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Genetic Architecture of Alzheimer's Disease in the Korean Population Revealed by a Large-Scale GWAS

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Alzheimer's disease (AD) is an increasing global health concern that demands extensive genetic studies to gain a better understanding of its etiology, particularly in underrepresented populations. This study is the largest pathologically well-defined genome-wide association study (GWAS) of AD conducted in a Korean population. We examined approximately 80,000 individuals, including 4,000 with whole-genome sequencing data and over 10,000 with array-based genotyping from the Gwangju Alzheimer's & Related Dementias (GARD) cohort, alongside 70,000 array-genotyped participants from three cohorts of the Korean Genome and Epidemiology Study (KoGES), all supported by comprehensive epidemiological data. Given the genetic homogeneity of the Korean population, this research offers a unique opportunity to explore both the similarities and differences in genetic architecture between Korean and primarily Caucasian populations, which have been the focus of most prior GWAS studies. Our findings contribute to a more comprehensive understanding of AD across diverse populations and enhance knowledge of its genetic underpinnings.