

## Uncover Genetic Influences on Aging-Related Factors Using SV-based Genome-wide Association Studies

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Genome-wide association studies (GWAS) based on single nucleotide polymorphisms (SNPs) have identified numerous genetic regions associated with various diseases. However, they account for only a limited proportion of the heritability of polygenic disorders. To address this limitation, structural variants (SVs) that extend beyond SNPs have gained increasing attention, as they can profoundly affect gene expression and function and are thus considered important contributors to disease susceptibility. Recently, computational tools have been developed to estimate SVs from whole-genome sequencing (WGS) data, enabling the simultaneous analysis of copy number variants (CNVs), short tandem repeats (STRs), and insertions/deletions within a single dataset. In this study, we analyzed WGS data from a large cohort of elderly Korean individuals with Alzheimer's disease (Gwangju Alzheimer's & Related Dementia, GARD) to identify SV regions and performed GWAS to examine their associations with brain function-related phenotypes, including MRI measures, neuropsychological test scores, and dementia diagnoses, all obtained from the same individuals. By integrating multiple types of SVs from a single WGS dataset, our approach provides a cost-effective strategy to enhance the genetic explanatory power for complex traits. Moreover, the genetic factors identified in this study provide important insights into additional genetic contributors to cognitive decline related to dementia and aging.