

Further defining the genetic architecture of Alzheimer's disease

<https://neurodegenerationresearch.eu/survey/further-defining-the-genetic-architecture-of-alzheimers-disease/>

Principal Investigators

Professor J Williams

Institution

Cardiff University

Contact information of lead PI

Country

United Kingdom

Title of project or programme

Further defining the genetic architecture of Alzheimer's disease

Source of funding information

MRC

Total sum awarded (Euro)

€ 3,713,838

Start date of award

29/08/2013

Total duration of award in years

5.0

The project/programme is most relevant to:

Alzheimer's disease & other dementias

Keywords

Research Abstract

Approximately half a million people have Alzheimer's disease (AD) in the UK, incurring an annual care cost of £23 billion. 35 million have dementia world-wide and it is estimated that these numbers will double by 2040. Identifying genes that affect the development of AD is important in pin-pointing potential disease mechanisms, testing new therapeutics and in predicting individual risk of disease development. Our programme of research will focus on

identifying rare, exonic susceptibility variants of moderate/strong effect, using novel, powerful, genome-wide approaches and extended and enriched clinical samples. We will undertake a case-control association study comprising 20,000 AD cases and 49,000 controls focusing on coding regions throughout the genome, using the Illumina exome chip. We will also collect a sample of 500 cases with early-onset AD (EOAD), an uncommon form of the disease (<5% cases) that manifests before the age of 65, and in which heritability is especially high (92-100%). We will sequence the exomes of the 500 EOAD individuals and analyse them together with 500 EOAD exomes available to us through collaboration. Susceptibility variants identified will be replicated in an independent sample of 10,000 AD cases and 10,000 controls. We aim to detect rare variants of larger effect than those observed for common susceptibility variants; these effects should prove easier to model and will facilitate the further understanding of disease mechanisms and the development of new therapeutics. We will combine all genetic data we have generated to extend and develop complex analyses including pathway analysis, sub-phenotypic analysis and cross-disease analysis. Finally, we will establish and extend research resources such as DNA and additional sample banking from all EOAD cases collected, and iPSC programmable cell lines from 50 EOAD cases to facilitate functional analyses. This resource will be made available to research and pharmaceutical communities.

Lay Summary

Further information available at:

Types:

Investments > €500k

Member States:

United Kingdom

Diseases:

Alzheimer's disease & other dementias

Years:

2016

Database Categories:

N/A

Database Tags:

N/A