Plan Overview

A Data Management Plan created using DMPTool

DMP ID: https://doi.org/10.48321/D16317

Title: Molecular mechanisms enabling nematophagous fungi to parasitize Heterodera schachtii females and that enable H. schachtii female development

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Funding opportunity number: USDA-NIFA-AFRI-009003

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 worldwide. One of our **Long-Term Goals** is to create safe, cost-effective and sustainable strategies to reduce crop damage caused by cyst nematodes. Toward that goal, we **hypothesize** that we will be able to create new and more effective cyst nematode management strategies by obtaining a mechanistic understanding of: (i) the host-microbe interactions between highly effective, hyperparasitic fungi (*Hyalorbilia oviparasitica* clade) and cyst nematodes – which will enable the identification of the most effective fungal strains for biocontrol and (ii) the physiology of developing nematode females emerging from the roots – which will enable the identification of cyst nematode targets for novel nematicide development. The **objective** of this project is to perform transcriptomics experiments to identify both key genes associated with biocontrol of *H. oviparasitica* clade fungi, including fungal attraction, penetration, and parasitism of *H. schachtii* females, as well as the genes associated with the development of *H. schachtii* females as they emerge from the roots. We expect that these proposed seed grant studies will provide the results needed for a successful submission of a larger grant that will **causally test and validate the associations identified in this seed project**. This project specifically addresses one of the Program Area Priorities of the Pests and Beneficial Species Program, "Biotic and abiotic factors affecting the abundance or spread of agriculturally-important plant pests, disease vectors, or beneficial species relevant to pest management."

Start date: 01-01-2023

End date: 12-31-2023

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Copyright information:

Molecular mechanisms enabling nematophagous fungi to parasitize Heterodera schachtii females and that enable H. schachtii female development

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 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.

Planned Research Outputs

Publication in open access journal - "Publication in Open Access Scientific Journal"

Publication in Open Access Scientific Journal

Scientific results - "Molecules & Pathways to Causally Test"

We expect that our innovative experimental design will enable us to identify important molecular mechanisms – which will enable the creation of cost-effective and sustainable strategies to manage cyst nematodes.

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?
Publication in Open Access Scientific Journal	Publication in open access journal	Unspecified	Open	None specified		None specified	None specified	No	No
Molecules & Pathways to Causally Test	Scientific results	Unspecified	Open	None specified		None specified	None specified	No	No