

**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**

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

**Project Director**

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**Recipient Organization**

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**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, 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. 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 the genetic 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 characterize *Sinorhizobium meliloti* during 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.

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### **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.