

Element 1: Data Type:

A. Types and amount of scientific data expected to be generated in the project:

As detailed in the Research Strategy Section, this project is to investigate how several newly-identified proteins regulate the expression and functionality of Slo2 channels using *C. elegans* and *Xenopus* oocytes as the model systems. The project will yield diverse data sets, including electrophysiological recordings, microscopy images, whole-genome sequencing data, plasmids, transgenic worm strains, mutant worm strains, and worm behavioral observations. The volume of data generated will be contingent on the outcomes of our investigations.

B. Scientific data that will be preserved and shared and the rationale for doing so:

Both raw and processed data of electrophysiological recordings, microscopy images, and worm behavior will be stored on secure servers with regular backups. The raw whole-genome sequencing data will be deposited in public repositories, with corresponding accession numbers cited in our publications. Cryogenic storage of worm strains will be employed using established protocols, with regular backups and redundancy measures in place. Strain information, including genetic background, construction, and phenotypic data, will be recorded in an electronic database. Plasmids will be cataloged and stored in a designated -20°C freezer with proper labeling and documentation. Data generated from this project will be made available to the wider scientific community through established repositories and databases, following our publication, to ensure transparency, encourage reproducibility, and promote scientific collaboration.

C. Metadata, other relevant data, and associated documentation:

We will furnish a comprehensive methods section delineating the acquisition of scientific data generated in this study. Additionally, any step-by-step protocols devised in the course of this project will be made available in a supplementary protocol document. Detailed information regarding the instruments and technologies utilized in data generation will also be included.

In tandem with the publications linked to this research, we will furnish a thorough, step-by-step protocol as a Supplementary Protocol document. Furthermore, we are committed to maintaining up-to-date protocols for each technology and workflow employed in our research.

Element 2: Related Tools, Software, and/or Code:

- Electrophysiological recording data will be stored as ABF files, which can be easily analyzed and exported using the Clampex software provided by Molecular Devices.
- Microscopy images will be provided as the accessible .TIFF files and can be viewed with common image viewing software.
- Whole-genome sequencing data will be supplied in FASTQ file format, which is the standard format and can be used as input for a wide variety of secondary data analysis pipelines.
- Phenotypic variables will be documented in tab-separated files and can be managed using ubiquitous spreadsheet software like Microsoft Excel.
- Statistical analyses of the data will be performed using the versatile OriginPro software developed by OriginLab Corporation.

Element 3: Standards:

Community standard file formats will be provided for various data types, including ABF files for electrophysiological recordings, .TIFF files for microscopy imaging, FASTQ files for whole-genome sequencing results, and spreadsheets for gene expression and phenotypic results.

Element 4: Data Preservation, Access, and Associated Timelines

A. Repository where scientific data and metadata will be archived:

Whole-genome sequencing datasets will be deposited in Sequence Read Archive (SRA), NIH's primary archive of high-throughput sequencing data. For worm phenotypic datasets, we will utilize WormBase, a comprehensive online resource dedicated to sharing diverse data types and offering the research community precise, up-to-date, and easily accessible information on the genetics, genomics, and biology of *C. elegans* and related nematodes.

B. How scientific data will be findable and identifiable:

Each dataset will be assigned a unique identifier and referenced in associated publications. Persistent identifiers and metadata will be provided for easy identification.

C. When and how long the scientific data will be made available:

Scientific data will be shared as soon as possible, with datasets associated with publications available at the time of publication. All other data will be made available no later than the end of the project. This information will be preserved and accessible for a minimum of five years. Both raw and processed data will be provided at the time of data submission or publication, and will remain available for at least five years.

Element 5: Access, Distribution, or Reuse Considerations

A. Factors affecting subsequent access, distribution, or reuse of scientific data:

There are no use limitations associated with the scientific data generated in this study. There are no ethical or legal issues that can have an impact on data sharing. No personal data will be published in this project.

B. Whether access to scientific data will be controlled:

Data will be made publicly available, and access will not be controlled.

C. Protections for privacy, rights, and confidentiality of human research participants:

No human samples or research participants will be involved in this study.

Element 6: Oversight of Data Management and Sharing:

The Principal Investigator, Dr. Bojun Chen, will oversee the adherence of all project researchers to the Data Management and Sharing Plan. The University of North Texas' Grants and Contracts Administration office, in partnership with the library, will establish a streamlined procedure for facilitating Public Access to Research based on this plan. They will conduct yearly assessments of data submissions and publication updates, and will verify that the PI submits a confirmation statement, ensuring that all data and publications have been duly disclosed to the library and that all requirements of this plan have been met upon the conclusion of the award.