Supplementary Online Content

Marini S, Crawford K, Morotti A, et al; the International Stroke Genetics Consortium. Association of apolipoprotein E with intracerebral hemorrhage risk by race/ethnicity: a meta-analysis. *JAMA Neurol.* Published online February 6, 2019. doi:10.1001/jamaneurol.2018.4519

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This supplementary material has been provided by the authors to give readers additional information about their work.

Apolipoprotein E and Intracerebral Hemorrhage: A Trans-Ethnic Meta-Analysis

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eMethods

Participating Studies

Case and control subjects included in the study were gathered from 3 multicenter studies in the US and from 8 distinct European sites participating in the ISGC, based on availability of directly ascertained APOE ε genotypes. US studies included The Genetics of Cerebral Hemorrhage with Anticoagulation (GOCHA) study¹, the Genetic and Environmental Risk Factors for Hemorrhagic Stroke (GERFHS) study², the Ethnic/Racial Variations of Intracerebral Hemorrhage (ERICH) study³. European studies included The Hospital del Mar and Vall d'Hebron Hospital ICH studies 4.5 in Barcelona, Spain, the Jagiellonian University Hemorrhagic Stroke Study⁶ in Krakow, Poland, the Lund Stroke Register study⁷ in Lund, Sweden, the Edinburgh Stroke Study and LINCHPIN⁸ study in Scotland, UK, the University Medical Center (UMC) Utrecht ICH study, and the Brescia Stroke Registry⁹. Because of variable sample sizes from contributing centers, data from the European studies (ISGC Europe) were analyzed together for association testing in meta-analysis, as done previously^{10,11}. We analyzed primary ICH cases, CT or MRI confirmed, aged >18 years (GOCHA enrolled subjects aged > 50 years). ICH cases where there was evidence of secondary cause (such as trauma, tumor, hemorrhagic transformation of ischemic stroke, or vascular malformation) were excluded. More specific inclusion and exclusion criteria for each of the included studies are reported in eTable 1.

Phenotypic and Genetic variables

Demographic variables, including self-identified race and ethnicity (according to the recommendation of the Standards for Maintaining, Collecting, and Presenting Federal Data on Race and Ethnicity¹²) were systematically obtained from structured patient and family member interview within each site^{3,13}. Additional covariates previously associated with ICH¹⁴ risk were also collected: medical history of hypertension, previous stroke, hypercholesterolemia, warfarin, antiplatelet and statin use, smoking history, and alcohol exposure (more than twice per week)¹⁵. Given the heterogeneity among the studies, other variables were not available. Number of medications used to treat hypertension (taken in the 2 weeks before ICH onset or before the interview, for cases and controls respectively) and systolic and diastolic blood pressure readings (measured on enrollment with index ICH for cases, and at the time of interview with controls) were also available for ERICH participants. CT images on admission were analyzed at each participating site for hematoma classification as lobar (involving predominantly the cortex and underlying white matter), and non-lobar (involving predominately the basal ganglia, periventricular white matter, or internal capsule), following prespecified criteria¹¹.

APOE genotype was determined as part of an ongoing GWAS of ICH. Taqman (Applied Biosystems, Foster City, CA) and iPLEX (Sequenom, San Diego, CA) methodologies were adopted at the University of Miami and Massachusetts General Hospital genotyping centers, respectively for all the sample. The genotypes obtained for rs429358 (C/T) and rs7412 (C/T) were used to define the three standard human APOE ε haplotypes of ε 2, ε 3, and ε 4¹⁶. Genomewide data were available for a subgroup of subjects, from Affymetrix 6.0 in GERFHS, and Illumina HumanHap610-Quad in GOCHA and ISGC Europe. IRB approval was obtained at all participating centers, and informed consent was obtained from all participants or their legally authorized representative.

Population Stratification

Fifteen ancestry informative markers were selected among the polymorphisms directly genotyped in ERICH 17 (eTable 2). These markers, distributed across the genome, showed difference in allele frequency (δ) of at least 0.5 between any two of the recruited ancestral populations (African American, Hispanic American, non-Hispanic European). GWAS data for GOCHA, GERFHS, ISGC Europe samples were analyzed as previously described¹⁰. Briefly

Standardized prespecified quality control procedures¹⁸, imputation via IMPUTE2 v.2.2¹⁹ and 1000 Genomes integrated reference panels (Phase I interim release in NCBI build 37), and post imputation filtering (MAF <0.01, IMPUTE2 information score <0.7) were implemented. Samples with < 90% call rates, or SNPs with call rates <95% or deviation from Hardy-Weinberg equilibrium at P-value < 2.5 × 10−4 were excluded. Based on these 15 selected markers, principal component analysis was implemented in GOCHA, GERFHS, ISGC Europe and ERICH subjects in accordance with previously published methods^{20–22}. The first four principal components were included in regression models to adjust for population stratification. We have previously shown the reliability of this approach in defining ancestries of populations¹⁷. This PC analysis was not used to reclassify participants, as self-identified race/ethnicity may capture exposures that transcend genetic ancestry and could contribute to explain the stratification among different populations.

eTable 1. ICH Case Inclusion and Exclusion Criteria by Recruitment Site

* This study was used to recruit controls for the Edinburgh – ESS and Edinburgh – LINCHPIN cases

eTable 2. Ancestry Informative Markers Selected

AIM: ancestry informative marker; A1 and A2: allele frequency; AFR: Afro-American; AMR: Mixed American; EUR: European

eTable 3. Comparison Between With Subjects With and Without Ancestry Informative Markers Available for Population Stratification Analysis

eTable 4. Frequencies of Additional Diseases and Risk Factors Among Cases and Controls of the Available Data

* χ2 test and Mann Whitney u test; CV: cerebrovascular

eFigure. Distribution of Subjects in Principal Component (PA) Space and the Relation with Selfidentified Race and Ethnicity (Ellipses Cluster 95% of PC Analysis Data)

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