High-density Genetic Mapping of Intermediate Wheatgrass QTLs Associated with Disease and Agronomic Traits

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Intermediate wheat grass breeding nursery on the St. Paul Campus that will lead to the release of the first perennial grain variety for the University of Minnesota.
Abstract

Intermediate wheatgrass (*Thinopyrum intermedium*), also known as Kernza, has been identified as a candidate for domestication and improvement as a perennial grain, forage, and biofuel crop and is actively being improved by several breeding programs. To accelerate this process using genomics assisted breeding, efficient genotyping methods and genetic marker reference maps are needed. As part of this Forever Green project, we contributed to the development of the first consensus genetic map for intermediate wheatgrass. Genotyping-by-sequencing was used to identify 10,029 markers that were mapped to 21 linkage groups. Some of the same populations used to develop the genetic maps were characterized for their seed weight, seed area size, seed width, seed length, and resistance to the diseases Fusarium head blight and Bacterial leaf streak. Thirty-three quantitative trait loci (QTL) associated with seed weight and size were identified using association mapping, of which 23 were verified using linkage mapping in the bi-parental populations. The consensus map and QTLs identified for agronomic and disease resistance traits can help lead to rapid improvement of IWG and development of high-yielding cultivars of this perennial grain that would facilitate the sustainable intensification of agricultural systems.
Background of the Project: The main goals of the project were to develop genetic maps and map QTLs for agronomic and disease resistance traits of intermediate wheatgrass (IWG). This research helps characterize the genetic variation for important traits in IWG and identify quantitative trait loci that can be used to more efficiently breed for these traits.

Progress made toward the original goals of the project: Objective 1: Develop genetic maps using three populations. We developed genetic maps in 3 populations:

- Population SS: C3-2331/C3-2595, 178 genets 3,317 GBS markers with less than 20% missing data were mapped into 21 linkage groups corresponding to 21 chromosomes of IWG.
- Population BA: WG116216/WG115302, 133 genets 1,585 GBS markers with less than 10% missing data into 20 linkage groups.
- Population CA: WG117703/WG112027, 131 genets, 1,564 GBS markers with less than 10% markers were mapped into 21 linkage groups.

These three maps were combined with maps developed at Kansas State University and USDA ARS, UT, making an integrated map containing a total of ~10,000 high quality GBS markers across all populations and published in 2016:


Objective 2: Map QTLs for resistance to bacterial leaf streak and Fusarium head blight. Collaborating with plant pathologists Drs. Carol Ishimaru and Ruth Dill-Macky at the Department of Plant Pathology, we screened the parents of the three mapping populations in greenhouse trials in 2014. One parent of Population CA is resistant to Fusarium head blight (FHB), but susceptible to bacterial leaf streak (BLS) and the other parent is resistant to BLS but susceptible to FHB. Thus, population CA was selected for screening with BLS and FHB in greenhouse assays. In total, 105 genets of Population CA were screened for FHB (one experiment, 2 reps) and BLS (2 experiments, 2 reps) under greenhouse conditions. Due to the departure of Postdoc Dr. Xiaofei Zhang in February, 2017, the QTL mapping for this objective has not been completed but will be done later this year by the new project postdoc, Dr. Prabin Bajgain.

Objective 3: Map QTLs for shattering, threshing ability, seed size, and height by characterizing three F1 populations.

- Population SS was established in 2013. We recorded the traits height, heading date, head weight, seed weight and size, and shattering resistance in 2013-2014 and 2014-2015 growth seasons. Populations BA and CA was established in 2014. In the growth season 2014-2015, the height, heading data and BLS resistance were recorded in the field. The head weight and shattering resistance were from 10 spikes of individual plants.

This research was recently published in The Plant Genome:
**Long-term sustainability and impact of the project** The research material is derived from the intermediate wheatgrass breeding program and the results and materials developed will contribute to sustained breeding efforts to develop intermediate wheatgrass varieties to meet the needs of growers and end-users.

**Additional funds secured or applied for to support continuation of the project**

2. “Dissecting the genetic architecture of agronomic traits in intermediate wheatgrass using genome-wide analysis”, funded by The Land Institute, $193,000, 7/16-6/19. This grant will complement our existing research by using a Nested Association Mapping panel to map QTLs for these agronomic traits in a broader genetic context. One of the main objectives of this project is to map QTLs for seedling vigor, stem angle, heading date, height, lodging resistance, head weight, shattering, threshability and seed size.

3. “Accelerate the Improvement of Intermediate Wheatgrass in Grain Yield and Fusarium Resistance Using Genomic Selection”, funded by FGI, $171,125, 9/16-6/19. This proposal specifically focuses on expanding the intermediate wheatgrass (IWG) breeding program and increasing the breeding efficiency using genomic selection. A representative breeding population with 560 plants will be evaluated in field nurseries at Crookston and St. Paul and in a Fusarium head blight nursery at St. Paul.

4. “Increasing the capacity of an applied, genomics-assisted Kernza breeding program at the University of Minnesota”, funded by MN Dept. of Agriculture, $161,241, 7/17-6/20. This proposal provides additional technician support and funding to genotype an additional 1,500 intermediate wheatgrass plants as part of our breeding activities.

**Undergraduate, graduate student and post-doc education and opportunities provided by the grant** This grant supported postdoc Dr. Xiaofei Zhang and its activities provided learning opportunities for several undergraduate students including Max Fraser and Jennifer LaValley. Max is now a Ph.D. candidate on our wheat genetics and breeding project.