

# Plant Pathology Seminar Series



## “Wheat Genotype-Specific Recruitment of Rhizosphere Microbiomes that are Suppressive to Rhizoctonia Root Rot”

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### Abstract

The soilborne fungal pathogen *Rhizoctonia solani* AG8 causes root-rot and bare patch disease and is an important disease of wheat especially in the dryland areas of the Pacific Northwest. Despite large scale screening for resistance, resistance is limited in the wheat germplasm. Harnessing suppressive soils with the use of specific wheat genotypes that recruit suppressive rhizosphere microbiomes is a potential alternative in managing the disease. To determine wheat genotype-specific recruitment of microbiomes, growth chamber cycling experiments using six winter wheat genotypes were initially done and suppression assays were performed to determine suppression against *R. solani* AG8. Furthermore, a more diverse wheat panel was assembled for a two-year field cycling experiment to explore more suppressive microbiomes. Soils cultivated with PBW343 a spring wheat variety, exhibited more suppressiveness compared with PI561725, a winter wheat breeding line that was identified to have a suppressive microbiome in the initial growth chamber cycling experiment. Disease suppression observed in the field was further validated in the growth chamber. To identify bacterial taxa that constitute the suppressive microbiome, 16S rRNA sequencing was done and revealed that bacterial taxa belonging to Proteobacteria, Bacteroidetes and Actinobacteria were differentially more abundant in the rhizosphere of PBW343 and were associated with pathogen suppression. Furthermore, bacterial isolation from the rhizosphere soil of PBW343 was done to isolate suppressive bacterial taxa and to determine direct antagonism to the pathogen. Of the 13 isolates, *Pseudomonas baetica*, *Stenotrophomonas maltophilia* and *Pseudomonas fluorescens* significantly reduced the radial growth of the pathogen. Our research demonstrated that disease suppression elicited by microbiomes are recruited by specific wheat genotypes. With this, specific wheat genotypes can be used to manipulate soil as part of a cropping system to manage root rot and bare patch disease in wheat.

### References

- Mahoney, A. K., Yin, C., and Hulbert, S. H. (2017). Community structure, species variation, and potential functions of rhizosphere-associated bacteria of different winter wheat (*Triticum aestivum*) cultivars. *Front. Plant Sci.* 8, 132.
- Mazzola, M., and Gu, Y. (2002). Wheat genotype-specific induction of soil microbial communities suppressive to disease incited by *Rhizoctonia solani* anastomosis group (AG)-5 and (AG)-8. *Biol. Control* 92, 1300–1307.
- Yin, C., Hulbert, S. H., Schroeder, K. L., Mavrodi, O., Mavrodi, D., Dhingra, A., ... Paulitz, T. C. (2013). Role of bacterial communities in the natural suppression of *Rhizoctonia solani* bare patch disease of wheat (*Triticum aestivum* L.). *Appl. Environ. Microbiol.* 79, 7428–7438.

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**ZOOM Link:** <https://wsu.zoom.us/j/93395333254?pwd=OVlwWk8xcnNadVluVjFYUW5hWWx1dz09>

**Meeting ID:** 933 9533 3254

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