

Washington Grain Commission
Wheat and Barley Research Annual Progress Report

Project #: 3690

Progress Report Year: 1 of 3 (maximum of 3 year funding cycle)

Title: Developing Washington Wheat with Stable Falling Numbers (FN) through Resistance to Preharvest Sprouting and LMA.

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Executive summary: The goal of this project is to breed for stable Falling Numbers (FN) in Washington wheat through selection for genetic resistance to preharvest sprouting and late maturity alpha-amylase (LMA). The project identified cultivars with low FN problems through evaluation of the WSU cereal variety trials, and with sprouting and LMA problems through greenhouse and field testing. We have identified molecular markers linked to PHS resistance and are in the process of identifying molecular markers linked to LMA resistance loci to allow selection in as many as 5000 early breeding lines per year. We are improving field and greenhouse testing for use in screening elite breeding lines.

Objective 1. Identify varieties with stable FN by performing FN tests and statistical analysis of variety trials in environments that have preharvest sprouting and/or LMA

FN data from the soft white winter WSU variety trials was analyzed using five statistical methods designed to examine how traits are impacted both by genetics and the environment. FN is difficult to analyze due to the fact that it is impacted by multiple environmental factors leading to preharvest sprouting or to LMA. The factor analytic model seemed to provide the best approach to compare both how well a variety performs for falling number and how stable that falling number is over changing environments.

Objective 2. Screen winter and spring wheat breeding lines for preharvest sprouting and/or LMA. In 2018, 1,335 lines were screened for LMA susceptibility using in the field, and 708 lines were screened for preharvest sprouting susceptibility by spike-wetting test.

Objective 3. Identify molecular markers linked to LMA susceptibility in northwest wheat.

a. We have completed three greenhouse and two field experiments screening the 250 lines of the spring TCAP population for LMA. b. Based on one greenhouse experiment, 3 of 10 spring RIL populations and 3 of 20 winter RIL populations were chosen as good candidates for LMA mapping.

Objective 4. Develop molecular markers for selection of PHS resistance in northwest wheat. A preliminary genome-wide association mapping was conducted. Some loci linked to good seedling emergence did not correspond to loci for preharvest sprouting resistance, suggesting that we may be able to select preharvest sprouting resistant without compromising seedling emergence. Molecular markers associated with preharvest sprouting resistance will be confirmed using spike-wetting tests of 461 doubled haploids descended from parents in the original association mapping study.

Impact: Wheat in all market classes is dramatically discounted for low falling numbers (below 300s). Moreover, a consistent problem with low FN could damage the reputation of Washington wheat in foreign markets. Screening for low FN, LMA, and sprout-susceptibility will the selection of new varieties with more stable FN. Posting of FN data on the WSU small grains website and the PNW FN website makes this data available to farmers and to breeders.

WGC project number: 3690
WGC project title: Developing Washington Wheat with Stable Falling Numbers (FN) through resistance to preharvest sprouting and LMA
Project PI(s): Camille M. Steber, Michael O. Pumphrey, Arron H. Carter, and Kimberly Garland Campbell
Project initiation date: July 1, 2018
Project year (X of 3-yr cycle): This is year 1 of 3 of the funding cycle.

Objective	Deliverable	Progress	Timeline	Communication
<p>1. Identify varieties with stable FN by performing FN tests and statistical analysis of variety trials in environments that have PHS and/or LMA.</p>	<p>1. FN testing results posted on the PNW FN website (steberlab.org). 2. Development of statistical methods to compare varieties for performance and stability of FN. 3. A new FN comparison tool.</p>	<p>1. FN testing of susceptible spring and winter varieties has been completed for all variety trial locations. 2. FN data from the WSU soft white winter variety testing in 2013, 2014, and 2016 has been analyzed using five different statistical approaches. A first article about the statistical analysis of falling number data has been submitted to Crop Science. Ongoing research using a factor-analytic model in AMSREML appears to provide the best tool for comparing both how well a variety performs for falling number, and how stable the falling number is over changing environments. 3. We used half-seed assays to examine whether of subset of variety trial samples with FN below 300 seconds had alpha-amylase distribution consistent with LMA or preharvest sprouting. We had some samples that had FN below 300 that did not have elevated alpha-amylase enzyme levels. These results are just anecdotal. But it appears that this phenomenon of low FN without alpha-amylase was associated with low protein of around 6%. This supports a previous report by Andrew Ross of Oregon State University saying that low protein can cause a lower FN.</p>	<p>1. Annually, FN testing of susceptible varieties will be used to determine which WSU Cereal Variety locations will be subject to FN testing. 2. In 2018 and 2019, compare various methods for ranking varieties for FN. 3. In 2019, complete statistical analysis of soft white winter FN data from 2013, 2014, and 2016. 4. In 2020, select a method for annual analysis of variety trial FN data.</p>	<p>Results of annual FN testing will be made available on the PNW FN website and on the WSU small grains website. Information will be published in peer-reviewed journals, summarized in a Wheat Life article, presented during field days, and presented at the annual Wheat Review.</p>
<p>2. Screen winter and spring wheat breeding lines for PHS and LMA susceptibility.</p>	<p>Data obtained will allow selection for increased resistance to LMA and preharvest sprouting in winter and spring wheat breeding programs at WSU. This should indirectly lead to release of varieties with increased resistance to low FN.</p>	<p>1. The LMA field-testing method was used to induce LMA in a total of 1,335 lines. This included 72 spring wheat breeding lines, 168 winter wheat breeding lines, 185 variety trial and parental lines, 426 TCAP spring wheat mapping plots, and 484 QAM winter wheat mapping lines. FN testing of this material is still in progress. 2. Preharvest sprouting resistance was tested using greenhouse spike-wetting tests of spikes harvested at physiological maturity from the field. Testing results were obtained for 495 soft white winter and 213 spring wheat lines. 3. Experiments were performed to optimize the temperature, humidity, and developmental timing of LMA induction. The goal of using the Chemwell-T robot to optimize alpha-amylase enzyme assays (Megazyme SD assay) met with serious problems in 2018. The programming of the robot does not allow it to maintain a consistent 5 minute reaction time, making results inconsistent. This meant that over 1000 samples had to be repeated using the Phadebas enzyme assay.</p>	<p>1. Perform field LMA testing annually of about 1000 lines annually for breeding and mapping. 2. Perform spike-wetting tests annually. 3. Continue improving methods to increase efficiency.</p>	<p>Information will be published in peer-reviewed journals, summarized in a Wheat Life article, presented during field days, and presented at the annual Wheat Review.</p>

<p>3. Identify molecular markers linked to LMA susceptibility in northwest wheat.</p>	<p>1. Molecular markers linked to LMA resistance allowing selection in earlier generation breeding lines. 2. Mapped LMA genes/loci linked to LMA resistance and susceptibility in the soft white spring TCAP population. 3. Mapped LMA genes/loci linked to LMA resistance and susceptibility in recombinant inbred line populations.</p>	<p>1. We have completed 3 greenhouse and two field LMA testing experiments for the spring TCAP population. Only the third greenhouse experiment showed good LMA induction due to optimized conditions. We will need to repeat the greenhouse screening one more time to obtain publication-worthy data. Preliminary genome-wide association mapping is in progress. 2. The parents for 10 spring RIL populations were screened for LMA in a single greenhouse experiment. Of these 3 populations, AVS*2xJD, UI-Platinum x LCS Star, and UI-Platinum x LCS Atomo, are likely to show clear segregation of LMA resistant and susceptible lines. The parents of 20 winter RIL population have been screened in a single greenhouse LMA experiment. Of these, three look promising for LMA mapping including, Xerpha x Munstertaler, Cara x Xerpha, and Finch x Eltan. Analysis of additional samples from the 2018 field season are still in progress, and will be used to confirm identification of useful populations for LMA testing. Promising populations have been and will be planted for the 2019 field season.</p>	<p>1. The goal to complete TCAP LMA screening in 2018 must be extended into 2019. 2. Genome-wide association mapping in the TCAP will be performed in 2019. 3. RIL populations for LMA mapping will be identified by 2019, and LMA screening initiated in 2019 and 2020.</p>	<p>Information will be published in peer-reviewed journals, summarized in a Wheat Life article, presented during field days, and presented at the annual Wheat Review.</p>
<p>4. Develop molecular markers for selection of preharvest sprouting resistance in northwest wheat.</p>	<p>1. Molecular markers that can be used to select for resistance to preharvest sprouting. 2. Identify markers that can select for sprouting resistance without compromising field emergence.</p>	<p>1. Mapping results for preharvest sprouting were based on FN and sprouting scores from spike-wetting tests. Mapping was also preformed for emergence based on field emergence and coleoptile/seedling elongation. Comparison found that there were some strong genes/loci lined to emergence that were not linked to preharvest sprouting susceptibility. This is a preliminary result, but suggests that this mapping approach may be used successfully in soft white winter wheat populations. 2. Spike-wetting tests were performed for 461 doubled-haploid winter wheat breeding lines derived from parents in the QAM and SNP winter wheat mapping populations. These data can be used to confirm marker-trait associations for molecular markers.</p>	<p>1. In 2018, GWAS was performed in a second population to confirm marker-trait associations. 2. In 2018, spike-wetting tests were performed on winter doubled haploid populations. 3. In 2019 and 2020, we will develop a genomic prediction model.</p>	<p>Information will be published in peer-reviewed journals, summarized in a Wheat Life article, presented during field days, and presented at the annual Wheat Review. The goal in to summarize these markers on the PNW falling number website to make it easier for wheat breeders to access this information.</p>