Development of Intermediate Wheatgrass as a Next-Generation Sustainable Crop Using Genomics-Assisted Breeding & Domestication

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Background
Intermediate wheatgrass (IWG, Thinopyrum intermedium) is a novel perennial grain crop. It is a distant relative of wheat and is widely known as Kernza®, the crop’s trade name. In addition to producing nutritious grain, IWG has an extensive root structure and provides year-round soil coverage thereby offering the following benefits that contribute towards sustainable & regenerative agriculture:
- Reduced soil erosion
- Increased carbon sequestration
- Reduced N and P contamination of freshwater and marine ecosystems by lowering runoff of surface nutrients
- Minimal need of tillage, herbicide, fungicide applications

The world’s first food-grade IWG cultivar, ‘MN-Clearwater’, was released by the University of Minnesota in 2019.

Breeding & Domestication
IWG breeding and domestication program at the University of Minnesota was initiated in 2011. The major goal of the program is to improve the crop’s profitability by improving IWG germplasm in following areas:
- Grain yield
- Larger grain size
- Improved spike characteristics
- Reduced seed shatter
- Higher free grain threshing
- Disease resistance
- Reduced lodging
- Better end-use quality traits

In order to expedite breeding grains and increase selection efficiency, we rely on genomic tools such as genome-wide molecular markers, genetic mapping of important traits, and genomic selection.

Approach: Traditional Breeding
We evaluate our single-plant selection nursery at two MN locations for 2-3 years for several agronomic and domestication traits.

The best plants are replicated and intermated in crossing-blocks to develop synthetic populations which are evaluated for 2-3 years in state-wide variety trials.

Genomics-assisted Breeding
Our traditional breeding pipeline is supported by genomic prediction based selection approach. We first carry out association mapping in a breeding population (single plant selection nursery) to identify regions associated with important traits of interest.

Genomic prediction is then carried out in a larger population (~3000 individuals) with genetic information but no field data.

Genomic Prediction in IWG
Our genomic prediction models are trained using 5000-7000 genome-wide markers and phenotypic data obtained on a population evaluated at two locations for 2-3 years.

Trained models are then applied to a non-phenotyped breeding population to obtain genome estimated breeding values (GEBVs). Plants with the best GEBV estimates are used as parents of next breeding cycle. Prediction models that include genotype by environment (GxE) interaction effects give best predictions, as shown in the figure below.

Genetic gain estimates from the prediction models were relatively high for important traits. Our results confirm that GS can accelerate IWG domestication by increasing genetic gain per breeding cycle and assist in selection of genotypes with promise of better performance in diverse environments.

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