# Plan Overview

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*A Data Management Plan created using DMPTool*

**DMP ID:** https://doi.org/10.48321/D11G6C

**Title:** Understanding a Natural Disease Tolerance Phenomenon Using a Metabolic Modeling-Based Approach

**Creator:** James Borneman - **ORCID:** 0000-0003-0661-4970

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**Funder:** United States Department of Agriculture (usda.gov)

**Funding opportunity number:** A1141

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

**Project abstract:**

Huanglongbing (HLB) is a devastating citrus disease that threatens the existence of the citrus industry in the United States and worldwide, and there currently are no effective and sustainable strategies to manage HLB. This project is to use a novel integrated experimental and computational approach to understand a natural HLB disease tolerance phenotype, and then translate that knowledge into HLB management solutions. More specifically, the Long-Term Goal of this proposed project is to create citrus trees that are resistant or tolerant to Huanglongbing (HLB) disease, and/or to create effective prophylactic or curative HLB treatments. The Objective of this Seed Proposal is to use metabolic models and multi-omics data to identify the metabolic pathways and molecules in citrus and its associated microbes that are responsible for the Survivor Tree Phenotype in Florida. Survivor Trees exhibit a very slow rate of decline even though they are in orchards where most of the trees exhibit the normal rapid HLB decline. After 4.5 years of an ongoing study, we have identified trees that have only declined by 0.5 in a 0 to 5 disease rating system. Since this proposed project is to identify the metabolic pathways and molecules in citrus and its associated microbes that are responsible for the Survivor Tree Phenotype, it specifically addresses one of the Program Area Priorities of the Pests and Beneficial Species Program, which is "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:** 11-01-2021

**End date:** 10-31-2023

**Last modified:** 01-17-2024

**Copyright information:**

## Understanding a Natural Disease Tolerance Phenomenon Using a Metabolic Modeling-Based Approach

Primary non-digital and digital data generated will come from computational work and lab work. Data will be diverse and include hand-written observations, images, videos, nucleotide and protein sequences, genome sequences, genome annotations, metabolic models, metabolomics and transcriptomics data, as well as genetic and phenotypic data. Metadata will include collaborating institution, researcher, date, experimental methods, HLB disease severity rating, Survivor or Non-Survivor Tree status, 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. The format of the metabolic models follows 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), meet all format requirements. A University of California librarians specializing in data services is 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 for publications will be submitted in Dryad for curation and preservation. The project will also use the University of California Curation Center (UC3) Merritt Repository Service to manage, archive, and share digital content. Merritt provides public access via persistent URLs, tools for long-term data management, and permanent storage options, with built-in contingencies for disaster recovery. 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 at Fort Collins, Colorado. 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 (e.g. CRISPR-based genome editing vectors and citrus-specific promoters) 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.

During the grant, data will be deposited in Merritt (as described above) 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 or Dryad. Progress and final reports will include a persistent identifier that provides links to the full text. 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 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 with assistance from Co-PD Karsten Zengler (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 - "Annotated Citrus Genomes"

1. Annotated Citrus Genomes

### Model representation - "Metabolic Models will be archived at BIGG Models https://bigg.ucsd.edu"

Metabolic Models will be archived at BIGG Models https://bigg.ucsd.edu

### Dataset - "Omics Datasets"

Omics Datasets

### Text - "Putative Molecules and Pathways that explain the Survivor Tree Phenotype - Provided in Publications and at https://escholarship.org"

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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? |
|---|---|---|---|---|---|---|---|---|---|
| Annotated Citrus Genomes | Dataset | 2023-10-30 | Open | NCBI | 800 MB | Creative Commons Attribution Non Commercial 4.0 International | None specified | No | No |
| Metabolic Models will be archived at BIGG Models h ... | Model representation | 2023-10-30 | Open | None specified | 1,000 MB | Creative Commons Attribution Non Commercial 4.0 International | None specified | No | No |
| Omics Datasets | Dataset | 2023-10-30 | Open | NCBI | 50 GB | Creative Commons Attribution Non Commercial 4.0 International | None specified | No | No |
| Putative Molecules and Pathways that explain the S ... | Text | 2023-10-30 | Open | None specified | 1 MB | Creative Commons Attribution Non Commercial 4.0 International | None specified | No | No |