

University of Minnesota Annual Potato Breeding Progress Report to the Minnesota Department of Agriculture

Submitted January 15, 2023 by Laura Shannon (lshannon@umn.edu), Assistant Professor of Potato Breeding Genetics and Genomics for the UMN College of Food, Agricultural and Natural Resource Sciences (CFANS) in the Department of Horticultural Science AGREET funding her program receives.

Per the requirements set forth in Minnesota Statutes 3.197, the cost to prepare this report was \$153.00.

Abstract:

Researchers from the Shannon Lab at the University of Minnesota College of Food, Agricultural, and Natural Resources Sciences in the Department of Horticultural Science have collaborated with a multitude of research institutions in breeding new potato cultivars for distinct market classes with characteristics such as skin and flesh color (red, yellow, russet), chipping suitability as well as increasing our understanding of potato genomics, genetic diversity, and evolutionary history. Understanding the structure and history of genomes and how diversity is partitioned within populations has facilitated genetic gain in a variety of crops. Because of the complexity of the potato genome there are a range of outstanding questions about potato history including: the number and timing of domestication events, the identity of a wild progenitor, and the number of cultivated species. This report summarizes and provides a progress report for this project and its objectives.

Objectives:

1. Breed new potato cultivars for distinct market classes with increased resistance to biotic and abiotic stresses and enhanced nutrition and quality traits, while requiring fewer inputs such as nitrogen fertilizer, pesticides, and water use.
2. Increase our understanding of potato genomics, genetic diversity, and evolutionary history.

Activities Performed and Outcomes:

Objective 1A Actions

- Breeding potatoes is a multi-year, multi-institutional effort. Our collaborations have resulted in planting a large number of genotypes for evaluation. As part of this process we have been very selective to only continue the best genotypes into further trials. As an example, we planted 26,000 single genotypes from a number of institutional partners

covering different market classes. We selected 3.44% of the individuals over all to continue on in the program to year 2.

- We have also been supported by a number of grower organizations such as the Area II Potato Growers and the Northern Plains Potato Grower Association, as well as successfully obtaining grants to evaluate new and legacy genotypes within the program. We had a tasting event so growers and interested individuals could see the breadth of the traits the program continues to evaluate. The Good Acre, a Minnesota nonprofit focusing on improving local food systems, hosted us and our project produced the tubers at Andrew Cardinal's farm, All Good Organics.
- We have released a long season fresh market yellow potato with low internal defects called Polaris Gold

Objective 1B Actions

- Growers have highlighted the need for nitrogen (N) efficient varieties. Our work thus far suggests that early screening is necessary to identify varieties that use less N without sacrificing yield and quality. The goal is to determine which genotypes are N efficient and build a machine learning model to use drone imagery to predict N use efficiency in the field.
- When screening the germplasm for lower N applications, we are using a single pre-plant application of N. Since different varieties respond to N differently, we assume that ideal timing for N application may be genotypically dependent. Therefore, we trialed 8 red cultivars with 3 different N application patterns – pre plant, half at pre plant/half at emergence, and one third at pre plant one-third at emergence/one third at flowering. We measured the effect on yield and skin finish and will continue this grant funded project into 2023.

Objective 2A Actions

- As part of an international collaboration to sequence 6 potato genomes, our research group analyzed introgressions from wild species into the potato genome and found evidence for a long history of mixing among potatoes and wild species suggesting a history of adaptive introgression. Our group also contributed genetic diversity, defining deleterious alleles and genotyping for phasing for this international collaboration.
- As part of the diploid breeding efforts we have sequenced 91 dihaploid potatoes we have used this data to examine relatedness among genotypes and determine the comparative diversity in different market classes to guide our sequencing and extraction strategies going forward.

Objective 2B Actions

- To determine ploidy level, our research group developed a method used to correct errors in databases we and others have been working from.

- The International Potato Center (CIP) in Peru has genotyped their entire potato catalog and we are currently working to determine diversity and trait analysis.

University of Minnesota Annual Wild Rice Breeding and Related Research Progress Report to the Minnesota Department of Agriculture

Submitted January 15, 2023 by Dr. Jennifer Kimball (jkimball@umn.edu), Assistant Professor of Wild Rice Breeding, Genetics, and Conservation for the UMN College of Food, Agricultural and Natural Resource Sciences (CFANS) in the Department of Agronomy and Plant Genetics AGREETT funding her program receives.

Per the requirements set forth in Minnesota Statutes 3.197, the cost to prepare this report was \$170.00.

Abstract:

The wild rice breeding, genetics, and conservation program's work centers on wild rice (*Zizania palustris*) as a cultivated crop as well as a natural resource in the state of Minnesota. Our breeding efforts focus on improving the sustainability and growth of the Minnesota Cultivated Wild Rice Industry and its growers through the development of new and improved varieties. We are currently focused primarily on improving seed shattering resistance and disease resistance. Our research focuses on 1.) investigating the genetic and physiological bases of quantitative traits in wild rice and 2.) evaluating and monitoring the genetic diversity and changing environment of natural stands of wild rice in Minnesota to ensure their protection and conservation.

Program Accomplishments:

1. Released a new high yielding, long seeded cultivated wild rice variety, 'RayGun', that caters to both grower and end-use marketers needs.
2. Sequenced, assembled, and annotated the wild rice genome (Haas et al., 2021). This new available public resource will be useful for a wide range of wild rice researchers, including both breeders and conservationists alike.
3. Investigating the genetic architecture of the seed shattering trait in wild rice, a major limiting factor in its production. Within the year, we aim to have molecular markers that can track seed shattering resistance, which can help to quickly and efficiently identify plants with higher resistance to seed shattering. This is a primary trait of concern for Minnesota cultivated wild rice growers.
4. Investigating the genetic architecture of disease resistance in wild rice for fungal brown spot, a major fungal pest in cultivated wild rice production. The identification of molecular markers to track disease resistance will enable the rapid development of new varieties with improved disease resistance, which will improve the productivity and environmental sustainability of cultivated wild rice production.
5. Addressing concerns about pollen-mediated gene flow from cultivated to natural stands of wild rice. Independent studies evaluating gene flow based on molecular markers (Haas et al., 2022) and pollen travel (Gietzel et al., 2022) have confirmed that pollen travel and thus gene flow is not only minimal in *Zizania palustris* but the entire *Zizania* genus, which consists of four species, 3 North American and 1 Asian species. We did not identify gene flow between cultivated and natural stands of wild rice in Minnesota, which indicates that cultivated wild rice production is not changing the natural stands of wild rice in any way.

6. Monitoring natural stand populations for changes in genetic diversity, which was listed as the primary concern in the Department of Natural Resources 2008 report on the current status of natural stands of wild rice in Minnesota. Thirteen natural stand populations were evaluated in 2018, which serves as a snapshot of genetic diversity from that time. Future efforts to monitor the health of these populations can use the publicly available data in future conservation efforts.
7. Investigating the unique seed physiology of wild rice, which hinders our ability to store seed long-term. For both breeding and conservation purposes, this poses extreme challenges. For example, there is currently no wild rice seed stored in any *ex-situ* conservation seed bank worldwide, which makes the preservation of wild rice populations in Minnesota incredibly important. Improving seed longevity in storage would help to reduce the potential catastrophic impacts on wild rice as a species if an ecological disaster were to occur.

Result Dissemination:

1. Haas, M., Kono, T., Macchietto, M., Millas, R., McGilp, L., Shao, M., ... & Kimball, J. (2021). Whole-genome assembly and annotation of northern wild rice, *Zizania palustris* L., supports a whole-genome duplication in the *Zizania* genus. *The Plant Journal*, 107(6), 1802-1818.
2. Haas, M. W., McGilp, L., Shao, M., Millas, R., Castell-Miller, C., Shannon, L. M., ... & Kimball, J. (2022). Genetic Analysis of Wild and Cultivated Populations of Northern Wild Rice (*Zizania palustris* L.) Reveal New Insights into Gene Flow and Domestication. *bioRxiv*.
3. Gietzel, C., Duquette, J., McGilp, L., & Kimball, J. (2022). Recessive male floret color for tracking gene flow in cultivated northern wild rice (*Zizania palustris* L.). *Crop Science*, 62(1), 157-166.
4. McGilp, L., Semington, A., & Kimball, J. (2022). Dormancy breaking treatments in Northern Wild Rice (*Zizania palustris* L.) seed suggest a physiological source of Dormancy. *Plant Growth Regulation*, 98(2), 235-247.
5. Gietzel, C., McGilp, L., & Kimball, J. (2022). Spatiotemporal Profiling of Seed-Associated Microbes of an Aquatic, Intermediate Recalcitrant Species, *Zizania palustris* L. and the Impact of Anti-Microbial Seed Treatments. *bioRxiv*.

Significant Impacts:

While training undergraduate and graduate students as well as post-doctoral researchers, the wild rice breeding, genetics, and conservation program's breeding and research efforts have led to the development of a new variety for cultivated wild rice growers as well as substantial research in the areas of breeding and conservation. As a regionally important species, this program has the unique opportunity and skillsets to cater to a wide variety of stakeholders in the state.