

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

Project #: 5195
Progress Report Year: 3 of 3
Title: Use of biotechnology for wheat improvement
Investigator/Cooperators: **AH Carter**, KG Campbell, D See, M Pumphrey

Executive summary: In 2014 we continued our effort to advance breeding lines as quickly and efficiently as possible by employing both molecular marker analysis and doubled-haploid technology. The traits of main focus for marker-assisted selection are foot rot resistance, stripe rust resistance, herbicide tolerance, and end-use quality. These are our primary focus due to very good markers having been developed and the importance of these traits in Washington. Additional traits include aluminum tolerance, SBWMV, dwarfing genes, photoperiod sensitivity, and nematode resistance. Over 900 lines were selected out of those tested which had the desired genes based on marker profiling. These have been advanced to field testing to confirm presence of the selected genes. Markers were also used to screen all advanced breeding lines to identify presence of known genes. This information was used for selection and advancement purposes (in conjunction with field data) as well as for selecting lines which should be cross-hybridized to create future populations. The process of marker-assisted selection is an ongoing process, and at any given point we either have lines planted for analysis, in the laboratory undergoing marker profiling, or on increase in the greenhouse after selection to advance seed into field evaluations. Our genomic selection efforts are proceeding and we have completed our third year of phenotypic evaluations in the field. We submitted this population for GBS analysis. We will begin establishing the prediction model to apply to material in the field in the summer of 2015.

In the greenhouse, we made approximately 1,000 crosses consisting mainly of soft white, hard white, and hard red germplasm. These are being advanced to the F2 generation. We planted 1,100 DH plants in the field in 2014 for evaluation in 2015. In 2014 we attempted nearly 6,000 DH crosses, of which about 3,000 were successful. These will be advanced under greenhouse conditions and planted in the field in 2015.

We continue to introgress and select for (both phenotypically and with markers) germplasm containing herbicide resistance, foot rot, cold tolerance, snow mold tolerance, end-use quality, and stripe rust resistance. Multiple tools are being used in the greenhouse to screen this material for the selected traits and prepare seed for field evaluations. For these select traits, screening in the greenhouse can help ensure germplasm advanced to field conditions has the required level of resistance needed for variety release.

Impact: This project covers all market classes and rainfall zones in the state of Washington. This work will improve end-use quality, genetic resistance to pests and diseases, and agronomic adaptability and stability of released cultivars. Incorporating novel genes into cultivars will enhance the profitability of winter wheat production. Growers will save time and money by getting superior cultivars into their hands much quicker. The full impact of this work will depend on the adoption of wheat producers to the new cultivars developed, the perceived losses avoided through genetic resistance, and the varying price of wheat and input costs.

WGC project number: 5195
WGC project title: Use of biotechnology for wheat improvement
Project PI(s): AH Carter
Project initiation date: July 1, 2012
Project year: 3 of 3

Objective	Deliverable	Progress	Timeline	Communication
Marker-assisted selection				Results are presented through annual progress reports, the research review, field tours, and grower meetings
	Foot rot resistant lines	In 2014, 12 populations were screened for the Pch1 gene for foot rot resistance. Of these, lines with the gene were advanced in the greenhouse and field selection will occur this coming year.	Each year new crosses are made to Pch1 containing lines. These are subsequently developed, screened, and advanced to state-wide yield trials. At any given time, lines are in every stage of development	
	Stripe rust resistant lines	In 2014, 15 populations for Yr5 and Yr15 were screened for and selected upon for upcoming field testing. Additionally, crosses were made in the field with lines carry diverse stripe rust genes that survived the cold and looked to perform well in the field. Field crosses were done to expedite the development process. An additional 5 populations were screened for a rust gene from the cultivar Stephens.	Each year new crosses are made to stripe rust resistant lines. These are subsequently developed, screened, and advanced to state-wide yield trials. At any given time, lines are in every stage of development	
	Gpc-B1 and Bx7oe lines	In 2013, 34 F2 populations were screened for the genes Gpc-B1 and Bx7oe. Of these, 472 lines were selected and advanced in the greenhouse. In 2014 these were selected under field conditions and lines selected are now undergoing end-use quality screening. In 2014, 12 populations for Gpc-B1 were selected upon, and additional populations have been initiated with these two traits for selection in 2015.	Each year new crosses are made to lines containing unique end-use quality genes. These are subsequently developed, screened, and advanced to state-wide yield trials. At any given time, lines are in every stage of development	

	Reduced height lines	In 2013, 5 populations were screened for incorporation of various Rht genes. These lines were tested in 2014 for emergence potential and lines which emerged well have been planted again at Lind for further screening while proceeding through the breeding process.	In 2013 these lines will be planted and in 2014 evaluated for performance under field conditions. Once it is confirmed these lines reduce height without hindering emergence or yield potential, more crosses will be initiated to more fully incorporate into our germplasm.	
	Genomic selection	Our genomic selection training panel was genotyped with 9K SNP markers in 2011. In 2012 and 2013, we collected our additional phenotypic data. In 2014 we did GBS on this population. We have combined agronomic data on this population into one file. With the assistance of Dr. Zhang, we will begin genomic selection in 2015. Prediction model development will begin and refinement will be made as more data is added at the end of the 2015 season. Once the model is developed, we will use it to predict performance of our advanced breeding lines currently in field trials.	Each year we will continue to phenotype the training panel, add more lines to the training panel (and genotype them), and refine the prediction model	Results are presented through annual progress reports, the research review, field tours, and grower meetings
Genotyping advanced breeding lines	Provide useful information regarding genetic diversity and gene profiles to better estimate crossing potential	In 2014, the advanced germplasm was screened with DNA markers for traits of interest. In 2015 we plan to continue this screening and progress to earlier generations.	This is done annually	Results are presented through annual progress reports, with the outcomes of this research being realized in new cultivars
Greenhouse				Results are presented through annual progress reports, with the outcomes of this research being realized in new cultivars
	Hybridization and propagation	In 2014 we made approximately 1200 crosses which were targeted for herbicide resistance, low rainfall and high rainfall production, and specific gene introgressions. These crosses were advanced to the F2 stage.	This is done annually, with the number of crosses/populations varying	
	Single-seed descent	Four existing (high rainfall SWW, Lo rainfall SWW, HWW and HRW Populations) single seed decent populations were increased to the F4 generation in the green house in 2013 and evaluated in the field in 2014. Due to lack of greenhouse space we did not make additional populations for 2014 increase. We have plans to do SSD populations in 2015.	This is done annually, with the number of crosses/populations varying	

	Doubled haploid	In 2014, we planted 1100 DH plants in the field. In 2014 we attempted approximately 6,000 DH plants, of which about 3,000 were successful and will be planted in the Fall of 2015. We are currently developing DH plants for another 100 populations.	This is done annually, with the number of crosses/populations varying	
	Trait Introgression	We made crosses to germplasm containing resistance to snow mold, stem rust, stripe rust, end use quality, foot rot resistance, preharvest sprouting, Al tolerance, Ceph Stripe, SBWMV, and vernalization duration. The populations are being increased in the greenhouse for field selection. Currently there are no markers for many of these genes, although some are in development. The idea was either to select based on field conditions or have populations ready once the markers were identified. These will be planted in 2015 as rows at various locations and stages of development, depending on the trait of interest.	This is done annually, with the number of crosses/populations varying	
Trait assessment				Results are presented through annual progress reports, with the outcomes of this research being realized in new cultivars
	Coleoptile length	All advanced breeding lines are screened and selected for coleoptile length (funded by the Amen Foundation)	Screening and selection will be completed in 2015. Superior lines will be planted in the field and crossed back into the breeding program.	
	Foot rot	Advanced populations are being screened for foot rot resistance. Resistant lines will be used in the breeding program to incorporate this trait through a diversity of backgrounds	Screening and selection will be completed in 2015. Superior lines will be planted in the field and crossed back into the breeding program.	
	Cold Tolerance	All advanced breeding lines are screened for cold tolerance through the USDA funded WGC grant.	Screening and selection will be completed in 2015. Superior lines will be planted in the field and crossed back into the breeding program.	
	Stripe rust	An advanced population was screened for stripe rust resistance and that analysis is now complete. We identified over 20 QTL in PNW germplasm, about half of which appear to be novel. These lines are now being crossed to additional breeding lines and cultivars, and selection will be done with the recently identified markers to incorporate this resistance through a diversity of backgrounds.	Screening and selection will be completed in 2015. Superior lines will be planted in the field and crossed back into the breeding program.	