

Washington Grain Commission
Wheat and Barley Research Annual Progress Reports and Final Reports

Project #: 3673

Progress Report Year: 1 of 3

Title: Increasing Genetic Opportunities for Stripe Rust Resistance

Investigator/Cooperators: **AH Carter, KG Campbell, M Pumphrey**, X. Chen, S. Hulbert, D. See

Executive summary: Significant SNP markers associated with novel resistant genes and known genes such as *Yr17*, *Yr5* and the Coda resistance have been identified through Winter wheat and/or Spring wheat panels. Additionally, novel stripe rust resistance genes from tetraploid wheat have also been identified. Although some of these genes identified have already been described, the identification of SNP markers linked to these genes will allow breeders to more effectively transfer these useful genes into new breeding lines. The resistance genes from tetraploid wheat are in the process of being transferred to spring wheat for use in breeding. Spring wheat lines were initially chosen for speed, but will eventually be moved into winter germplasm as well. The JD/Avocet S and Finch/Eltan populations have been tested in the field for QTL analysis and we have identified the stripe rust genes from Finch and Eltan. Mutant populations for *Yr5* and the Coda resistance have been developed for further analysis and were screened under field conditions in 2014. Association mapping has been completed on various panels and a list of resistance loci, markers, and germplasm containing each resistance source has been identified. These lines are in the process of being crossed to other breeding material and marker assisted selection will take place to carry forward breeding lines with multiple sources of resistance. We now have multiple effective sources of resistance to PNW races of stripe rust, as well as markers associated with them, to begin selecting resistant germplasm. Additional studies are being conducted to further evaluate selected sources of resistance to better characterize these genes.

Impact: Throughout the project, we identified SNP markers which showed significant association with novel resistant genes and known resistant genes. We are now able to add them in our MAS protocols and routinely screen for these resistance genes in our breeding material. We also have developed SNP markers linked to the Louise and Coda resistance and successfully have applied them in MAS. It is a significant accomplishment to develop elite wheat cultivars with durable rust resistance in PNW wheat breeding programs. The impact of identifying new SNP markers will allow all breeding programs the ability to use and pyramid useful stripe rust resistance genes into new germplasm. The effective use of resistance genes will mitigate the damage caused by the stripe rust pathogen as well as the amount of fungicides applied each year. Wheat producers in Washington have access to wheat cultivars with better stripe rust resistance than they did three years ago. The markers identified in this project will continue to ensure that future releases from breeding programs have resistance to stripe rust, thereby maintaining or improving upon the level of resistance they already experience in current cultivars.

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Project PI(s): A Carter, K Garland-Campbell, M Pumphrey
Project initiation date: July 1, 2014
Project year: 1 of 3

Objective	Deliverable	Progress	Timeline	Communication
Use DNA markers to pyramid stripe rust resistance into PNW breeding material	Breeding lines and cultivars with multiple resistance genes conferring both seedling and adult plant resistance	Association mapping has been completed and QTL have been identified. Lines carrying these QTL have also been identified. In some cases, crosses have already been made to these lines and populations are being developed for selection. In other cases, crosses have been initiated with lines carrying the desired QTL. QTL have been identified which would work well to be pyramided together and population selection will begin in 2015.	Population creation and selection with DNA markers will be done annually as populations are established. Once populations have been selected upon, field screening will be completed to ensure resistance has been captured.	Results will be communicated through field days, grower meetings, seminars, journal articles, annual progress reports, and the wheat research review, as well as through other venues as requested.
Transfer resistance genes from Emmer wheat into hexaploid wheat	Additional novel genes currently effective against PNW stripe rust races moved into new breeding lines and cultivars	37 BC1F2 populations have been made and are currently being grown in the greenhouse. DNA markers will be used to identify progeny with stripe rust resistance genes of interest and then phenotyping will be done to confirm resistance. These lines will then be further used to introgress this resistance into other PNW germplasm.	Crosses between Emmer wheat and hexaploid wheat have been completed. Additional crosses will be done as necessary and once populations are established markers will be used to select for resistance.	Results will be communicated through field days, grower meetings, seminars, journal articles, annual progress reports, and the wheat research review, as well as through other venues as requested.
Develop 'near-perfect' markers for Yr5, Yr15, and YrCoda that can be used for marker-assisted selection.	DNA markers associated with genes resistant to currently known stripe rust races in Washington	Mutation populations have been generated. Phenotyping was completed in 2014. Additional phenotyping will be done in 2015. Crosses have been made to verify if YrCoda is novel or not. Genetic linkage maps are in their final stages and new markers tightly linked to these genes are in their final stages of validation.	Phenotyping will be done for two to three years. Genotyping will be done concurrently. Markers will be identified at the end of the funding period.	Results will be communicated through field days, grower meetings, seminars, journal articles, annual progress reports, and the wheat research review, as well as through other venues as requested.

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