Alzheimer’s disease genetics has seen significant progress by implementing genome-wide association studies (GWASs). However, differences in GWAS design and focus—association with disease risk (i.e., case-control status) versus related phenotypes (e.g., cognitive decline, family history) and inclusion of different populations—limit the AD community’s ability to leverage the richness of these findings.

Dr. Yuk Yee Leung (co-investigator of NIAGADS) and colleagues created the Alzheimer’s Disease Variant Portal (AVDP), an easy-to-use resource that houses the newest curated, harmonized, and searchable collection of genetic association study results (Kuksa et al.).

The uniqueness and necessity of having a curated and harmonized interactive platform that provides unified access and visualization of a uniquely extensive up-to-date collection of GWAS data for AD.

As of August 2021, the ADVP includes data from 125 curated AD GWAS publications and contains 6,990 associations across more than 900 loci, 1,800 variants, 80 cohorts, and eight populations.

In describing the usefulness of the ADVP, Dr. Leung describes this resource as “great for people who want introductory knowledge or in-depth understanding of AD genetics findings.”

To learn more about ADVP, click here.

ADVP is freely accessible at http://advp.niag-ads.org.

New Datasets available at https://www.niagads.org/datasets

NG00105 - MiGA – Microglia Genomic Atlas
NG00108 - Profiling microglia expression profiles in AD using single-nuclei RNA-seq
NG00109 - Genetic architecture of subcortical brain structures in 38,851 individuals summary statistics - Satizabal et al. 2019
NG00110 - Exome-wide age-of-onset analysis reveals exonic variants in ERN1 and SPPL2C associated with Alzheimer’s disease
NG00111 - Genome-wide association identifies the first risk loci for psychosis in Alzheimer disease
NIAGADS presents at AAIC 2021

Heather Issen presented the 2021 update for The National Institute on Aging Genetics of Alzheimer’s Disease Data Storage Site (NIAGADS).

As of January 2021, NIAGADS houses 74 datasets comprised of >90,000 samples including GWAS, sequencing, gene expression, annotations, deep phenotypes, and summary statistics. Qualified investigators can retrieve ADSP sequencing data with ease and flexibility through the NIAGADS DSS. As of February 2021, the ADSP and other contributing studies have completed whole exome sequencing (WES) of 20,504 samples and whole-genome sequencing (WGS) of 16,896 samples. Raw WES and WGS files, quality controlled VCF files, and phenotype data files are available via qualified access. The next round of sequencing currently underway will generate around 18,000 additional genomes to be released at the end of 2021.