

# Identifying Genetic Risk for Late-onset Alzheimer's Disease: The GERAD Consortium

<https://neurodegenerationresearch.eu/survey/identifying-genetic-risk-for-late-onset-alzheimers-disease-the-gerad-consortium/>

## Title of project or programme

Identifying Genetic Risk for Late-onset Alzheimer's Disease: The GERAD Consortium

## Principal Investigators of project/programme grant

Title	Forname	Surname	Institution	Country
Professor Julie		Williams	Cardiff University	UK

## Address of institution of lead PI

Institution	Cardiff
Street Address	Henry Wellcome Building, Heath Park
City	Cardiff
Postcode	CF14 4XN

## Country

- United Kingdom

## Source of funding information

Medical Research Council

## Total sum awarded (Euro)

1322519.23

## Start date of award

01-09-2010

## Total duration of award in months

24

## The project/programme is most relevant to

Alzheimer's disease and other dementias

## Keywords

### Research abstract in English

Alzheimer's disease (AD) is a common, heritable, genetically complex disorder. Genome-wide association studies (GWAS) have succeeded in identifying over 400 genetic variants contributing to

complex phenotypes, in less than two years. Recently, our consortium performed a GWAS in 16,000 AD and control samples, which succeeded in identifying two new susceptibility genes (CLU:  $p = 8.5 \times 10^{-10}$ , odds ratio (OR) = 0.86 & PICALM:  $p = 1.3 \times 10^{-9}$ , OR = 0.86), provided strong evidence for the existence of several more (13 variants observed  $p < 1 \times 10^{-5}$ , 4 expected by chance:  $p = 7.5 \times 10^{-6}$ ) and confirmed a third susceptibility gene CR1. We will undertake a powerful GWAS (+55,000 individuals) of AD, aiming to identify 10 new susceptibility genes contributing to disease risk, modifying age at onset or contributing to copy number variation. Findings will be screened for AD susceptibility pathways and tested for relationships with clinical symptoms. This proposal will produce a definitive study of common genetic risk in AD and will deliver around 20 new susceptibility genes, CNVs and pathways in 2 years. Identifying new susceptibility genes will pinpoint primary causal pathways to disease and provide the basis for future preventative and therapeutic interventions, contribute to early susceptibility testing and increase UK research capacity.

### **Lay summary**