

High-Throughput Phenotyping Meets Single Plant Analysis

Efficient and robust integration of phenomics and genomics data is the key to revolutionizing plant breeding. One important but unexplored area to leverage the combined power of phenomics and genomics is field-based single plant phenotyping in the early generations of selection. Cost-effective high-throughput evaluation of single plants that enables breeders to select as well as advance populations during early generations could significantly increase the rate of genetic gain and resource efficiency. A USDA NIFA project “**Unified Big Data in Genomics and Phenomics for Plant Breeding**” led by Kansas State University is focused on advancing the field of high-throughput phenotyping to the scale of single plants using unmanned aerial vehicles (UAVs) equipped with high-resolution imaging. Using multispectral digital imagery throughout the growing season, data from single spaced wheat plants was collected and evaluated. The methods developed will also be relevant for researchers that are screening populations seeking key phenotype changes such as those induced by mutation breeding, double haploids or genetic editing where there is insufficient seed to evaluate full size test plots.

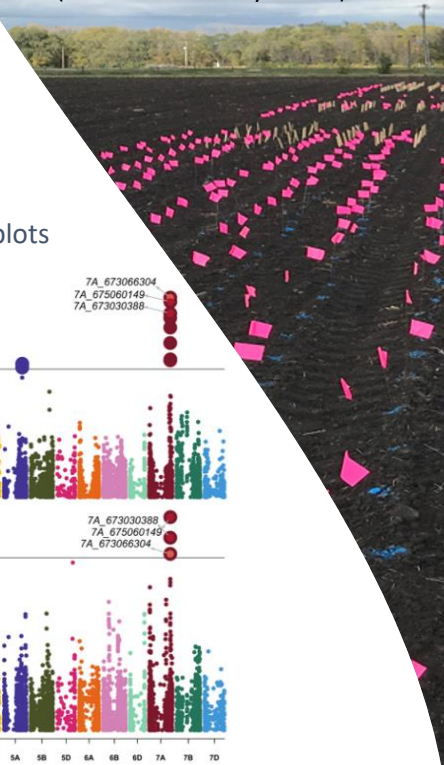
High throughput imaging single spaced plants
(Photo credit Byron Evers)



What Solutions have been Identified?

- An association mapping panel of 340 winter wheat lines was grown as both full plots and single plants in the field to compare plant traits from individual plants to the traits in a larger, dense commercial-type planting.
- During two growing seasons, UAV imagery was collected for the single plants and full plots. Image data include red, blue, green, and near-infrared measurements to calculate a normalized difference vegetation index (NDVI) and other growth indices.
- Pipelines for extracting plot-level data were modified to extract single plant data.
- NDVI was correlated to both single plant yield and full plot yield.
- Common genetic loci were found among hand-measured traits in single plants and full plots (Figure 1).

Preparing field for planting single plants
(Photo credit Haley Ahlers)



Anticipated Impacts of this Research

- Application of single plant analysis could provide plant breeders with improved tools to select plants in early, segregating generations thus increasing genetic progress.
- Data of enhanced quantity and quality to inform selection decisions.
- A workflow for single plant image extraction has been deposited in the Zenodo digital repository <https://doi.org/10.5281/zenodo.6515042>.

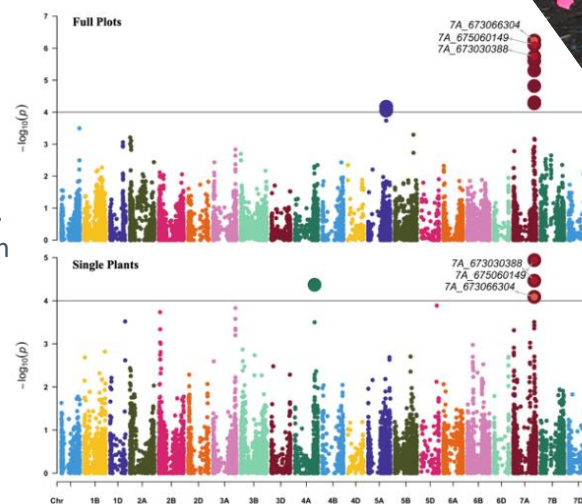


Figure 1. Manhattan plot of spikelets per spike in full plots (top) and single plants (bottom). Common significant markers on chromosome 7A have been highlighted.

Adapted from [Crain et al. \(2022\)](#).