

Effect of APOE ϵ 4 Genotype on Amyloid- β and Tau Accumulation in Alzheimer's Disease

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Research

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Abstract

Background

To assess effects of apolipoprotein E (ApoE) $\epsilon 4$ genotype on A β and tau burden and their longitudinal changes in Alzheimer's disease (AD) spectrum.

Methods

Among 272 individuals who underwent PET scans (^{18}F -florbetaben for A β and ^{18}F -flortaucipir for tau) and ApoE genotyping, 187 individuals completed 2-year follow-up PET scans. After correcting for partial-volume effect, we compared the standardized uptake value ratio (SUVR) for A β and tau burden between the $\epsilon 4+$ and $\epsilon 4-$ groups. By using a linear mixed-effect model, we measured changes in SUVR in the ApoE $\epsilon 4+$ and $\epsilon 4-$ groups.

Results

The $\epsilon 4+$ group showed greater baseline A β burden in the diffuse cortical regions and greater tau burden in the lateral, and medial temporal, cingulate, and insula cortices. Tau accumulation rate was higher in the parietal, occipital, lateral, and medial temporal cortices in the $\epsilon 4+$ group. In A $\beta+$ individuals, baseline tau burden was greater in the medial temporal cortex, while A β burden was conversely greater in the $\epsilon 4-$ group. Tau accumulation rate was higher in the $\epsilon 4+$ group in a small region in the lateral temporal cortex. The effect of ApoE $\epsilon 4$ on enhanced tau accumulation persisted even after adjusting for the global cortical A β burden.

Conclusions

Progressive tau accumulation may be more prominent in $\epsilon 4$ carriers, particularly in the medial and lateral temporal cortices. ApoE $\epsilon 4$ allele has differential effects on A β burden depending on the existing amyloidosis and enhances vulnerability to progressive tau accumulation in the AD spectrum independent of A β .

Background

Except for the rare dominantly inherited Alzheimer's disease (AD), most AD patients are sporadic [1, 2]. The apolipoprotein E (ApoE) gene encodes an 35-kDa extracellular lipid and cholesterol carrier glycoprotein, and its $\epsilon 4$ allele is a major genetic risk factor for sporadic AD [1, 3]. The presence of this allele increases the risk of AD in a dose-dependent manner and lowers the age at onset [4, 5]. However, its effect on the regional accumulation rates of two major pathological proteins—amyloid- β (A β) and tau—remains unclear.

Greater amounts of A β burden are demonstrated in $\epsilon 4$ carriers than in non-carriers in the previous postmortem and ^{11}C -Pittsburgh compound B (PIB) positron emission tomography (PET) studies [6–8]. Longitudinal change in A β burden was also greater in $\epsilon 4$ carriers than non-carriers in the previous studies [9–11], while the other longitudinal study did not find this association [12].

Postmortem studies showed more frequent neurofibrillary tangle pathology in $\epsilon 4$ carriers in a dose-dependent manner [7], a greater tangle pathology in AD patients with $\epsilon 4$ homozygote [13], and an association of $\epsilon 4$ allele with tangle pathology in the presence of A β [14]. In contrast, the other study did not find this association [15]. Recent tau PET study exhibited an effect of ApoE $\epsilon 4$ on A β -independent increase in tau load in the entorhinal cortex and hippocampus [16],

while the other studies found this effect was associated with the global A β burden [17] or even greater tau burden in the prodromal AD and AD dementia patients without ϵ 4 allele, particularly in the parietal cortex, than in ϵ 4 carriers [18].

In this study, we investigated the effects of the ϵ 4 allele on regional A β and tau burden and their longitudinal changes in cognitively unimpaired (CU) individuals, mild cognitive impairment (MCI), and AD patients.

Materials And Methods

Participants

From January 2015 to August 2017, 272 individuals completed a baseline tau PET study at Gangnam Severance Hospital. The baseline study included magnetic resonance (MR) and two PET scan (^{18}F -florbetaben for A β and ^{18}F -flortaucipir for tau) studies, neuropsychological tests with Seoul Neuropsychological Screening Battery (tests for global cognition and six cognitive domains) [19], and ApoE genotyping. In 187 individuals who agreed to a follow-up study, the same neuroimaging and neuropsychological tests were performed after a mean of 2.0 ± 0.3 years.

We used clinical diagnostic criteria for probable AD dementia proposed by the National Institute of Neurological and Communicative Disorders and Stroke and the Alzheimer's Disease and Related Disorders Association and Petersen's criteria for diagnosing MCI [20, 21]. Thereby, baseline study included 96 CU, 105 MCI and 71 AD dementia patients, and longitudinal study included 80 CU, 42 MCI, and 65 AD dementia patients. Baseline A β -positivity was determined by two nuclear medicine specialists using the validated visual assessment methods [22, 23]. Detailed information for the inclusion of participants is described in our previous works [24, 25].

Acquisition of PET and MR images

PET images were acquired in a Biograph mCT PET/CT scanner (Siemens Medical Solutions; Malvern, PA, USA) for 20 min at 90 min after the injection of ^{18}F -florbetaben and at 80 min after the injection of ^{18}F -flortaucipir. Prior to the scan, brain computed tomography images were acquired for attenuation correction. 3D PET images were reconstructed using the ordered-subsets expectation maximization (OSEM) algorithm in a $256 \times 256 \times 223$ matrix with a $1.591 \times 1.591 \times 1$ mm voxel size. In a 3.0 T MR scanner (Discovery MR750, GE Medical Systems, Milwaukee, WI), T1-weighted MR images were acquired using 3D-spoiled gradient-recalled sequences (repetition time = 8.3 ms, echo time = 3.3 ms, flip angle = 12° , 512×512 matrix, voxel spacing $0.43 \times 0.43 \times 1$ mm).

Image processing steps

We used FreeSurfer 5.3 (Massachusetts General Hospital, Harvard Medical School; <http://surfer.nmr.mgh.harvard.edu>) software to obtain participant-specific volumes-of-interest (VOIs). In brief, T1-weighted MR images were resliced to a 1-mm isovoxel space in FreeSurfer, corrected for inhomogeneity and segmented into gray and white matter. After tessellation, 3D-surfaces for gray and white matter were reconstructed. Subcortical regions were segmented with the probabilistic registration method [26], and cortical regions were probabilistically labelled based on the curvature information overlaid on inflated white matter surface [27, 28]. Finally, participant-specific composite VOI images, including 16 and 4 subcortical regions, were created by merging anatomically related regions.

Statistical parametric mapping 12 (Wellcome Trust Centre for Neuroimaging, London, UK) and in-house software implemented in MATLAB 2015b (MathWorks, Natick, MA, USA) were used for the processing of PET images. PET images were first coregistered to MR images resliced to the FreeSurfer isovoxel space. Using participant-specific composite VOI images, PET images were corrected for partial volume effect (PVE) with a region-based voxel-wise (RBV) method [29]. Standardized uptake value ratio (SUVR) images were created using the cerebellar crus median obtained by overlaying a template mask on PET images spatially normalized with diffeomorphic anatomical registration through an

exponentiated Lie algebra tool [30]. Finally, regional SUVR values were obtained by overlaying the participant-specific composite VOI images on individual PET images.

For visualization, cortical activities were mapped on the white matter surface by assigning the values of voxels corresponding to the mid-point between the gray and white matter surface, corrected for PVE with the RBV method, and then converted to SUVR maps using the cerebellar crus median as a reference. Surface SUVR images were spatially normalized and finally smoothed on a 2D surface using a Gaussian kernel with 8-mm full-width half-maximum.

Statistical analysis

SPSS 23 (IBM Corp., Armonk, NY, USA) was used for the statistical analysis of demographic data and baseline VOI data. Continuous and categorical demographic variables were compared between the ApoE $\epsilon 4^-$ and $\epsilon 4^+$ groups using independent t-test and chi-square test, respectively. Using the general linear model with age, years of education, sex, and baseline MMSE scores as covariates, baseline SUVR values were compared between the ApoE $\epsilon 4^-$ and $\epsilon 4^+$ groups. *P*-values for trends were calculated using analysis of covariance (ANCOVA) after adjusting for age, sex, years of education, and baseline MMSE scores as covariates. Region-wise multiple comparisons were corrected for using Benjamini-Hochberg's false discovery rate method [31]. Likewise, baseline surface images were compared between the two groups using the same general linear model implemented in FreeSurfer. Longitudinal changes in the regional SUVR values and surface images were compared between the groups using a linear mixed effect model in MATLAB with age, sex, years of education, baseline MMSE scores, and an interaction term between the presence of ApoE $\epsilon 4$ and time intervals as fixed factors under the assumption of a random intercept and slope by setting the intervals and subject as random factors.

Results

Demographic characteristics

Baseline and follow-up demographic data are summarized in Table 1 and e-1. In individuals included in the baseline and follow-up studies, age, sex, and education were not different between the $\epsilon 4^-$ and $\epsilon 4^+$ groups. The $\epsilon 4^+$ group showed higher proportions of A β -positivity and clinical dementia and worse global cognition measured at baseline than the $\epsilon 4^-$ group. However, all demographic characteristics and global cognition were not different in each group stratified by A β -positivity. Compared to baseline, global cognition worsened at follow-up in both the $\epsilon 4^-$ and $\epsilon 4^+$ groups. The number of $\epsilon 4$ carriers was greater in patients with dementia than that in CU and MCI patients.

Table 1
Baseline demographic characteristics of 272 participants who completed the baseline study

	A β \pm		A β -		A β +	
	ϵ 4-	ϵ 4+	ϵ 4-	ϵ 4+	ϵ 4-	ϵ 4+
N	195	77	134	24	61	53
Baseline age (years)	70.4 \pm 10.3	70.0 \pm 8.6	68.4 \pm 10.3	65.5 \pm 8.3	74.7 \pm 8.7	72.1 \pm 7.9
Females (%)	127 (65%)	51 (66%)	90 (67%)	16 (67%)	37 (61%)	35 (66%)
Education (years)	11.1 \pm 4.9	11.2 \pm 5.0	11.0 \pm 4.9	11.4 \pm 4.2	11.2 \pm 4.8	11.1 \pm 5.3
Duration (years)	2.6 \pm 1.5	3.1 \pm 1.4	2.3 \pm 1.5	2.4 \pm 1.3	3.0 \pm 1.5	3.2 \pm 1.4
Aβ-positivity (%)	61 (31%)	53 (69%) ^a	0 (0%)	0 (0%)	61 (100%)	53 (100%)
ϵ2/2 : ϵ2/3 : ϵ3/3	1 : 37 : 157	n.a.	1 : 31 : 102	n.a.	0 : 6 : 55	n.a.
ϵ2/4 : ϵ3/4 : ϵ4/4	n.a.	2 : 60 : 15	n.a.	2:21:1	n.a.	0 : 39 : 14
Baseline diagnosis	79/75/41	17/30/30 ^a	72/49/13	15/7/2	7/26/28	2/23/28
CU/MCI/DEM (%)	(41/38/21%)	(22/39/39%)	(54/37/10%)	(63/29/8%)	(11/43/46%)	(4/43/53%)
MMSE	25.4 \pm 4.7	23.5 \pm 5.3 ^a	26.8 \pm 3.2	26.7 \pm 2.5	22.2 \pm 5.7	22.1 \pm 5.7
CDR-SB	1.6 \pm 2.3	2.7 \pm 2.5 ^a	0.9 \pm 1.5	0.8 \pm 1.4	3.1 \pm 3.0	3.6 \pm 2.4
Data are presented as mean \pm SD. ^a <i>P</i> < 0.05 for the comparisons between the ϵ 4- and ϵ 4+.						
Abbreviations: CU = cognitively unimpaired, MCI = mild cognitive impairment, DEM = dementia, A β +/- = A β -positivity, ApoE = apolipoprotein-E, MMSE = Mini-Mental State Examination, CDR-SB = Clinical Dementia Rating sum-of-boxes						

Baseline A β and tau burden

In all 272 individuals, the ApoE ϵ 4 + group exhibited greater A β burden in the global cortex, prefrontal, parietal, lateral temporal, parahippocampal, and cingulate cortices and hippocampus than the ϵ 4- group, and all regions survived correcting for multiple comparisons. Conversely, in A β + individuals, A β burden was greater in the ϵ 4- group in the global cortex, sensorimotor, superior parietal, occipital, and insula cortices than in the ϵ 4 + group, although all regions did not survive correcting for multiple comparisons (Fig. 1A). Surface-based statistics showed similar results as VOI-based comparisons (Fig. 1B).

In all individuals, greater tau burden was observed in the ϵ 4 + group in the lateral and medial temporal, cingulate, and insula cortices, and all regions survived multiple comparisons (Fig. 1A). In A β + individuals, the ϵ 4 + group showed greater tau burden in the medial temporal regions, and only the amygdala and hippocampus survived correcting for multiple comparisons. When the baseline global cortical A β burden was included as an additional covariate in the model, ApoE ϵ 4 + group exhibited greater tau burden in all medial temporal regions when compared to ϵ 4- group (Additional file 1: Figure S1A). Surface-based statistics showed greater tau burden in the medial temporal and anterior cingulate regions

in the $\epsilon 4 +$ group than in the $\epsilon 4 -$ group, however, none of the regions survived after correcting for multiple comparisons (Fig. 1B).

Increased baseline A β burden in the hippocampus was associated with the number of $\epsilon 4$ alleles. Likewise, tau burden in the medial temporal regions showed an association with $\epsilon 4$ allele in a dose-dependent manner (Fig. 4A). In A β + individuals, increased tau burden in the hippocampus and amygdala was associated with the $\epsilon 4$ allele in a dose-dependent manner (Fig. 4B).

Longitudinal changes in A β and tau burden

Examples of baseline A β and tau burden and their changes at follow-up are demonstrated in Fig. 2. In all 187 individuals, the $\epsilon 4 +$ group exhibited a higher A β accumulation rate than the $\epsilon 4 -$ group in the global cortex, superior parietal, occipital, lateral temporal, parahippocampal cortices and amygdala, however, none of the regions survived correcting for multiple comparisons (Fig. 3A). A surface-based comparison showed a higher A β accumulation rate in the $\epsilon 4 +$ group in the diffuse cortical areas than in the $\epsilon 4 -$ group, and small regions in the lateral temporal cortex survived correcting for multiple comparisons (Fig. 3B). In A β + individuals, there was no difference in the A β accumulation rate between the two groups.

In all individuals, tau accumulation rate in the $\epsilon 4 +$ group was higher in the global cortex, prefrontal, parietal, occipital, lateral and medial temporal, posterior cingulate, and insula cortices compared to the $\epsilon 4 -$ group. Except for the prefrontal, superior parietal, and posterior cingulate cortices, all regions survived correcting for multiple comparisons (Fig. 3A). In addition, the increase in tau accumulation rate is associated with the number of ApoE $\epsilon 4$ allele (Fig. 4B). Similar to the VOI-based results, a surface-based comparison of the annual increase in tau showed a higher tau accumulation rate, particularly in the diffuse parietotemporal cortex in the $\epsilon 4 +$ group (Fig. 3B). In A β + individuals, the $\epsilon 4 +$ group exhibited a greater annual increase in tau burden in the middle temporal and hippocampus, although none of the regions survived correcting for multiple comparisons (Fig. 3A). Surface-based statistics also showed a higher tau accumulation rate in the small regions in the basal and lateral temporal and sensorimotor cortices (Fig. 3B).

Even after the inclusion of baseline global cortical A β burden as an additional covariate in the model, statistical results for the VOI-based comparison of tau accumulation rates between the two ApoE groups were almost similar (Additional file 1: Figure S1B).

Discussion

In this study, we assessed the effects of ApoE $\epsilon 4$ genotype on A β and tau burden and found a greater baseline A β and tau burden and higher tau accumulation rate in the $\epsilon 4 +$ group than in the $\epsilon 4 -$ group. The A β accumulation rate in the $\epsilon 4 +$ group was higher in small areas in the lateral temporal cortex. In A β + individuals, baseline tau burden in the $\epsilon 4 +$ group was greater in the medial temporal regions and tau accumulation rate in the $\epsilon 4 +$ group was higher in the small regions in the basal and lateral temporal cortices compared to the $\epsilon 4 -$ group.

Transgenic mice model with neuron-specific overexpression of ApoE $\epsilon 4$ showed greater phosphorylated tau burden in the neocortex and hippocampus [32], and tau transgenic mice with human ApoE $\epsilon 4$ exhibited greater tau burden in the hippocampus than those with $\epsilon 2$ or $\epsilon 3$ [33]. A postmortem study showed $\epsilon 4$ gene dose-dependent increase in neurofibrillary tangle (NFT) pathology and thereby greater NFT pathology in the diffuse cortical areas in the AD patients with $\epsilon 4$ allele than those without [7]. Another study showed greater cortical NFT pathology only in the AD patients homozygous for $\epsilon 4$ allele than those with a single $\epsilon 4$ allele or those without the allele [13]. Unlike these transgenic mice and human postmortem studies, human cerebrospinal fluid (CSF) biomarker studies showed no differences in the level of CSF T-tau and P-tau between the $\epsilon 4 +$ and $\epsilon 4 -$ groups [34, 35]. Moreover, one cross-sectional tau PET study in A β + MCI

and AD patients demonstrated that the $\epsilon 4$ - group conversely exhibited greater tau burden in the parieto-occipital cortex than the $\epsilon 4+$ group [18]. However, our study results showed greater tau burden in the medial temporal areas even in the $A\beta+$ individuals with the $\epsilon 4$ allele than in those without, although the result for the hippocampus was limited by the off-target binding in the choroid plexus neighboring hippocampus. This discrepancy may be attributable to the disproportionate frequency of the $\epsilon 4$ allele in different subtypes of AD. The hippocampal sparing type of AD is associated with a younger age at onset, lower frequency of the ApoE $\epsilon 4$ allele, greater tau burden particularly in the parietal cortex, faster cortical atrophy, and faster cognitive decline than the typical AD subtype [36–39]. Therefore, we suspect that the inclusion of a greater proportion of the hippocampal sparing subtype in the study cohort diluted an effect of $\epsilon 4$ on tau burden or even caused contrary results.

Although there has been a report demonstrating a longitudinal increase in CSF tau in AD patients [40], one longitudinal tau PET study in a small number of AD patients did not find an association between the ApoE genotypes and longitudinal changes in tau burden [41]. In our results for all $A\beta \pm$ individuals, the regional tau accumulation rate was higher in the $\epsilon 4+$ group in the diffuse regions in the medial and lateral temporal and parieto-occipital cortices than that in the $\epsilon 4$ - group. Moreover, even in the $A\beta+$ individuals, higher tau accumulation rate was observed in the $\epsilon 4+$ group in the small regions in the temporal cortex suggesting the impact of ApoE $\epsilon 4$ genotype on progressive tau accumulation.

One recent tau PET study including 325 individuals (90% cognitively-unimpaired and 10% cognitively-impaired) showed an association of ApoE $\epsilon 4$ with increased tau burden in the entorhinal cortex, but they lost significance after adjusting for global cortical $A\beta$ burden [17]. In contrast, the other study including 489 individuals with more balanced distribution of cognitive status (57% cognitively-unimpaired and 43% cognitively-impaired) demonstrated an effect of ApoE $\epsilon 4$ on increased tau burden in the entorhinal cortex and hippocampus, and it persisted even after adjusting for global cortical $A\beta$ burden like our study result [16]. Moreover, the effect of ApoE $\epsilon 4$ on progressive tau accumulation was replicated after adjusting for global cortical $A\beta$ burden in our longitudinal study. Therefore, tau accumulation may be accelerated by the presence of ApoE $\epsilon 4$ independent of $A\beta$ burden.

The ApoE $\epsilon 4$ isoform was more likely to stimulate neuronal $A\beta$ production than the other isoforms *in vitro* [42], and transgenic mice expressing the ApoE $\epsilon 4$ isoform showed less effective clearance of soluble $A\beta$ from the brain interstitial fluid [43]. Human autopsy findings demonstrated greater $A\beta$ burden in the $\epsilon 4+$ than in the $\epsilon 4$ - group not only in AD patients [13], but also in the MCI patients and CU individuals [44]. Likewise, when compared to the individuals without the $\epsilon 4$ allele, a greater $A\beta$ burden was observed in the global cortex in CU and MCI patients with $\epsilon 4$ allele [8], and in the temporo-parietal cortex in AD patients with $\epsilon 4$ allele in the PET studies [45]. Our study also demonstrated greater $A\beta$ burden in the diffuse cortical areas in individuals with the $\epsilon 4$ allele than in those without. In contrast to the strong association between the $\epsilon 4$ allele and baseline $A\beta$ burden, we found a weak effect of ApoE $\epsilon 4$ on progressive $A\beta$ accumulation in small regions in the lateral temporal cortex only in all $A\beta \pm$ individuals. The $A\beta$ accumulation rate in the $A\beta+$ individuals was not different between the $\epsilon 4+$ and $\epsilon 4$ - groups like previous studies [9, 11], suggesting an effect of the ApoE $\epsilon 4$ allele on $A\beta$ deposition only in the early stage of the disease.

Interestingly, $A\beta$ burden in the $A\beta+$ individuals was paradoxically greater in the $\epsilon 4$ - group than in the $\epsilon 4+$ group, similar to the previous ^{11}C -PIB and ^{18}F -fluorodeoxyglucose PET studies that demonstrated lower $A\beta$ burden and contrarily greater cortical hypometabolism in the AD patients with $\epsilon 4$ allele than in those without [46, 47]. This paradoxical effect of the ApoE $\epsilon 4$ allele on $A\beta$ deposition can be expected by clinical studies that found an impact of the ApoE $\epsilon 4$ allele on $A\beta$ burden in CU and MCI but not in those with AD [8, 34]. Furthermore, a study with transgenic mice demonstrated enhanced $A\beta$ aggregation by ApoE4 in the early seeding stage but not in the later $A\beta$ growth stage [48]. An *in vitro* experiment demonstrated that ApoE $\epsilon 4$ binds to toxic $A\beta$ oligomers and more potently delays further aggregation of $A\beta$ into the PET-detectable fibril form than the other ApoE isoforms [49]. Therefore, ApoE $\epsilon 4$ may play an important role in $A\beta$ accumulation in the early stages of AD pathogenesis rather than in the advanced stages and may be more likely to be

exposed to toxic oligomers. Subsequently, events toward final neurodegeneration may be induced, thereby shifting the hypothetical biomarker curves for tau and neurodegeneration to the A β curve [47]. It is also interesting to note that a transgenic mice model expressing both A β and tau exhibited a smaller number of plaque than that expressing only A β [50]. Greater microgliosis and reduction of the amyloid-precursor protein-producing neurons due to greater tau accumulation in ϵ 4 carriers may be another possible mechanism explaining the paradoxically lower A β burden [50]. However, this hypothesis cannot fully explain the mechanism due to mismatch between the cortical areas with greater A β burden in the ϵ 4- group and those with greater tau burden in the ϵ 4 + group (Fig. 1).

Limitations

This study has several limitations. First, different time intervals for each participant between baseline and follow-up studies (mean of 2.0 ± 0.3 years) may affect the results, however, the linear mixed effect model with random intercept and slope adopted in this study was considered more appropriate for the study design with variable time intervals compared to the repeated measures-ANOVA test. In addition, longer follow up duration would be promising to observe more conclusive pathologic changes between the ϵ 4 + and ϵ 4- groups.

Conclusions

Our study revealed that progressive tau accumulation occurs more prominently in ϵ 4 carriers, particularly in the medial and lateral temporal cortices. The presence of the ϵ 4 allele not only has differential effects on A β burden depending on the existing amyloidosis but also enhances vulnerability to progressive tau accumulation in the AD spectrum independent of A β .

Abbreviations

ApoE
apolipoprotein E;
CU
cognitively unimpaired;
MCI
mild cognitive impairment;
SUVR
Standardized uptake value ratio;

Declarations

Ethics approval and consent to participate

This study was approved by the institutional review board of Gangnam Severance Hospital (Ref# 3-2017-0054), and written informed consent was obtained from all participants and/or their legal guardians. All procedures performed in this study were in accordance with the ethical standards of the 1964 Helsinki declaration and its later amendments.

Consent for publication

Not applicable

Availability of data and materials

Data generated by this study are available from the corresponding author on reasonable request. The data are not publicly available due to privacy restriction.

Competing interests

The authors declare that they have no competing interests

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Authors' contributions

MSB contributed with: conception and design, collection and assembly of data, data analysis and interpretation, and manuscript writing. HC contributed with: collection and assembly of data, and data analysis and interpretation. HSL contributed with: data analysis and interpretation. JHL contributed with: collection and assembly of data, data analysis and interpretation. YHR contributed with: conception and design, administrative support, collection and assembly of data, data analysis and interpretation, manuscript writing, and final approval of manuscript. CHL contributed with: conception and design, administrative support, and final approval of manuscript.

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Figures

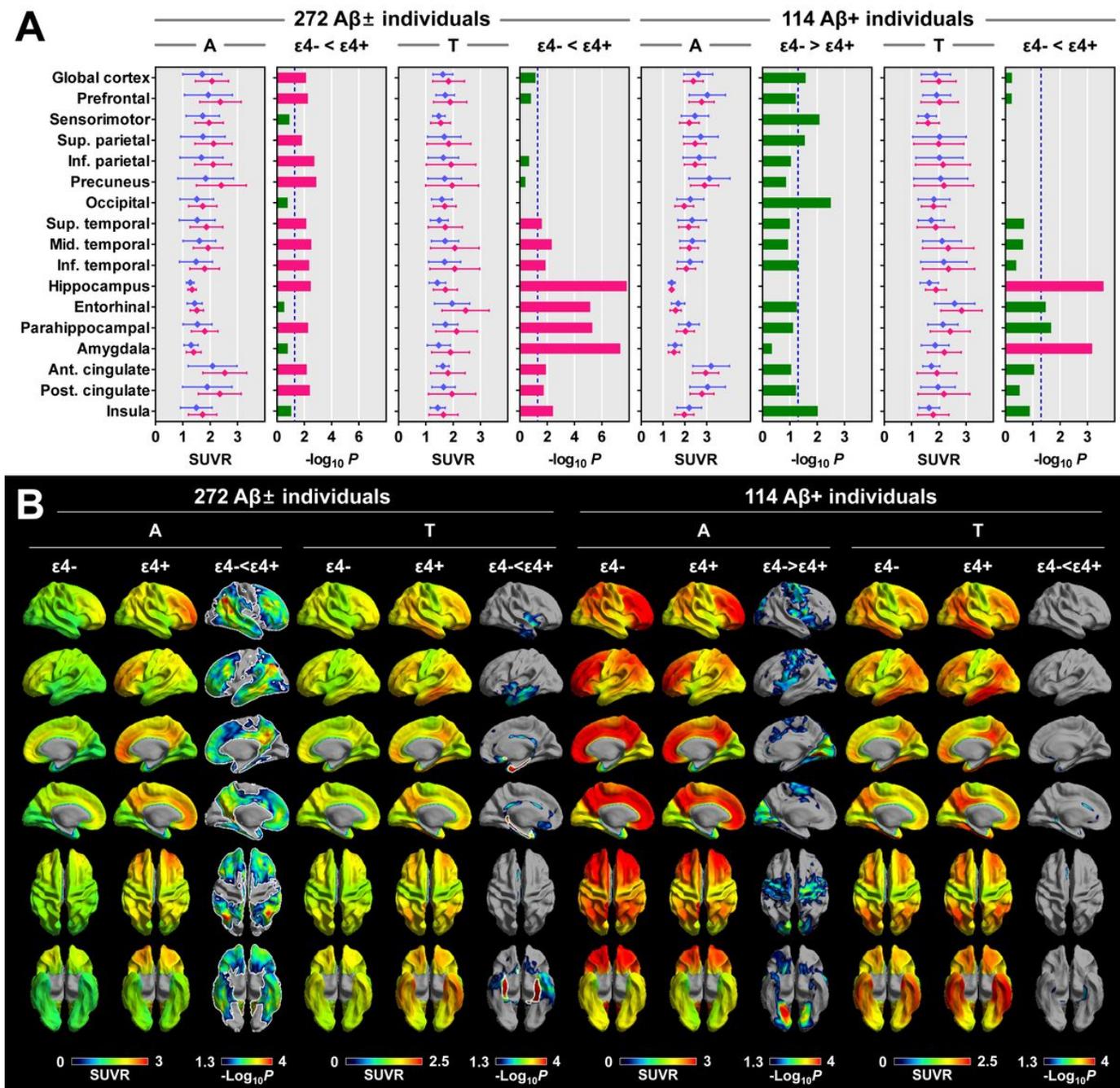


Figure 1

Comparison of baseline 18F-florbetaben and 18F-flortaucipir SUVR between the ApoE $\epsilon 4^-$ and $\epsilon 4^+$ groups. (A) VOI-based comparisons between the ApoE $\epsilon 4^-$ and $\epsilon 4^+$ groups. Data are presented as means (dots) and standard deviations (error bars) of the $\epsilon 4^-$ (blue) and $\epsilon 4^+$ (red) groups. P-values for the comparison between the $\epsilon 4^-$ and $\epsilon 4^+$ groups are expressed as $-\text{Log}_{10}P$. Red bars represent the regions that survived correcting for region-wise multiple comparisons (false discovery rate-corrected $P < 0.05$), and blue dotted lines represent uncorrected $P = 0.05$. (B) Surface-based comparisons between the ApoE $\epsilon 4^-$ and $\epsilon 4^+$ groups. Regions surrounded by white lines ($\epsilon 4^- < \epsilon 4^+$ in $A\beta$ and tau burden in all individuals) represent the cortical areas that survived correcting for multiple comparisons (false discovery rate-corrected $P < 0.05$). P-values for the comparison between the $\epsilon 4^-$ and $\epsilon 4^+$ groups are expressed as $-\text{Log}_{10}P$. Abbreviations: $A\beta^{+/-}$ = $A\beta$ -positivity, ApoE = apolipoprotein-E, SUVR = standardized uptake value ratio, A = 18F-florbetaben, T = 18F-flortaucipir

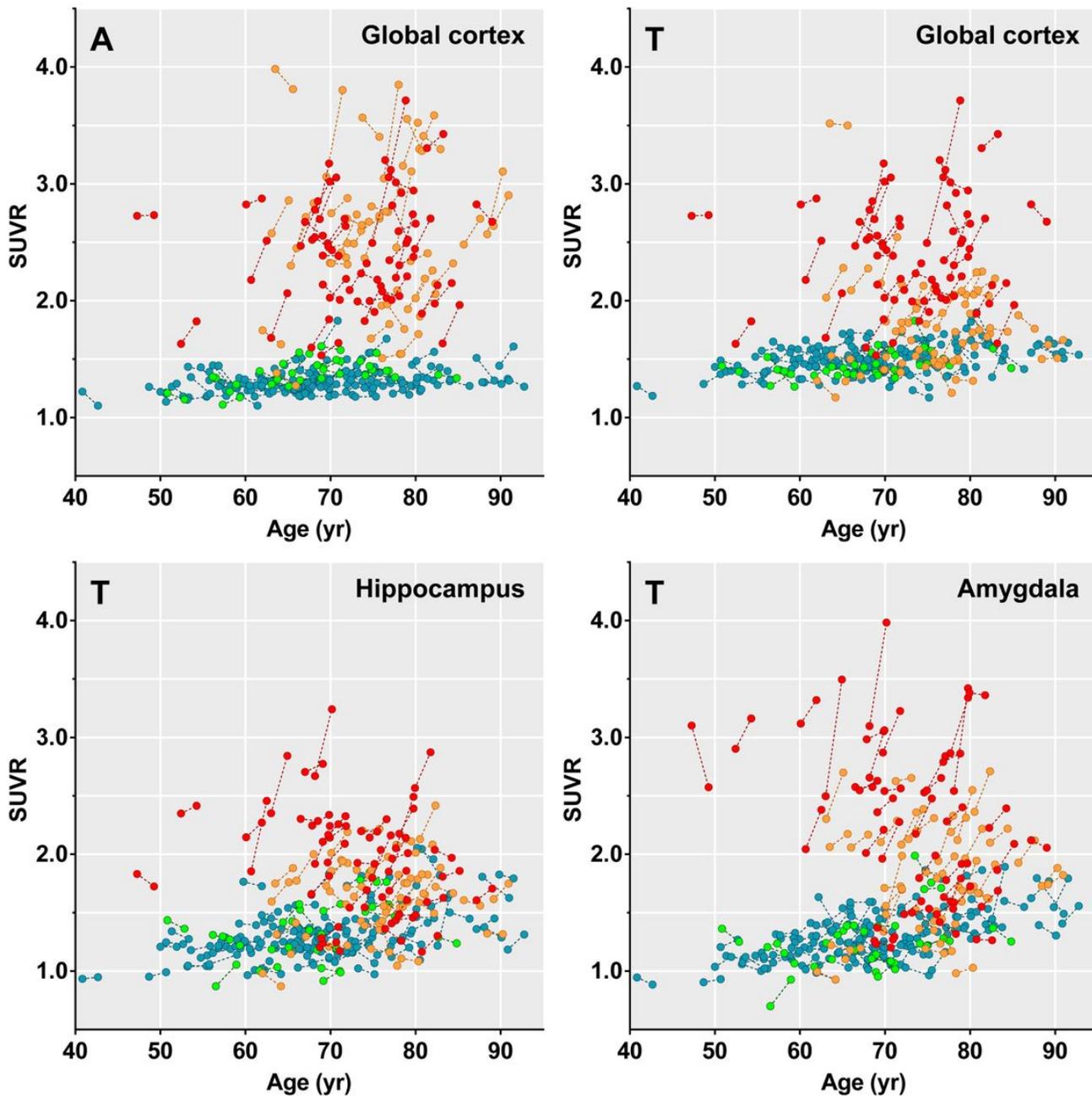


Figure 2

Spaghetti plots showing individual changes in regional SUVR values In 187 A β \pm individuals, the individual data points measured at baseline and follow-up are displayed as color-coded dots (cyan = A β ⁻ / ApoE ϵ 4⁻, green = A β ⁻ / ApoE ϵ 4⁺, orange = A β ⁺ / ApoE ϵ 4⁻, red = A β ⁺ / ApoE ϵ 4⁺). Abbreviations: A β ^{+/-} = A β -positivity, ApoE = apolipoprotein-E, SUVR = standardized uptake value ratio, A = 18F-florbetaben, T = 18F-flortaucipir

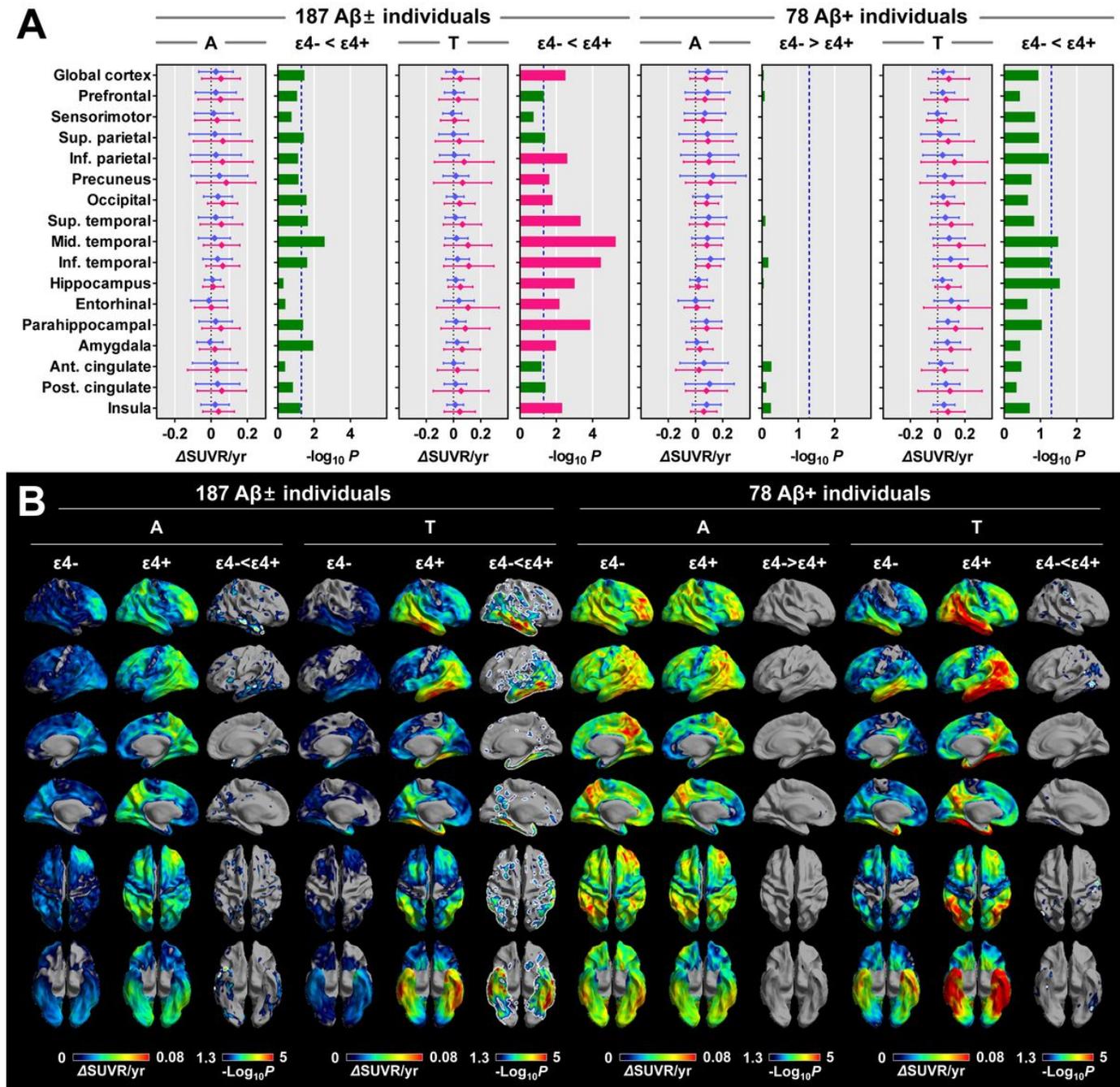


Figure 3

Comparison of annual changes in 18F-florbetaben and 18F-flortaucipir SUVR between the ApoE ϵ 4⁻ and ϵ 4⁺ groups. (A) VOI-based comparison between the ApoE ϵ 4⁻ and ϵ 4⁺ groups. Data are presented as means (dots) and standard deviations (error bars) of the ϵ 4⁻ (blue) and ϵ 4⁺ (red) groups. P-values for the comparison between the ϵ 4⁻ and ϵ 4⁺ groups are expressed as $-\log_{10} P$. Red bars represent the regions that survived correcting for region-wise multiple comparisons (false discovery rate-corrected $P < 0.05$), and blue dotted lines represent uncorrected $P = 0.05$. (B) Surface-based comparisons between the ApoE ϵ 4⁻ and ϵ 4⁺ groups. Regions surrounded by white lines (ϵ 4⁻< ϵ 4⁺ in A β and tau accumulation rates in all individuals, and ϵ 4⁻< ϵ 4⁺ in tau accumulation rate in A β ⁺ individuals) represent the cortical

areas that survived correcting for multiple comparisons (false discovery rate-corrected $P < 0.05$). P-values for the comparison between the $\epsilon 4^-$ and $\epsilon 4^+$ groups are expressed as $-\log_{10}P$. P-values for the comparison between the baseline and follow-up are expressed as $-\log_{10}P$. Abbreviations: $A\beta_{+/-}$ = $A\beta$ -positivity, ApoE = apolipoprotein-E, SUVR = standardized uptake value ratio, A = 18F-florbetaben, T = 18F-flortaucipir

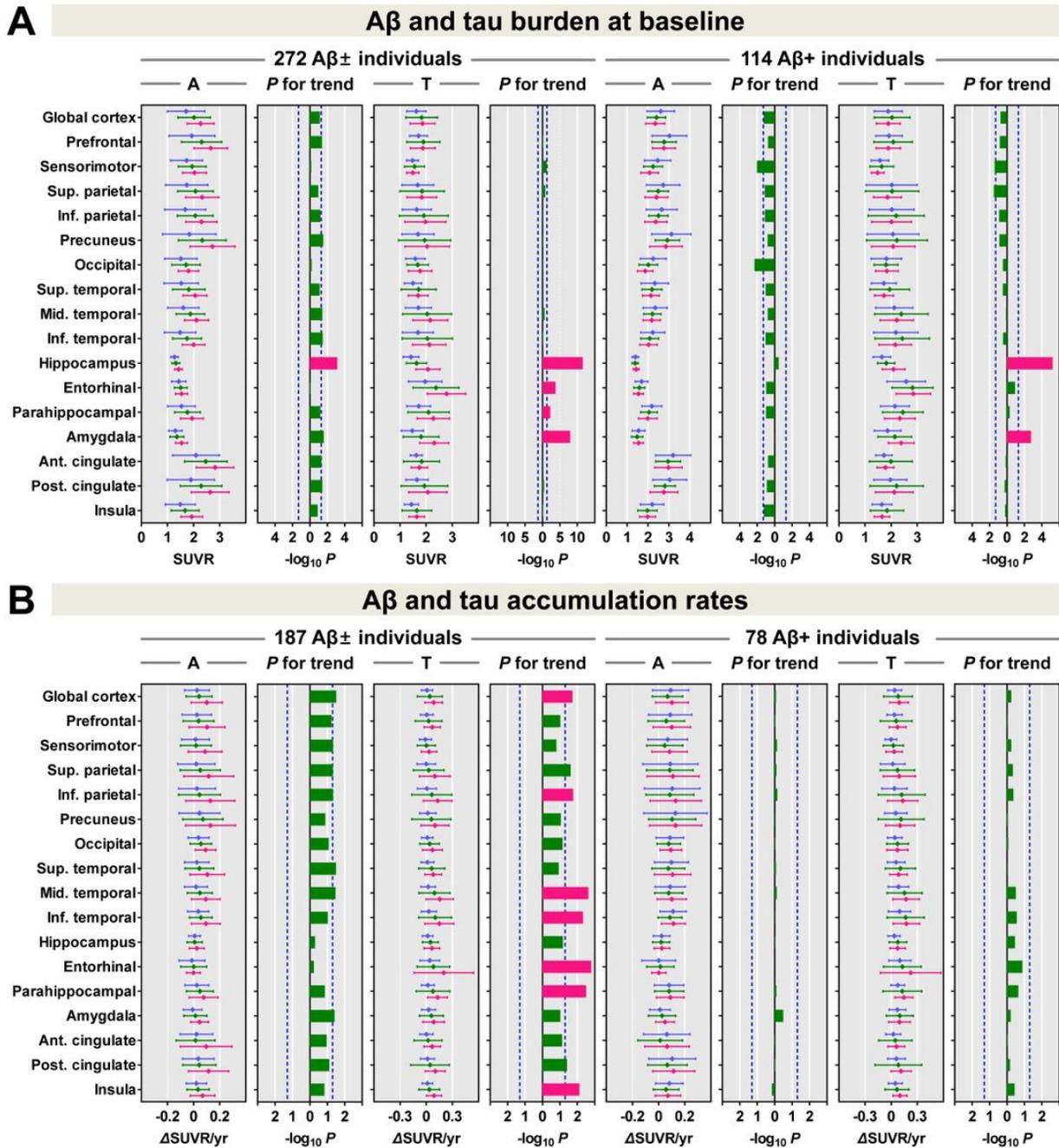


Figure 4

P for trend analysis of baseline 18F-florbetaben and 18F-flortaucipir SUVR and their longitudinal accumulation rates across the ApoE $\epsilon 4^-$, heterozygous, and homozygous groups. Data are presented as means and standard deviations (error bars) of $\epsilon 4^-$ (blue), $\epsilon 4^-$ heterozygous (green), and $\epsilon 4^-$ homozygous (red) groups. Regions that showed significant differences in a dose-dependent manner after adjusting for sex, age, duration of education, and MMSE score (uncorrected P for trend < 0.05) and additionally survived correcting for region-wise multiple comparisons (false discovery rate-corrected $P < 0.05$) are presented as red bars. Blue dotted lines represent uncorrected P for trend = 0.05. Rightward direction of horizontal bars represents an SUVR values increased with higher numbers of $\epsilon 4$ alleles,

while the leftward direction represents a SUVR values decreased with higher numbers of $\epsilon 4$ alleles. Abbreviations: $A\beta+/-$ = $A\beta$ -positivity, ApoE = apolipoprotein-E, SUVR = standardized uptake value ratio, A = 18F-florbetaben, T 18F-flortaucipir.

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