

RESEARCH USE STATEMENT AND NON-TECHNICAL SUMMARY

Research Use Statement for Application for Genomic Data from NIAGADS Please limit to 2,200 characters max. The statement should include the following components:

- Objectives of the proposed research;
- Study design;
- Analysis plan, including the phenotypic characteristics that will be evaluated in association with genetic variants

Research Use Statement:

Our lab recently showed that repressor element 1-silencing transcription factor (REST) is induced in human cortical and hippocampal neurons during aging. In Alzheimer's disease (AD), however, REST is lost from the nucleus. In cell culture, REST protects neurons from oxidative stress and amyloid b-protein toxicity by repressing genes involved in cell death and inducing stress response genes. Additionally, a mouse model of loss of REST in the brain leads to age-related neurodegeneration. Finally, REST levels during aging are correlated with cognitive preservation. Thus, the regulation of REST may distinguish neuroprotection from neurodegeneration. Based on these results, the objective of our proposed research is to use SNP array datasets (ng00030, ng00028, ng00026, ng00017, ng00034) to determine if there are genetic variants in REST or REST-regulating genes that associate with increased or decreased risk of developing late onset Alzheimer's disease, age of onset, or severity of the course of the disease as determined by well-established criteria. Candidates will be prioritized by predicted function of the variant, effect size and frequency.

Non-Technical Summary for Application for Genomic Data from NIAGADS Investigators will provide a non-technical summary of their proposed research. If the project is approved, this statement will be publicly available for lay audiences to read the purpose and objectives of the research. Please limit to 1,100 characters.

Our lab recently showed that repressor element 1-silencing transcription factor (REST) is induced in human cortical and hippocampal neurons during aging. In Alzheimer's disease (AD), however, REST is lost from the nucleus. In cell culture, REST protects neurons from oxidative stress and amyloid b-protein toxicity by repressing genes involved in cell death and inducing stress response genes. Additionally, a mouse model of loss of REST in the brain leads to age-related neurodegeneration. Finally, REST levels during aging are correlated with cognitive preservation. Thus, the regulation of REST may distinguish neuroprotection from neurodegeneration. Based on these results, the objective of our proposed research is to use these SNP array datasets to determine if there are genetic variants in REST or REST-regulating genes that associate with increased or decreased risk of developing late onset AD, age of onset, or severity of the course of the disease as determined by well-established criteria. Candidates will be prioritized by predicted function of the variant, effect size and frequency.