

## 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:**

The goal of this study is to perform pleiotropy analysis of multiple public datasets representing the taupathy spectrum. Identification and characterization of genetic risk across all neurodegenerative diseases resulting from tau pathology, including progressive supranuclear palsy (PSP), Alzheimer's disease, corticobasal degeneration and frontotemporal lobar degeneration, will be critical for identifying common mechanisms of pathogenesis that can serve as targets for therapeutic intervention.

We will perform cross-sectional analysis of multiple GWAS datasets reflecting tau-mediated neurodegeneration—including the PSP dataset—using pleiotropy analysis methods developed by our collaborators.

**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.

We will use PSP GWAS data in conjunction with existing data from other large GWAS to identify shared genetic risk factors for neurodegeneration due to tau pathology. Strong candidate variants will be followed up through additional association testing in other, independent cohorts of individuals with the relevant neurodegenerative disease diagnoses and may be corroborated through the functional studies of gene expression using existing datasets from brain tissue and/or cellular models of taupathy. Results from this study have the potential to identify novel, shared risk factors that may be the strongest candidates for disease modifying compounds with broad impacts across all tau-mediated degeneration.