

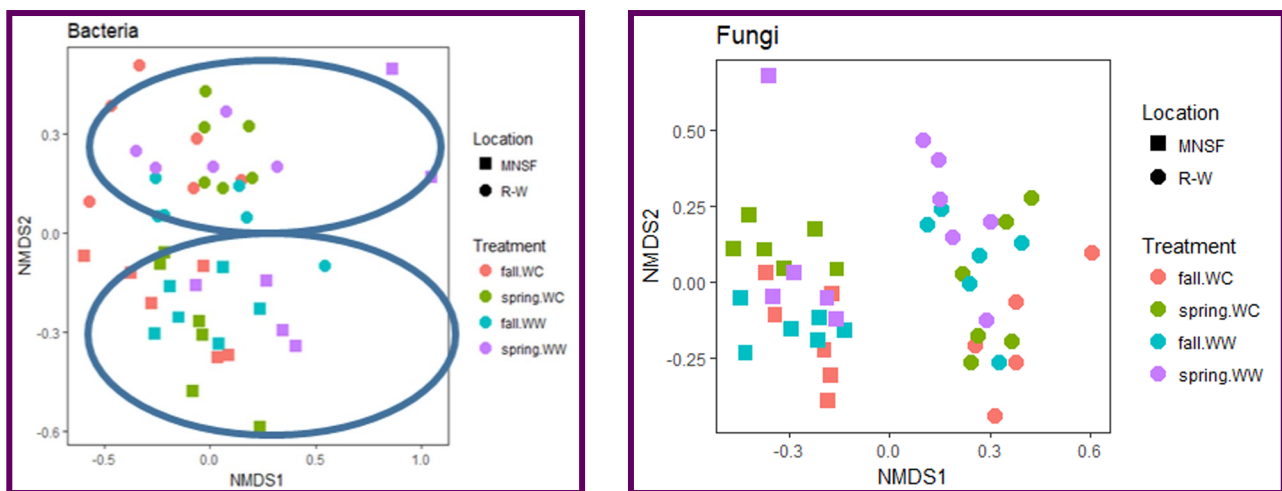
## The Rhizosphere Microbiome of Wheat and Canola in Eastern Washington



DANIEL SCHLATTER<sup>1</sup>, JEREMY HANSEN<sup>1</sup>, WILLIAM SCHILLINGER<sup>2</sup>, TARAH SULLIVAN<sup>2</sup>, AND TIMOTHY PAULITZ<sup>1</sup>

<sup>1</sup>USDA-ARS; <sup>2</sup>DEPT. OF CROP AND SOIL SCIENCES, WSU

In a series of replicated field trials over 6 years in the Davenport area, spring wheat grown after winter canola had an average of a 17% yield decrease, compared to when grown after winter wheat. Diseases, water use, and nutrient use could not explain this reduction (see article on page 40). We explored the potential role of microbial communities in explaining this yield decline (see articles on page 54). With samples from a related study (see article on page 45), we used next-generation sequencing (Illumina MiSeq) to look at fungal and bacterial communities to examine the differences in microbial communities between crop species. Six fields were sampled, three in Douglas County and three in Adams County. The soil around the roots (rhizosphere) was sampled on winter canola and winter wheat in fall and spring. Community analysis showed that location was a primary driver of both fungal and bacterial communities, with the three locations in Douglas County clustering together, and the Adams County sites similar to each other (Fig. 1, 2). Season had the next strongest effect, followed by the crop. Differences between the two crops was more evident in the spring than the fall. A more detailed comparison of bacteria showed that *Pseudomonas*, *Flavobacterium* and *Pedobacter* were more abundant on the wheat rhizosphere compared to canola. A few genera including *Opitius* and *Sporocytophaga* were more abundant on canola. Many groups highly abundant in the rhizosphere of both crop species, especially *Janthinobacterium* and *Kaistobacter*. Another interesting finding was that the bacterial community on winter wheat in the fall was dominated by Actinomycetes and Acidobacteria. These are slow growing bacteria that can survive the hot, dry summer. But in the spring, these communities were dominated by fast growing bacteria adapted to high levels of nutrients coming off the root and wetter conditions, including *Pseudomonas*, Oxalobacteraceae, and Sphingobacteriaceae. We identified almost 1,000 groups of fungi. Some fungi were very abundant on both crops- *Ulocladium*, *Mortierella*, *Cryptococcus*, *Chaetomium*, *Penicillium* and *Trichoderma*. These are very abundant in soils as saprotrophs and decay residue. The only distinct differences were the identification of wheat root pathogens in higher levels in winter wheat- *Rhizoctonia*, *Ceratobasidium*, *Typhula*, and *Microdochium*. The latter two are snow molds. In conclusion, we did not find a "smoking gun" of a group that was increased by canola. Most of the community of fungi and bacteria are not "host specific" but colonize around the roots of both wheat and canola.



Figures 1 (left) and 2 (right). Non-metric multidimensional scaling (NMDS) of bacterial and fungal communities. MNSF= Douglas County, R-W = Adams County. WC= winter canola, WW= winter wheat