A Data Management Plan created using DMPTool

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Title: Determining the Traits that Enable a Biocontrol Fungus to Consistently Suppress Cyst Nematodes in Different Non-Sterile Soils

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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 biocontrol treatments that are consistently effective across varying agronomic conditions such as different soils. Prior research has shown that a group of nematophagous fungi – the Hyalorbilia oviparasitica clade – are able to consistently suppress cyst nematodes below the damage threshold in different non-sterile soils. This proposed project builds on those prior studies by endeavoring to determine why these fungi have this unusual capability. Specifically, the Goal of this project is to determine the traits that enable members of the H. oviparasitica clade to effectively suppress the sugarbeet cyst nematode (Heterodera schachtii) in different soils. While biocontrol traits such as the ones we propose to examine have been previously studied in other systems, we are unaware of studies that have linked such traits to consistent biocontrol efficacies in different soils. We hypothesize that the findings from this proposed project will provide a blueprint that allows our group and others to more effectively search for and identify additional biocontrol agents that have this important property. This project addresses one of the Program Area Priorities, which is: "Biotic and abiotic factors, affecting the abundance or spread of agriculturally-important ... beneficial species relevant to pest management; ..." Our project addresses this priority because the goal is to identify traits that enable consistent efficacy in different soils which have varying abiotic and biotic features.

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Determining the Traits that Enable a Biocontrol Fungus to Consistently Suppress Cyst Nematodes in Different Non-Sterile 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 James Borneman and PD Jiue-in Yang (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.