United States Department of Agriculture
Project Initiation

Project Data for Accession Number 1033765

Project Title

ENHANCING CROP HEALTH THROUGH THE ROOT: UNDERSTANDING MECHANISMS OF BACTERIAL INVASION OF RHIZOSPHERE COMMUNITIES

Project Details

Sponsoring Institution National Institute of Food and Agriculture	**Project Status** ACTIVE
Funding Source NIFA Non Formula	**Grant Year** 2026
Grant No. 2026-67039-45654	**Cumulative Award Amt.** $850,000.00
Proposal No. 2024-12632	**Multistate No.** (N/A)
Project Start Date Jan 15, 2026	**Project End Date** Jan 14, 2029
Program Code [A1402] Agricultural Microbiomes in Plant Systems and Natural Resources	

Project Director

Handelsman, J.

Recipient Organization

UNIVERSITY OF WISCONSIN SYSTEM

21 N PARK ST STE 6301

Madison, WISCONSIN 537151218

Performing Department

(N/A)

Non Technical Summary

Crop production needs to increase to meet the future food needs of the Earth's population. Addressing this challenge will require effective,sustainablemethodstobolster yields and improve plant health.Microbial inoculants offer promising technologies but have behaved inconsistently in the past. Our incomplete understanding of how microorganisms invade communities on roots or in soil prevents design of more successful inoculants. Therefore, the goal of the proposed work is to understand the ability of a beneficial bacterium to invade the natural rhizosphere community. Specifically, we will characterize thegenetic drivers of microbial invasiveness. This will enable the design or selection of bacterial crop inoculants that are more successful in reaching their target and accomplish their intended function, such as protecting crop plants from disease or providing them with nutrients. The goal is to reduce the use of chemical pesticides and fertilizers.

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Animal Health Component

Animal Health Component: 0%

Research Effort Categories

Basic	80%
Applied	20%
Developmental	0%

Classification

Knowledge Area (KA)	Subject of Investigation (SOI)	Field of Science (FOS)	Percent
102	1640	1100	100%

Knowledge Area

[102] Soil, Plant, Water, Nutrient Relationships

Subject Of Investigation

[1640] Alfalfa

Field Of Science

[1100] Bacteriology

Keywords

microbial community dynamics, rhizosphere, soil, bacterial invasion, multiomics

Goals / Objectives

Crop production needs to increase to meet the future food needs of the Earth's population. Addressing this challenge will require effective, sustainable methods to bolster yields and improve plant health. Microbial inoculants offer promising technologies but have behaved inconsistently in the past. Our incomplete understanding of how microorganisms invade communities on roots or in soil prevents design of more successful inoculants. The goal of the proposed work is to understand the ability of a beneficial bacterium to invade the natural rhizosphere community. Specifically, we will characterize the genetic drivers of microbial invasiveness.Using a simple model rhizosphere community developed by our lab, we will functionally characterizeSinorhizobium melilotiduring community invasion with metatranscriptomics and metabolomics. We will also use a functional, non-targeted approach to find genes that contribute to or diminish invasion with a massively parallel screen that will identify mutants that are either over- or under-represented after invasion on a plant-host. From these experiments we will select candidate genes predicted to drive invasion success and functionally validate their role during invasion. Finally, we will determine whether there are trade-offs between invasion ability and symbiotic behavior with the plant host. This will be accomplished by determining whether mutants affected in invasion are altered in plant root colonization and nodulation. This work will produce a mechanistic understanding of the genes and functions involved in community invasion, which has not been subjected to genetic characterization, and inform design of reliable and effective microbiological interventions to improve crop production.

Project Methods

Methods will include scientific experiments to identify genes involved in community invasion. This will entail transposon mutagenesis, DNA sequencing, computational analysis of DNA sequences, cloning and mutating genes of interest, community invasion experiments in a model community in vitro followed by invasion experiments on plant roots.