NIAAA Policy for Submission of Applications Containing Genome-Wide Association Studies

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Key Dates
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Related Announcements
PA-16-160
PA-16-161

Issued by
National Institute on Alcohol Abuse and Alcoholism (NIAAA)

Purpose

The purpose of this notice is to communicate the NIAAA Policy regarding grant applications seeking to identify common variants conferring genetic risks for alcohol use disorder (AUD) and related phenotypes. The policy is based on recommendations from the Genetics and Genomics Advisory Meeting NIAAA convened on October 26, 2016. The Advisory Panel determined that Genome-Wide Association Studies (GWAS) are currently the preferred approach for the identification of and the confirmation of genes that harbor variants that contribute to AUD, since results from these studies will likely to provide potential insights into translational studies and new therapeutic targets. GWAS can be accomplished with moderate resources and within a short to midrange timeframe. To achieve the sample sizes needed to detect robust associations with risk for AUD, it will likely be necessary to combine GWAS data across multiple studies into large datasets and to harmonize and use appropriate metrics of alcohol misuse and related phenotypes to ensure comparability across independent analyses.

Please note that investigators interested in submitting applications in this research area that, beginning with June 5, 2017 submission date and all subsequent applicable deadlines,

NIAAA will:

- only support collection of human samples that contain many subjects who are severely affected, either through new data collection projects or collaboration with existing large-scale studies. It is of particular interests to NIAAA how genetic backgrounds influence the effects of common variants as well as those variants that are found preferentially in different subpopulations for AUD and related phenotypes. Collection of new cohorts with a focus on more extreme individuals and on diversity in ethnicity and SES is an important consideration. Active involvement of investigators from those communities and/or experienced in working with these communities is encouraged, as they could play an important role in recruitment and ascertainment of the subjects.

- require each application to develop and use a core set of questions, or utilize available assessment instruments, such as SSAGA, PhenX Toolkit, and ANA. The instrument should be compatible across all studies for the evaluation of DSM IV/-5 criteria for AUD and key co-occurring disorders.

Some examples for domains for assessing alcohol exposure phenotypic risk-factors and environmental risk-measures may include but not limited to:

- alcohol use and misuse across the lifetime or at period of maximum use
- drinking across adolescent period on both quantity and frequency
- longitudinal data and family history
- medical history on treatments sought and outcome

- externalizing phenotypes such as impulsivity and conduct/antisocial traits, other psychoactive substance use and abuse, alcohol problems/alcoholism and comorbidity with other psychiatric disorders especially depression
- neurophysiological endophenotype approaches that utilize electrophysiological measures, such as EEG may also be included.

- expect each application to collect and make available high-quality DNA samples for genotyping at the facility NIAAA designates and supports, such as NIH Center for Inherited Disease Research (CIDR) Program (http://www.cidr.jhmi.edu/), or RUCDR Infinite Biologics at Rutgers University in New Jersey (http://www.rucdr.org/). Thus, NIAAA requires investigators to include a budget in their applications based on the NIAAA-negotiated costs for GWAS genotyping.

- expect broad sharing, in compliance with *NIH Genomic Data Sharing Policy* (NOT-OD-14-124), of GWAS datasets and their accompanying key phenotypic data generated by NIAAA-supported studies for both existing and new samples, consistent with achieving the goals of the NIAAA programs for AUD. NIAAA expects these datasets be deposited in a timely manner into the designated databases such as NIH database of Genotypes and Phenotypes (dbGaP) (https:// www.ncbi.nlm.nih.gov/ gap), NIH/NIMH Data Archive (NDA) (https://data-archive.nimh.nih.gov/), or The Psychiatric Genomics Consortium (PGC) (https://www.med.unc.edu/pgc).

- encourage collaborative efforts for sharing and harmonizing genotype and phenotype datasets for large-scale meta-analyses. The Psychiatric Genomics Consortium Substance Use Disorder (PGC-SUD) working group may provide such a conduit for data sharing, harmonization and analysis.

- encourage and support innovative, novel, and creative research by individual groups that are complementary to large-scale gene discovery efforts.

Inquiries

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