

ML 2015, Ch. 76. Art. 2, Sec. 6a Project Abstract
Amended December 8, 2022

PROJECT TITLE: Sub-project #6: Distribution and traits of the fungal pathogen *Fusarium virguliforme* that influence current and future risks to soybean and other legumes in Minnesota

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APPROPRIATION AMOUNT: \$383,651

AMOUNT SPENT: \$383,651

AMOUNT REMAINING: \$ 0

Sound bite of Project Outcomes and Results

This project has discovered factors that influence the ability of the fungus *Fusarium virguliforme* to become established as a destructive pathogen on crops in new areas of Minnesota. The results are foundational to understanding this pathogen and contribute to managing the diseases it causes on soybean and other crops.

Overall Project Outcome and Results

The fungal pathogen *Fusarium virguliforme*, which causes sudden death syndrome (SDS) on soybean and root rot of other legumes, is an expanding problem for crop producers in Minnesota. Our research team has made discoveries regarding the pathogen's ability to spread and cause disease. First, a survey has confirmed the spread of the pathogen for the first time into seven counties in central and western MN. Second, studies of nutrient use suggest that *F. virguliforme* grows on a larger number of carbon and nitrogen sources than many other fungi in crop fields, likely giving it a competitive advantage. Analysis of competition between *F. virguliforme* and other fungi from crop fields revealed that while several fungi can inhibit its growth, multiple others are overcome by the pathogen, indicating it is a good competitor in soil and roots. Third, we determined it can survive to -40°C and thus its spread is not likely limited by cold temperatures. Fourth, in field and greenhouse experiments investigating host range, multiple crop species (black bean, pinto bean, kidney bean, and pea) showed symptoms of disease, and multiple other plant species were infected asymptotically. Fifth, we completed a study and a publication on genetic and pathogenic variation among *F. virguliforme* populations in Minnesota and the Midwest. While genetic groups did not correspond to aggressiveness, three genetic clusters were identified, with two clusters likely contributing most to spread of this fungus. Sixth, we completed initial analysis of genomes from 35 isolates to investigate genes involved in pathogenicity and abilities to invade new environments. The project trained one M.S. level and one postdoctoral level scientist, expanding expertise for addressing invasive plant pathogens. This project significantly advances fundamental and applied knowledge of *F. virguliforme* that can be harnessed for disease management and risk analysis by scientists, agricultural professionals, and crop producers.

Project Results Use and Dissemination

This project has discovered multiple factors that influence the ability of *F. virguliforme* to spread and become established as a destructive pathogen on crops in new areas. Results have been presented via University of Minnesota Extension programs to key agricultural professionals and crop producers across Minnesota that contribute to managing this pathogen and the crop diseases it causes. Results have also been presented at scientific conferences and are being published in scientific journals.