Apolipoprotein E Polymorphism and Alzheimer Disease

The Indo-US Cross-National Dementia Study

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Background: The APOE*E4 allele of the gene for apolipoprotein E (APOE) has been reported as a risk factor for Alzheimer disease (AD) to varying degrees in different ethnic groups.

Objective: To compare APOE*E4-AD epidemiological associations in India and the United States in a cross-national epidemiological study.

Design: Case-control design within 2 cohort studies, using standardized cognitive screening and clinical evaluation to identify AD and other dementias and polymerase chain reaction to identify APOE genotyping.

Participants: Rural community samples, aged 55 years or older (n=4450) in Ballabgarh, India, and 70 years or older (n=886) in the Monongahela Valley region of southwestern Pennsylvania.

Main Outcome Measures: Criteria of the National Institute of Neurological and Communicative Disorders and Stroke–Alzheimer's Disease and Related Disorders Association for probable and possible AD and Clinical Dementia Rating (CDR) scale for dementia staging.

Results: Frequency of APOE*E4 was significantly lower (P<.001) in Ballabgarh vs the Monongahela Valley (0.07 vs 0.11). Frequency of probable or possible AD, with CDR of at least 1.0, in the Indian vs US samples, was as follows: aged 55 to 69 years, 0.1% (Indian sample only); aged 70 to 79 years, 0.7% vs 3.1%; aged 80 years or older, 4.0% vs 15.7%. Among those aged 70 years or older, adjusted odds ratios (95% confidence interval) for AD among carriers of APOE*E4 vs noncarriers were 3.4 (1.2-9.3) and 2.3 (1.3-4.0) in the Indian and US samples, respectively, and not significantly different between cohorts (P=.20).

Conclusion: This first report of APOE*E4 and AD from the Indian subcontinent shows very low prevalence of AD in Ballabgarh, India, but association of APOE*E4 with AD at similar strength in Indian and US samples.

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Dementia affects 5% to 10% of individuals aged 65 years or older in Europe and North America at any given time. Alzheimer disease (AD) is the most frequent cause of dementia.1 Of the many putative genetic risk factors for AD, only the gene for apolipoprotein E (APOE) has thus far been shown to be associated with both early- and late-onset AD of sporadic and familial varieties.2,4 The *E4 allele of the APOE gene has been consistently shown to be associated with AD in many studies of white populations, whereas the *E2 allele has in some studies appeared to be protective against AD.6 Findings appear similar in a Chinese population6 but, based on a number of studies in African, African American, and Hispanic populations, the evidence of an APOE-AD association is mixed.6-8 Thus, there may be interactions between APOE and racial or ethnic group as well as environmental factors that might modify the increased risk of AD conferred by the APOE*E4 allele in different populations.7 To our knowledge, there are no previous reports from the Indian subcontinent, of which the population represents approximately one sixth that of the world.9

Under a National Institute on Ageing-sponsored program of cross-national investigations,10 the Indo-US Cross-National Dementia Epidemiology Study was funded as a collaborative venture between the University of Pittsburgh, Pittsburgh, Pa, and the Centre for Ageing Research in India (CARI), New Delhi. The study was designed to compare the prevalence, incidence, risk factors, and outcome of AD and other...
The prevalence of AD and other dementias among the elderly in Ballabgarh was recently reported to be the lowest thus far reported in the world, suggesting that different risk and protective factors might be operating in this Indian community than in other populations. We herein report and compare the relationship between AD and the APOE polymorphism in large, community-based samples of the elderly populations of Ballabgarh and the Monongahela Valley, to answer the following 3 primary research questions: (1) Is the frequency of the APOE*E4 allele different between study cohorts from both populations? (2) Is the APOE*E4 allele associated with AD in both cohorts? (3) If so, is the strength of the association similar in the two cohorts?

When the APOE gene was first reported as a risk factor for AD in 1993, the MoVIES cohort was in its third biennial data collection wave. From January 26, 1994, through October 23, 1997, blood specimens for APOE genotyping were collected from surviving members of the MoVIES cohort, who by that time were all older than 70 years. Of the 1681 subjects in the original (1987-1989) MoVIES cohort, 886 white individuals who were still alive and participating in the study and had not moved to nursing homes underwent blood sample draws for genotyping. The likely survival bias in the genotyped subsample of the MoVIES cohort precludes its use for prevalence estimation but does not affect its usefulness for case-control and other risk and protective factor studies.

Blood samples were collected by venipuncture (88%) or by finger- or earlobe-stick (12%). The DNA was isolated with the use of a commercially available kit (QI Amp Kit; QIAGEN Inc, Chatsworth, Calif). The APOE genotyping was performed by means of a polymerase chain reaction protocol as described previously.

### BALLABGARH STUDY SITE

Ballabgarh is a rural agricultural area in the state of Haryana in northern India. The initial phase of the study was devoted to developing appropriate assessment tools for the Hindi-speaking Ballabgarh elderly population, approximately three quarters of whom were totally illiterate. The development of the cognitive screening battery, the functional ability scale, and the clinical diagnostic protocol used in our study and designed to maximize comparability to the MoVIES study have been described in detail elsewhere.

After instrument development, the entire population aged 55 years or older in the 28 villages in the Ballabgarh study area was recruited and surveyed from December 4, 1993, through December 9, 1997. Recruitment for the present study was extended to all adults aged 55 years or older, rather than 65, because of the relatively short life expectancy (62.1 years at birth) of individuals in this area. Demographic data collected included age confirmation (reported previously), education (years of formal schooling), and literacy (ability to write a sentence and read the local language in their native tongue).

### RESULTS

#### DEMOGRAPHICS

As of the reference dates, the MoVIES cohort (n=886) had a mean age of 79.3 (4.8) years, with a median of 78.7 years; 61.1% were aged 70 to 79 years, and 38.9% were aged 80 years or older. Women constituted 64.2% of the sample. For education, 38.3% did not graduate from high school, 36.0% were high school graduates, and 25.7% had more than a high school education.

In the Ballabgarh cohort (n=4450), the mean age was 67.1 (7.2) years, with a median of 65.7 years as of the reference dates; 72.0% were aged 55 to 69 years, 21.8% were aged 70 to 79 years, and 6.2% were aged 80 years or older. Women constituted 48.0% of the sample. Although 73.9% had no formal schooling, 1.6% of unschooled individuals had some literacy as defined ear-
Gene counting was used to calculate APOE allele frequencies in each cohort. In each cohort, adherence to Hardy-Weinberg expectation was tested by means of χ² goodness-of-fit tests. Within each cohort, APOE allele frequencies were calculated by and compared among the age groups to determine whether APOE*E4 frequency decreased with age. The χ² tests were used to compare frequencies of each allele between cohorts.

Within each cohort, the proportion of subjects by CDR stage and with diagnosis of probable or possible AD were calculated for the entire cohort and by age group as of the reference date (date of blood sample draw for genotyping). As with any cross-sectional study, it was recognized that dementia would develop subsequently in some individuals classified as nondemented for the purpose of the current analyses.

A case-control design, with cases and controls identified as of the reference date, was used to examine cross-sectional relationships of APOE genotype with all dementias and with AD in both cohorts. Logistic regression was used to calculate the odds ratios (ORs) and the associated 95% confidence intervals (CIs) for a diagnosis of AD in APOE*E4 carriers (subjects with at least one copy of the APOE*E4 allele) compared with noncarriers. Logistic regression models were also fit to look for associations of APOE*E4 with all dementias combined (ie, including non-AD dementias). Four different logistic regression models were fit for each cohort, with outcome variables being probable or possible AD with CDR of at least 1.0, probable or possible AD with CDR of at least 0.5, all dementia with CDR of at least 1.0, and all dementia with CDR of at least 0.5. Models restricted to probable or possible AD excluded subjects with other dementias; models restricted to subjects with CDR of at least 1.0 treated subjects with CDR of 0.5 as not demented. The ORs were adjusted for age (continuous variable) and education (MoVIES cohort, high school graduates vs subjects with less than high school) or literacy (Ballabgarh cohort, literate vs illiterate subjects.) The logarithms of the ORs for AD in both cohorts were then compared using a z test. Similar logistic regression models were fit to calculate ORs and CIs for AD among APOE*E2 carriers compared with noncarriers in each cohort. Models were also fit to MoVIES data, adjusting for random or volunteer status.

**FREQUENCY OF AD AND OTHER DEMENTIAS**

In the MoVIES cohort, 132 subjects (14.9%) had any or all dementia according to DSM-III-R and a CDR stage of at least 0.5 as of the reference date. Of those with any
dementia, 115 (87.1%) had probable or possible AD according to NINCDS-ADRDA criteria. Restricting the analyses to subjects with CDR stage of at least 1.0, 75 subjects (8.5%) had any dementia, 71 (94.7%) of whom had probable or possible AD.

In the Ballabgarh cohort, 36 (0.8%) had any dementia according to DSM-III-R and a CDR stage of at least 0.5. Of the demented, 28 (77.8%) had probable or possible AD according to NINCDS-ADRDA criteria. Among those with CDR stage of at least 1.0, there were 29 (0.7%) subjects with any dementia, 21 (72.4%) of whom had probable or possible AD. Further breakdown of these diagnosis and stage categories in both samples by age groups is shown in Table 1, and by genotype in Table 2.

ASSOCIATIONS BETWEEN AD AND APOE GENOTYPES

Adjusted ORs used to estimate cross-sectional associations between APOE genotypes, and AD and dementia in both cohorts are shown in Table 3.

APOE*E4 ALLELE

After adjustment for age and education (in the MoVIES cohort), and for age and literacy (in the Ballabgarh cohort), the OR (with 95% CI) for probable or possible AD with CDR stage of at least 1.0, in APOE*E4 carriers compared with noncarriers, was 2.26 (1.29-3.95) in the MoVIES cohort and 3.35 (1.20-9.39) in the Ballabgarh cohort aged 70 years or older. Odds ratios for all dementias and for CDR of at least 0.5 in both cohorts, including the entire Ballabgarh cohort (all age groups), are shown in Table 3. In the MoVIES data, controlling for selection (random vs volunteer) status by including it as an independent variable in the models barely changed the ORs or CIs.

Since the MoVIES subjects undergoing genotyping were all aged 70 years or older, we restricted cross-national comparisons across Indian and US cohorts to subjects in the category aged 70 years or older. The ORs reported for AD with CDR of at least 1.0 were not significantly different across cohorts (P=.25), to the extent that a difference could be detected with available power. Essentially, the APOE*E4 allele was associated with AD at similar strength in both cohorts.

APOE*E2 ALLELE

After adjustment for age and education (in the Monongahela Valley), and for age and literacy (in Ballabgarh), the OR for probable or possible AD with CDR stage of at least 1.0, given the presence of at least 1 APOE*E2 allele, was calculated for both cohorts. No significant association was found between APOE*E2 and AD as all CIs included 1, most likely because of lack of power.

All models had adequate fit by Hosmer-Lemeshow goodness-of-fit test.28

The frequencies of AD and the APOE*E4 allele were higher among those who underwent genotyping within our US sample than in our Indian sample. The APOE*E4 carrier status and the presence of probable or
possible AD were positively associated in both cohorts. In each cohort, the elevated risk was about 2- to 3-fold, ie, the ORs were lower than those reported from the highly selected populations of Alzheimer’s Disease Centers and similar referral centers. The ORs in our cohorts were within the range reported from other community-based studies of white populations in East Boston and Rotterdam, which included mild dementias and similar referral centers. The ORs in our study population were white, a term often used interchangeably with Caucasian. However, our nonwhite Asian Indian population would also have to be classified as Caucasian, as natives of India and western Asia are described as forming “a Caucasoid cluster when compared with Asians from further north and east.”

Previous studies of APOE polymorphism in individuals of Indian ancestry have reported APOE*E4 allele frequencies of 0.101, 0.127, 0.127, and 0.103 (M. Ilyas Kamboh, PhD, and A. Ramesh, PhD, unpublished data, 1990), which appear marginally higher than the frequency of 0.07 in Ballabgarh inhabitants aged 55 years or older. None of the previous studies provided the age distributions of their populations, which appeared to represent small convenience (eg, blood bank) samples rather than defined representative communities. None of the previous reports included diagnostic information on AD or other diseases. Although ours is the largest Indian sample from which APOE allele frequencies have been reported, it is not representative of the population of India as a whole.

On the basis of a multicenter meta-analysis, Farrer et al recently concluded that the APOE*E4 allele “represents a major risk factor for AD in all ethnic groups studied, across all ages between 40 and 90 years, and in both men and women.” Studies included in the meta-analysis were of ethnic groups described as Caucasian, African American, Hispanic, and Japanese. Our US study population was white, a term often used interchangeably with Caucasian. However, our nonwhite Asian Indian population would also have to be classified as Caucasian, as natives of India and western Asia are described as forming “a Caucasoid cluster when compared with Asians from further north and east.”

Previous genetic studies have suggested that linguistic (ie, ethnic) differences account for much of the genetic diversity of present-day Indian populations; the ethically diverse population of India is politically divided into linguistic states. Our study was conducted in Haryana, a northern Indian state whose inhabitants speak an Indo-European language (the Haryanvi dialect of Hindi). A study of Indians in 2 adjacent states, where the Punjabi and Hindi languages are spoken, demonstrated Caucasoid genetic features in addition to at least 1 marker suggesting ancient East Asian lineage. Thus, there is likely to be genetic admixture even in our Indian study population, which is probably more ethnically homogeneous than our Monongahela Valley study population of mixed European ancestry. Cross-ethnic comparisons can reveal important environmental differences (including, eg, cultural, geographic, socioeconomic, or dietary factors) that may be relevant to disease and that may interact with genetic risk. However, the genetic basis of conventional racial and ethnic distinctions per se is far from clear. Given the recent proliferation in reports of genetic studies from unique national, geographic, linguistic, racial, and ethnic groups, caution is warranted in comparing genetic data between studies that use different or overlapping ethnic classifications.

Our study had some limitations. The current report excluded the 17 African American subjects in our US genotyped cohort because of their small numbers. In both cohorts, the category of all dementias was
largely composed of probable or possible AD; we had too few cases of non-AD dementias to allow separate analyses of their relationship with APOE. As with most community-based studies, both cohorts included too few *E4/*E4 homozygotes to allow the exploration of dose-dependent risk of AD conferred by APOE*E4. Although the US cohort at its inception was representative of its base population, some natural attrition had occurred during the 6 years of follow-up before genotyping was performed. Although our clinical and genetic measures were comparable across the Indian and US cohorts, the two cohorts are very different from each other in a variety of cultural and environmental aspects that cannot easily be compared. Despite these differences, the cohorts revealed similar strength of association between APOE*E4 and AD; thus, the difference in disease occurrence between both study populations cannot be explained by differential risk, or modification of risk, with respect to the APOE polymorphism. As alternative explanations, differences in additional genetic risk and protective factors, survival effects, or environmental factors are promising directions for future research.

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