

the *Yr8* near-isogenic wheat line. To answer the questions why race-specific all-stage resistance is not durable and non-race specific HTAP resistance is durable, we completed experiments to elucidate mechanisms of stripe rust resistance using the microarray technology. In 2008, we made wheat custom gene chips based on genes identified in the previous studies to determine common and unique genes regulated by various genes for either all-stage or HTAP resistance. Molecularly, HTAP resistance is more broadly based than all-stage resistance. Through collaborating with Dr. Dubcovsky's program at UC Davis, we cloned resistance gene *Yr36*. In 2008, we evaluated 18 fungicide treatments including different rates and application combinations of Topguard, BAS 556 01, and Evito for control of stripe rust in experimental fields near Pullman, WA. Better formulations and applications of fungicides were identified.

Rhizoctonia Resistant Wheat -- Potential New Resources for Control for Soilborne Pathogens

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Pacific Northwest (PNW) wheat, barley, legume and canola varieties are susceptible to the broad host-range soilborne pathogens that cause *Rhizoctonia* root rot and *Pythium* root rot. Effective control of these diseases will likely require additional approaches and resources. We have identified promising new sources of genetic resistance against *Rhizoctonia solani* AG-8 and *R. oryzae*, *Pythium ultimum* and *P. irregulare* group I. These four pathogens are among the most damaging to PNW dryland cereal production systems. Until the generation of the *Rhizoctonia*-resistant wheat genotype Scarlet-Rz1 by mutagenesis, non-GMO resistance to root diseases has been elusive. The resistance in Scarlet-Rz1 is readily deployable by wheat breeders, making it unique. In greenhouse trials, Scarlet-Rz1 seedlings are resistant to about ten-fold more pathogen than is detected in symptomatic field soils. Field trials are being planned to determine how seedling resistance impacts field traits, such as heading date and yield. Chromosome 4 from the wild grass *Thinopyrum* confers resistance to eyespot, an important disease of winter wheat caused by the soilborne pathogen *Tapesia yallunde*, when introduced into hexaploid wheat Chinese Spring. We have determined that seedlings of Chinese Spring carrying *Thinopyrum* chromosome 4 also are resistant to *R. solani* AG-8 and *P. ultimum*. Scarlet-Rz1, Chinese Spring-chromosome 4 addition lines and other genotypes of wheat under development offer novel genetic resources for combating *Rhizoctonia* and *Pythium* in the PNW.

Real-time detection and quantification of *Rhizoctonia* and *Pythium* species on the Cook Agronomy Farm.

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Populations of *Rhizoctonia* and *Pythium* are diverse in eastern Washington, with multiple species/anastomosis groups present throughout the region and within individual fields. The process of identifying the pathogen present in a sample is laborious and the high diversity increases the difficulty in accurately identifying and quantifying the important species present in a field. Recently, real-time PCR assays were developed for both of these organisms to provide a new tool for more accurate measurements of pathogen populations. With this new tool, the biology and disease management strategies for these organisms can be better evaluated. Evidence from recent surveys for the presence of these pathogens suggests that various environmental and soil factors may influence the species composition and populations of these pathogens. This composition may also be influenced by crop rotation. To further evaluate the impact of crop rotation and spatial distribution of these pathogens, soil samples were collected from the Cook Agronomy Farm near Pullman, WA. This research farm was established in 1999 to test direct-seed cropping systems on a field scale and includes 369 GPS sampling locations spaced every 30 m. A three-year rotation was established to include winter wheat-alternate crop-spring wheat, with each rotation occurring every year. The alternate crops consisted of a winter and/or spring variety of pea, lentil, barley or canola. Soil samples were collected from about 115 sites from the spring wheat portion of the field following the alternate crop. DNA was extracted from each soil sample using a Barocycler™ and Mo-Bio Soil DNA kit, and

quantified with species-specific primers and real-time PCR. *Rhizoctonia solani* AG-2-1 occurred more frequently in fields with a history of canola, with a higher frequency following spring canola (48% of sites) compared to winter canola (28%). *Rhizoctonia oryzae* was detected more often following winter alternate crops (39-44%) than spring crops (24-37%). Of four *Pythium* species examined, *P. irregulare* group IV and *P. rostratiformis* had the highest incidence of occurrence (66% and 67% respectively). These species of *Pythium* were also higher following winter canola and pea versus spring canola and pea. *Pythium ultimum* and *P. irregulare* group I, two of the more virulent species of *Pythium*, were seldom observed on this farm.

Ten Years of Plant Pathology Research at the Cook Agronomy Farm: What Have We Learned?

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The Cook Agronomy Farm has provided important information for understanding root diseases under direct-seeded conditions in the higher rainfall annual cropping zones of the Palouse, at a landscape scale. This farm has served as an important outdoor laboratory to test disease management techniques such as chemical fallow, residue management and precision N application. The primary *Rhizoctonia* species on the farm is *R. oryzae*, which has an aggregated, patchy distribution and is not influenced by crop rotation. On the other hand, *R. solani* AG 2-1, a brassica pathogen, was strongly influenced by rotation, and was found almost exclusively in the plots that had either spring or winter canola the previous 1 or 2 years. Surprisingly, *R. solani* AG-8, the cause of bare patch, is almost completely absent from the farm, despite 10 years of direct-seeding. Chemical fallow reduced *R. solani* AG-2-1 but not *R. oryzae*, only after 3 years in the absence of a host, although the fallow was not completely weed-free. This indicates that *Rhizoctonia* can survive for long periods in intact roots in chemical fallow, or as microsclerotia, in the case of *R. oryzae*. The predominant *Pythium* species on the farm are *P. irregulare* group IV and *P. rostratiformis*. The most virulent species, *P. ultimum*, is very rare on the farm. Unlike *Rhizoctonia*, *Pythium* is more evenly distributed across the landscape. *P. irregulare* group I is also less prevalent, but highly pathogenic on legumes such as lentils, peas and chickpeas. Fusarium crown rot probably has been the most yield-limiting disease on the Cook Farm, especially since the wheat varieties were hard red, managed with high N levels to attain protein. This disease is exacerbated by drought and excess N fertilizer levels. We have been able to see crown rot every year, especially on dry sites and in low rainfall years. *F. culmorum* is the predominant species, with less *F. pseudograminearum*. Rotation does not have a large effect on these pathogens, which mainly infect grassy hosts. Splitting N application in the fall and spring, as opposed to all in the spring, did not consistently reduce Fusarium crown rot averaged across the entire landscape. Precision application of N, based on landscape position and amount in the soil, also did not consistently reduce disease when averaged over the entire field, but may reduce disease at specific locations. Take-all, caused by *Gaeumannomyces graminis* var. *tritici*, has occurred at very low levels on the Cook Farm. This disease is primarily controlled by rotating with non-host broadleaf crops such as pea or canola every 3rd year.

Screening Wheat and Brassica Germplasm for Resistance to *Rhizoctonia* Root Diseases

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Rhizoctonia solani infection can cause poor stands of both wheat and canola and even bare or severely stunted patches when inoculum levels are high. Crop rotation alone will not control the disease because there are different taxonomic groups of the pathogen that can infect multiple crops. For example, *Rhizoctonia solani* AG-2-1 is particularly virulent on canola and *R. solani* AG-8 affects both wheat and canola. The disease is particularly troublesome in direct-seed systems or when the crops are planted into dying weeds or volunteers treated with herbicides. Genetic resistance in various crops would be an efficient means to control the disease. Up to now, no wheat or canola varieties have been identified with good levels of resistance. We examined the levels of resistance in a diverse set of *Brassica* genotypes collected from different breeding programs with both winter and spring growth habit types. A total of eighty five genotypes of *Brassica napus*, *B. rapa*, *B. carinata*, *B. juncea* and *Sinapis alba* were evaluated in the growth chamber for their resistance to both *R. solani* AG-2-1 and AG-8. The percentage