

## Plan Overview

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*A Data Management Plan created using DMPTool*

**DMP ID:** <https://doi.org/10.48321/D1C071>

**Title:** Obtaining the Materials, Results and Collaborations to Submit Grant Proposals on Nematode-Fungal Interactions and Nematode-Suppressive Soils

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**Funder:** United States Department of Agriculture ([usda.gov](http://usda.gov))

**Funding opportunity number:** A1112

**Template:** USDA-NIFA: National Institute of Food and Agriculture

### **Project abstract:**

Cyst nematodes are one of the most damaging groups of obligate pathogens of economically important crops in the USA. The Long-Term Goal of this project is to create safe, cost-effective, and sustainable strategies to reduce crop damage caused by cyst nematodes. Toward that goal, the Objective of this Seed Grant project is to identify agricultural field soils from different geographic regions that harbor fungi belonging to the *Hyalorbilia oviparasitica* clade, and to create a fungal strain collection from those soils. We hypothesize that obtaining these results will allow us to create more effective and more sustainable cyst nematode management strategies by: (i) Determining why certain strains of *H. oviparasitica* clade fungi are more effective than others at suppressing nematodes and by (ii) Determining how to create and maintain nematode suppressive soils utilizing fungal amendments and/or indigenous fungi. We expect that these proposed studies will provide the preliminary results needed for the successful submission of two larger grants. These results will include identifying agricultural field soils from different geographic regions that harbor indigenous populations of *H. oviparasitica* clade fungi, and that come from regions with any of the three most damaging types of cyst nematodes – *Heterodera schachtii*, *glycines*, and *avenae*. These preliminary results will also include constructing a *H. oviparasitica* clade fungal strain collection from these soils. This project addresses one of the Program Area Priorities, which is: "Biotic and abiotic factors ... relevant to pest management; ...," because it is to create more effective and sustainable cyst nematode management strategies.

**Start date:** 02-01-2024

**End date:** 01-31-2026

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## **Obtaining the Materials, Results and Collaborations to Submit Grant Proposals on Nematode-Fungal Interactions and Nematode-Suppressive Soils**

Primary non-digital and digital data generated by this project will come from sources such as computational work and lab work. Data will be diverse and include things such as hand-written observations, images, videos, nucleotide and protein sequences, genome sequences, genome annotations, metabolic models, metabolomics and transcriptomics data, and genetic and phenotypic data. Metadata will include things such as collaborating institution, researcher, date, experimental methods, disease severity ratings, plant weights, microbe and nematode population densities, conditions, locations, and digital file names associated with individual experiments. We will also incorporate the FAIR Framework that can be found at this link – <https://www.go-fair.org/fair-principles>.

Data formats will be non-proprietary, unencrypted, machine-readable, recognizable by the scientific community, and interoperable among platforms and applications (e.g., TXT, DOC, XML, PDF, CSV, TIFF, and JPEG). In the unlikely event of using a proprietary data format, clear instructions for data access and software source (i.e., software name, version, and company) will be included as a simple text file in the data directory. For metabolic models, the format will follow the guidelines presented at BIGG Models (<http://bigg.ucsd.edu/>), which is the recognized standard in this field. Non-digital data will be digitized by scanning or manual input. Data submitted to public databases (e.g. NCBI) will meet all format requirements. University of California librarians specializing in data services are available to assist with annotation of research data, formatting, and metadata workflows for submission to archiving and for use by the scientific community. We will also incorporate the FAIR Framework that can be found at this link – <https://www.go-fair.org/fair-principles>.

Labs using digital notebooks and LIMS systems will be backed up on hard drives. Laboratory computers are routinely backed up on hard drives and a cloud system. Lab members' personal computers are backed up monthly on an external hard drive. Datasets and digital content will be available via open access journal tables, figures, and supplements, and/or deposited in storage services such NCBI and/or Dryad. UC Riverside is a partner of Dryad, an open-source, research data curation and publication platform. All records created in Dryad are searchable, with metadata indexed in Clarivate's Data Citation Index, Scopus, and Google Dataset Search. Dryad may be used as a permanent archive with stable URLs. All deposits to Dryad are sent to a CoreTrustSeal-certified preservation repository called Merritt. All data will be preserved for a minimum of five years after project completion. High-value genome-edited plants will be maintained in greenhouses and tissues sent for long-term storage in the USDA cryopreservation facility. Products including plasmids, nucleic acids, will be retained for at least three years and often longer by storage at -20C and -80C. Plasmids of potential general use will be deposited at Addgene. We will also incorporate the FAIR Framework that can be found at this link – <https://www.go-fair.org/fair-principles>.

Datasets and digital content will be available via open access journal tables, figures, and supplements, and/or deposited in storage services such NCBI and/or Dryad, which allows public sharing. Research data will also be cataloged in the Ag Data Commons as required. Final published data will be made publicly available. PDs will deposit papers published without open access in the UC "eScholarship" digital repository. All publications and presentations acknowledge USDA-NIFA support. Datasets on genomes, gene expression, or metabolomics profiling will be available through NCBI and/or Dryad. All final data associated with the project will be retained for a minimum of five years after project conclusion or any project publication. If requested, data will be shared with qualified parties, as long as such a request does not compromise intellectual property interests or interfere with a publication. All members of the research team will make presentations at stakeholder events and/or scientific conferences. We will also incorporate the FAIR Framework that can be found at this link – <https://www.go-fair.org/fair-principles>.

PD Jiue-in Yang and Co-PI James Borneman (or if needed their replacements, which would likely be the other project participants), will provide oversight of all data management activities and responsibilities. No funds will be needed for data management because will be using all public domain databases, software, and/or services. All members of the project's research team with access to data will receive instruction in the Responsible Conduct of Research, which includes proper maintenance of laboratory notebooks. We will also incorporate the FAIR Framework that can be found at this link – <https://www.go-fair.org/fair-principles>.

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## Planned Research Outputs

Dataset - "Strain rRNA ITS sequences"

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### Planned research output details

Title	Type	Anticipated release date	Initial access level	Intended repository(ies)	Anticipated file size	License	Metadata standard(s)	May contain sensitive data?	May contain PII?
Strain rRNA ITS sequences	Dataset	Unspecified	Open	National Center for Biotechnology Information		None specified	None specified	No	No