Review: apolipoprotein E ε4 allele is a risk factor for Alzheimer’s disease in different ethnic groups


Question
What is the effect of age, sex, and ethnicity on the association between apolipoprotein E (APOE) genotype and Alzheimer’s disease (AD)?

Main results
Among white patients from clinic or autopsy studies, the risk of AD was greater in patients with genotypes ε2/ε4 (OR 2.6, 95% CI 1.6 to 4.0); ε3/ε4 (OR 3.2, CI 2.8 to 3.6); and ε4/ε4 (OR 14.9, CI 10.8 to 20.6) and the risk was decreased in patients with genotype ε2/ε3 (OR 0.6, CI 0.5 to 0.8). Similarly, in population based studies of white patients, the ε3/ε4 and ε4/ε4 genotypes were associated with AD (OR 2.7, CI 2.2 to 3.2 and OR 12.5 CI 8.8 to 17.7, respectively) and the ε2/ε3 genotype was protective (OR 0.6, CI 0.5 to 0.9). The association between the ε4/ε4 genotype and AD was strongest among Japanese patients (OR 33.1, CI 13.6 to 80.5) and weakest among African-American (OR 5.7, CI 2.3 to 14.1) and Hispanic patients (OR 2.2, CI 0.7 to 6.7). Substantial heterogeneity existed in studies of African-American patients. In white patients with the ε3/ε4 or ε4/ε4 genotypes, the risk of AD increased between 40 and 60 years of age. Age affected Japanese patients with the ε3/ε4 similarly but did not affect risk in Hispanic patients. The risk of AD in patients with the ε3/ε4 and ε2/ε4 genotypes, compared with those with the ε3/ε3 genotype, was greater in women than in men.

Conclusions
The apolipoprotein E ε4 allele is strongly associated with Alzheimer’s disease in white, African-American, Hispanic, and Japanese people. The risk is evident between 40 and 90 years of age.

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Commentary
A positive association between the ε4 allele of the APOE gene and AD was first reported in 1995. It has become the most statistically robust and biologically important example of a genetic risk factor for a common psychiatric disorder. As such, the main conclusion of the meta-analysis by Farrer et al, that the APOE ε4 allele is a determinant of risk of AD, is hardly unexpected. The real value of this review is that it clarifies the magnitude of the risk in population based and in clinic based samples, and it highlights some of the complexities in the association. For example, it confirms suspicions that possession of an ε2 is protective, but shows that this effect is more than cancelled out if ε2 is inherited with an ε4 allele. The meta-analysis also makes clear that the size, although not the existence, of risk conferred by the ε4 allele differs considerably not only between groups but also within the African-American population (which is usually considered as a single entity in genetic research). Establishing these details about the influence of APOE on AD provides clearer pointers as to populations and experimental strategies which may be informative when looking for additional genetic and environmental contributors to the disease.

The APOE association is of undoubted importance to the understanding of AD, ranking alongside the seminal discoveries of the cholinergic deficits and the genes causing the dominant familial form of the disease. This meta-analysis should not, however, be seen as bearing directly upon the possible use of APOE testing in the differential diagnosis of AD, let alone the prediction of its occurrence or its response to treatment.

These crucial issues await clarification about the sensitivity, specificity, and predictive value of APOE testing in each of these clinically relevant situations. This information requires more extensive research in several areas, including the association of the APOE genotype with other disorders, and prospective studies of younger, cognitively normal cohorts.

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