

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.