#071

Accelerating breeding efficiency by applying high-throughput phenotyping and genomic prediction methods in canola

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Background:

North Dakota leads the U.S. in canola acreage (over 82% of the planted area) and production (around 85% of the U.S. canola). To better support canola growers in the state and across the region, a canola breeding program was established at North Dakota State University in 2006.

Objective:

Recently, high-throughput phenotyping (HTP) and genomic prediction have been alluring in crop research in both public and private sectors around the world. These methods can significantly accelerate breeding efficiency in canola, as well as in other crops. As part of efforts to implement HTP into our canola breeding program, we are currently using DJI Matrice 200 equipped with a 10-band multispectral camera (MicaSense Dual Camera system) and small plot autonomous ROBOT for different agronomic traits.

Methods:

The unmanned aerial system (UAS) multispectral images were taken at 100 ft above ground level (AGL) at 51, 66, 72, and 77 days after seeding (DAS) of the canola. The experimental trials used in this study were wide-area yield trial (WAT) with 108 research plots and advanced yield trial (AYT) with 243 research plots. The images were stitched into orthomosaic using Pix4DMapper from Pix4D, then we use an in-house developed Python script to calculate and extract single plot statistics (mean, median, max, min, range, and standard deviation) for 38 vegetation indices (VIs). Pearson's correlations were conducted with the VIs and four agronomic traits such as early vigour, breeder's score, seed yield, and seed oil.

Results:

The breeder's score and seed yield showed a significant correlation with many indices. NDVI, ENDVI, VEG, GRRI, NGRDI, MGRVI, VDVI, VARI, SAVI, OSAVI at 66 DAS showed significantly higher correlation (0.60**** to 0.74****) with breeder's score and seed yield in both experimental trials. A very strong correlation was observed between seed yield and breeder's score (0.98**** for WAT, and 0.98**** for AYT). This result indicates that the breeder's scores and UAV multispectral images could be used as the proxy of seed yield. Small plot robot has been used in the greenhouse and in the field to measure stem diameter and stand count. The genomic prediction was conducted for pod shatter resistance with 24k SNPs using 14 prediction models. The prediction ability of all models for pod shatter resistance ranged from 0.18 – 0.50. To determine the minimum number of markers needed to estimate the predictive ability, we used 25 to 20000 randomly selected markers where 3000 to 20000 markers gave a similar prediction ability (≈0.47).