Project #: 

Progress Report Year: 1 of 1 (maximum of 3 year funding cycle)

Title: Imaging and Rhizosphere Microbial Analysis of Wheat Seedlings Experiencing Root Rot Caused by *Rhizoctonia solani* AG8

PI: Isaac Madsen

Cooperators: Rick Lewis, Tarah Sullivan, Christine Jade Ermita

Executive summary:

Root rot is a yield reducing fungal disease in the inland Pacific Northwest. *Rhizoctonia solani* AG8 is a fungal pathogen responsible root rot and bare patch in wheat. The present methods for assessing disease severity are subjective and/or expensive disease analysis. This project set out to initiate the development of objective and inexpensive methods for assessing disease severity. The method proposed in this project is an innovative imaging method which uses a scanner based rhizobox and allows for non-destructive observations of disease progression. Four successful experimental runs have been conducted and the project is currently in the analysis phase. The initial experiments demonstrated the ability of the rhizobox methods to detect disease symptoms on infected roots, but has not successfully led to the differentiation between tolerant and susceptible wheat genotypes. The current difficulties in detecting varietal differences are likely due to a lack of variation in tolerance between the wheat varieties used in the study. In a corresponding screening experiments utilizing the conventional screening methods, no differences were found between the varieties used in the trial of the rhizobox method. However, as we are endeavoring to find a more sensitive technique than the conventional technique we intend to continue using image processing and analysis to attempt to delineate between the genotypes. Additionally, we intend to use different wheat genotypes in at least two more experimental runs with the rhizoboxes. These additional runs will focus on using what are known to be highly susceptible varieties of wheat in order to maximize the variation. In addition to the development of the imaging methods described above the soil microbiome of the rhizosphere (soil near the root) and the bulk soil are being analyzed. To date the rhizosphere and bulk soil have been sampled and the DNA has been successfully extracted from the soil. DNA sequencing will be completed by the spring of 2020 and analysis will follow shortly after.

Impact:

The primary immediate impact of the project is the demonstration of rhizoboxes as an effective means of differentiating between diseased and non-diseased wheat plants. These results have been presented at two international meetings. In the short-term we plan to demonstrate the effectiveness of this technique in differentiating between susceptible and tolerant wheat lines. The successful differentiation between wheat lines will lead to accelerated wheat breeding. In the long-term we hope the microbial analysis conducted in this study may help develop biocontrol agents for root pathogens.
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**Project PI(s):** Isaac Madsen, Ph.D., Rick Lewis, Ph.D., Tarah Sullivan Ph.D., Scot H. Hulbert, Ph.D. and Christine Jade  
**Project initiation date:** July 1, 2019  
**Project year (1 of 3-yr cycle):**

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