Role of Family History for Alzheimer Biomarker Abnormalities in the Adult Children Study

Chengjie Xiong, PhD; Catherine M. Roe, PhD; Virginia Buckles, PhD; Anne Fagan, PhD; David Holtzman, MD; David Balota, PhD; Janet Duichuk, PhD; Martha Storandt, PhD; Mark Mintun, MD; Elizabeth Grant, PhD; Abraham Z. Snyder, PhD, MD; Denise Head, PhD; Tammie L. S. Benzinger, MD, PhD; Joseph Mettenburg, MD, PhD; John Csernansky, MD; John C. Morris, MD

Objective: To assess whether family history (FH) of Alzheimer disease (AD) alone influences AD biomarker abnormalities.

Design: Adult Children Study.

Setting: Washington University’s Charles F. and Joanne Knight Alzheimer’s Disease Research Center.

Participants: A total of 269 cognitively normal middle- to older-aged individuals with and without an FH for AD.

Main Outcome Measures: Clinical and cognitive measures, magnetic resonance imaging–based brain volumes, diffusion tensor imaging–based white matter microstructure, cerebrospinal fluid biomarkers, and molecular imaging of cerebral fibrillar amyloid with positron emission tomography using the \([11C]\) benzothiazole tracer, Pittsburgh compound B.

Results: A positive FH for AD was associated with an age-related decrease of cerebrospinal fluid Aβ42; the ε4 allele of apolipoprotein E (APOE4) did not alter this effect. Age-adjusted cerebrospinal fluid Aβ42 was decreased for individuals with APOE4 compared with the level for those without, and the decrease was larger for individuals with a positive FH compared with the decrease for those without. The variation of cerebrospinal fluid tau and Pittsburgh compound B mean cortical binding potential increased by age. For individuals younger than 55, an age-related increase in mean cortical binding potential was associated with APOE4 but not FH. For individuals older than 55, a positive FH and a positive APOE4 implied the fastest age-related increase in mean cortical binding potential. A positive FH was associated with decreased fractional anisotropy from diffusion tensor imaging in the genu and splenium of the corpus callosum.

Conclusion: Independent of APOE4, FH is associated with age-related change of several cerebrospinal fluid, Pittsburgh compound B, and diffusion tensor imaging biomarkers in cognitively normal middle- to older-aged individuals, suggesting that non-APOE susceptibility genes for AD influence AD biomarkers.

Arch Neurol. 2011;68(10):1313-1319

Recent advances suggest that Alzheimer disease (AD) has a lengthy period in which cerebral lesions gradually accumulate in the absence of symptoms, eventually causing sufficient synaptic and neuronal damage to result in symptomatic AD.\(^1\) Since 2005, Antecedent Biomarkers for AD: The Adult Children Study (ACS) has enrolled a cohort of cognitively normal 43- to 76-year-old individuals in an extensive study of biomarkers for AD before its symptomatic stages. In addition to clinical and cognitive measures, a broad spectrum of candidate antecedent biomarkers for AD were assessed, including magnetic resonance imaging (MRI)–based brain volumes, diffusion tensor imaging–based measures of white matter microstructure, cerebrospinal fluid (CSF), and molecular imaging of cerebral fibrillar amyloid with positron emission tomography (PET) using the \([11C]\) benzothiazole tracer, Pittsburgh compound B (PIB). Because the ACS cohort is cognitively normal, changes in these well-established biomarkers for AD likely reflect the insidious pathogenesis of AD well before the development of symptoms, i.e., during the preclinical stage of AD.

The ACS cohort is stratified by family history (FH) for AD to genetically enrich the participants at risk of AD. Therefore, analysis on FH and biomarkers allows a linkage of biomarker abnormality to susceptibility genes for AD, especially non–apolipoprotein E (APOE) genes (i.e., PICALM, CR1, and CLU discovered from recent genome-wide association studies\(^6\)\(^7\) if the effect of FH is independent of APOE. Whereas several studies reported changes in isolated biomarkers with rela-
tively small samples of elderly normal individuals with an FH of AD8–10 or the ε4 allele of APOE (APOE4) (OMIM +107741),11 the ACS facilitates a comprehensive analysis of both FH and APOE for a wide array of candidate antecedent biomarkers in cognitively normal individuals of middle to older age (43–76 years).

The objective of this study was to assess whether FH alone conveys AD risk beyond that of APOE4 by examining the influence of FH for AD, both together and independent of APOE4, on biomarker abnormalities using the baseline data of the ACS.

METHODS

PARTICIPANTS

As of October 2009, the ACS cohort included 269 community-living volunteers from the greater St Louis metropolitan area. Recruitment primarily was through word of mouth and personal inquiries. A positive FH for AD was defined as at least 1 biological parent with age at onset for dementia of the Alzheimer type (DAT) of less than 80 years, and a negative FH was defined as both biological parents living to age 70 or longer without DAT. If a parent living to age 70 without DAT later developed DAT by age 80, the participant was reassigned to the positive FH group. About one-third of the participants were children of parents enrolled in longitudinal studies of the Washington University Alzheimer’s Disease Research Center. Eligibility criteria for the ACS were age 45 to 75 (2 early enrollees were age 43 and 76 years), availability of an informant who knew the participant well, normal cognition (defined as Clinical Dementia Rating12 of 0), and willingness in principle to complete all procedures. Comorbid conditions, including depressive features short of major affective disorder, were acceptable if the patient was clinically stable at time of enrollment. Exclusion criteria included conditions such as end-stage cancer or end-stage renal disease that would preclude longitudinal participation and/or confound cognitive assessment. Another exclusion criterion was membership in families with a dominantly inherited pattern of AD and/or a known causative mutation for AD. The Washington University Human Research Protection Office approved the study.

CLINICAL AND COGNITIVE ASSESSMENTS

The primary clinical assessment protocol was that of the National Alzheimer Coordinating Center Uniform Data Set.13 Additional clinical information, such as an assessment of autobiographical memory using events in which the participant recently engaged,14 was obtained. The standard definitions and criteria14 of the Uniform Data Set for detection of dementia and its differential diagnosis were used.14 The presence or absence of dementia and, when present, its severity were operationalized with the Clinical Dementia Rating.12 The Clinical Dementia Rating is based on the judgment of an experienced physician, with informant information and examination of the participant, as to whether the individual performs accustomed activities at his or her previously attained level17 and was completed independently of neuropsychological test results. The Clinical Dementia Rating is highly reliable18–20 and sensitive and accurate for even very mild cognitive decline caused by AD.17,21,22 The clinical assessment takes 90 minutes to complete.

Participants completed psychometric testing 1 to 2 weeks after they received the clinical assessment. The 5 cognitive domains assessed in the 2-hour battery were episodic memory (Wechsler Memory Scale–III Logical Memory I and II, Verbal Paired Associates I,23 and Free and Cued Selective Reminding24), working memory (Wechsler Memory Scale–III Letter-Number Sequencing, Auditory Consonant Trigrams,25 and Reading Span26), semantic knowledge (Wechsler Adult Intelligence Scale–III Similarities and Information27 and Animal Naming28), executive function and attention (Trailmaking Test A and B,29 Simon Task,30 and Switching Task31), and visuospatial ability (Wechsler Adult Intelligence Scale–III Block Design,32 Benton Line Orientation,33 and Woodcock-Johnson Visual Spatial Relations34). The clinical and cognitive assessments are obtained at baseline and every 3 years thereafter except for participants aged 65 years or older, for whom they are obtained annually.

CSF COLLECTION AND ANALYSIS

Cerebrospinal fluid (20–30 mL) was collected by routine lumbar puncture, free from any blood contamination, in polypropylene tubes at 8:00 AM after overnight fasting, as previously described.34 The samples were analyzed for total tau, tau phosphorylated at threonine-181 (ptau181), and Aβ1-42 by commercial enzyme-linked immunosorbent assay (Innotest; Innogenetics, Ghent, Belgium). Cerebrospinal fluid Aβ40 was assayed by enzyme-linked immunosorbent assay as previously described.30 For all CSF measures, samples were continuously kept on ice, and assays were performed on sample aliquots after a single thaw following initial freezing.

IMAGE ACQUISITION AND PROCESSING

Magnetic resonance imaging scans were obtained on either a Sonata 1.5T, Vision 1.5T, or Trio 3.0T scanner (Siemens Corporation, Malvern, Pennsylvania). Structural MRI processing procedures have been reported elsewhere.40 Brain PET imaging was conducted using a Siemens 961 HR ECAT PET scanner or a Siemens 962 HR+ ECAT PET scanner (both, Control Technology, Inc, Knoxville, Kentucky). Radiochemical synthesis of [11C]PIB was performed in accordance with the published literature.41 After a transmission scan to measure attenuation, approximately 12 mCi of [11C]PIB was administered intravenously simultaneously with initiation of a 60-minute dynamic PET scan in 3-dimensional mode (septa retracted; twenty-four 5-second frames, nine 20-second frames, and ten 1-minute frames). The measured attenuation factors, scatter correction, and a ramp filter were used to reconstruct the dynamic PET images. Analysis of PIB images was performed for specific regions of interest as detailed pre-
The dissociation task. The 2 span tasks involved participants making a series of true/false judgments, with the working memory component being to remember in order the parts of the stimulus across the judgments. The Stroop is a computerized color-naming task, which includes 60 trials for the congruent (e.g., RED in BLUE), neutral (e.g., DEEP in BLUE), and incongruent (e.g., RED in BLUE) conditions. The process dissociation task in estimates of the binding potential for each region of interest were averaged to calculate a mean cortical binding potential (MCBP).

ATTENTIONAL ASSESSMENT

A 2-hour attentional battery was administered separately from the psychometric testing. The attentional control tasks were computation span, letter rotation span, Stroop, and a process dissociation task. The 2 span tasks involved participants making a series of true/false judgments, with the working memory component being to remember in order the parts of the stimulus across the judgments. The Stroop is a computerized color-naming task, which includes 60 trials for the congruent (e.g., BLUE in BLUE), neutral (e.g., DEEP in BLUE), and incongruent (e.g., RED in BLUE) conditions. The process dissociation task places recollection in direct conflict with familiarity via opposition procedures during retrieval. A Consonant-Vowel/Odd-Even Switching task was also administered.

GENOTYPING

We extracted DNA from peripheral blood samples using standard procedures. Apolipoprotein E genotyping was performed as previously described.

STATISTICAL ANALYSIS

The analysis was done on ACS baseline data. Each marker was analyzed as a function of age, FH (yes or no), and APOE4 genotype (ε4 allele present or absent) by the analysis of covariance. The interactive effects among these 3 risk factors were first tested and reported if confirmed. Otherwise, independent effects of each risk factor were reported. Preliminary analysis suggested differential variances as a function of age (e.g., younger vs older than 55), which were tested and then accommodated in the associational analyses with FH and APOE4 if confirmed. The software PROC MIXED/SAS (SAS Institute, Cary, North Carolina) was used to implement these analyses. The Satterthwaite approximation was used to estimate the denominator df in the approximate F or t tests.

Table 1. Characteristics of the ACS Cohort at Baseline

<table>
<thead>
<tr>
<th>Variable</th>
<th>Family History of AD (n=160)</th>
<th>No Family History of AD (n=109)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Clinical (n=126)</td>
<td>Imaginga (n=128)</td>
</tr>
<tr>
<td></td>
<td>Attention (n=126)</td>
<td>Attention (n=136)</td>
</tr>
<tr>
<td></td>
<td>All (n=55)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Clinical (n=91)</td>
<td>Imaginga (n=94)</td>
</tr>
<tr>
<td></td>
<td>Attention (n=96)</td>
<td>All (n=53)</td>
</tr>
<tr>
<td>Age group, No.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;55 y</td>
<td>54</td>
<td>18</td>
</tr>
<tr>
<td>≥55 y</td>
<td>106</td>
<td>30</td>
</tr>
<tr>
<td>Female sex, %</td>
<td>73.1</td>
<td>79</td>
</tr>
<tr>
<td>MMSE score, mean (SD)</td>
<td>29.22 (1.11)</td>
<td>29.25 (1.09)</td>
</tr>
<tr>
<td>Educational level, mean (SD)</td>
<td>15.99 (2.34)</td>
<td>16.11 (2.15)</td>
</tr>
<tr>
<td>Presence of APOE4, %</td>
<td>49.4</td>
<td>56.4</td>
</tr>
</tbody>
</table>

Abbreviations: ACS, Adult Children Study; AD, Alzheimer disease; APOE4, the ε4 allele of apolipoprotein E; CSF, cerebrospinal fluid; MMSE, Mini-Mental State Examination.

RESULTS

Table 1 presents the demographic characteristics of the entire sample and subgroups with each modality of assessments. All 269 participants completed baseline clinical and psychometric assessments. Two hundred seventeen participants (80.7%) had a lumbar puncture to obtain CSF, 206 (76.6%) completed PET PIB, 147 (54.6%) had an MRI, and 232 (86.2%) completed the attentional battery. One hundred eight participants (40.1%) completed all baseline procedures (clinical, psychometric, attention, lumbar puncture, MRI, and PET PIB).

As shown in the Figure, the mean (SE) level of CSF Aβ42 decreased significantly with age at a rate of −7.76 (2.14) pg/mL per year (P<.001) in those with a positive FH but not in those without (P=.35). The presence of an APOE4 allele did not alter the effect of FH on the age-related decrease in CSF Aβ42 (P=.50). Those with an ε4 allele had lower levels of age-adjusted CSF Aβ42 compared with the corresponding level in those without (P<.001), and the decrease was larger if FH was positive compared with the decrease if FH was negative (F1,209=5.29, P=.02). Sensitivity analyses with multiple imputations on CSF Aβ42 confirmed these findings.
The variance increased among individuals aged 55 or older compared with that of the younger age group for CSF tau ($\chi^2=9.71; P=.002$) and MCBP ($\chi^2=98.35; P<.001$). Table 2 presents the estimated slope (per year of age) for MCBP and CSF tau on younger (<55 years) and older individuals (≥55 years) as a function of FH and APOE4. No significant effect of FH or APOE4 was found for CSF tau on the age-related rate of change, but individuals with a positive FH had a higher level of CSF tau than those otherwise ($F_{1,152}=4.60; P=.03$) at age 55. For individuals younger than 55, MCBP increased by age at a significantly faster pace for individuals with APOE4 compared with the pace for those without APOE4 ($F_{1,62}=.4.72; P=.03$), eventually leading to a higher level of MCBP for those with APOE4 compared with the level for those without ($P=.01$). For individuals older than 55, a trend ($P=.09$) was found to suggest a faster age-related increase of MCBP for individuals with APOE4 compared with the increase for those without APOE4. Individuals with a positive FH and a positive APOE4 had the largest age-related increase of MCBP ($P<.001$).

Brain volumes as determined by MRI decreased with age, but the decrease was not statistically significant by FH (total cerebral brain volume: $F_{1,132}=0.90; P=.34$; right hippocampal volume: $F_{1,130}=1.85; P=.18$; left hippocampal volume: $F_{1,130}=0.31; P=.58$).

From a subsample of 165 participants who had diffusion tensor imaging data, the age-adjusted mean level of fractional anisotropy was lower for individuals with an FH of AD compared with the level for those without an FH of AD in the genu ($F_{1,114}=3.91; P=.05$) and in the splenium ($F_{1,142}=4.12; P=.04$) of the corpus callosum. In the gyrus rectus, individuals with APOE4 had a lower level of fractional anisotropy ($F_{1,142}=4.75; P=.03$) and a higher level of radial diffusivity ($F_{1,142}=4.3; P=.04$) than those without APOE4. The age-related increase in radial diffusivity in the precuneus was faster if FH was positive, compared with the increase if FH was negative, only among individuals with APOE4 ($F_{1,42}=4.67; P=.03$). The mean (SE) performance level of auditory consonant trigrams decreased significantly with age at the rate of −0.411 (0.125) per year ($P=.001$) for those with a positive FH but not for those with a negative FH ($P=.52$).

One hundred fifteen and 52 participants reported their mother’s and their father’s age of onset of DAT, respectively. An earlier mother’s age of onset was correlated with a larger reaction time difference between pure blocks and switched blocks of trials from the Consonant–Vowel/Odd–Even Switching task (Spearman $r=−0.21; P=.04$), and an earlier father’s age of onset was correlated with poorer performance in Wechsler Adult Intelligence Scale–III Similarities ($r=0.44; P=.01$).

Exploratory correlational analyses across the entire modalities of biomarkers confirmed those previously reported in the literature. Significant correlations between MCBP and CSF biomarkers (tau $r=0.22$, $p_{tau181}=0.19$, and CSF Aβ42 $r=−0.41$) were observed in the entire ACS cohort. Some of these are potentially modulated by age but not by FH. In the younger cohort (age <55 years), MCBP was not significantly correlated with CSF biomarkers or brain volumes. In the older cohort (age ≥55 years), however, MCBP was significantly correlated with CSF biomarkers (tau $r=0.24$, $p_{tau181}=0.22$, and Aβ42 $r=−0.53$). Furthermore, CSF and imaging biomarkers were correlated with Stroop performance in the younger sample in only 2 occasions (Aβ42 with greater interference in reaction times $r=−0.28$, and MCBP with Simon coefficient of variation $r=0.31$). In the older sample, however, CSF and imaging biomarkers were correlated with poorer performance across many attention measures (eg, Aβ42 with task switching coefficient of variation $r=−0.22$ and interference errors $r=−0.20$; MCBP with task switching coefficient of variation $r=0.19$, interference RT $r=0.17$ and errors $r=0.19$, incongruent errors $r=0.19$, and Simon coefficient of variation $r=0.17$). Brain volumetric measures were also correlated with attentional and working memory measures (eg, total cerebral brain volume with rotation span $r=0.22$, and left hippocampal volume with rotation span $r=0.33$) in the older sample. Because of a large number of correlations assessed across all modalities of markers, these findings were subjective to a higher false-positive rate (>5%). Therefore, they were preliminary and will serve only to generate scientific hypotheses that need to be critically tested in future studies.

Analyses were repeated on the subgroup of individuals who completed all procedures. The findings were con-
Family history for AD as a risk factor for AD and cognitive decline has been well documented, many times jointly with APOE4 genotypes. Several studies reported reduced gray matter volume and brain glucose metabolism as well as increased semantic memory activation in healthy individuals with a maternal history of AD. These reports, however, focused mostly on a small number of biomarkers assessed on the elderly population aged 65 or older. We reported the influence of FH for AD for a wide array of candidate antecedent biomarkers in the ACS cohort of cognitively normal middle- to older-aged individuals (aged 43–76 years). In addition to clinical and cognitive measures, we analyzed MRI-based brain volumes, diffusion tensor imaging–based estimates of white matter microstructure, biofluid assays, and molecular imaging of fibrillar amyloid measure with PET PIB.

No difference was found on cognitive and clinical measures as a function of FH of AD among cognitively normal ACS individuals. The only possible exception comes from the performance on the auditory consonant trigrams, and the difference is no longer significant after multiplicity adjustment.

Family history for AD, however, was associated with several CSF and imaging biomarkers in the cognitively normal ACS cohort, suggesting their potential role as antecedent biomarkers of AD. These findings support the design of the ACS that genetically enriched the sample of cognitively normal individuals at risk of AD by FH and are consistent with a recently reported meta-analysis of diffusion tensor imaging. The current results point to several CSF and imaging biomarkers on a cohort of cognitively normal middle-aged individuals (aged 43–76 years). In additional to clinical and cognitive measures, we analyzed MRI-based brain volumes, diffusion tensor imaging–based estimates of white matter microstructure, biofluid assays, and molecular imaging of fibrillar amyloid measure with PET PIB.

Accepted for Publication: March 15, 2011.

Author Affiliations: Charles F. and Joanne Knight Alzheimer’s Disease Research Center (Drs Xiong, Roe, Buckles, Fagan, Holtzman, Balota, Duchek, Storandt, Mintun, Grant, Snyder, Head, Benzinger, Mettenburg, Csernansky, and Morris), and Departments of Neurology (Drs Roe, Buckles, Fagan, Holtzman, Storandt, and Morris), Pathology and Immunology (Dr Morris), Physical Therapy (Dr Morris), Occupational Therapy (Dr Morris), Biostatistics (Drs Xiong and Grant), Psychology (Drs Balota, Duchek, Storandt, and Head), Radiology (Drs Mintun, Snyder, Benzinger, Mettenburg, and Head), and Development Biology (Dr Holtzman), Washington University School of Medicine, St Louis, Missouri; and Departments of Psychiatry and Behavioral Sciences, Stone Institute of Psychiatry, and Northwestern Memorial Hospital, Chicago, Illinois (Dr Csernansky).

Correspondence: Chengjie Xiong, Department of Biostatistics, Washington University School of Medicine, 660 S Euclid Ave, Campus Box 8067, St Louis, MO 63110 (chengjie@wubios.wustl.edu).

Author Contributions: Dr Xiong had full access to all the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis. Study concept and design: Xiong, Roe, Buckles, Mintun, Csernansky, and Morris. Acquisition of data: Fagan, Balota, Duchek, Storandt, Mintun, Grant, Head, Benzinger, Mettenburg, and Morris. Analysis and interpretation of data: Xiong, Roe, Buckles, Holtzman, Duchek, Snyder, Benzinger, and Morris. Drafting of the manuscript: Xiong, Balota, and Snyder. Critical revision of the manuscript for important intellectual content: Xiong, Roe, Buckles, Fagan, Holtzman, Duchek, Storandt, Mintun, Grant, Head, Benzinger, Mettenburg, Csernansky, and Morris. Statistical analysis: Xiong, Roe, and Duchek. Obtained funding: Xiong, Balota, Storandt, Head, and Morris. Administrative, technical, and material support: Buckles, Fagan, Holtzman, Duchek, Mintun, Grant, Snyder, Csernansky, and Morris. Study supervision: Storandt, Mintun, Benzinger, and Morris.
Financial Disclosure: Dr Holtzman reports that he receives research funding from Eli Lilly and Company, AstraZeneca, Pfizer, and C2N Diagnostics through Washington University; he is a member of the scientific advisory board for En Vivo, Satori, and C2N Diagnostics; and he is a consultant for Innogenetics. Dr Mintun reports that he is the chief medical officer for Avid Radiopharmaceuticals.

Funding/Support: This study was supported by grant P01 AG026276 from the National Institute on Aging (Dr Morris), the American Roentgen Ray Scholar Award (Dr Benzerger), and grant P50 AG05681 from the Charles F. and Joanne Knight Alzheimer’s Research Initiative of the Washington University Alzheimer’s Disease Research Center (Dr Morris).

Additional Contributions: We thank the Genetics Core (Alison Goate, DPhil, Core Leader) of the Alzheimer’s Disease Research Center for the APOE data.

REFERENCES


