

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

Project #: 3673

Progress Report Year: 2 of 3

Title: Increasing Genetic Opportunities for Stripe Rust Resistance

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Executive summary: Work has been completed identifying markers linked to *Yr5*. This manuscript has been submitted for publication and will allow breeders the ability to more effectively track this important gene. Fine mapping populations for the *YrCoda* gene have been completed. Phenotyping will begin in 2016. Additional work on this region has redeveloped the genetic map to better clarify this region. The additional work on the QAM panel has clarified there are multiple genes for resistance in this region. The resistance genes from tetraploid wheat are in the process of being transferred to spring wheat for use in breeding. Crosses have been made and additional backcrosses need to be made to recover the 42 chromosomes of hexaploid wheat. The JD/Avocet S and Finch/Eltan populations have been tested in the field for QTL analysis. The JD/Avocet S population is undergoing genotyping to complete the analysis. The Finch by Eltan work is completed and we have identified markers associated with each of these genes. Results have been published. 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. The spring wheat, winter wheat, and USDA breeding programs are all using different sets of markers to move stripe rust resistance genes into their respective germplasm bases. 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. Progress is measured by the excellent stripe rust resistance that has been incorporated into recent releases such as Puma, Jasper, Melba, Seahawk, Alum, and Chet. These lines are gaining in popularity in part due to their rust resistance.

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WGC project title: Increasing Genetics Opportunities for Stripe Rust Resistance
Project PI(s): A Carter, K Garland-Campbell, M Pumphrey
Project initiation date: July 1, 2015
Project year: 2 of 3

| Objective | Deliverable | Progress | Timeline | Communication |
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| 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 using PNW soft white winter wheat ('QAM panel') has been carried out and new QTL and consistent QTL from previous panel ('SNP panel') 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 such as a cross between 'Bitterroot X WA8115'. In other cases, crosses have been initiated with lines carrying the desired QTL such as a cross between 'Coda X WA8115'. | Markers will be used to verify that these lines carry target resistance along with field and/or greenhouse phenotyping in 2016. Coda X WA8115 lines will be tested for few races in greenhouse. | 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. Association mapping with 'SNP panel' has been published in Theoretical and Applied Genetics 128: 1083-1101. A integrated work from association mapping with 'QAM panel' and QTL mapping in 'Coda X Brundage' will be presented in Plant and Animal Genome conference in 2016. |
| 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 | 22 of BC1F2 populations have been tested in field. Only two out of these showed segregation on disease response. These two BC1F2 are being advanced in greenhouse. | Unsuccessful crosses will be repeated in 2016. The advanced populations will be tested in field again, and DNA markers will be used to identify progeny with stripe rust resistance genes of interest to confirm resistance. These lines will be further used to introgress this resistance into other PNW germplasm. | 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 | 'Near perfect' markers for Yr5 have been developed and verified their usefulness with other germplasm. Re-mapping for Coda X Brundage population with additional SNP markers was carried out and verified YrCoda is novel. A population derived from a cross between JD (potentially carrying YrCoda and other resistance) and Avocet S was phenotyped in field and genotyping by sequencing has been completed. Populations developed for Yr15 showed complex segregation and markers did not seem to be associated with Yr15. | Fine-mapping for YrCoda will be carried out using backcross populations which currently being developing. 'JD X Avocet S' will be phenotyped in field again and QTL mapping will be carried out in 2016. | 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. 'Near perfect' markers for Yr5 have been presented in Borlaug Global Rust Initiative workshop in 2015 and currently prepared for manuscript. |

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