

OPTIMIZING WHEAT BREEDING WITH TECHNOLOGY

A changing and more unpredictable climate is increasing the need for the agricultural sector to respond aggressively and develop solutions to substantially increase global wheat yields. This would provide a buffer against predicted yield losses and the means to meet the increasing demands from consumers for wheat and wheat-based products. One solution is to breed new wheat varieties that are better adapted to a range of environments. A recent grant from USDA NIFA of US \$15M was awarded at the beginning of 2022 to a coalition of US wheat scientists led by the University of California, Davis. This new Coordinated Agricultural Project (CAP) “**Leveraging high-throughput genotyping and phenotyping technologies to accelerate wheat improvement and mitigate the impacts of climate change**” is a 5-year project, aligned with IWYP, and will be conducted by 41 collaborators at 22 institutions with active breeding and/or genomics programs in 20 states. It includes international collaborations with partners from CIMMYT, the UK and Canada. Building on previous research where multiple genes linked to different yield components were identified and the phenotypic value of specific alleles determined, this new project will utilize existing phenotypic and genotypic data supplemented by new high throughput phenotypic and SNP genetic marker data to fully evaluate gene x genotype x environment interactions using new innovative analytical tools and pipelines (see below). Project success will be measured by (i) the volume of data deposited into the T3/Breedbase database (<https://wheat.triticeaetoolbox.org/>), (ii) the number and economic impact of released varieties and the genomic resources developed, (iii) the number of publications, the number of students trained as plant breeders and the type of careers they pursue in industry or academia.

Key Objectives and Outputs

- 🌾 Develop and make widely available to the wheat scientific community, low cost, medium-density SNP assays for accurate genome-wide imputation using haplotype graphs in an easily accessible and automated platform for genomic selection (**Figure 1**).
- 🌾 Implement a centralized pipeline for the storage, processing and analysis of large volumes of high-throughput phenotypic data collected by unmanned aircraft systems (UAS-HTP).
- 🌾 Develop improved and additional analytical tools for the T3/BreedBase database management system.
- 🌾 Train a new generation of plant breeders by integrating them into active wheat breeding programs while developing improved wheat varieties.

Anticipated Impact of this Research

- 🌾 High yielding commercial wheat varieties that are more resilient to changes in climate.
- 🌾 Widespread adoption of UAS-HTP data and technologies by public and private wheat breeding programs for better data-driven decisions in selection of new wheat varieties.
- 🌾 Analytical tools and large genotypic and agronomic datasets from public wheat breeding programs deposited in public wheat databases as global resources for the development of new and improved wheat varieties.

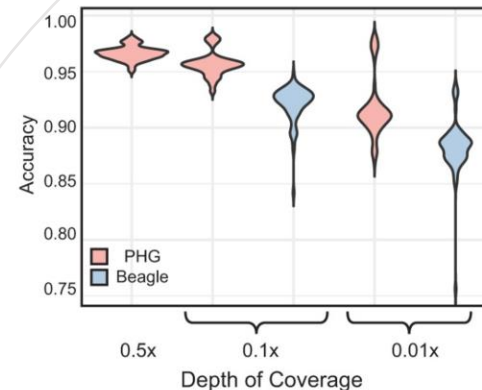


Figure 1. Accuracy of imputation using the Wheat Practical Haplotype Graph (PHG) compared to other low-coverage imputation methods. The mean accuracy of PHG imputation was 95.7% with 0.1× coverage depth, and 91.7% with 0.01× coverage depth. This method was able to adequately capture the haplotypic diversity of a panel of US breeding lines used in the study. Jordan *et al.* (2022) doi.org/10.1093/g3journal/jkab390



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