

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

Project # 3019-3685

Progress Report Year: __1__ of __3__ (*maximum of 3 year funding cycle*)

Title: **Fusarium Crown Rot on Wheat: Prebreeding and Development of Tools for Genetic Disease Management**

M. Pumphrey, K. Garland-Campbell, and T. Paulitz

Cooperators: Yvonne Thompson, WSU, Nuan Wen, WSU, Arron Carter, WSU; Chris Mundt and Christina Hagerty, OSU

Executive summary:

- A modified method was developed to increase the disease pressure of Fusarium crown rot under greenhouse conditions. This method resulted in less variation and was used to a diverse global spring wheat collection, a set of wheat synthetic lines, a backcross population derived from the spring wheat cultivar Louise and an Iranian land race with multiple root disease resistance and the winter wheat variety trials.
- A genome-wide association study (GWAS) was conducted to determine the genetic architecture of resistance to *F. culmorum* in the global spring wheat collection and QTLs for resistance were identified on chromosomes 1A, 2B, 4D, 5A, 6B, and 7A. Chromosome 2B, 4D, and 7A may reflect novel sources of resistance.
- Resistance was discovered in the set of synthetics. Synthetic wheat is derived from crosses between durum wheat and *Aegilops squarrosa*, the donor of the wheat D genome. Since durum is susceptible, to *Fusarium*, resistance is from the D genome. This germplasm represents potential new sources of resistance and has been crossed with winter wheat breeding lines from the USDA and WSU breeding programs.
- We evaluated the Louise/IWA860877 (AUS285451) backcross population in the field for resistance to *Fusarium*. The results were skewed towards susceptibility as would be expected from a backcross population but some resistant lines were identified. We are following up to identify the loci responsible for this resistance using QTL analysis.

Impact: The economic impact of this disease continues to be large and affects all growing areas of Washington including both high and low precipitation zones

What measurable impact(s) has your project had in the most recent funding cycle?

- A list of the most susceptible and resistant varieties
- Better methods for greenhouse screening
- The first QTLs for resistance to *F. culmorum* have been identified.

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WGC project title: Fusarium Crown Rot on Wheat: Prebreeding and Development of Tools for Genetic Disease Management
Project PI(s): M. Pumphrey, K. Garland-Campbell, and T. Paulitz
Project initiation date: 7/1/2018
Project year: Year 1 2018-2019

Objective	Deliverable	Progress	Timeline	Communication
Objective 1. Screen spring and winter variety trials and breeding lines for resistance in the greenhouse.	Ratings of varieties for <i>Fusarium</i> tolerance in the the WSCIA seed buyers guide and other publications.	We have screened almost 500 lines from regional nurseries and variety testing for resistance to <i>F. culmorum</i> , and are identifying the most resistant and susceptible. We have further optimized our greenhouse testing protocol to maximize disease and reduce variability by using a cold vernalization period followed by a water stress treatment at the end. Using this protocol we have screened the following: 2018 Winter Variety Trials- 97 entries in 3 replications, 291 cones total Cara Xerpha- 128 entries in 3 replications, 384 cones total DNAM tauschii- 8 entries in 3 replications, 24 cones total DNAM RIL- 54 entries in 4 replications, 216 cones total CIMMYT Synthetics- 20 entries in 4 replications, 80 cones total	Greenhouse screening will continue with optimized methods in 2019-2020	Yvonne Manning. 2018. Identification of Quantitative Trait Loci (QTL) for Resistance to Soil-Borne Pathogens <i>Fusarium culmorum</i> and <i>Heterodera filipjevi</i> in Wheat (<i>Triticum aestivum</i> L). PhD Thesis, Washington State University, Pullman, WA
Objective 2. Select for QTLs associated with resistance in segregating populations	Resistant sources that can be used for variety development.	A mini-core collection of 600 lines was developed for the spring core collection. Phenotyping and screening of mapping population in the greenhouse has been completed. We conducted 6 replications of this populations for a total of 3600 containers screened. The student has completed the analysis and written the PhD thesis. QTLs were identified on chromosomes 1A, 2B, 4D, 5A, 6B, and 7A. Chromosome 2B, 4D, and 7A may reflect novel sources of resistance.	Verification of QTLs will continue in 2019-2020	Yvonne Manning. 2018. Identification of Quantitative Trait Loci (QTL) for Resistance to Soil-Borne Pathogens <i>Fusarium culmorum</i> and <i>Heterodera filipjevi</i> in Wheat (<i>Triticum aestivum</i> L). PhD Thesis, Washington State University, Pullman, WA.
Objective 3. Look for new sources of resistance in a new set of synthetic wheat that was developed by CIMMYT in Turkey.	Resistant sources that can be used for variety development.	Resistance was discovered in the set of synthetics. Synthetic wheat is derived from crosses between durum wheat and <i>Aegilops squarrosa</i> , the donor of the wheat D genome. Since durum is susceptible, to <i>Fusarium</i> , resistance is from the D genome. This germplasm represents potential new sources of resistance and has been crossed with winter wheat breeding lines from the USDA and WSU breeding programs.	Greenhouse screening of synthetics will continue in 2019-2020.	

