**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 201 we continued our effort to advance breeding lines as quickly and efficiently as possibly 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 8,500 data points were collected on 178 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 third year of phenotypic evaluations in the field. We are analyzing the GBS data from the 2015 and 2016 field entries, and are submitting our 2017 entries for GBS. Developed genomic selection models will be used for selection in 2017. We also screened 111 populations for 2-gene resistance in the laboratory, of which 41 made it to the field in for 2017 evaluations and the remaining will be for 2018 evaluation. 45 of these populations were also screened with markers for the traits listed above.
In the greenhouse, we made approximately 700 crosses consisting mainly of soft white and hard red germplasm. These are being advanced to the F2 generation. We planted ~2,200 DH plants in the field in 2017 for evaluation. The remaining DH lines are undergoing increase in the greenhouse and will have a similar number ready for yield evaluation in 2018. 90 crosses have been submitted for DH production in 2017. We also have about 100 specialty crosses to introgress traits such as nematode resistance, Hessian fly resistance, herbicide tolerance, FHB tolerance, low PPO, and novel stripe rust resistance genes.

**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 have benefited through this project by incorporation of disease and end-use quality genes. Released lines have gained popularity and are growing in demand in part due to the gene combinations they were selected for. 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 |
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| Marker-assisted selection | | | | Results are presented through annual progress reports, the research review, field tours, and grower meetings |
| | Foot rot resistant lines | In 2016, 55 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 2016, 79 populations for stripe rust resistance (Yr5, Yr15, Yr17, Yr18, YrEltan, etc) 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 2016, 30 F2 populations were screened for the genes Gpc-B1. Lines which had previously been selected for Gpc-Bi and Bx7oe have been advanced to yield testing. Lines previously selected for GBSS genes (waxy) and the glutenin genes have also been advanced to yield testing. | 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 2016, 14 populations were screened for incorporation of various Rht genes. Previous populations were planted at Lind to be screened for emergence potential. | Each year new crosses are being made to incorporate different 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. | |

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| | Genomic selection | With the assistance of Dr. Zhang, we have begun genomic prediction model building. Lines from the 2015 and 2016 breeding program have been genotyped as well as a large training panel. The 2017 breeding program has been submitted for genotyping. Models built will be used to assist with selection in the 2017 crop year. | 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 2016, the advanced germplasm was screened with DNA markers for about 20 traits 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 2016 we made approximately 700 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 100 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 2016 we submitted 90 crosses for DH production. We are advancing roughly 4,000 DH lines in the greenhouse to get enough seed to plant in yield plots in the fall of 2017. We planted about 2,200 DH lines in the field for 2017 observations and yield testing at both Pullman and Lind. | This is done annually, with the number of crosses/populations varying | |
| | Trait Introgression | We made crosses to germplasm containing resistance/tolerance to snow mold, stem rust, 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 will be planted in 2016 as rows at various locations and stages of development, depending on the trait of interest. Some will be screened in the greenhouse for traits of interest before being moved to field testing. | This is done annually, with the number of crosses/populations varying | |

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| 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 2016. 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 2016. 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 2016. 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. We continue to work on other populations to identify new genes for stripe rust resistance and develop markers for them. We also screen material in the greenhouse for resistance. | Screening and selection will be completed in 2016. Superior lines will be planted in the field and crossed back into the breeding program. | |

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