Serum triglycerides in Alzheimer's disease: Relation to neuroimaging and CSF biomarkers

Megan M. Bernath, B.S.[1,2,3,4]*, Sudeepa Bhattacharyya, Ph.D.[5]*, Kwangsik Nho, Ph.D.[1,2]*, Dinesh Kumar Barupal, Ph.D.[6], Oliver Fiehn, Ph.D.[6,7], Rebecca Baillie, Ph.D.[8], SL Risacher, Ph.D. [1,2], Matthias Arnold, Ph.D.[9,12], Tanner Jacobson, B.S.[1,2,3], John Q. Trojanowski, M.D., Ph.D.[10], Leslie M. Shaw, Ph.D.[10], Michael W. Weiner, M.D.[11], Rima Kaddurah-Daouk, Ph.D.[12,13,14]**, Andrew J. Saykin, Psy.D.[1,2,3]**, for the Alzheimer's Disease Neuroimaging Initiative[§] and Alzheimer's Disease Metabolomics Consortium

[1]Center for Neuroimaging, Department of Radiology and Imaging Sciences, Indiana University School of Medicine, Indianapolis, IN

[2]Indiana Alzheimer Disease Center, Indiana University School of Medicine, Indianapolis, IN

[3]Medical and Molecular Genetics Department, Indiana University School of Medicine, Indianapolis, IN

[4]Medical Scientist Training Program, Indiana University School of Medicine, Indianapolis, IN

[5]Department of Pediatrics, University of Arkansas for Medical Sciences, Little Rock, AR, USA

[6]NIH-West Coast Metabolomics Center, University of California, Davis, 451 Health Sciences Drive, Davis, California 95616, United States

[7]Department of Biochemistry, Faculty of Sciences, King Abdulaziz University, Jeddah 21589, Saudi Arabia

[8] Rosa & Co LLC, San Carlos, CA, USA

[9]Institute of Bioinformatics and Systems Biology, Helmholtz Zentrum München, German Research Center for Environmental Health, Neuherberg, Germany

[10]Department of Pathology & Laboratory Medicine, University of Pennsylvania, Philadelphia, PA, USA

[11]Center for Imaging of Neurodegenerative Diseases, Department of Radiology, San Francisco VA Medical Center/University of California San Francisco, San Francisco, CA, USA

[12]Department of Psychiatry and Behavioral Sciences, Duke University, Durham, NC, USA

[13]Duke Institute of Brain Sciences, Duke University, Durham, NC, USA

[14]Department of Medicine, Duke University, Durham, NC, USA

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* Contributed equally to this report

** Corresponding Authors:

Statistical analyses were completed by Bernath, MM, Indiana University School of Medicine, Indianapolis, IN

Andrew J Saykin, PsyD

Department of Radiology and Imaging Sciences, Indiana University School of Medicine, 355 West 16th Street, Suite 4100, Indianapolis, IN USA 46202

Tel: 317-963-7501

Fax: 317-963-7547

Email: asaykin@iupui.edu

Rima Kaddurah-Daouk, Ph.D.

Duke University Medical Center

Durham, NC, USA

Tel: 1-919-684-2611

Email: kaddu001@mc.duke.edu

Author information:

Bernath MM, bernath@iu.edu; Bhattacharyya, S, SBhattacharyya2@uams.edu; Nho K, knho@iupui.edu; Barupal, DK, dinkumar@ucdavis.edu; Fiehn, O, ofiehn@ucdavis.edu; Baillie, R, rbaillie@rosaandco.com; Risacher, SL, srisache@iupui.edu; Arnold, M, matthias.arnold@helmholtz-muenchen.de; Jacobson, T, tanjacob@iupui.edu; Trojanowski, JQ, trojanow@upenn.edu; Shaw, LM, les.shaw@uphs.upenn.edu; Weiner, MW, Michael.Weiner@ucsf.edu; Kadduah-Daouk, R, rima.kaddurahdaouk@duke.edu; Saykin, AJ, asaykin@iupui.edu

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Abstract (216/250 words)

Objective: To investigate the association of serum levels of triglyceride (TG) species with Alzheimer's disease (AD) and the "A/T/N/V" (Amyloid, Tau, Neurodegeneration, and Cerebrovascular disease) biomarkers for AD.

Methods: Serum levels of 84 TG species were measured using untargeted lipid profiling of 714 participants from the Alzheimer's Disease Neuroimaging Initiative (ADNI) cohort including 194 cognitively normal older adults (CN) and 351 mild cognitive impairment (MCI) and 169 AD. Principal component (PC) analysis with factor rotation was used for dimension reduction of TG species. Association of PCs with AD risk and biomarkers was assessed for CSF, MRI and [^{18}F]FDG-PET using Bonferroni-adjusted *p*-values.

Results: The 84 TGs yielded 9 PCs, one of which consisting of long-chain, polyunsaturated fatty acid-containing TGs (PUTGs), was significantly associated with MCI and AD (corrected *p*-value < 0.05). Lower levels of PUTGs were observed in MCI and AD compared to CN. This PC was also significantly associated with hippocampal volume and entorhinal cortical thickness (corrected *p*-value < 0.05). In participants carrying *APOE* ε4 allele, this PC was significantly associated with CSF amyloid-$\beta_{1\text{-}42}$ values and entorhinal cortical thickness (corrected *p*-value < 0.05).

Conclusions: This study shows PUTGs significantly associated with diagnostic group and AD biomarkers, a finding that was more pronounced in *APOE* ε4 carriers. Replications in independent larger studies and longitudinal follow-up are warranted.

Introduction: 250/250

Triglycerides (TGs) may represent a risk factor for Alzheimer's disease (AD), yet this relationship is not well understood. TGs are lipids that are comprised of three fatty acids (FA) linked a glycerol backbone. Blood total TG levels are measured in routine clinical check-ups. Depending on the FAs that contribute to the TG, many combinations of carbon chains and double bonds result, leading to more than 6,000 species encompassed by the term "triglyceride". Conflicting reports exist in the literature regarding TG homeostasis in AD. No relationship between AD and total TGs has been reported,[1] while others suggest that elevated TGs early in life represented a risk factor for increased amyloidosis 20 years later.[2,3] Finally, others found that individuals with probable AD had significantly decreased serum TG levels.[4,5]

Apolipoprotein E (*APOE*) ε4 carrier status may serve as a risk factor for altered TG levels in AD. TGs are transported by lipoproteins, due to their lipophilic nature. APOE regulates TG homeostasis by acting as a ligand for the TG-rich lipoproteins. *APOE* is composed of three allele types: ε2, ε3, and ε4. The *APOE* ε4 allele is a major genetic risk factor for sporadic AD and is associated with a significant decrease in blood TG levels in AD.[5] Here, we examined the association between TGs and AD biomarkers, with and without medication adjustment. We also investigated the effect of *APOE* ε4 by stratifying for *APOE* ε4 carriers and non-carriers. This study shows that serum-based TG species are associated with diagnostic group and AD biomarkers.

Methods

Study sample: All individuals used in this study were participants from the Alzheimer's Disease Neuroimaging Initiative Phase 1 (ADNI-1), which is a longitudinal study aimed to explore clinical, genetic, imaging, and biological biomarkers for early AD progression. ADNI-1 is a

multicenter consortium across 59 sites in the U.S. and Canada, composed of approximately 200 cognitively normal (CN) older adults, 400 adults diagnosed with mild cognitive impairment (MCI) and 200 adults diagnosed with probable Alzheimer's disease (AD), ranging in age from 47 to 91 years old.[6,7] In partnership with ADNI, the Alzheimer's Disease Metabolomics Consortium (ADMC) provided serum metabolic data for this group of participants. Demographic information, *APOE*, clinical information, neuroimaging and CSF biomarker data were downloaded from the ADNI data repository (http://adni.loni.usc.edu).

Lipid analysis: Lipid analyses were performed as previously described.[8] In summary, an untargeted lipidomics dataset was generated by the NIH West Coast Metabolomics Center (http://metabolomics.ucdavis.edu) using an ultra-high performance liquid chromatography-quadrupole time-of-flight (UHPLC-QTOF) mass spectrometer (Agilent, Santa Clara, California) for 807 baseline serum samples from ADNI-1 participants of the ADMC initiative. Lipid species were annotated by matching accurate mass, isotope abundance, retention times and MS/MS fragmentation spectra in LipidBlast[9] in-silico mass spectral library and measured by signal intensities on the precursor mass level. After data processing, the quality of data was assessed and low-quality lipid species were removed. These quality control (QC) analyses resulted 349 annotated lipids, including 84 triglyceride species. The TG values obtained from the QC step were unadjusted and adjusted[10] for the effect of medication use at baseline.

Neuroimaging analysis: MRI scans were processed prior to download as previously described.[11,12] These scans were further processed locally using FreeSurfer version 5.1.[13–15] Regions of interest were extracted, including the bilateral hippocampal volumes, entorhinal cortical thickness, and total intracranial volume (ICV). [^{18}F]fluorodeoxyglucose (FDG) PET scans were pre-processed prior to download.[13,16] Standardized uptake value ratio (SUVR) images

were created by intensity-normalization using a pons reference region. Mean SUVR values were extracted for each participant from an overall cortical ROI representing regions where CN>AD from the full ADNI-1 cohort. White matter hyperintensity volumes (WMHI) were assessed using previously described methods.[17,18]

CSF biomarker analysis: The CSF biomarker data were downloaded from the ADNI data repository. As previously described,[19] CSF measurements for amyloid β 1-42 peptide ($A\beta_{1-42}$), total tau (t-tau), and tau phosphorylated at threonine 181 ($p\text{-}tau_{181P}$) were obtained by the validated and highly automated Roche Elecsys electrochemiluminescence immunoassays.

Cognitive Assessment: We used the modified Alzheimer's Disease Assessment Scale-cognition sub-scale (ADAS-Cog 13)[20] and composite scores for executive functioning (ADNI-EF) and memory (ADNI-MEM) as indices of general cognitive performance.[21,22]

A/T/N/V biomarkers: We used CSF $A\beta_{1-42}$ levels as a biomarker of amyloid-β ("A"), CSF p-tau levels as a biomarker of tau ("T"), structural atrophy on MRI, FDG PET metabolism, and CSF t-tau levels as biomarkers of neurodegeneration ("N"), and white matter hyperintensity volume as a biomarker for microvascular disease burden ("V"), as described in the National Institute of Aging- Alzheimer's Association (NIA-AA) Research Framework.[23]

Medication adjustment: Triglyceride data was corrected for 41 major medication classes used to treat psychiatric (including different categories of benzodiazepines, antipsychotics, and antidepressants) and cardiovascular conditions (including different categories of antihypertensives, cholesterol treatment, and antidiabetics), as well as dietary supplements (Co-Q10, fish oil, nicotinic acid, and acetyl L-carnitine). For complete medication list and procedures, please see previously reported methods.[10]

Statistical analysis: Dimension reduction was performed on the original 84 triglycerides using Principal Component Analysis (PCA) as implemented in SPSS (v 24). Initial principal component (PC) extraction was followed by orthogonal rotation to yield PC-based factor scores. Number of PCs extracted was pre-specified using the standard eigenvalues greater than 1 criterion. "Top contributors" of each rotated PC were defined as those with a factor loading $\geq$ 0.8. All other contributors for each rotated PC (with a factor loading < 0.8) were excluded from further consideration. Potential covariates of interest were screened for possible inclusion in analyses of the PCA results including age, sex, body mass index (BMI), total triglycerides, and *APOE* ε4 status using linear regression. Covariates assessed for the diagnosis and AD-related biomarkers included age, sex, BMI, total triglycerides, and *APOE* ε4 status. Years of education for cognitive performance, and years of education and intracranial volume (ICV) for MRI biomarkers were added as additional covariates. We did not use total serum cholesterol levels as a covariate because total serum cholesterol levels had no effect on all 6 PCs. Significant associations were defined as $p<0.05$ after Bonferroni adjustment to correct for multiple testing.

Whole brain surface-based analysis: As previously described, we performed a multivariate analysis of cortical thickness over the whole brain using SurfStat software (http://www.math.mcgill.ca/keith/surfstat/). We constructed a general linear model (GLM) using age, sex, *APOE* ε4 status, BMI, total triglycerides, years of education, and ICV as covariates. We corrected for multiple comparisons using the random field theory (RFT) correction method at $p < 0.05$ significance level. [24]

Data Availability Statement: All data used in the analyses reported here are available in the ADNI data repository (http://adni.loni.usc.edu).

Standard Protocol Approvals, Registrations, and Patient Consents: Written informed consent was obtained at the time of enrollment for imaging and genetic sample collection and protocols of consent forms were approved by each participating sites' Institutional Review Board (IRB).

Results

In the analysis, we included 714 ADNI participants who had baseline data for the 84 TGs (194 cognitively normal older adults (CN), 351 mild cognitive impairment (MCI) and 169 AD) after quality control procedures including removing participants with non-fasting status (n=69). Demographic information is shown in **Table 1**.

Principal component analysis (PCA) for dimension reduction of TGs: Dimension reduction with PCA resulted in 9 PCs with eigenvalues >1 (**Table e-1**). After selecting for the "top contributors" with a factor loading $\geq$ 0.8 in each component, 6 of 9 components remained for further analysis (**Table e-2**).

Association of TG PCs with diagnosis: Figure 1 shows significant associations between diagnostic groups (CN, MCI, AD) for principal component 3 ("PC3") and "PC5" after adjusting for multiple testing. We identified significant associations in "PC5" between CN and AD (corrected *p*-value= 4.32E-04) and between CN and MCI (corrected *p*-value= 1.84E-03; **Figure 1**). There was not a significant association between MCI and AD. "PC5" consists of six long-chain, polyunsaturated TGs (PUTGs), with all species containing 8 or more double bonds. Lower levels of PUTGs belonging to "PC5" are seen in MCI and AD compared to CN. In addition, among the six PUTGs, four (TG 60:11, TG 58:9, TG 58:8, and TG 56:8) were significantly associated with diagnosis (corrected *p*-value < 0.05) (**Figure e-1**). We also identified "PC3" as marginally associated with AD (corrected *p*-value=0.054; **Figure 1**). "PC3" consisted of seven

PUTGs, with almost all species containing 2 or more double bonds. Similar to "PC5", AD patients compared to CN showed lower levels of TGs belonging to "PC3."

Association of TG PCs with AD biomarkers: The principal components significantly or marginally associated with diagnosis ("PC3" and "PC5") were further investigated to assess their associations with A/T/N/V biomarkers for AD. **Figure 2** shows associations of "PC3" and "PC5" with AD biomarkers. From our linear regression analysis, we found a significant association between "PC5" and hippocampal volume ("N") after adjusting for multiple testing (corrected *p*-value =0.0243, β=0.106; **Figure 2**). Lower levels of "PC5" were associated with greater brain atrophy. As "PC5" is associated with hippocampal volume, we investigated the association of "PC5" with cognitive performance using ADAS-Cog13 scores, ADNI-MEM, and ADNI-EF. The analysis revealed associations between ADAS-Cog13 (*p*-value =0.012, β= -0.093), ADNI-MEM (*p*-value =0.035, β= 0.078), and ADNI-EF (*p*-value =0.028, β= 0.082) with "PC5." We also found marginal associations between "PC5" with entorhinal cortical thickness ("N") (*p*-value=0.015, β=0.0919) and CSF $A\beta_{1\text{-}42}$ level ("A") (*p*-value=0.047, β=0.0977). In addition, we found a significant association between "PC3" and entorhinal cortical thickness ("N") (corrected *p*-value=3.61E-03, β=0.147; **Figure 2**) and a marginal association between "PC3" with hippocampal volume (*p*-value =0.0383; β=0.0751). We then performed a detailed whole-brain surface-based analysis of cortical thickness on the brain surface to investigate the effects of "PC3" and "PC5" on structural atrophy in an unbiased way. Lower levels of "PC3" were significantly associated with reduced cortical thickness in bilateral frontal and parietal lobes and right temporal lobe including the entorhinal cortex (corrected *p*-value < 0.05; **Figure 3(A)**). Also, lower levels of "PC5" were significantly associated with reduced cortical thickness in right temporal lobe including the entorhinal cortex (corrected *p*-value < 0.05; **Figure 3(B)**).

Effect of *APOE* ε4 on TGs: In order to investigate the effect of *APOE* ε4 on TGs, we first investigated the presence of an interaction between *APOE* ε4 status and PCs with diagnosis and A/T/N/V biomarkers for AD. We did not find evidence of significant interactions for any PCs after correcting for multiple comparisons. We then performed an association analysis of PCs with diagnosis and A/T/N/V biomarkers for AD after stratifying on *APOE* ε4 carrier status. In the both *APOE* ε4 carrier group and *APOE* ε4 non-carrier group, we did not find any significant associations of PCs with diagnosis (**Figure e-2**). However, in the *APOE* ε4 carrier group, "PC5" was significantly associated with CSF $A\beta_{1-42}$ levels (corrected *p*-value= 0.0360, β=0.239; **Figure 4**) and marginally associated with entorhinal cortical thickness (corrected *p*-value=0.054, β=0.161; **Figure 4**). "PC3" was also significantly associated with entorhinal cortical thickness (corrected *p*-value= 9.62E-04, β=0.245) (**Figure 4**). In the *APOE* ε4 non-carrier group, we did not identify any significant associations of PCs with A/T/N/V biomarkers for AD.

Effect of medication use on TGs: Using TG values adjusted for the effect of medication use at baseline as a potential confounder, we repeated all analyses. All key findings remained significant after adjustment for medication use (see **Figures e-3 and e-4**).

Discussion

In this study, we found that long-chain, polyunsaturated FA-containing triglycerides (PUTGs) were significantly associated with diagnosis and AD biomarkers, including hippocampal volume and entorhinal cortical thickness measured from MRI scans. In addition, we observed a significant *APOE* ε4 effect on TGs. In *APOE* ε4 carriers, we found significant, positive correlations between serum levels of PUTGs and entorhinal cortical thickness and CSF $A\beta_{1-42}$ levels, but no significant associations in *APOE ε4* non-carriers. These results suggest that the observed PUTGs are associated with early-disease changes in AD.

The association of PUTGs with atrophy in the entorhinal cortex and hippocampus is noteworthy as these regions are affected in early stages of AD pathophysiology. Aβ accumulation is an important early change in AD and is associated with *APOE* ε4 carrier status. Triglycerides (TGs) have been shown to be particularly associated with Aβ. For example, mouse studies showed that serum TG levels were elevated prior to amyloid deposition,[25] while human studies showed increased serum TGs were associated with increased amyloidosis in cognitively normal individuals.[3] Longitudinal studies showed that increased midlife TGs predicted amyloidosis and tau pathology 20 years later,[2] providing additional evidence for the early influence of TGs in AD. Thus, it is particularly interesting that we found a selective association of PUTGs with CSF Aβ only in *APOE* ε4 carriers. The specific mechanistic role underlying the association of decreased PUTGs and early processes involved in AD pathogenesis remains to be determined, but our results suggest a relationship between a decrease in serum levels of PUTGs and early-stage biomarkers in AD. Results remained significant after adjusting for medication use. Thus, exposure to medication by AD and some MCI patients does not appear to account for these results, although some roles cannot be entirely ruled out.

The relationship between TGs and amyloid-β may be explained through role of TGs in the lipoprotein peripheral transport of Aβ. Apolipoprotein E (ApoE) is a plasma protein that is involved in lipid transport and metabolism in lipoproteins, including TG-rich lipoproteins.[26] Studies suggest that TG-rich lipoproteins may participate in peripheral Aβ transport and delivery, as evidenced by a study that showed Aβ accumulated in TG-rich lipoproteins.[27] As discussed above, ApoE exists in three major isoforms, ApoE ε4, ApoE ε3, and ApoE ε2. ApoE ε4 has been shown unable to complex with Aβ and, peripherally, to associate with triglyceride-rich, very low-density lipoproteins (VLDLs) in contrast to high-density lipoproteins.[28,29] These studies

suggest an important relationship between Aβ and peripheral TG lipoprotein carriers that may provide further insight into aberrant serum PUTG levels in AD.

Omega-3 polyunsaturated fatty acids such as docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA), have anti-inflammatory and neuroprotective roles, as evidenced by their associations with cognitive improvement in the elderly.[30] In blood, polyunsaturated fatty acids travel in different states: esterified, bound to complex lipids (such as TGs) or lipoproteins, or free-floating. Triglycerides are created by incorporating three fatty acids onto a carbon backbone, which can then serve to transport and store fatty acids. A previous study, using the same TG dataset, identified EPA and DHA as the primary polyunsaturated fatty acids contributing to PUTG fatty acids of "PC5" (Barupal DK, et al., "in press"). Recently published studies have shown that serum DHA and EPA levels were decreased in AD,[31] and that polyunsaturated fatty acid intake acted to reduced risk for AD.[32] We found that lower levels of PUTGs were associated with poorer cognitive performance. Due to the importance of these polyunsaturated fatty acids in cognition and neuroinflammation, we believe our findings need further study to determine the overlapping mechanism that may underlie PUTG and polyunsaturated fatty acid aberrations.

PUTGs and, by extension, polyunsaturated fatty acids represent links in the gut-liver-brain axis. Triglycerides are synthesized in the liver or absorbed from the gut and have recently been found to cross the blood-brain barrier and accumulate in the brain.[33] PUFAs are rapidly and preferentially incorporated into TGs following postprandial ingestion, suggesting an important role for TGs in PUFA supplementation.[34] The gut-liver-brain communicate through neuronal, neuroimmune, and neuroendocrine pathways. These pathways overlap polyunsaturated fatty acids and AD and may serve an interesting direction to study PUTGs.

A Lipid Hypothesis has been proposed, suggesting that lipid oxidation is the initiating factor for late-onset AD.[35] Lipid oxidation is a key early event in AD that precedes amyloid and neurofibrillary tangle deposition. When lipids are exposed to free radicals, they progress through autoperoxidation, where reactive oxidative species are released. Previous studies have shown that Aβ aggregation occurred more readily in membranes composed of oxidized lipids,[36] and that polyunsaturated lipids were most vulnerable to oxidative stress.[37] Early-stage AD is characterized by an accumulation of Aβ, potentially resulting from impaired clearance of pathogenic species by microglia. Early microglial activity is neuroprotective, but progressive cytokine production from microglia, due to aging and disease progression, can reduce Aβ clearance and promote its accumulation. Peripheral inflammatory cytokines have been shown to interact with or pass through endothelial cells on the blood-brain barrier to activate microglia. It is well established that polyunsaturated fatty acid intake is associated with an anti-inflammatory effect. Polyunsaturated fatty acids have been directly linked to the regulation of cytokines by decreasing the expression of proinflammatory pathways.[38] Moreover, polyunsaturated fatty acid intake has been shown to decrease microglial inflammatory activation of Aβ, supporting a neuroprotective role.[39] Decreases in PUTGs could presumably result in decreased availability for polyunsaturated fatty acids and loss of neuroprotective metabolites, thereby suggesting the need for further study into this relationship.

Neural connections between the brain and the gut exist through the vagus nerve and enteric system. The vagus nerve originates in the brain stem and complexes onto the enteric plexus in the gut. These neural connections are important for gastric motility and have been implicated in relaying inflammatory, microbial and nutrient information from the gut to the brain.[40] Interestingly, dietary fat has shown to activate the vagus nerve and neuroimmunologic

pathways.[41] Recent work in Parkinson's disease found that severance of the vagal trunk was protective against PD, suggesting that central nervous system (CNS) invasion may occur from the gut, through the vagus nerve.[42] This study provides an interesting avenue of study for AD due to many links between PD and AD.

The gastrointestinal tract is home to more than 10 times the number of bacteria than cells in the human body, functioning in a mutualistic relationship with their human host.[43] Gut microbiota are known to function in immune responses, nutrient absorption, and regulate gut motility. [44,45] When gut microbiota is no longer homeostatic (gut dysbiosis), the CNS receives signals to activate inflammatory processes. Alterations in gut microbiota have been linked to neurological conditions, including AD,[46] where gut dysbiosis was associated with memory dysfunction and decreased hippocampal neurogenesis.[47] Polyunsaturated fatty acid intake has been associated with changes in gut microbiota and intestinal excretion of mucosal defense factors that exhibit anti-inflammatory effects.[48] The data suggests an interesting relationship between polyunsaturated fatty acids, gut microbiota and AD and an interesting direction to study PUTGs. We did not see a significant association between saturated TGs and AD, although we did find a significant difference in PUTGs between diagnostic groups. A recent meta-analysis revealed that, over time, saturated fat intake was associated with an increase in AD risk.[49] It is possible that blood TG levels do not accurately represent long-term saturated TG intake and, rather, BMI may better represent the effects of highly saturated diets over time.[50] Further studies are required to investigate these findings.

There are some limitations to our study. This is a cross-sectional study investigating early changes in AD. Longitudinal and model system studies are required to determine the role and mechanisms of specific classes of TGs in AD initiation and progression. Mechanistic

investigations into the cause of decreased PUTGs using mouse models of AD may provide insight relevant to early detection and treatment for AD. Replication in independent samples and longitudinal follow-up of the present cohort will also be important.

In summary, our study investigated the relationship between TG species, AD risk and biomarkers for AD. To our knowledge, this is the first study to show decreased levels of highly unsaturated, long-chain triglycerides in MCI and AD compared to cognitively normal older adults, an association between PUTGs and extent of brain atrophy and amyloid-β deposition, and the effect of *APOE* ε4 carrier status on PUTGs in AD. Moreover, our results provide a potential mechanism to study the relationship of PUFA supplements with memory in AD. Overall, our findings suggest that PUTGs may have potential as an early detection biomarker and a target for therapeutic development.

Appendix: authors

Name	Location	Role	Contribution
Megan Bernath, BS	Indiana University, Indianapolis	Author	Study design, statistical analysis, drafted and revised manuscript
Sudeepa Bhattacharyya, PhD	University of Arkansas for Medical Sciences	Author	Initial analysis of data and edited manuscript
Kwangsik Nho, PhD	Indiana University, Indianapolis	Author	Design and conceptualization of study, edited manuscript
Shannon L Risacher, PhD	Indiana University, Indianapolis	Author	MRI and PET image processing
Dinesh Kumar Barupal, PhD	Genome Center, University of California, Davis, California	Author	Contributed lipidomics data and edited manuscript.
Oliver Fiehn, PhD	Genome Center, University of California, Davis, California	Author	Contributed lipidomics data and edited manuscript.
Rebecca Baillie, PhD	Rosa & Co LLC, San Carlos, CA	Author	Interpretation of data and edited manuscript
Matthias Arnold, PhD	Helmholtz Zentrum munchen, Neuherberg, Germany	Author	Contributed to quality control of data set

Tanner Jacobson, BS	Indiana University, Indianapolis	Author	Contribution to data analysis and interpretation
John Q. Trojanowski, MD, PhD	University of Pennsylvania, Philadelphia	Author	Biomarker core coleader, provided samples and data interpretation
Leslie M. Shaw, PhD	University of Pennsylvania, Philadelphia	Author	Biomarker core coleader, provided samples and data interpretation
Michael W. Weiner, MD	University of California, San Francisco and San Francisco VAMC	Author	PI of ADNI, study design, data interpretation
Rima Kaddurah Daouk, PhD	Duke University Medical Center	Author	PI of ADMC the consortium that conceptualized design, secured funding and executed study
Andrew J. Saykin, PsyD	Indiana University, Indianapolis	Author	Design and conceptualization of study, statistical analysis and interpretation, edited manuscript

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Table 1. Demographics of ADNI participants included in the analysis by diagnosis.

	N	CN (N=194)	N	MCI (N=351)	N	AD (N=169)
Age	194	75.26 (4.96)	351	74.34 (7.48)	169	74.62 (7.30)
Sex (Male/Female)	194	97/97	351	227/124	169	86/83
Education	194	15.94 (2.66)	351	15.65 (3.01)	169	14.56 (3.07)
APOE ε4 status (presence/absence)	194	53/141	351	185/166	169	112/57
BMI	193	26.71 (4.53)	351	26.13 (4.01)	169	25.54 (3.96)
Total triglycerides	191	140.26 (79.56)	339	154.41 (142.53)	160	156.83 (99.09)
CSF $A\beta_{1-42}$	91	1257.01 (640.59)	172	858.92 (499.29)	88	665.53 (389.28)
CSF t-tau	88	2.36 (0.15)	172	2.46 (0.17)	87	2.52 (0.17)
CSF p-tau_{181P}	88	1.33 (0.16)	172	1.44 (0.20)	87	1.52 (0.19)

Data are reported as mean (standard deviation) unless otherwise indicated.

Abbreviations: CN: cognitively normal older adult controls; MCI: mild cognitive impairment; AD: Alzheimer's disease; BMI: body mass index; CSF: cerebrospinal fluid;

Figure 1: Association of principal components of triglycerides with CN, MCI, and AD

(*<0.05, ** <0.0056, ***<0.001)

ANCOVA performed for PCs with diagnosis; mean +/- standard error. *Abbreviations*: PC: principal component; CN: cognitively normal older adult controls; MCI: mild cognitive impairment; AD: Alzheimer's disease.

Figure 2: Association of two principal components (PC3 and PC5) with A/T/N/V biomarkers for AD

(*<0.05, ** <0.0035, ***<0.001)

Linear regression performed for "PC3" and "PC5" with AD endophenotypes. *Abbreviations*: PC: principal component; CSF: cerebrospinal fluid; CSF Aβ: CSF amyloid β 1-42 peptide ($A\beta_{1-42}$); CSF p.tau: CSF tau phosphorylated at threonine 181 (CSF $p\text{-}tau_{181P}$); CSF t.tau: CSF total tau (CSF t-tau); WMHI: white matter hyperintensity total volume, FDG Global cortex: cortical glucose SUVR measured from [^{18}F]FDG PET scans; Hippocampal.volume: hippocampal volume; Entorhinal.thickness: entorhinal cortical thickness, "A"= $A\beta_{1-42}$ levels as a biomarker of amyloid-β, "T"= CSF p-tau levels as a biomarker of tau, "N"= structural atrophy on MRI, FDG PET metabolism, and CSF t-tau levels as biomarkers of neurodegeneration, and "V"= white matter hyperintensity volume as a biomarker for microvascular disease burden.

Figure 3: Whole-brain surface-based analysis of cortical thickness for two principal components ("PC3" and "PC5").

A whole-brain multivariate analysis of cortical thickness across the brain surface was performed to identify the association of two PCs ((a) "PC3" and (b) "PC5") with brain structure shown as a T-value map and a corrected P-value map. Statistical maps were thresholded using a random field theory for a multiple testing adjustment to a corrected significance level of 0.05. Positive t

values (red, yellow) indicate thicker cortical thickness. The *p*-value for clusters indicates significant corrected *p* values with the lightest blue color.

Figure 4: Association of two principal components (PC3 and PC5) with A/T/N/V biomarkers for AD in the *APOE* ε4 carrier group

(*<0.05, ** <0.0035, ***<0.001)

Linear regression performed for "PC3" and "PC5" with AD endophenotypes in *APOE* ε4 carrier stratified groups. *Abbreviations*: PC: principal component; CSF: cerebrospinal fluid; CSF Aβ: CSF amyloid β 1-42 peptide ($A\beta_{1-42}$); CSF p.tau: CSF tau phosphorylated at threonine 181 (CSF $p\text{-}tau_{181P}$); CSF t.tau:CSF total tau (CSF t-tau); WMHI: white matter hyperintensity volume, FDG Global cortex: : cortical glucose SUVR measured from [^{18}F]FDG PET scans; Hippocampal.volume: hippocampal volume; Entorhinal.thickness: entorhinal cortical thickness, "A"= $A\beta_{1-42}$ levels as a biomarker of amyloid-β, "T"= CSF p-tau levels as a biomarker of tau, "N"= structural atrophy on MRI, FDG PET metabolism, and CSF t-tau levels as biomarkers of neurodegeneration, and "V"= white matter hyperintensity volume as a biomarker for microvascular disease burden.

Figure 1: Association of principal components of triglycerides with CN, MCI, and AD

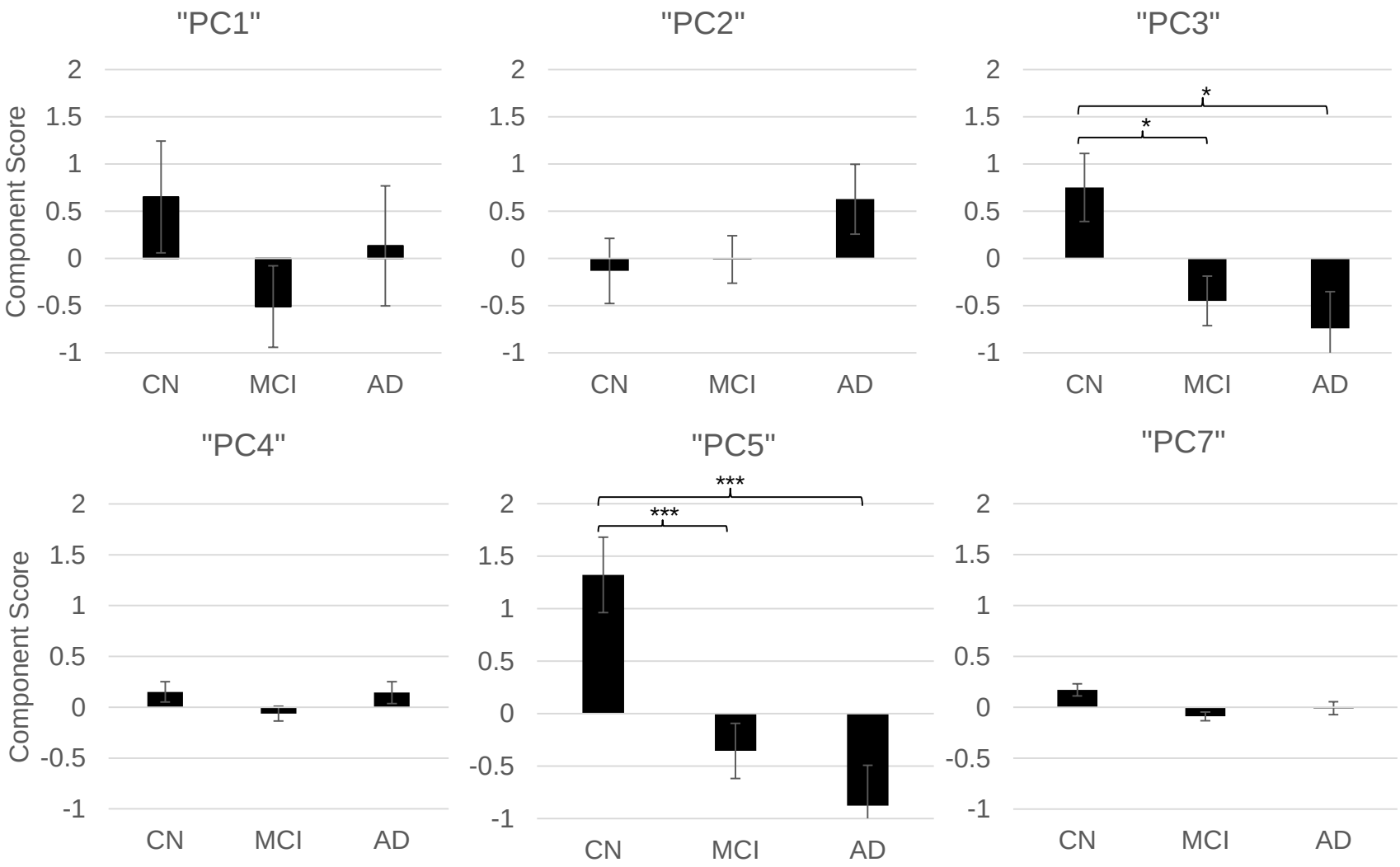

Figure 2: Association of two principal components (PC3 and PC5) with A/T/N/V biomarkers for AD

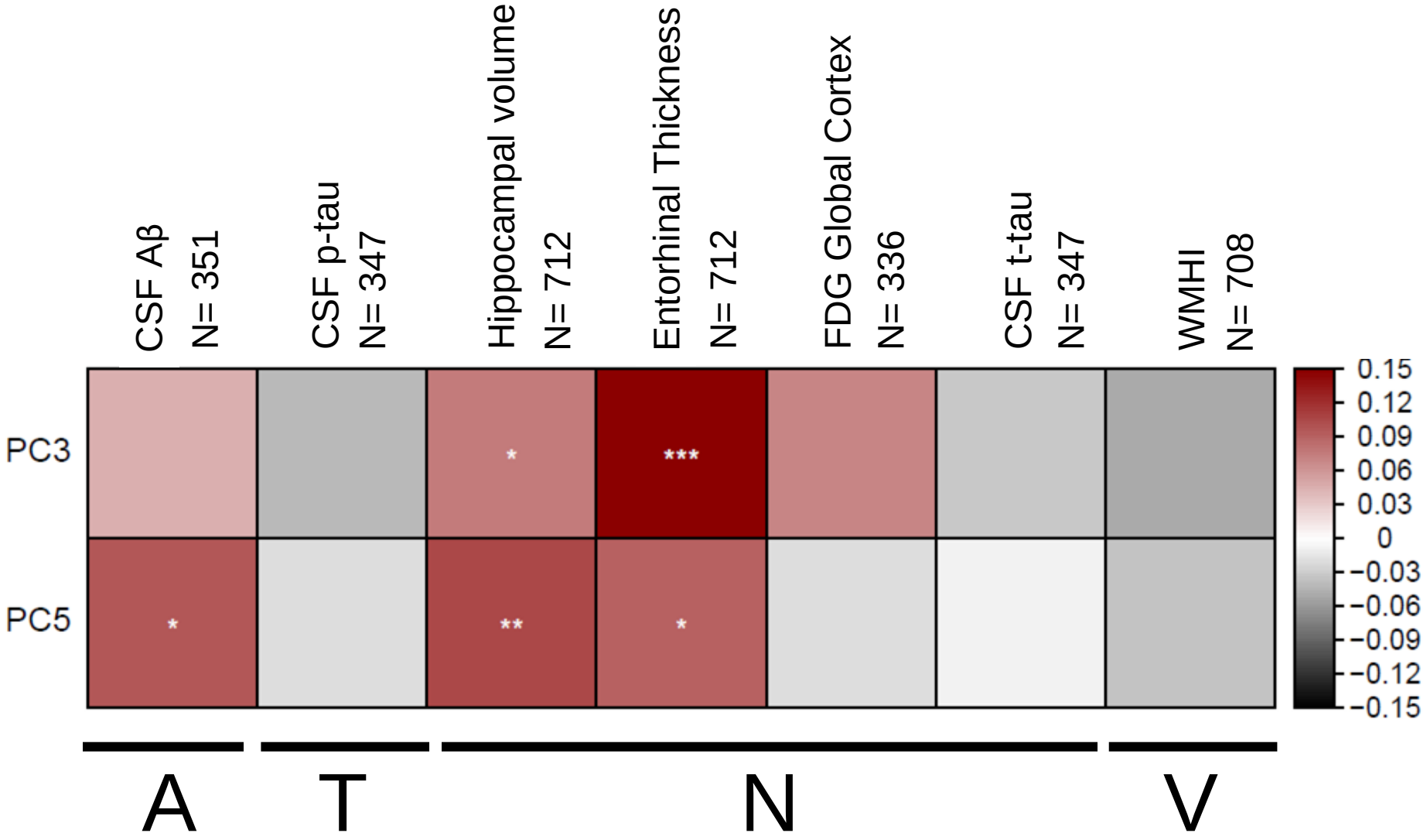

Figure 3

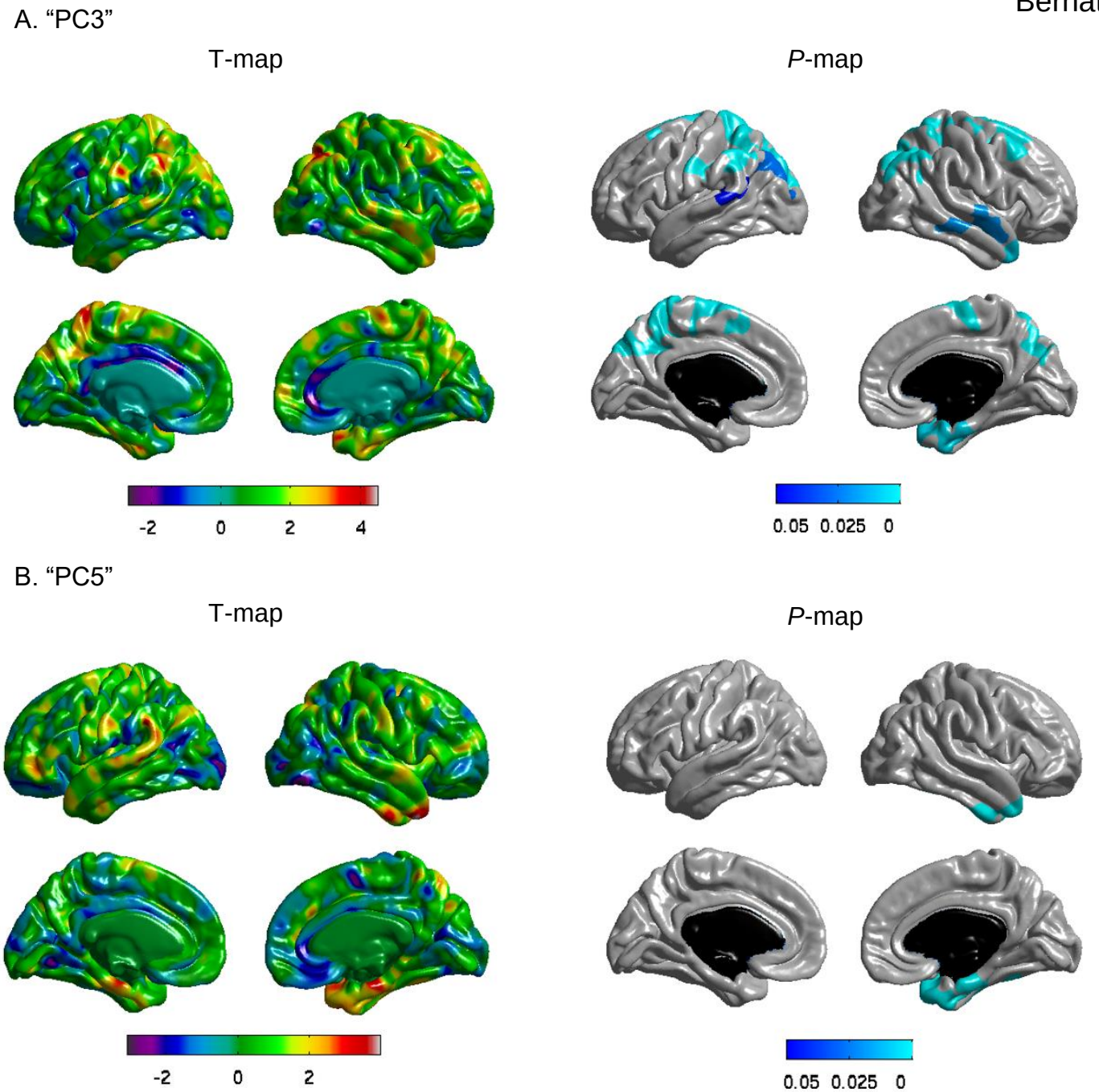
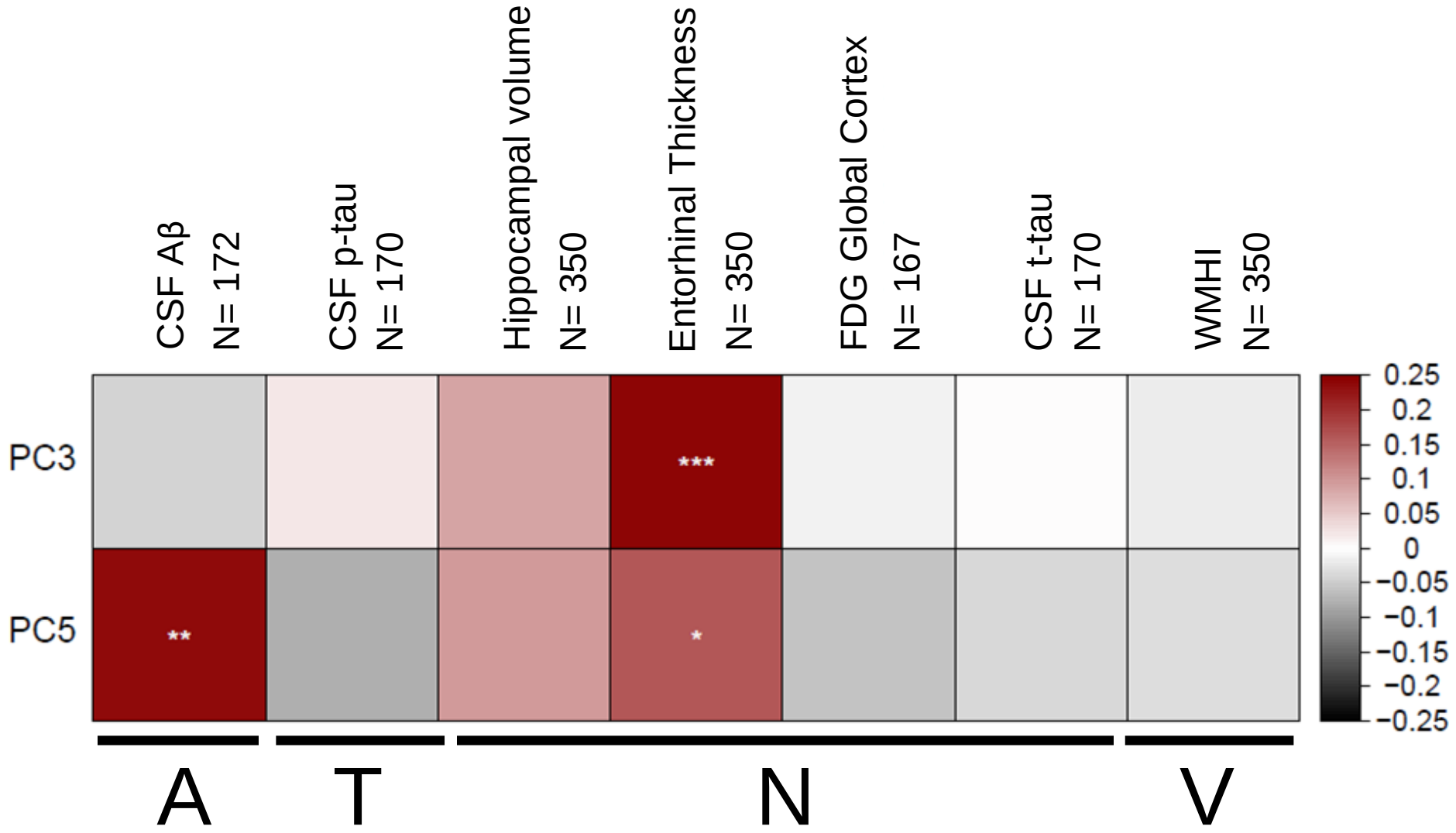
Figure 4: Association of two principal components (PC3 and PC5) with A/T/N/V biomarkers for AD in the *APOE* ε4 carrier group