

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

**Project #:** 5195  
**Progress Report Year:** 2 of 3  
**Title:** Use of biotechnology for wheat improvement  
**Investigator/Cooperators:** AH Carter, KG Campbell, D See, M Pumphrey

**Executive summary:** In 2019 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, low PPO, Fusarium head blight, Hessian fly, and nematode resistance. Over 15,000 data points were collected on 230 populations to confirm presence of 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 fourth year of phenotypic evaluations in the field and genotyping. Data is being used to validate end-use quality selection models. In the greenhouse, we made approximately 550 crosses consisting mainly of soft white and hard red germplasm. These are being advanced to the F1 generation, and then divided between our DH production and MAS protocol. We planted ~2,600 DH plants in the field in 2020 for evaluation. The remaining DH lines are undergoing increase in the greenhouse and will have a similar number ready for yield evaluation in 2021. Our screening process has been slightly altered to allow for marker selection after some field selection is completed.

**Impact:** This project covers all market classes and rainfall zones in the state of Washington, with about 70% of the effort on soft white crosses. This work will improve end-use quality, genetic resistance to pests and diseases, and agronomic adaptability and stability of released cultivars. All cultivars released (Otto, Puma, Jasper, Sequoia, Devote, Stingray CL+, Scorpio, Purl) have benefited through this project by incorporation of disease and end-use quality genes. Released lines have gained popularity and are growing in demand due to the gene combinations they were selected for. The breeding program as a whole has become more efficient in the selection process, and more focus is placed on field evaluations since known genes are already confirmed to be present in the breeding lines. Continued success will be measured by increases in acreage of these lines as well as enhanced cultivar release through DH production, marker-assisted, and genomic selection.

**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:** 2 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 2019, 115 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. Since more lines are being advanced with Pch1, fewer populations are segregating for the gene as we recycle lines back into the breeding program.	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	In 2019 we communicated results of this project through the following venues: 9 peer-reviewed publications; 1 field day abstracts; 3 invited speaker presentations; 8 poster presentations; 4 popular press interviews; 2 grower meeting presentations; 1 wheat workshop presentations; 10 field day presentations; 3 seed dealer presentations; participation in the Tri-State Grain Growers Convention; and hosted 4 trade teams.
	Stripe rust resistant lines	In 2019, 100 populations for stripe rust resistance (Yr5, Yr15, Yr17, Yr18, YrEltan) were screened for and selected upon for upcoming field testing.	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	
	End-use quality lines	In 2019, populations were selected for combinations of the GBSS genes ( <i>waxy</i> ) and the glutenin genes. We also had a high school student intern with us and select lines null for all three PPO genes. Field testing also evaluated previously identified waxy wheat families for advancement in the program.	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 2019, all breeding lines in field trials were screened to identify which dwarfing gene they carry in order to aid in selection and crossing decisions. Selection is then made on which genes are present rather than incorporating new genes as they already exist in our breeding program. All lines are field tested for emergence potential.	Each year new crosses are being made to incorporate Rht genes into the breeding program. We also verify presence of dwarfing genes in all material to assist with selection of lines with enhanced emergence potential.	

	Genomic selection	With the assistance of Dr. Zhang and Dr. Lozada, we have begun genomic prediction model building. Lines from the 2015-2019 breeding program have been genotyped as well as a large training panel. Models built were used to assist with selection in the 2019 crop year. End-use quality models are being explored, as well as models for agronomic traits and spectral reflectance traits.	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. Validation of results is proceeding.	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 2019, the advanced germplasm was screened with DNA markers for about 22 markers of interest. This information was used to enhance selection of field tested material, as well as assist in parent cross-combinations to develop populations with desired traits of interest.	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 2019 we made approximately 550 crosses which were targeted for herbicide resistance, low rainfall and high rainfall production. These crosses were mainly in soft white backgrounds. Crosses were advanced to the F2 stage. We also made about 60 crosses for introgression of the below mentioned traits.	This is done annually, with the number of crosses/populations varying	
	Single-seed descent	No SSD populations were developed this year.		
	Doubled haploid	In 2019 we submitted all crosses for DH production. We are advancing roughly 2,600 DH lines in the greenhouse to get enough seed to plant in field trials in the fall of 2019.	This is done annually, with the number of crosses/populations varying	
	Trait Introgression	We made crosses to germplasm containing resistance/tolerance to snow mold, stripe rust, end use quality, foot rot resistance, preharvest sprouting, Al tolerance, Ceph Stripe, SBWMV, vernalization duration, low PPO, Fusarium head blight, and certain herbicides (in coordination with Dr. Burke). The populations are being made and 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 populations are either currently planted in the field for observations, undergoing marker screening, or undergoing phenotypic selection in the greenhouse.	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.	Screening and selection will be completed in 2020. 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 2020. 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 2020. Superior lines will be planted in the field and crossed back into the breeding program.	
	Stripe rust	Previously, 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. because selection with markers is difficult for these QTL, we have begun looking at genomic selection as an improved method to introgress these QTL. We continue to work on other populations to identify new genes for stripe rust resistance and develop markers for them.	Screening and selection will be completed in 2020. Superior lines will be planted in the field and crossed back into the breeding program.	

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