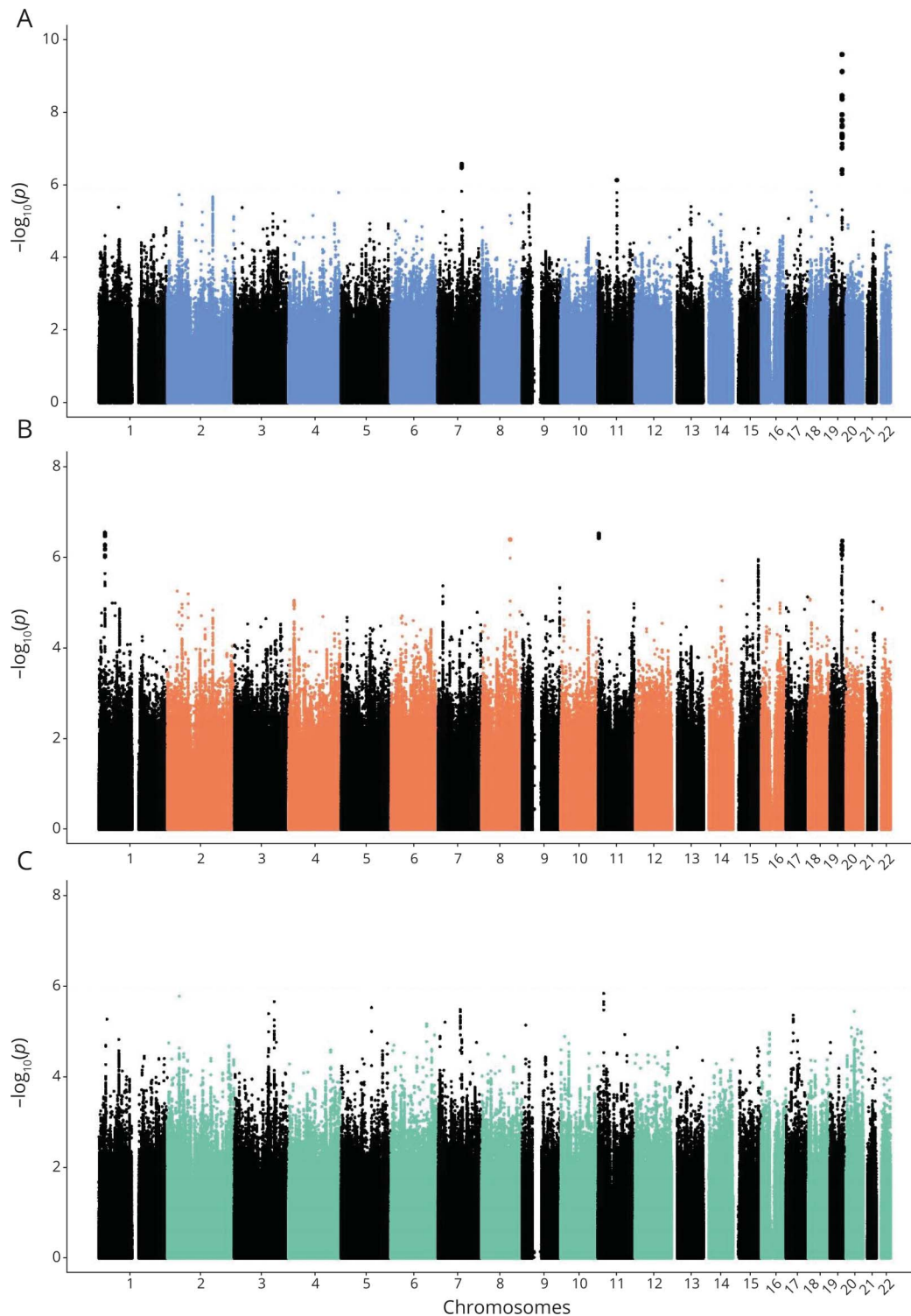
In the combined CHARGE with additional studies and UK Biobank multiethnic meta-analysis, genetic and BMB rating

data were available for 25,862 participants, of whom 3,556 (13.7%) had BMB. In 2,179 (8.4%), these were lobar and in 1,293 (5.0%) mixed. The prevalence of any BMB ranged from 6.5% to 34.3% for studies using T2*-weighted sequences for the assessment of BMB, and from 7.0% to 36.8% for studies using SWI sequences. After excluding participants with dementia and stroke, 23,032 individuals remained, of whom 2,889 (12.5%), 1,843 (8.0%), and 969 (4.2%) had any, lobar, and mixed BMB, respectively. A complete overview of the included studies is shown in table 1.

Genome-wide association studies

A quantile–quantile plot showed mild enrichment of genome-wide associations with any BMB (supplementary figure e-1, doi.org/10.5061/dryad.mcvdncjz4), and limited genomic inflation was observed ($\lambda = 1.02$, LD score regression intercept = 1.02, supplementary table e-3, doi.org/10.5061/dryad.mcvdncjz4). One locus in the APOE region on chromosome 19 reached genome-wide significance (lead genetic variant

Figure 1 Common genetic variants associated with brain microbleeds

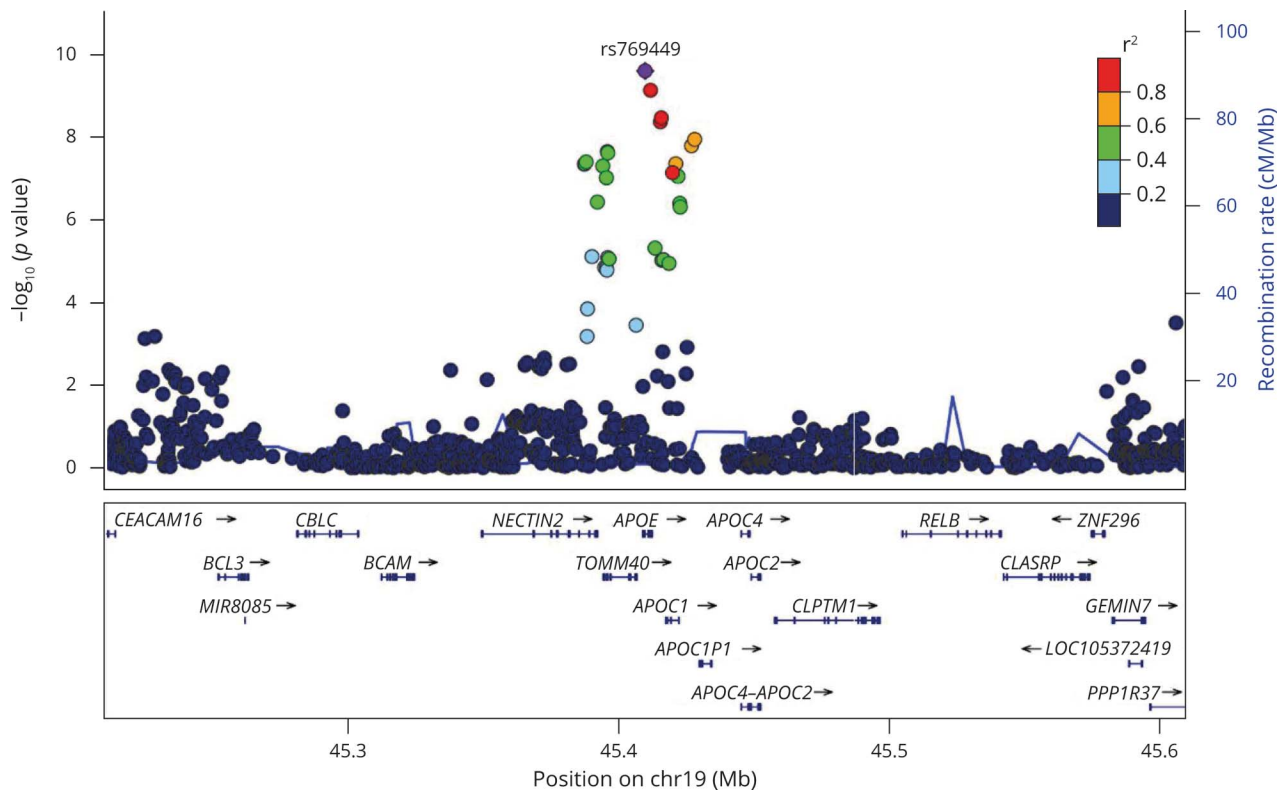


Manhattan plots show genome-wide associations by chromosomal position for (A) any, (B) lobar, and (C) mixed microbleeds.

rs769449; odds ratio [OR] [95% confidence interval (CI)] 1.33 [1.21–1.45]; $p = 2.5 \times 10^{-10}$; table 2, figures 1 and 2, and supplementary figure e-2, doi.org/10.5061/dryad.mcvdncjz4). This effect was stronger for lobar (OR [95% CI] 1.32 [1.19–1.47]; $p = 4.3 \times 10^{-7}$) than for mixed microbleeds (OR [95% CI] 1.27 [1.11–1.46]; $p = 5.4 \times 10^{-4}$), albeit not

significantly. Similar associations were observed for the different participating studies (CHARGE with additional studies $I^2 = 0$, $p_{\text{heterozygosity}} = 0.68$; CHARGE with additional studies and UK Biobank combined $I^2 = 0$, $p_{\text{heterozygosity}} = 0.78$, supplementary figure e-3, doi.org/10.5061/dryad.mcvdncjz4). Functional annotation of the genome-wide significant variants and

Figure 2 Regional association of genome-wide significant locus for any brain microbleeds



Regional plot shows association of genetic variants in the *APOE* region with any brain microbleeds.

genetic variants in LD ($r^2 > 0.8$) are presented in supplementary table e-4, doi.org/10.5061/dryad.mcvdncjz4). In the analysis excluding individuals with dementia and stroke, the effect estimate for the lead SNP rs769449 did not attenuate, although the level of significance slightly decreased, reflecting the smaller sample size (OR [95% CI] 1.32 [1.20–1.46], $p = 2.1 \times 10^{-8}$, supplementary table e-5 and supplementary figure e-4, doi.org/10.5061/dryad.mcvdncjz4).

***APOE* ε2 and ε4 count analysis**

To further elucidate whether 1 of the 2 *APOE* genotypes were driving this identified genetic association between the *APOE* region and BMB, we performed a follow-up analysis of this finding, assessing the association of *APOE* ε2 and ε4 allele counts with BMB in the 2 largest cohorts (Rotterdam Study and UK Biobank). The *APOE* ε4 allele count was significantly associated with the number of BMBs (OR [95% CI] 1.27 [1.14–1.42]; $p = 1.3 \times$

Table 3 The effects of *APOE* ε2 and ε4 allele count on the number of brain microbleeds (BMBs) overall and by location

| Outcome | β | SE | OR (95% CI) | p Value |
|------------------------------------|--------|-------|------------------|----------------------|
| <i>APOE</i> ε2 allele count | | | | |
| All BMBs | 0.026 | 0.089 | 1.03 (0.86–1.22) | 0.769 |
| Lobar BMBs | 0.130 | 0.121 | 1.14 (0.90–1.44) | 0.283 |
| Mixed BMBs | –0.243 | 0.178 | 0.78 (0.55–1.11) | 0.171 |
| <i>APOE</i> ε4 allele count | | | | |
| All BMBs | 0.242 | 0.055 | 1.27 (1.14–1.42) | 1.3×10^{-5} |
| Lobar BMBs | 0.285 | 0.069 | 1.33 (1.16–1.52) | 3.5×10^{-5} |
| Mixed BMBs | 0.069 | 0.117 | 1.07 (0.85–1.35) | 0.553 |

Abbreviations: CI = confidence interval; OR = odds ratio.

Table 4 Two-sample mendelian randomization of cardiovascular traits and brain microbleeds overall and by location

| Analysis | Estimate (95% CI) | p Value |
|--------------------------------|--------------------------|--------------------|
| Any brain microbleeds | | |
| Type 2 diabetes | -0.072 (-0.176 to 0.031) | 0.170 |
| Systolic blood pressure | 0.026 (0.005 to 0.046) | 0.013 ^a |
| Diastolic blood pressure | 0.046 (0.010 to 0.082) | 0.011 ^a |
| Pulse pressure | 0.021 (-0.008 to 0.049) | 0.156 |
| Body mass index | -0.037 (-0.131 to 0.057) | 0.445 |
| Low density lipoprotein | 0.057 (-0.085 to 0.198) | 0.431 |
| High density lipoprotein | -0.001 (-0.159 to 0.157) | 0.990 |
| Triglycerides | 0.290 (0.090 to 0.489) | 0.004 ^b |
| Lobar brain microbleeds | | |
| Type 2 diabetes | -0.053 (-0.180 to 0.074) | 0.414 |
| Systolic blood pressure | 0.027 (0.003 to 0.051) | 0.029 ^a |
| Diastolic blood pressure | 0.046 (0.003 to 0.088) | 0.035 ^a |
| Pulse pressure | 0.023 (-0.010 to 0.057) | 0.174 |
| Body mass index | -0.023 (-0.141 to 0.094) | 0.697 |
| Low density lipoprotein | 0.145 (-0.015 to 0.306) | 0.076 |
| High density lipoprotein | -0.024 (-0.206 to 0.159) | 0.799 |
| Triglycerides | 0.250 (0.015 to 0.486) | 0.037 ^a |
| Mixed brain microbleeds | | |
| Type 2 diabetes | -0.074 (-0.222 to 0.073) | 0.323 |
| Systolic blood pressure | 0.024 (-0.005 to 0.054) | 0.108 |
| Diastolic blood pressure | 0.034 (-0.019 to 0.086) | 0.209 |
| Pulse pressure | 0.025 (-0.017 to 0.066) | 0.243 |
| Body mass index | -0.047 (-0.191 to 0.097) | 0.524 |
| Low density lipoprotein | -0.078 (-0.315 to 0.159) | 0.519 |
| High density lipoprotein | -0.050 (-0.263 to 0.162) | 0.642 |
| Triglycerides | 0.374 (0.094 to 0.654) | 0.009 ^a |

Abbreviation: CI = confidence interval.

^a Nominally significant associations ($p < 0.05$).

^b Significant after adjustment for the number of risk factors ($p < [0.05/8]$).

10^{-5} ; table 3). This effect was stronger for lobar than for mixed microbleeds (OR [95% CI] 1.33 [1.16–1.52]; $p = 3.5 \times 10^{-5}$ and OR [95% CI] 1.07 [0.85–1.35]; $p = 0.553$, respectively). These results did not change after excluding individuals with the *APOE* $\epsilon 2\epsilon 4$ genotype (supplementary table e-6, doi.org/10.5061/dryad.mcvdncjz4). No significant association was found between the *APOE* $\epsilon 2$ allele count and the number of BMBs (OR [95% CI] 1.03 [0.86–1.22]; $p = 0.769$), also not after removing

individuals with the *APOE* $\epsilon 2\epsilon 4$ genotype (table 3 and supplementary table e-6, doi.org/10.5061/dryad.mcvdncjz4).

Two-sample mendelian randomization

Mendelian randomization analyses testing the influence of cardiovascular risk factors on BMBs showed positive nominal associations of systolic blood pressure, diastolic blood pressure, and triglycerides with any BMB and of systolic and diastolic blood pressure and triglycerides with strictly lobar BMBs as well as triglycerides with deep, infratentorial, or mixed BMBs (table 4). Only the association of triglycerides with any microbleeds survived multiple testing adjustments ($\beta = 0.29$, 95% CI 0.09–0.49, $p = 0.004$); the effect estimate of this association was stronger for mixed microbleeds ($\beta = 0.37$, 95% CI 0.09–0.65, $p = 0.009$).

Related phenotypes

One genetic variant previously associated with deep ICH and WMH (rs2984613 in the 1q22 locus) was associated with BMB (OR [95% CI] 1.12 [1.05–1.18], $p = 1.8 \times 10^{-4}$), with slightly stronger effects on mixed BMB than lobar BMB (OR [95% CI] 1.14 [1.05–1.25], $p = 3.2 \times 10^{-3}$ vs OR [95% CI] 1.09 [1.01–1.17], $p = 2.2 \times 10^{-2}$) (table 5). One variant known to be associated with lacunar stroke (rs9515201 in the 13q34 locus) also associated with mixed BMB (OR [95% CI] 1.12 [1.02–1.22], $p = 0.014$), but did not associate with lobar BMB (OR [95% CI] 0.98 [0.91–1.06], $p = 0.684$). No other CSVD variants were individually associated with BMB. Cumulatively, genetic variants identified for cerebral WMH burden were associated with mixed BMB (OR [95% CI] 1.78 [1.15–2.77]; $p = 0.01$), but not with lobar BMB (OR [95% CI] 1.02 [0.71–1.45]; $p = 0.93$). Also, a cumulative effect of previously identified variants for any stroke was found for mixed BMB (OR [95% CI] 1.78 [1.09–2.91]; $p = 0.02$), which was similar for variants of any ischemic stroke (OR [95% CI] 2.00 [1.22–3.27]; $p = 0.006$). Full results of the genetic variants previously identified for AD and stroke are presented in supplementary table e-7 (doi.org/10.5061/dryad.mcvdncjz4).

Discussion

We report the first large-scale multiethnic genome-wide study of BMBs in 25,862 individuals, including 3,556 participants with any BMB, of whom 2,179 had strictly lobar and 1,293 mixed BMB. We identified an association with BMB in the *APOE* region, in particular for strictly lobar BMBs, most likely due to risk associated with *APOE* $\epsilon 4$ allele counts.

Our findings are in line with previous studies showing an association between *APOE* $\epsilon 4$ genotypes and BMB, in particular with strictly lobar BMB.¹² One genetic variant in LD with the identified lead SNP (rs769448) is rs429358, which is an *APOE* missense variant and 1 of the 2 SNPs constituting *APOE* $\epsilon 2/3/4$ polymorphisms; this variant was more strongly associated with strictly lobar than mixed BMB. In an

Table 5 Association of cerebral small vessel disease–associated genetic variants with brain microbleeds (BMBs) overall and by location

| Trait | Locus | SNP | All BMBs | | Lobar BMBs | | Mixed BMBs | |
|------------------|---------|------------|------------------|---------------------|------------------|--------------------|------------------|--------------------|
| | | | OR (95% CI) | p Value | OR (95% CI) | p Value | OR (95% CI) | p Value |
| ICH deep | 1q22 | rs2984613 | 1.12 (1.05–1.18) | 0.0002 ^a | 1.09 (1.01–1.17) | 0.022 ^a | 1.14 (1.05–1.25) | 0.003 ^a |
| | 13q34 | rs4771674 | 1.03 (0.97–1.09) | 0.350 | 0.99 (0.93–1.07) | 0.879 | 1.06 (0.97–1.15) | 0.218 |
| Lacunar stroke | 16q24 | rs12445022 | 1.07 (1.00–1.13) | 0.034 ^b | 1.04 (0.97–1.12) | 0.277 | 1.10 (1.00–1.20) | 0.039 ^b |
| | 10q26 | rs79043147 | 1.02 (0.91–1.14) | 0.785 | 1.04 (0.90–1.21) | 0.601 | 1.05 (0.87–1.27) | 0.582 |
| | 13q34 | rs9515201 | 1.04 (0.98–1.10) | 0.206 | 0.98 (0.91–1.06) | 0.684 | 1.12 (1.02–1.22) | 0.014 ^a |
| WMH ^c | 2p21 | rs11679640 | 0.95 (0.88–1.01) | 0.111 | 0.96 (0.88–1.04) | 0.300 | 0.98 (0.88–1.10) | 0.768 |
| | 10q24 | rs12357919 | 1.01 (0.94–1.08) | 0.881 | 1.00 (0.91–1.10) | 0.970 | 0.97 (0.86–1.09) | 0.598 |
| | 6q25 | rs275350 | 1.01 (0.95–1.06) | 0.775 | 0.98 (0.91–1.05) | 0.519 | 1.08 (0.99–1.17) | 0.084 |
| | 1q22 | rs2984613 | 1.12 (1.05–1.18) | 0.0002 ^a | 1.09 (1.01–1.17) | 0.022 ^b | 1.14 (1.05–1.25) | 0.003 ^a |
| | 17q25 | rs7214628 | 1.00 (0.94–1.08) | 0.902 | 1.04 (0.95–1.13) | 0.404 | 1.02 (0.91–1.13) | 0.779 |
| | 10q24 | rs72848980 | 1.00 (0.93–1.08) | 0.947 | 1.00 (0.91–1.10) | 0.970 | 0.98 (0.87–1.10) | 0.687 |
| | 2q33 | rs72934505 | 1.05 (0.96–1.15) | 0.264 | 1.01 (0.91–1.12) | 0.886 | 1.11 (0.97–1.27) | 0.141 |
| | 2p16 | rs78857879 | 1.06 (0.97–1.17) | 0.206 | 1.02 (0.91–1.16) | 0.695 | 1.08 (0.93–1.25) | 0.300 |
| | 10q24 | rs7894407 | 1.04 (0.98–1.10) | 0.212 | 1.01 (0.94–1.09) | 0.772 | 1.02 (0.94–1.12) | 0.605 |
| | 10q24 | rs7909791 | 0.99 (0.94–1.05) | 0.784 | 0.99 (0.92–1.06) | 0.737 | 0.96 (0.88–1.05) | 0.420 |
| | 14q32 | rs941898 | 0.95 (0.89–1.01) | 0.117 | 0.91 (0.84–0.99) | 0.025 ^b | 1.01 (0.92–1.12) | 0.817 |
| | 13q34 | rs9515201 | 1.04 (0.98–1.10) | 0.206 | 0.98 (0.91–1.06) | 0.684 | 1.12 (1.02–1.22) | 0.014 ^b |
| | 17q21 | rs962888 | 1.02 (0.96–1.08) | 0.570 | 1.01 (0.93–1.09) | 0.868 | 1.02 (0.93–1.12) | 0.641 |
| | Overall | | 1.29 (0.97–1.72) | 0.074 | 1.02 (0.71–1.45) | 0.927 | 1.78 (1.15–2.77) | 0.010 ^b |

Abbreviations: CI = confidence interval; ICH = intracerebral hemorrhage; OR = odds ratio; SNP = single nucleotide polymorphism; WMH = white matter hyperintensities.

ORs aligned to risk allele from original studies.

^a Significant after Bonferroni correction ($p < 0.05/\text{number of genetic variants}$).

^b Nominally significant ($p < 0.05$).

^c In the overall score for WMH, rs12357919 was left out because this genetic variant was in linkage disequilibrium ($r^2 > 0.2$) with rs72848980.

additional analysis performed in a subset of the cohorts, we confirmed the known link between *APOE* $\epsilon 4$ allele count and the number of BMBs, with stronger effect estimates for the strictly lobar BMB subtype compared to the mixed subtype. This association was less pronounced and non-significant for the *APOE* $\epsilon 2$ allele count, which is also in accordance with previous studies,¹² although this might be due to a lack of power. Other studies did find a significant association between *APOE* $\epsilon 2$ alleles and cerebral angiopathy–related ICH,⁹ with stronger estimates for the lobar compared to the deep phenotype, which is similar to our study. Stronger effects for ICH in the previous study than for BMBs in the current study might be due to sampling variability or biological differences between the 2 traits. The *APOE* locus remained significant with a similar effect estimate in the GWAS meta-analysis performed in a dementia- and stroke-free sample, indicating that this association was not driven by individuals with disease, and

suggesting that *APOE* may already affect BMB risk in a preclinical phase of dementia or stroke.

Our findings further suggest that higher triglyceride levels may be causally related to the presence of BMBs. This relationship between the genetics of triglycerides and BMBs, in particular for mixed BMBs, confirms other studies showing a contribution of cardiovascular risk factors to BMB risk, mainly for deep or infratentorial BMBs.⁶ A previous 2-sample mendelian randomization study did not find a significant association between the genetics of triglycerides and ICH, although the direction of effect for the triglycerides analysis was the same as for BMBs in the current study.⁴⁴ However, this positive link between the genetics of triglyceride levels and the presence of BMBs is in contrast with previous phenotypic association studies showing an inverse relationship between triglyceride levels and BMB risk in elderly population-based individuals.^{45,46} Similarly, lower triglyceride levels have been associated with an increased ICH risk.^{45,47,48}

Thus, our finding should be interpreted with caution and further studies are needed to elucidate the exact causal mechanisms underlying lipid profiles over time and BMB risk.

We also showed that genetic variation previously associated with risk of CSVD (i.e., WMH burden, lacunar infarcts, and subcortical ICH) are associated with an increased risk of BMB, and that this association is restricted to mixed rather than lobar BMB. This suggests that mixed BMBs have a shared pathophysiologic pathway with other features of the CSVD spectrum. This is consistent with recent data showing genetic sharing between WMH, lacunar infarcts, and subcortical ICH.⁴⁹ Increasing evidence suggests that small vessel arteriopathy may lead to WMH, acute lacunar infarction, and ICH.⁵⁰ Our data suggest that mixed BMBs are likely to be related to the same underlying arterial pathology.

Associations of the *APOE* $\epsilon 4$ genotype with decreased cognitive function in the elderly are well-established.⁵¹ Although part of this decline is due to the predisposition to AD pathology conferred by *APOE* $\epsilon 4$, our results suggest that another part might be due to vascular mechanisms predisposing to BMBs, most likely via cerebral amyloid angiopathy. Apart from the *APOE* locus, no enrichment of previously reported genetic variants for AD was found. This is in line with a previously published WMH GWAS, in which no significant association was found between the identified loci for WMH and AD.¹¹ It might indicate that *APOE* is mainly responsible for the genetic overlap between BMB and AD. Alternatively, the current BMB and AD GWAS could be underpowered to identify biological pathways playing a role in the development of CSVD subsequently leading to AD. As another possibility, environmental factors might primarily play a role in the link between BMB and neurodegenerative diseases later in life. Although the 19q13 locus was the only significant BMB locus, we did observe a cumulative effect of stroke SNPs on mixed BMB, suggestive of overlapping biological mechanisms underlying the two.

In this study, we were able to collate most of the GWAS data available worldwide on BMBs, enabling us to perform by far the largest GWAS meta-analysis of BMB to date. Our study also has limitations. Despite being the largest study to date, the number of individuals with BMB was still modest, resulting in a limited power to identify genetic factors related to BMB. Significantly larger sample sizes are needed to fully elucidate the genetic contribution to BMB. Because of the relatively small number of participants with BMBs, we combined the presence of deep, infratentorial, and mixed BMBs into one group of mixed BMBs, even though previous research has suggested there may be differences between strictly deep and mixed BMBs.²⁰ With larger sample sizes, it would be interesting to investigate whether there are differences in the genetics between deep and infratentorial BMBs. The percentage of individuals with microbleeds varied across studies, which may be due to a true difference in the presence of BMBs or population differences, e.g., age distributions, ethnicities, and lifestyle factors. However, the differences in the presence of BMBs might

also be partially attributable to different sensitivities of the used methodologies, e.g., the magnetic field strength of the MRI scanner or the sequence used for rating BMB. Another limitation of the current study is the large majority of individuals of European ancestry included in the analyses; previous studies have shown differences in the occurrence, distribution, and associated risks of BMBs across different ethnicities.^{52–54} Therefore, it would be valuable for future studies to increase the sample size of individuals of non-European ancestry in order to be able to perform ancestry-specific analyses. Also, larger reference panels would enable us to investigate rare genetic variants as well. Lastly, it may be worthwhile to take into account the number of microbleeds instead of treating the phenotype as a dichotomous trait, which results in a loss of information.

We identified genetic variants located in the *APOE* region associated with BMB, which were more strongly associated with lobar than mixed BMB. Our data also demonstrated genetic overlap between mixed BMB and other features of CSVD, emphasizing that they represent part of the CSVD spectrum.

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funding from the Stroke Foundation/British Heart Foundation. H. Schmidt, J.M. Wardlaw, M.A. Ikram, S. Seshadri, L.J. Launer, and H.S. Markus report no disclosures relevant to the manuscript. Go to [Neurology.org/N](https://www.neurology.org/N) for full disclosures.

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Appendix (continued)

| Name | Location | Contribution |
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Continued

Appendix (continued)

| Name | Location | Contribution |
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Appendix (continued)

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| Lenore J. Launer, PhD | National Institutes of Health, Baltimore, MD | Acquired data, directed the work |
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Appendix 2 Coinvestigators

Coinvestigators are listed at links.lww.com/WNL/B222

References

1. Wardlaw JM, Smith EE, Biessels GJ, et al. Neuroimaging standards for research into small vessel disease and its contribution to ageing and neurodegeneration. *Lancet Neurol* 2013;12:822–838.
2. Poels MM, Vernooij MW, Ikram MA, et al. Prevalence and risk factors of cerebral microbleeds: an update of the Rotterdam Scan Study. *Stroke* 2010;41:S103–S106.
3. Debette S, Schilling S, Duperron MG, Larsson SC, Markus HS. Clinical significance of magnetic resonance imaging markers of vascular brain injury: a systematic review and meta-analysis. *JAMA Neurol* 2019;76:81–94.
4. Wilson D, Ambler G, Lee KJ, et al. Cerebral microbleeds and stroke risk after ischaemic stroke or transient ischaemic attack: a pooled analysis of individual patient data from cohort studies. *Lancet Neurol* 2019;18:653–665.
5. Wang Z, Soo YO, Mok VC. Cerebral microbleeds: is antithrombotic therapy safe to administer? *Stroke* 2014;45:2811–2817.
6. Vernooij MW, van der Lugt A, Ikram MA, et al. Prevalence and risk factors of cerebral microbleeds: the Rotterdam Scan Study. *Neurology* 2008;70:1208–1214.
7. van Rooden S, van der Grond J, van den Boom R, et al. Descriptive analysis of the Boston criteria applied to a Dutch-type cerebral amyloid angiopathy population. *Stroke* 2009;40:3022–3027.
8. Akoudad S, Portegies ML, Koudstaal PJ, et al. Cerebral microbleeds are associated with an increased risk of stroke: the Rotterdam Study. *Circulation* 2015;132:509–516.
9. Biffi A, Sonni A, Anderson CD, et al. Variants at APOE influence risk of deep and lobar intracerebral hemorrhage. *Ann Neurol* 2010;68:934–943.
10. Traylor M, Tozer DJ, Croall ID, et al. Genetic variation in PLEKHG1 is associated with white matter hyperintensities (n = 11,226). *Neurology* 2019;92:e749–e757.
11. Verhaaren BF, Debette S, Bis JC, et al. Multiethnic genome-wide association study of cerebral white matter hyperintensities on MRI. *Circ Cardiovasc Genet* 2015;8:398–409.
12. Maxwell SS, Jackson CA, Paternoster L, et al. Genetic associations with brain microbleeds: systematic review and meta-analyses. *Neurology* 2011;77:158–167.
13. Li HQ, Cai WJ, Hou XH, et al. Genome-wide association study of cerebral microbleeds on MRI. *Neurotox Res* 2020;37:146–155.
14. Psaty BM, O'Donnell CJ, Gudnason V, et al. Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium: design of prospective meta-analyses of genome-wide association studies from 5 cohorts. *Circ Cardiovasc Genet* 2009;2:73–80.
15. Traylor M, Zhang CR, Adib-Samii P, et al. Genome-wide meta-analysis of cerebral white matter hyperintensities in patients with stroke. *Neurology* 2016;86:146–153.
16. Greenberg SM, Vernooij MW, Cordonnier C, et al. Cerebral microbleeds: a guide to detection and interpretation. *Lancet Neurol* 2009;8:165–174.
17. Nandigam RN, Viswanathan A, Delgado P, et al. MR imaging detection of cerebral microbleeds: effect of susceptibility-weighted imaging, section thickness, and field strength. *AJNR Am J Neuroradiol* 2009;30:338–343.
18. Cheng AL, Batool S, McCreary CR, et al. Susceptibility-weighted imaging is more reliable than T2*-weighted gradient-recalled echo MRI for detecting microbleeds. *Stroke* 2013;44:2782–2786.
19. Goos JD, van der Flier WM, Knol DL, et al. Clinical relevance of improved microbleed detection by susceptibility-weighted magnetic resonance imaging. *Stroke* 2011;42:1894–1900.
20. Ding J, Sigurdsson S, Jonsson PV, et al. Space and location of cerebral microbleeds, cognitive decline, and dementia in the community. *Neurology* 2017;88:2089–2097.

21. Kantarci K, Gunter JL, Tosakulwong N, et al. Focal hemosiderin deposits and beta-amyloid load in the ADNI cohort. *Alzheimers Dement* 2013;9:S116–S123.
22. Qiu C, Cotch MF, Sigurdsson S, et al. Retinal and cerebral microvascular signs and diabetes: the Age, Gene/Environment Susceptibility–Reykjavik Study. *Diabetes* 2008;57:1645–1650.
23. Roob G, Lechner A, Schmidt R, Flooh E, Hartung HP, Fazekas F. Frequency and location of microbleeds in patients with primary intracerebral hemorrhage. *Stroke* 2000;31:2665–2669.
24. Graff-Radford J, Simino J, Kantarci K, et al. Neuroimaging correlates of cerebral microbleeds: the ARIC Study (Atherosclerosis Risk in Communities). *Stroke* 2017;48:2964–2972.
25. Wilson D, Ambler G, Shakeshaft C, et al. Cerebral microbleeds and intracranial haemorrhage risk in patients anticoagulated for atrial fibrillation after acute ischaemic stroke or transient ischaemic attack (CROMIS-2): a multicentre observational cohort study. *Lancet Neurol* 2018;17:539–547.
26. Cordonnier C, Potter GM, Jackson CA, et al. Improving interrater agreement about brain microbleeds: development of the Brain Observer MicroBleed Scale (BOMBS). *Stroke* 2009;40:94–99.
27. Romero JR, Preis SR, Beiser A, et al. Risk factors, stroke prevention treatments, and prevalence of cerebral microbleeds in the Framingham Heart Study. *Stroke* 2014;45:1492–1494.
28. Wardlaw JM, Bastin ME, Valdes Hernandez MC, et al. Brain aging, cognition in youth and old age and vascular disease in the Lothian Birth Cohort 1936: rationale, design and methodology of the imaging protocol. *Int J Stroke* 2011;6:547–559.
29. Altmann-Schneider I, van der Grond J, Slagboom PE, et al. Lower susceptibility to cerebral small vessel disease in human familial longevity: the Leiden Longevity Study. *Stroke* 2013;44:9–14.
30. Altmann-Schneider I, Trompet S, de Craen AJ, et al. Cerebral microbleeds are predictive of mortality in the elderly. *Stroke* 2011;42:638–644.
31. Willer CJ, Li Y, Abecasis GR. METAL: fast and efficient meta-analysis of genomewide association scans. *Bioinformatics* 2010;26:2190–2191.
32. Bulik-Sullivan BK, Loh PR, Finucane HK, et al. LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. *Nat Genet* 2015;47:291–295.
33. Ward LD, Kellis M. HaploReg: a resource for exploring chromatin states, conservation, and regulatory motif alterations within sets of genetically linked variants. *Nucleic Acids Res* 2012;40:D930–D934.
34. Xue A, Wu Y, Zhu Z, et al. Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. *Nat Commun* 2018;9:2941.
35. Warren HR, Evangelou E, Cabrera CP, et al. Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. *Nat Genet* 2017;49:403.
36. Yengo L, Sidorenko J, Kemper KE, et al. Meta-analysis of genome-wide association studies for height and body mass index in approximately 700000 individuals of European ancestry. *Hum Mol Genet* 2018;27:3641–3649.
37. Surakka I, Horikoshi M, Magi R, et al. The impact of low-frequency and rare variants on lipid levels. *Nat Genet* 2015;47:589–597.
38. Traylor M, Malik R, Nalls MA, et al. Genetic variation at 16q24.2 is associated with small vessel stroke. *Ann Neurol* 2017;81:383–394.
39. Rannikmäe K, Sivakumaran V, Millar H, et al. COL4A2 is associated with lacunar ischemic stroke and deep ICH: meta-analyses among 21,500 cases and 40,600 controls. *Neurology* 2017;89:1829–1839.
40. Woo D, Falcone GJ, Devan WJ, et al. Meta-analysis of genome-wide association studies identifies 1q22 as a susceptibility locus for intracerebral hemorrhage. *Am J Hum Genet* 2014;94:511–521.
41. Malik R, Chauhan G, Traylor M, et al. Multiethnic genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nat Genet* 2018;50:524–537.
42. Malik R, Rannikmäe K, Traylor M, et al. Genome-wide meta-analysis identifies 3 novel loci associated with stroke. *Ann Neurol* 2018;84:934–939.
43. Jansen IE, Savage JE, Watanabe K, et al. Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk. *Nat Genet* 2019;51:404–413.
44. Georgakis MK, Malik R, Anderson CD, Parhofer KG, Hopewell JC, Dichgans M. Genetic determinants of blood lipids and cerebral small vessel disease: role of high-density lipoprotein cholesterol. *Brain* 2020;143:597–610.
45. Wieberdink RG, Poels MM, Vernooij MW, et al. Serum lipid levels and the risk of intracerebral hemorrhage: the Rotterdam Study. *Arterioscler Thromb Vasc Biol* 2011;31:2982–2989.
46. Ding J, Sigurdsson S, Garcia M, et al. Risk factors associated with incident cerebral microbleeds according to location in older people: the Age, Gene/Environment Susceptibility (AGES)–Reykjavik Study. *JAMA Neurol* 2015;72:682–688.
47. Bonaventure A, Kurth T, Pico F, et al. Triglycerides and risk of hemorrhagic stroke vs. ischemic vascular events: the Three-City Study. *Atherosclerosis* 2010;210:243–248.
48. Sturgeon JD, Folsom AR, Longstreth WT Jr, Shahar E, Rosamond WD, Cushman M. Risk factors for intracerebral hemorrhage in a pooled prospective study. *Stroke* 2007;38:2718–2725.
49. Traylor M, Rutten-Jacobs LC, Thijs V, et al. Genetic associations with white matter hyperintensities confer risk of lacunar stroke. *Stroke* 2016;47:1174–1179.
50. Chung J, Marini S, Pera J, et al. Genome-wide association study of cerebral small vessel disease reveals established and novel loci. *Brain* 2019;142:3176–3189.
51. Caselli RJ, Reiman EM, Osborne D, et al. Longitudinal changes in cognition and behavior in asymptomatic carriers of the APOE ε4 allele. *Neurology* 2004;62:1990–1995.
52. Charidimou A, Kakar P, Fox Z, Werring DJ. Cerebral microbleeds and recurrent stroke risk: systematic review and meta-analysis of prospective ischemic stroke and transient ischemic attack cohorts. *Stroke* 2013;44:995–1001.
53. Copenhaver BR, Hsia AW, Merino JG, et al. Racial differences in microbleed prevalence in primary intracerebral hemorrhage. *Neurology* 2008;71:1176–1182.
54. Kakar P, Charidimou A, Werring DJ. Cerebral microbleeds: a new dilemma in stroke medicine. *JRSM Cardiovasc Dis* 2012;1:2048004012474754.

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