Minnesota Wheat Research and Promotion Council
For Crop Year 2026 (01/01/2026 to 12/31/2026)

Project Title: Early stage phenomic selection in the UMN wheat breeding program

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Project Period:1/1/26-12/31/26
Estimated cost: $10,250

Abstract:

This project aims to streamline the breeding of wheat experimental lines using a low-cost, high-throughput screening method. Accurate phenotyping is crucial in wheat breeding because it influences the breeder's ability to identify promising wheat genotypes early and is directly related to genetic gain. No specific traits will be targeted with this project; however, if successful, it can enhance the genetic gain for many traits, enabling growers to access higher-yielding varieties with good wheat quality, lodging resistance, disease resistance, and other desirable characteristics. The proposed technology relies on hyperspectral, or near-infrared spectroscopy (NIRS) of the wheat kernels, a technique already widely used in breeding and industry to estimate protein content. However, NIRS can also be used to predict the characteristics of the genotypes for other traits, with the hypothesis that the NIR spectrum of the kernels represents a fingerprint of genotypes. A proof-of-concept for this type of analysis has been developed in wheat, but it has yet to be applied in any breeding program.

Background and importance:

There are multiple successive steps of selection in a wheat breeding pipeline. It begins with a high number of candidates evaluated as few plants at one location, progressing to a wide evaluation across multiple locations and years for a few variety candidates. The selection of wheat entries at early stages is difficult due to the low and inaccurate phenotypic information available. This project aims to improve the breeding pipeline at the early stages of selection by utilizing NIRS data from wheat kernels. This project has the potential to discard the less promising genotypes more accurately, thereby increasing genetic progress.

Phenomic selection is a type of genotype analysis, utilizing NIR spectral data as a proxy for the genomic data. Several publications (Rincent et al., 2018; Robert, Auzanneau, et al., 2022; Robert, Brault, et al., 2022) outline the possibility of using spectra to speed up the breeding process in multiple species, including wheat, complementing the use of DNA fingerprinting, which is typically restricted to hundreds or a few thousand lines due to its cost and resources required. This hypothesis relies on the fact that NIRS data contains the fingerprint of the genotype, as the genomic information does. Here, NIRS is not used as a phenotyping method for wheat quality traits, but more as a screening of the genetic make-up.

Genotyping and genomic selection are still widely used and useful for predicting genetic values, but they are not well-suited for early selection when there are too many genotypes. Genetic progress is directly related to the accuracy of selection at each step of the breeding process. Our project aims to enhance the accuracy of selection at this critical stage, where significant genetic variation exists and current selection is relatively inaccurate. Our proposed method is inexpensive, easy to test, and scalable.

Research methods:

NIRS data will be collected on kernels from several wheat populations, which were collected from trials conducted at multiple locations over several years. Seeds from past yield trials conducted in 2025 and 2024 will also be used. Once the model has been calibrated on the yield trial population (preliminary and advanced yield trial, namely PYT and AYT), predictions will be made for an F4 generation. For this one, during the 2026 field season at maturity time, we will pick three spikes for each genotype in the field.

Table 1: Populations under study and their characteristics

Population	**Population size**	**Number of locations**	**Growing seasons**	**Phenotypic data**
AYT	250	3	2024-2026	Grain yield, test weight, grain protein, lodging, FHB, milling and baking quality, and other diseases as they occur
PYT	350	2	2024-2026	Grain yield, test weight, grain protein, lodging, FHB, milling and baking quality, and other diseases as they occur
F4 selected	1500	1	2026	No phenotypic data

The UMN oilseed crop lab's DA 7250 NIR machine (900–1700 nm wavelength range) is freely available to us. We will use it for scanning 2-3 g whole-kernel samples and exporting spectra.
A statistical model will be built from AYT and PYT genotypes, with a trait-specific predictive model to associate NIRS with the phenotype. Once the F4-stage genotypes are screened with NIRS, the phenotypic values for all the traits will be predicted. We will investigate the impact of location and population on the accuracy of prediction, as well as which traits have the most accurate predictions. All the plant material and phenotypic data will be provided by the University of Minnesota wheat breeding program at no cost for this project.

Outline the timeline for completion:

The screening of the 2024 and 2025 growing seasons AYT and PYT will be done in the spring of 2026. The F4 wheat spikes will be harvested during the 2026 growing season. During the fall 2026, the F4 wheat spikes will be threshed, and NIRS will be collected on all wheat populations grown that year. A predictive model will be built, and the model's ability to predict phenotypic values will be assessed during the winter. Then, phenotypic values will be predicted for the F4s, and the most promising individuals can be advanced in the breeding pipeline.

Dissemination of results:

If successful, the results will be replicated and applied more broadly to other locations and wheat populations. This new type of selection can be utilized in the breeding program and further extended to other public wheat breeding programs, such as North Dakota State University (NDSU) and South Dakota State University (SDSU). These results will be included in a scientific publication and might be presented at a scientific conference.

List potential collaborators:

This is a pilot study. If successful, we may encourage NDSU and SDSU breeders to collaborate in the future.

Budget requirements: See budget table with justification.

References:

R. Rincent *et al.*, "Phenomic Selection Is a Low-Cost and High-Throughput Method Based on Indirect Predictions: Proof of Concept on Wheat and Poplar," *G3 Genes|Genomes|Genetics*, vol. 8, no. 12, pp. 3961–3972, Dec. 2018, doi: 10.1534/g3.118.200760.

P. Robert et al., "Phenomic selection in wheat breeding: identification and optimisation of factors influencing prediction accuracy and comparison to genomic selection," Theor Appl Genet, vol. 135, no. 3, pp. 895–914, Mar. 2022, doi: 10.1007/s00122-021-04005-8.

P. Robert, C. Brault, R. Rincent, and V. Segura, "Phenomic Selection: A New and Efficient Alternative to Genomic Selection," in Genomic Prediction of Complex Traits: Methods and Protocols, N. Ahmadi and J. Bartholomé, Eds., New York, NY: Springer US, 2022, pp. 397–420. doi: 10.1007/978-1-0716-2205-6_14.