



Targeted genetic analysis of cerebral blood flow imaging phenotypes implicates the INPP5D gene



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ABSTRACT

The vascular hypothesis of Alzheimer's disease (AD) has proposed the involvement of brain hypoperfusion in AD pathogenesis, where cognitive decline and dysfunction result from dwindling cerebral blood flow (CBF). Based on the vascular hypothesis of Alzheimer's disease, we focused on exploring how genetic factors influence AD pathogenesis via the cerebrovascular system. To investigate the role of CBF endophenotypes in AD pathogenesis, we performed a targeted genetic analysis of 258 subjects from the Alzheimer's Disease Neuroimaging Initiative cohort to examine associations between 4033 single-nucleotide polymorphisms of 24 AD genes and CBF measures in 4 brain regions. A novel association with CBF measure in the left angular gyrus was identified in an *INPP5D* single-nucleotide polymorphism (i.e., rs61068452; $p = 1.48E-7$; corrected $p = 2.39E-3$). The gene-based analysis discovered both *INPP5D* and *CD2AP* associated with the left angular gyrus CBF. Further analyses on nonoverlapping samples revealed that rs61068452-G was associated with lower CSF t-tau/ $A\beta_{1-42}$ ratio. Our findings suggest a protective role of rs61068452-G in an AD-relevant cerebrovascular endophenotype, which has the potential to provide novel insights for better mechanistic understanding of AD.

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1. Introduction

Alzheimer's disease (AD) is a complex degenerative disease of the brain, characterized by neurodegeneration, memory impairment, and cognitive problems (Jack et al., 2010). As the leading cause of dementia, AD is influenced by environmental and genetic factors. It is critical to improve the understanding of molecular mechanisms of AD because of its high prevalence, burdens, and

currently no cure. Genomewide association studies (GWAS) of quantitative endophenotypes have successfully identified a number of loci susceptible for AD (Saykin et al., 2015); however, the underlying molecular mechanisms of how these genetic factors modulate AD or its biomarkers are not well characterized.

The vascular hypothesis of Alzheimer's disease (VHAD) (de la Torre, 2018) has proposed the involvement of brain hypoperfusion in AD pathogenesis, where cognitive decline and dysfunction result from dwindling neuronal energy supply and oxidative stress. In support of the vascular hypothesis, evidence suggests measurement of cerebral blood flow (CBF) may be a promising indicator of brain hypoperfusion useful for early detection of AD and assessing disease progression (Zhang et al., 2017). Consistent with the vascular hypothesis of AD, recent results have also demonstrated the potential of CBF as biomarker for preclinical detection of AD, as CBF changes present long before amyloid β ($A\beta$) load or brain atrophy (Hays et al., 2016). Other studies have discovered the association of CBF with AD stages as well as various brain structural and functional imaging quantitative traits (Bangen et al., 2017; Chen et al., 2011; Mattsson et al., 2014; Michels et al., 2016; Musiek et al., 2012; Wang et al., 2013). However, the molecular mechanisms of CBF changes underlying AD have not been fully understood.

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Given that large variations of CBF have been seen across AD studies, high scientific interests have aroused to examine whether they have a genetic basis. Reciprocally, assessing the genetic association with CBF might provide a better understanding of molecular mechanisms underlying changes of CBF as well as gaining additional insight into complex neurodegenerative diseases. To the best of our knowledge, the genetic contributions to CBF are an under-explored topic in AD research, except that a few studies examined the *APOE* effects on CBF (Hays et al., 2016; Kim et al., 2013b). Accordingly, in this study, we propose to investigate the genetic factors that affect AD through regulating the function of cerebrovascular system.

GWAS have successfully identified a number of loci susceptible for complex neurological traits and diseases (Saykin et al., 2015). Recently, a large-scale meta-analysis of GWAS identified a set of susceptibility loci for late-onset AD, including 9 known and 12 new single-nucleotide polymorphisms (SNPs) (Lambert et al., 2013). In addition to *APOE*, 23 genes underlying these 21 significant variants are discovered, most of which are associated with inflammation and immune system. For example, there are several genes encoding proteins relevant to microglial function and inflammation, including *TREM2*, *CD33*, *CR1*, *ABCA7*, and *INPP5D* (Malik et al., 2015). Mechanisms of how these genetic factors modulate AD or its biomarkers remain to be discovered.

Based on the VHAD, we hypothesized that some genetic factors impact AD pathogenesis via influencing brain hypoperfusion. Thus, this study is designed to improve the understanding of mechanisms by which genetic factors impact AD pathogenesis, in this case by investigating the role of cerebrovascular functions as an AD endophenotypes. Therefore, in this study, we perform a targeted genetic analysis for exploring the genetic effect on CBF measures in 4 brain regions using 24 AD candidate genes (*APOE* and the other 23 reported AD genes mentioned previously), to help provide novel insights for better revealing molecular interpretation of AD. To evaluate the CBF genetic findings, we further examine nonoverlapping samples from the Alzheimer's Disease Neuroimaging Initiative (ADNI) cohort regarding their associations with the CSF τ - $A\beta_{1-42}$ ratio and FDG-PET glucose metabolism, given that both are established AD biomarkers and their abnormalities have been suggested as downstream pathological events from initiation of brain hypoperfusion under VHAD (de la Torre, 2018). In addition, to examine whether our most significant CBF genetic finding has a direct effect on AD, we further evaluated its association with the AD status using the summary statistics from the most recent genomewide meta-analysis of AD (Jansen et al., 2019).

2. Materials and methods

2.1. Alzheimer's Disease Neuroimaging Initiative

Data used in the preparation of this article were obtained from the ADNI database (adni.loni.usc.edu). The ADNI was launched in 2003 as a public-private partnership, led by Principal Investigator Michael W. Weiner, MD. The primary goal of ADNI has been to test whether serial MRI, PET, other biological markers, and clinical and neuropsychological assessment can be combined to measure the progression of mild cognitive impairment and early AD. For up-to-date information, see www.adni-info.org.

2.2. Genomewide meta-analysis of AD

A large genomewide meta-analysis of clinically diagnosed AD and AD-by-proxy was recently conducted (Jansen et al., 2019). The study included 3 phases: (1) phase 1 was a meta-analysis of the AD status ($N = 79,145$) using 3 independent cohorts collected by

Alzheimer's disease working group of the Psychiatric Genomics Consortium, the International Genomics of Alzheimer's Project, and the Alzheimer's Disease Sequencing Project. (2) Phase 2 was a GWAS of the AD-by-proxy status ($N = 376,113$), using individuals of European ancestry from the UK Biobank with parental AD status weighted by age. (3) Phase 3 was a meta-analysis of the phase 1 and phase 2 findings, with totally 455,258 samples (71,880 cases and 383,378 controls). In this work, we downloaded the summary statistics of the phase 3 analysis (available at https://ctg.cncr.nl/software/summary_statistics) to examine whether our CBF finding is associated with AD.

2.3. Study participants

Participants for the present CBF study were limited to those with baseline scans from ADNI in the arterial spin labeling (ASL) MRI substudy as of May 2012. Full inclusion and exclusion criteria for ADNI are described at www.adni-info.org. Detailed quality control (QC) steps for phenotypic and genotypic data had been previously reported (Kim et al., 2013a; Wang et al., 2013) and were briefly described in the following. Participants were restricted to non-Hispanic Caucasian to reduce the likelihood of population stratification effects in the genetic analysis. A total of 258 non-Hispanic Caucasian subjects whose CBF data met all QC criteria were analyzed, including 72 healthy control, 16 significant memory concern, 71 early mild cognitive impairment, 57 late mild cognitive impairment, and 42 AD participants. Detailed characteristic information and the number of subjects in each subgroup are shown in Table 1. Besides participants included in the CBF analysis, nonoverlapping samples with various AD endophenotypes were studied further for evaluating their associations with the CBF findings. See Fig. 1 for detailed information of participant pool selection and study design of this work.

This study was approved by institutional review boards of all participating institutions and written informed consent was obtained from all participants or authorized representatives.

2.4. MRI data acquisition and processing

Both high-resolution structural MRI data and resting ASL data were downloaded from the ADNI website (adni.loni.usc.edu). Image processing used a SPM12 (<http://www.fil.ion.ucl.ac.uk/spm>) based toolbox, ASLtbx (Wang et al., 2008), as described previously (Wang et al., 2013). ASL images were processed with the following steps: motion correction (Wang, 2012), temporal denoising, spatial smoothing, CBF quantification, outlier cleaning, and partial volume correction (Hu et al., 2010), spatial registration to the Montreal Neurology Institute standard brain space, and CBF extraction in ROI.

Mean CBF for 4 ROIs were studied, including left angular, right angular, left temporal and right temporal gyri. The ROIs were selected on the basis of FDG-PET literature (Chen et al., 2011; Landau et al., 2011; Wang et al., 2013). In particular, meta-region of interest was previously found to be sensitive to AD-related CBF changes (Chen et al., 2011) and originally developed for FDG-PET data (Landau et al., 2011), where FDG-PET and ASL showed similar patterns of reduction in brain regions covered by these ROIs. A follow-up study also explored these ROIs using the same parcellation template and demonstrated the sensitivity of CBF on these ROIs for early AD. See Supplementary Methods for detailed MRI data acquisition, processing, and analysis.

A total of 299 subjects were included in the ASL-MRI processing. To restrict the present analysis to non-Hispanic Caucasians, 258 subjects were identified based on population stratification information from genotyping data processing. Considering the relatively small number of samples for the genetic analysis, we performed

Table 1
Participant characteristics in CBF genetic association analysis

Diagnosis	HC	SMC	EMCI	LMCI	AD	p Value
Number	72	16	71	57	42	-
Gender (M/F)	35/37	7/9	45/26	27/30	21/21	0.25
Age (mean ± SD)	75.03 ± 7.42	73.56 ± 6.87	74.01 ± 7.46	73.88 ± 7.66	73.67 ± 7.74	0.83
APOE ε4 present	30.99%	37.50%	40.85%	54.39%	69.05%	1.5E-03
MMSE (mean ± SD)	29.04 ± 1.16	29.40 ± 0.99	28.43 ± 1.55	27.23 ± 2.02	23.85 ± 2.96	2.2E-16
Left angular CBF (mean ± SD)	50.29 ± 23.96	51.77 ± 22.48	50.41 ± 20.48	51.47 ± 24.42	43.14 ± 21.11	0.39
Right angular CBF (mean ± SD)	52.90 ± 22.59	46.69 ± 16.93	49.25 ± 20.66	57.82 ± 27.14	50.99 ± 25.75	0.28
Left temporal CBF (mean ± SD)	44.76 ± 19.31	46.06 ± 15.51	44.34 ± 24.28	43.56 ± 21.65	37.45 ± 21.07	0.46
Right temporal CBF (mean ± SD)	46.36 ± 23.09	34.37 ± 17.91	40.90 ± 18.80	44.77 ± 23.31	37.23 ± 19.41	0.09

p Values were assessed because of significant differences among diagnosis groups, and were computed using one-way ANOVA (except for gender using χ^2 test). The p values < 0.05 are shown in bold.

Key: CBF, cerebral blood flow; AD, Alzheimer's disease; HC, healthy control; SMC, significant memory concern; EMCI, early mild cognitive impairment; LMCI, late mild cognitive impairment.

further QC to reduce the potential influence of extreme outliers. Mean and standard deviation of CBF measures for each ROI were calculated, blind to diagnostic information. Subjects who had at least 1 value greater or smaller than 6 standard deviations from the mean value of each of 4 CBF variables were detected as outliers. No subjects were identified as outliers and removed from this criterion. Finally, 258 subjects with 4 lists of quality controlled CBF measures were included (Fig. 1).

2.5. CSF biomarkers

The total tau (t-tau) and amyloid- β 1–42 peptide ($A\beta_{1-42}$) measured in the baseline CSF samples were obtained from the ADNI database (adni.loni.usc.edu). Sample acquisition and QC of CSF were performed as described previously (Shaw et al., 2009). The t-tau/ $A\beta_{1-42}$ ratio was calculated for 919 subjects who were non-Hispanic Caucasians as well as not included in the CBF analysis. Further QC was performed to reduce the potential influence of extreme outliers on statistical results. Mean and standard deviation of t-tau/ $A\beta_{1-42}$ ratio were calculated, whereas subjects with greater or smaller than 6 standard deviation from the mean value were regarded as outliers. 13 subjects were removed, where 12 subjects had missing t-tau/ $A\beta_{1-42}$ measures, and 1 subject had extremely high t-tau/ $A\beta_{1-42}$ ratio. Finally, 906 subjects with quality-controlled CSF t-tau/ $A\beta_{1-42}$ ratio were analyzed (Fig. 1).

2.6. FDG-PET data acquisition and processing

Given the certain agreement of CBF changes and cerebral metabolic rate of glucose on some brain regions (Chen et al., 2011; Musiek et al., 2012), considerable variability on some other regions was also observed. With this observation, we also examined the relationship between the CBF genetic findings and glucose metabolism measurements. Preprocessed FDG-PET scans were downloaded from the ADNI website (adni.loni.usc.edu) and processed as previously described in the study by Risacher et al., 2015. FDG-PET scans were then aligned to the corresponding MRI scans and normalized to the Montreal Neurology Institute space as $2 \times 2 \times 2$ mm³ voxels. ROI-level glucose metabolism measurements were further extracted based on the MarsBaR AAL atlas for 735 subjects who were not included in the CBF genetic analysis. Here we focused only on the left angular region (L-AG) on which the CBF genetic association was identified. Subjects were treated as outliers and excluded if their left angular FDG-PET measures were greater or smaller than 6 standard deviations from the mean value. No

subjects were removed under this criterion, and finally 735 subjects with quality-controlled left angular FDG-PET measured glucose metabolism were analyzed (Fig. 1).

2.7. Genotyping data

Genotyping data were obtained from the ADNI database (adni.loni.usc.edu). They were quality-controlled, imputed, and combined as described in the study by Kim et al., 2013a. Briefly, genotyping was performed on all ADNI participants following manufacturer's protocol using blood genomic DNA samples and Illumina GWAS arrays (610-Quad; OmniExpress, or HumanOmni2.5–4v1) (Saykin et al., 2010). QC was performed in PLINK v1.90 (Purcell et al., 2007) using the following criteria: 1) call rate per marker $\geq 95\%$, 2) minor allele frequency $\geq 5\%$, 3) Hardy Weinberg Equilibrium test $p \geq 1.0E-6$, and 4) call rate per participant $\geq 95\%$. Significant relatedness pairs with $PI_HAT > 0.45$ were

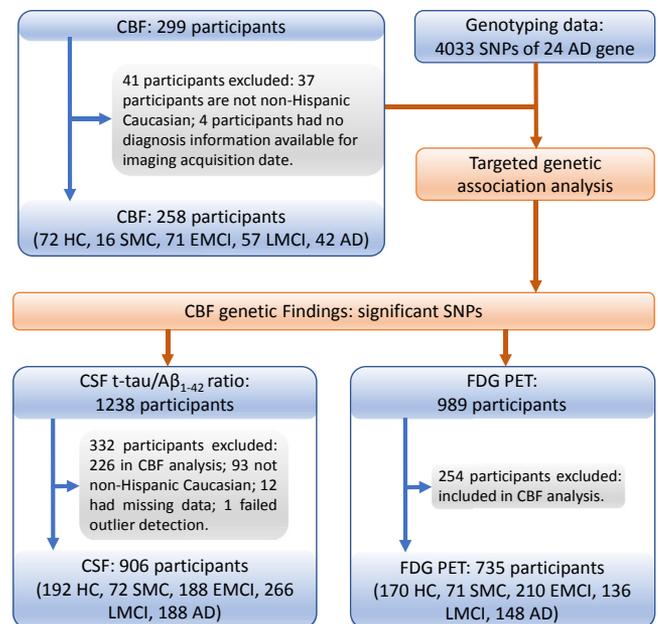


Fig. 1. Flowchart of participant selection and study design. Abbreviations: CBF, cerebral blood flow; AD, Alzheimer's disease; HC, healthy control; SMC, significant memory concern; EMCI, early mild cognitive impairment; LMCI, late mild cognitive impairment; SNP, single-nucleotide polymorphism.

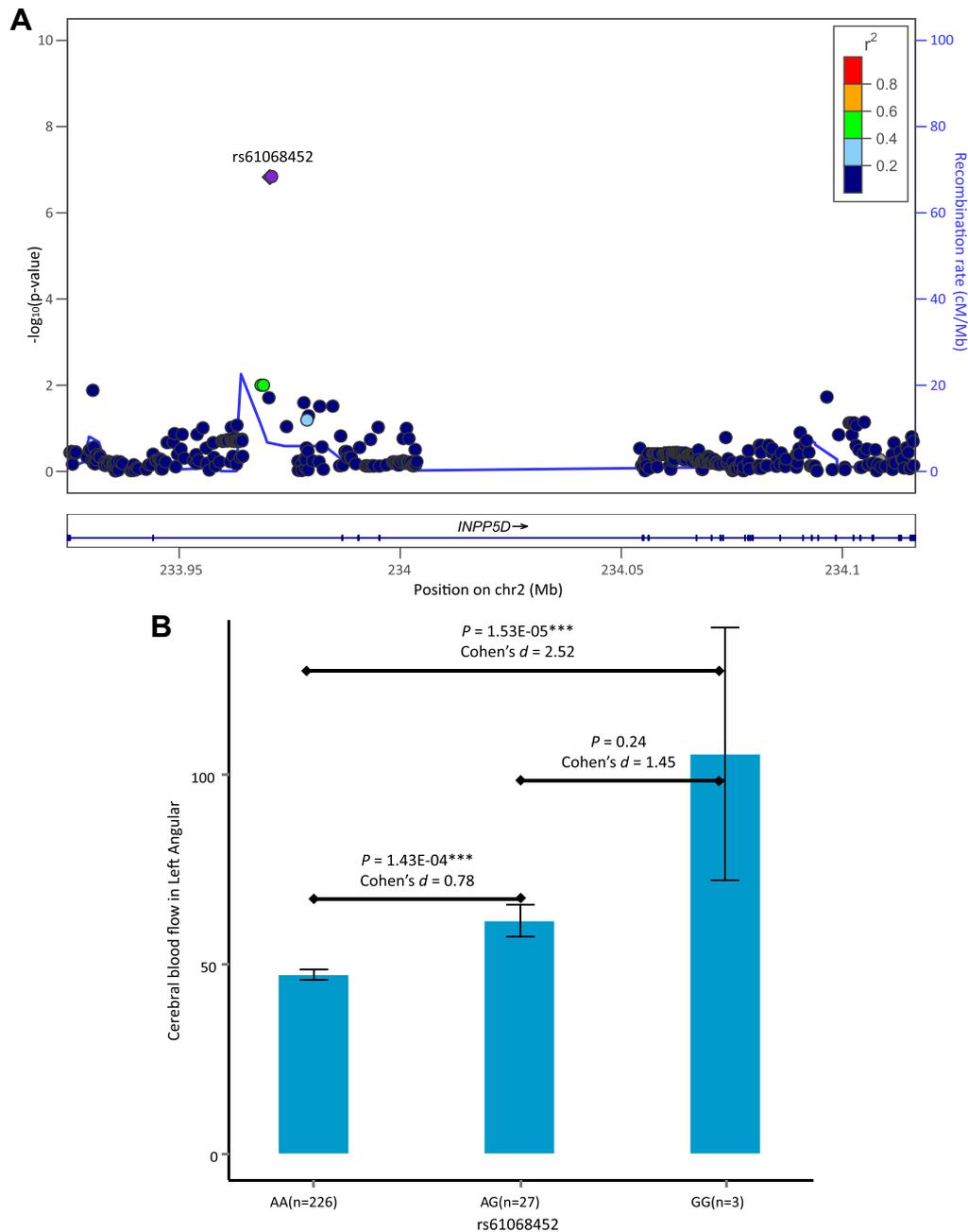


Fig. 2. Association and effect of *INPP5D* rs61068452 on left angular CBF. (A) All SNPs within *INPP5D* are plotted based on their genetic association statistics $-\log_{10} p$ values. NCBI build 37 genomic position and recombination rates are calculated from the 1000 Genome Project reference data. The color scale of r^2 values is used to label SNPs based on their degree of linkage disequilibrium with rs61068452. Genes in the region are labeled with arrows denoting 5' to -3' orientation. (B) Mean left angular CBF measures and standard errors are plotted against rs61068452 genotype groups (AA, AG, and GG). p value indicates the association significance of rs61068452 with left angular CBF. p values are calculated from linear regression with age, gender, *APOE* $\epsilon 4$ status and the top 4 principal components from population stratification analysis as covariates. Cohen's d indicates the effect size of minor allele G (1 copy or 2 copies) of rs61068452 on left angular CBF, after being adjusted for age, gender, *APOE* $\epsilon 4$ status and the top 4 principal components from population stratification analysis. Presence of minor allele G of rs61068452 suggests an additive effect of increasing left angular CBF and this SNP accounts for 9.57% of the phenotypic variance. Abbreviations: CBF, cerebral blood flow; SNP, single-nucleotide polymorphism. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

identified and thereafter 1 individual from each pair was randomly excluded (similar to the approach applied in the study by Ramanan et al., 2015). Participants were then checked for gender and identity-by-descent before imputation to identify genotyping or coding error and to avoid the potential confounding effect due to the gender ambiguity or consanguinity such as sibling pairs. To restrict the studied participants to non-Hispanic Caucasians, we further performed population stratification using 988 subjects with

known ancestry information from HapMap3 as reference data. We merged the ADNI and HapMap3 samples, and performed multidimensional scaling analysis using PLINK v1.90 with identity-by-state pairwise distance matrix on the merged data to clustering samples in the principal component analysis space. ADNI participants were identified as non-Hispanic Caucasians if 1) they were clustered with HapMap3 CEU or TSI subjects as well as had self-reported race/ethnicity as "non-Hispanic/white", or 2) they were not clustered

with any HapMap3 subjects while had self-reported race/ethnicity as “non-Hispanic/white”. Haplotype patterns from the 1000 Genomes Project reference panel were then applied to impute the SNPs that were not directly genotyped from arrays. 5,574,300 SNPs were obtained for all subjects involved in this work (see [Supplementary Methods](#) for more details about genotyping data imputation). To appropriately control for population stratification, we used PLINK v1.90 to generate the top 4 principal components to be included as covariates in our genetic association analyses.

A list of 24 AD candidate genes from the large-scale meta-analysis ([Lambert et al., 2013](#)) was analyzed. Given that the Genome Reference Consortium Human build 37 was used as reference genome for genotyping, gene annotation from Genome Reference Consortium Human build 37 was used to extract SNPs located within each AD gene. Two genes (HLA-DRB1 and HLA-DRB5) had no SNPs available in our imputed genotyping data. In total, 4033 SNPs were included in the genetic association analysis. Detailed information of these genes is available in [Supplementary Table 1](#).

2.8. Statistical analysis

Targeted genetic association analysis of CBF on each ROI was tested using linear regression under an additive genetic model in PLINK v1.90 ([Purcell et al., 2007](#)). Age, gender, APOE $\epsilon 4$ status, and the top 4 principal components from population stratification analysis were included as covariates. Post hoc analysis used Bonferroni correction for adjusting both the number of SNPs and the number of quantitative traits. Regional genetic association plot was generated using LocusZoom ([Pruim et al., 2011](#)). Gene-based association analysis was used to gain comprehensive statistical evidence of genetic findings. We used gene-based association test that uses extended Simes procedure ([Li et al., 2011](#)) to calculate a gene-level summary p -value for each gene by taking into account gene size, linkage disequilibrium and constituent SNP level p -values.

Phenotypic variance explained by an identified genetic variant was evaluated using the linear regression after removing effects from age, gender, APOE $\epsilon 4$ status, and the top 4 principal components from population stratification analysis. Both linear regression coefficient p value and Cohen's d statistic were used to illustrate the significance and effect size of identified variant, to facilitate the comparison among different genotyping groups.

The additive effects of the identified genetic variants from above association analysis were also assessed at each voxel using SPM12 under one-way ANOVA test with age, gender, APOE $\epsilon 4$ status, and the top 4 principal components from population stratification analysis as covariates. The statistical analysis results were assessed at $p < 0.001$ with no correction. The genetic effects were mapped onto the brain via voxel-based analysis.

Genetic findings from the CBF analysis were further investigated in nonoverlapping samples regarding their associations with the CSF t-tau/A β_{1-42} ratio and left angular FDG-PET glucose metabolism. For both association tests, linear regression models were used. In particular, we applied additive genetic models implemented in PLINK v1.90 ([Purcell et al., 2007](#)), with age, gender, APOE $\epsilon 4$ status, and the top 4 principal components from population stratification analysis as covariates.

3. Results

3.1. Participant characteristics

A total of 258 ADNI subjects were studied in the CBF genetic association analysis (see [Table 1](#) for their characteristics). There were 25 subjects with missing CBF measures in 1 or more ROIs (2 subjects for left angular region, 2 subjects for right angular region,

12 subjects for left temporal region, and 11 subjects for right temporal region). Using one-way ANOVA or χ^2 test, significant differences among diagnostic groups were observed for MMSE scores ($p = 2.20E-16$) and APOE $\epsilon 4$ status (present of APOE $\epsilon 4$ or not; $p = 0.0015$), while not observed for age, gender, or any CBF measure.

3.2. Targeted genetic association of CBF

To identify the genetic predictor of CBF, we performed a targeted genetic association analysis ($N = 258$) of CBF measurements in 4 brain ROIs using AD risk genes and controlling for age, gender, APOE $\epsilon 4$ status, and the top 4 principal components from population stratification analysis. A total of 4033 SNPs located in AD candidate genes were studied.

Genetic association analysis identified 1 significant association between rs61068452 with L-AG CBF ($p = 1.48E-7$; corrected $p = 2.39E-3$) after correcting for the number of variants and the number of phenotypes using the Bonferroni method. The minor allele G of rs61068452 (rs61068452-G) was associated with higher CBF in L-AG compared with its major allele A ([Fig. 2B](#)). It explained an additional 9.57% of the phenotypic variance of L-AG CBF that exhibited the protective effect on AD. Significant difference of L-AG CBF existed between AA and AG groups ($p = 1.43E-4$), between AA and GG groups ($p = 1.53E-5$), and between groups AG and GG ($p = 0.24$). The recessive homozygote showed higher Cohen's d statistics when compared with other 2 groups (i.e., Cohen's $d = 2.52$ between AA and GG groups, Cohen's $d = 1.45$ between AG and GG groups and Cohen's $d = 0.78$ between AA and AG groups). In addition, *INPP5D* rs61068452-G was associated with increased L-AG CBF in all diagnostic groups ([Supplementary Fig. 2A](#)).

The SNP rs61068452 resides in an intron of *INPP5D*, a reported AD candidate gene involved in inflammatory responses ([Fig. 2A](#)). Rs35349669, another SNP located within *INPP5D*, has been reported as risk AD variant in several studies ([Farfel et al., 2016](#); [Jing et al., 2016](#); [Lambert et al., 2013](#); [Ruiz et al., 2014](#)). In our CBF genetic studies, no significant association of rs35349669 was observed with CBF for any region ($p > 0.05$) based on the studied samples.

Owing to the possible opposite effects of our reported variant rs61068452 and previously reported variant rs35349669, we assessed their relationship. Correlation between these 2 SNPs was -0.22 , according to the genotyping data from the studied 258 subjects. There existed no linkage disequilibrium between these 2 SNPs, with $r^2 = 0.046$ computed from the genotyping data of the studied 258 samples (see [Supplementary Fig. 1](#)).

We further investigated the effect of the APOE $\epsilon 4$ allele (rs429358) because of its well-known association with AD diagnosis. We did not observe significant association of rs429358 with CBF in 4 ROIs in the studied sample. [Fig. 3](#) illustrated the additive effect of *INPP5D* rs61068452 on CBF under voxelwise analysis, adjusted for age, gender, APOE $\epsilon 4$ status, and the top 4 principal components from the population stratification analysis. The minor allele (G) of rs61068452 was associated with higher CBF, with significant clusters for this effect observed primarily in L-AG.

3.3. Gene-based association analysis of CBF

Complementary analysis was used to test the gene-based association with CBF measures in L-AG. We assessed the gene-based association with L-AG CBF using 4033 SNP statistics in gene-based association test that uses extended Simes procedure ([Li et al., 2011](#)). Two genes displayed significant associations with L-AG CBF including *INPP5D* ($p = 1.5E-3$) and *CD2AP* (CD2 associated protein;

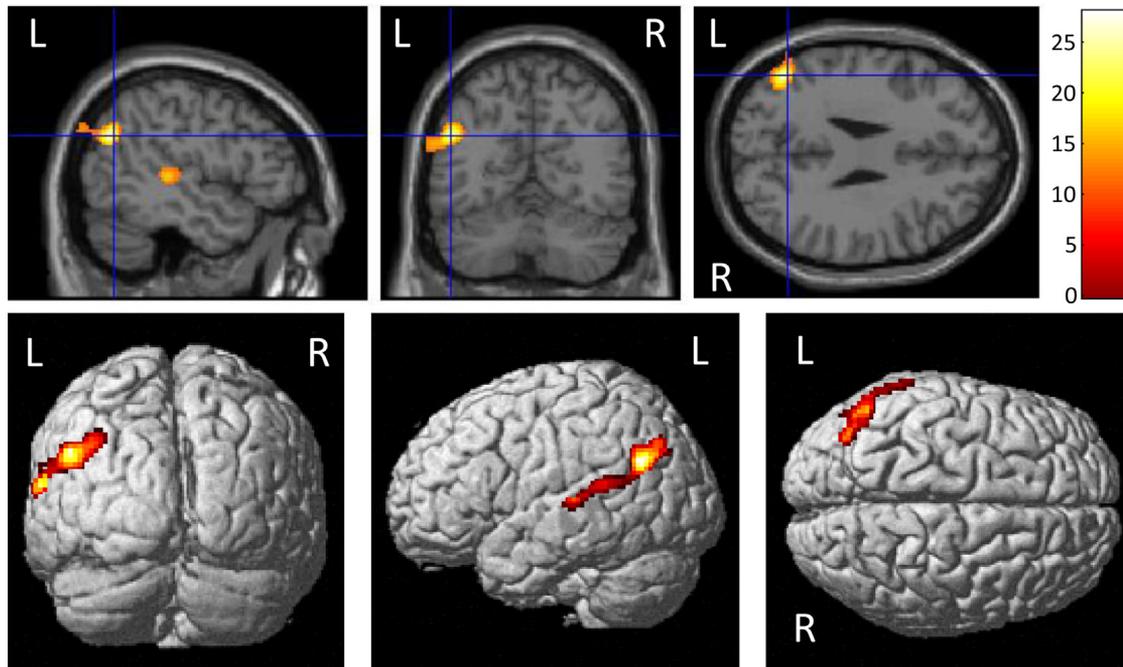


Fig. 3. Effect of *INPP5D* rs61068452 on cerebral blood flow. Selected sectional slices (top) and surface renderings (bottom) represent the voxelwise analysis of the additive effect of rs61068452-G on CBF. The color scale indicates significance ($-\log_{10} p$ value) of association between rs61068452 and CBF measure (i.e., GG > AG > AA). All comparisons are displayed at a voxelwise threshold of uncorrected $p < 0.001$ with minimum cluster size of 800 voxels (approximately responding to a clusterwise threshold of FDR-corrected $p < 0.05$). The most significant clusters are present in the left angular gyrus. Abbreviations: CBF, cerebral blood flow. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

$p = 2.0E-2$), after Bonferroni correction for the number of genes (Supplementary Table 2).

3.4. Association of *INPP5D* rs61068452 with CSF t-tau/A β_{1-42} ratio

Given the effect of rs61068452 with CBF measures in brain region, we hypothesized that *INPP5D* rs61068452 would also be associated with CBF-related AD biomarkers. We tested the hypothesis through assessing the association of rs61068452 with CSF t-tau/A β_{1-42} ratio in 906 subjects (Supplementary Table 3) from ADNI who were not included in the CBF genetic analysis. The minor allele (G) of rs61068452 was significantly associated with lower CSF t-tau/A β_{1-42} ratio ($p = 0.014$; Fig. 4A) under linear regression with age, gender, *APOE* $\epsilon 4$ status, and the top 4 principal components as covariates. We also tested the relevance of the previously reported *INPP5D* SNP rs35349669, and identified its association with higher CSF t-tau/A β_{1-42} ratio ($p = 0.028$). We observed that the minor allele (G) of rs61068452 was associated with decreased CSF t-tau/A β_{1-42} ratio across all diagnostic groups (Supplementary Fig. 2B).

3.5. Association of *INPP5D* rs61068452 with FDG-PET

Recent studies have reported different relationships between ASL MRI and FDG-PET in different brain regions, including the similar abnormalities in some regions (Chen et al., 2011; Musiek et al., 2012) and decoupling between perfusion and metabolism in other brain regions (Cha et al., 2013). We first explored the association of rs61068452 with glucose metabolism of left angular region measured by FDG-PET in 735 subjects from ADNI who were not included in our previous CBF analysis (Supplementary Table 4). There existed no significant association between rs61068452 and left angular glucose metabolic rate ($p = 0.111$, Fig. 4B) under linear regression with age, gender, *APOE* $\epsilon 4$ status, and the top 4 principal

components as covariates; while the minor allele (G) of rs61068452 showed a trend of association with increased glucose metabolic rate in L-AG for all diagnostic groups except healthy controls (Supplementary Fig. 2C).

3.6. Association of *INPP5D* rs61068452 with AD

To examine whether the genetic finding from our CBF analysis is directly associated with the AD status, we leveraged the valuable results available from the most recent large-scale genomewide meta-analysis of AD (Jansen et al., 2019). According to the summary statistics of the phase 3 analysis in this study, rs61068452 exhibited a significant association with AD ($p = 1.54E-04$; $N = 456,488$). The corresponding effect size is -0.0164 , indicating a protective role of rs61068452-G in AD. This aligns well with our CSF finding.

4. Discussion

Targeted genetic analysis of AD candidate genes discovered a novel association between the SNP rs61068452 in *INPP5D* and a regional CBF measure in 258 ADNI subjects. To the best of our knowledge, this is among the first genetic association analyses of CBF measured by ASL perfusion MRI in AD-related studies. We identify that *INPP5D* rs61068452-G is associated with higher CBF of left angular gyrus. The protective effect of the G allele of rs61068452 is further validated in a large meta-analysis of AD ($N = 456,488$), as well as shown in nonoverlapping samples from ADNI, where it is associated with AD CSF biomarker ($N = 906$) and left angular glucose metabolism measured by FDG-PET ($N = 735$).

INPP5D is a known negative regulator of inflammation, and has been reported to be associated with late-onset AD in a large meta-analysis of GWAS case-control study (Lambert et al., 2013; Yoshino et al., 2017). It has been further investigated and

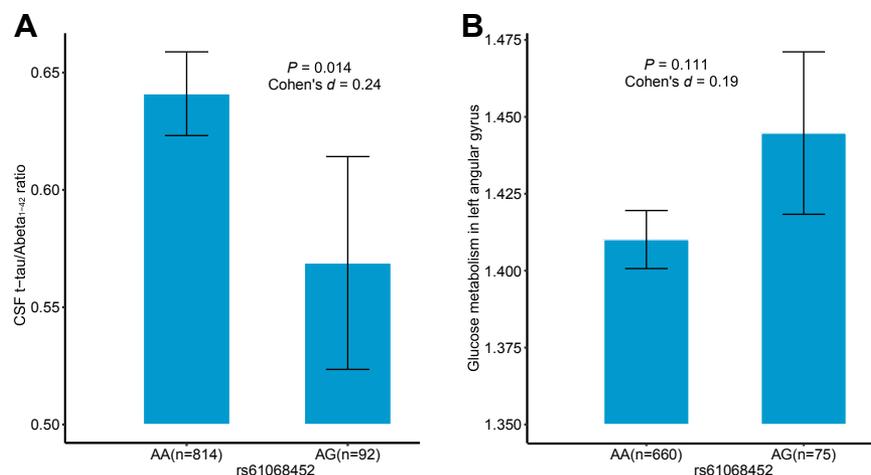


Fig. 4. Association of *INPP5D* rs61068452 on CSF t-tau/Aβ₁₋₄₂ ratio and FDG metabolism. (A) Mean CSF t-tau/Aβ₁₋₄₂ ratio with standard errors are plotted against the rs61068452 genotype groups (i.e., AA and AG, no GG participants in this sample). *p* value and Cohen's *d*, respectively, indicates the significance and effect size of the association between rs61068452 and CSF t-tau/Aβ₁₋₄₂ ratio, with age, gender, *APOE* ε4 status, and the top 4 principal components from population stratification analysis as covariates. Presence of minor allele (G) of rs61068452 is associated with decreasing CSF t-tau/Aβ₁₋₄₂ ratio. (B) Mean left angular FDG-PET glucose metabolism with standard errors are plotted against the rs61068452 genotype groups (i.e., AA and AG, no GG participants in this sample). Presence of minor allele (G) of rs61068452 is associated with increasing FDG-PET measured glucose metabolism in left angular gyrus. Abbreviations: Aβ, amyloid β.

reviewed for its function in a number of pathways including microglial activation, neuroinflammation, and immune response (López González et al., 2016; Malik et al., 2015; Yoshino et al., 2017). *INPP5D* mRNA analysis has revealed significantly higher expression in AD than in healthy control subjects, and suggested its involving role in microglial function via DAP12 (DNAX-activating protein of 12kD) (Yoshino et al., 2017).

INPP5D encodes a protein called *SHIP1* (phosphatidylinositol-3,4,5-trisphosphate-5-phosphatase 1). Our reported SNP rs61068452 is an intronic variant of *INPP5D*, locating nearby the *INPP5D* transcription starting site, which is related to the regulation of *SHIP1* by modulating the Src Homology 2 (SH2) domain. Therefore, 1 possible role which rs61068452 could play is to regulate the production of *SHIP1*. Another previously reported AD risk variant, *INPP5D* SNP rs35349669, is not associated with CBF phenotypes in the studied samples. However, it is significantly associated with CSF t-tau/Aβ₁₋₄₂ ratio in the subsequent biomarker analysis with opposite effect direction compared with rs61068452. There are multiple transcription factors of *INPP5D* for modulating the production of *SHIP1*. The SNPs rs61068452 and rs35349669 are located in different introns and independent from each other according to their linkage disequilibrium value. In addition, rs61068452 resides in regions that are related to the SH2-domain, whereas rs35349669 resides in regions regulating endonuclease. Thus, it warrants further investigation to examine how the molecular functions of rs61068452 and rs35349669 differ.

Recent studies of mouse model also indicate the important role of *INPP5D* in AD, especially in microglia. In particular, a recent work has demonstrated the conservative of transcriptomic between human and mouse microglia, and illustrated the higher expression level of *INPP5D* in them (Gosselin et al., 2017). In another study of AD immune basis, overlap of AD-associated variants within *INPP5D* with increasing enhancer has been identified in AD mouse model, as well as overlap with immune enhancer in human CD14⁺ primary cells (Gjoneska et al., 2015). Our reported variant, *INPP5D* rs61068452, overlaps with this enhancer region and is only ~10K bp from these variants. The transcription site nearby which rs61068452 is located encodes SH2 domain. Therefore, this may indicate a possible function of rs61068452 for modulating the transcription of *SHIP1* through affecting the SH2 domain. This

provides evidences for using mouse model to gain a better understanding of human neurodegenerative diseases.

In addition to *INPP5D*, our gene-based association analysis also discovered CD2AP (CD2-associated protein) associated with left angular CBF. Recent studies have identified interactions between *INPP5D* and several other AD candidates and studied their associations with AD pathogenesis. In particular, *SHIP1*, protein encoded by *INPP5D*, complexes with CD2AP to inhibit the ubiquitination of proinflammatory proteins Syk (spleen tyrosine kinase) and FcγRIIa (CD32) (Bao et al., 2012). *SHIP1* has also been investigated for inhibiting TREM2 (triggering receptor expressed on myeloid cell 2) signaling by binding to DAP12 and preventing the recruitment of PI3K (phosphatidylinositol 3-kinase) to DAP12 (Malik et al., 2015; Peng et al., 2010; Yoshino et al., 2017). Functional interactions among these genes may help supply meaningful information for understanding the underlying molecular mechanism.

Pathologically, interactions between CBF and neuroinflammation and their effects on neurodegenerative diseases have been explored. CBF is regulated by activations of neurons and glial cells, including microglia which are the main resident immune cells in brain. Increased activation of microglia has been shown linked to neurodegenerative diseases including AD. Relationships between microglia and brain blood flow have also been largely studied (Attwell et al., 2010; Szalay et al., 2016), further suggesting their involvements in AD.

In this work, we discover that rs61068452-G is associated with higher CBF in L-AG. Given that hypoperfusion of L-AG is an established imaging biomarker of AD and early AD (Liu et al., 2015; Suwa et al., 2015), increased L-AG CBF in the G-carriers of rs61068452 may represent a protective role in AD neuropathogenesis. It is further validated in a large meta-analysis of AD for the protective effect of G-carriers of rs61068452.

According to the discovery of rs61068452 from targeted genetic analysis, we test its association with other AD endophenotypes including CSF t-tau/Aβ₁₋₄₂ ratio and glucose metabolism measured by FDG-PET. The minor allele (G) of rs61068452 is significantly associated with lower CSF t-tau/Aβ₁₋₄₂ ratio and shows a trend toward higher glucose metabolic rate in left angular region. Both CSF and FDG-PET hold promise as early markers for preclinical of AD, whereas CSF biomarkers have been thought to be a type of “AD

signature” because of their predictive power for accurate and early diagnosis of AD (Blennow et al., 2015; De Deyn, 2015; Skillbäck et al., 2015). Therefore, these findings further suggest the protective effect of the G allele of rs61068452 for AD.

In conclusion, we have revealed a novel association between the minor allele (G) of *INPP5D* rs61068452 and higher left angular cerebral blood flow, and have related this genetic finding to AD endophenotypes including CSF t-tau/A β _{1–42} ratio. This study has focused on AD candidate genes, given the modest sample size in a genetic association study. Future investigation is warranted to conduct a replication study with larger sample(s) from independent cohorts. Another future direction is to perform the longitudinal CBF analysis for characterizing disease progression. The molecular mechanism of identified *INPP5D* rs61068452 warrants further investigation, including how it modulates *SHIP1* transcription, interacts with other AD genes such as *TREM2*, *CD2AP*, and affects the microglia activation and inflammation. Another future topic is to examine the biological role of *INPP5D* rs61068452 in vascular system, given the evolving of vascular system on CBF controlling and brain functions. In addition, AD animal models merit further investigation and may provide helpful information for filling the gap between neurodegenerative disease mechanisms and genetic risk and protective factors.

Disclosure

The authors have no actual or potential conflicts of interest.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.neurobiolaging.2019.06.003>.

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