

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

Project #: 3673
Progress Report Year: 3 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: Work has been completed identifying markers linked to *Yr5*. This manuscript has been published and will allow breeders the ability to more effectively track this important gene using KASP markers, which are fairly easy to use. Fine mapping populations for the *YrCoda* gene have been completed. Phenotyping was completed in 2016. Additional work on this region has redeveloped the genetic map to better clarify this region. We will continue this work with other funds to clarify this region associated with resistance in Coda, a highly resistant line. 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 final stages 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. This information has been published. 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 markers to move different 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 and KASP markers which showed significant association with novel and known resistant genes. This totals an estimated 20 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. We have developed reliable KASP marker for *Yr5* which are easy to use for breeders. We have published five manuscripts on stripe rust resistance and have seven in preparation. It is a significant accomplishment to develop elite wheat cultivars with durable rust resistance in PNW wheat breeding programs. The impact of identifying new 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. This will not only be beneficial to WSU and USDA breeding programs, but to all breeding programs in the PNW interested in using these technologies. 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, Sequoia, Melba, Seahawk, Alum, and Chet. These lines are gaining in popularity in part due to their rust resistance. Furthermore, progress is measured by other breeding groups requesting our germplasm and marker information so they can develop cultivars with stripe rust resistance.

Outputs:

Peer reviewed publications:

- Case AJ, Naruoka Y, Chen X, Garland-Campbell KA, Zemetra RS, Carter AH (2014) Mapping stripe rust resistance genes in a BrundageXCoda winter wheat population. PlosONE 9(3):e91758 doi: 10.1371/journal.pone.0091758.
- Naruoka Y, Garland-Campbell KA, and Carter AH (2015) Genome-wide association mapping for stripe rust (*Puccinia striiformis* f. sp. *tritici*) in US Pacific Northwest winter wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 128:1083-1101.
- Klarquist E, Chen XM, Carter AH (2016) Novel QTL for stripe rust (*Puccinia striiformis* f. sp. *tritici*) resistance on chromosomes 4A and 6B from soft white winter wheat (*Triticum aestivum*). Agronomy 6:4.
- Naruoka, Y, K. Ando, P. Bulli, K.T. Muleta, S. Ryneerson, and M.O. Pumphrey. 2016. Identificaiton and validation of SNP markers linked to the stripe rust reistance gene Yr5 in wheat. Crop Science 56:3055-3065.
- Weizhen Liu, Marco Maccaferri, Peter Bulli, Sheri Ryneerson, Roberto Tuberosa, Xianming Chen, Michael Pumphrey. 2017. Genome-wide association mapping for seedling and field resistance to *Puccinia striiformis* f. sp. *tritici* in elite durum wheat. *Theoretical and Applied Genetics*. In press.

Submitted or in Preparation:

- Kebede T. Muleta, Matthew N. Rouse, Sheri Ryneerson, Xianming Chen, Bedada G. Buta, Michael O. Pumphrey. Characterization of molecular diversity and genome-wide mapping of loci associated with resistance to stripe rust and stem rust in Ethiopian bread wheat accessions. Submitted to BMC Plant Biology.
- Kebede T. Muleta, Peter Bulli, Zhiwu Zhang, Xianming Chen, and Michael Pumphrey. Unlocking diversity in germplasm collection by genomic selection: a case study based on quantitative adult plant resistance to stripe rust (*Puccinia striiformis* f. sp. *tritici*) in spring wheat. Submitted to The Plant Genome.
- Weizhen Liu, Marco Maccaferri, Sheri Ryneerson, Tesfaye Letta, Habtemariam Zegeye, Roberto Tuberosa, Xianming Chen, Michael Pumphrey. Novel sources of stripe rust resistance identified by genome-wide association mapping in Ethiopian durum wheat (*Triticum turgidum* ssp. *durum*). *Frontiers in Plant Science*. Submitted
- Kebede T. Muleta, Peter Bulli, Sheri Ryneerson, Xianming Chen and Michael Pumphrey. Mapping of genomic loci associated with stripe rust (*Puccinia striiformis* f. sp. *tritici*)

resistance in a collection of spring wheat accessions. Manuscript under preparation

- Kebede T. Muleta, Peter Bulli, Xianming Chen and Michael Pumphrey. Identifying quantitative trait loci for resistance to stripe rust (*Puccinia f. sp. striiformis*) in a global collection of winter wheat population. Manuscript under preparation.
- Weizhen Liu, Marco Maccaferri, Xianming Chen, Michael Pumphrey, Roberto Tuberosa. Genome-wide association mapping reveals a rich genetic architecture of stripe rust resistance loci in emmer wheat (*Triticum turgidum* ssp. *dicoccum*). Manuscript in preparation
- Weizhen Liu, James Kolmer, Sheri Rynearson, Michael Pumphrey. Identifying durable rust resistance to wheat via genome-wide association mapping in a hexaploid wheat population. Manuscript in preparation

Ongoing projects leveraged from this funding:

- Fine mapping all-stage resistance genes in cultivar ‘Coda’ on chromosome 1B.
- QTL mapping of stripe rust resistance loci in ‘SWW10069’ population.
- QTL mapping of durable stripe rust resistance genes in JD x Avocet population.
- Genome-wide association mapping for resistance to stripe rust in cultivated emmer wheat using wheat 9K SNP array.
- Genome-wide association mapping for resistance to stripe rust in PNW soft white winter wheat.
- Validation and development of KASP markers for loci identified by genome-wide association analyses for conferring seedling and adult plant resistance to stripe rust.
- Development of breeder-friendly molecular marker for stripe rust resistance gene *Yr53* and its transfer into elite background through backcrossing.

WGC project number: 3673
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, 2014
Project year: 3 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	WSU and USDA breeding programs are routinely using DNA markers to pyramid effective resistance into breeding material.	Populations have been developed, phenotyped, and genotyped. Breeding programs annually use markers to ensure effective resistance genes are present in germplasm.	Results have been communicated through grower field days, international conferences, and peer-reviewed manuscripts.
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	Two BC1F2 were advanced in greenhouse. Lines confirmed to have the Emmer resistance genes will be given to breeding programs for crossing.	Confirmation of lines will be completed in the Spring, and seed will be distributed to breeding programs.	Results have been 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. Mapping the 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.	Yr5 markers have been developed and published. YrCoda markers are published, and work is ongoing to identify if this is one gene or two. Yr15 markers have been difficult to validate, and new research outside the scope of this project has been initiated to further investigate this gene.	Results have been 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 published.

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