Research Grants 2025

Alzheimer's disease | Discovering drivers of Alzheimer's disease using metabolomics

Doctor Sarah Holper

Dementia is the second leading cause of death of all Australians.1 Dementia is an umbrella term encompassing different brain disorders that cause loss of memory, language, and other thinking skills to the degree that they impact on a person's daily life. There are several causes of dementia, with Alzheimer's disease (AD) being the most common for older Australians. AD is typified by the toxic build-up of 2 proteins in the brain called tau and amyloid beta (A□). There is no known cure or effective treatment to reverse the disease.

Fifty million people worldwide are living with dementia, a number projected to triple by 2050.2 Currently, AD diagnosis is supported by specialized resource-heavy tests like brain scans and spinal fluid sampling. In the face of this expected surge in dementia cases, developing accessible diagnostic tests and treatments — blood tests and tablets — is essential.

Despite decades of research, significant gaps exist in our understanding of the disease-causing processes that drive AD. For instance, it remains unclear what triggers AD to develop, what drives the death of brain cells, what factors cause cognitive impairment to emerge, and why some people decline much faster than others. To answer these questions, we must understand at a chemical level the changes that are happening between molecules like proteins and genetic material in the brains of people with AD. Without this nuanced understanding, developing accurate diagnostic tests and therapies will be impossible.

In a pilot sub-study of a recently completed phase II placebo-controlled drug trial of SAMe (a putative anti-tau drug), we aim to analyse blood samples to explore the metabolomic changes that occur in people with Alzheimer's disease (AD) over 6 months.

Funding has already been secured to support another pilot sub-study in which we will use cutting-edge technology to perform a proteomics analysis of our samples. By adding this proposed metabolomics analysis, we will be able to leverage our proteomics data to molecularly profile our samples with exquisite granularity. Combining these powerful, complementary techniques in a novel multiomics approach, we will be ideally positioned to reveal new insights into AD's underlying mechanisms, with exciting opportunities for biomarker and drug development.

Grant $12,000

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