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#029

Whole genome predictions provide flexibility in the utilization of costly phenotypic data across environments with varying temperatures

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With > 8 M ha of canola (Brassica napus L.) grown in Canada and the crop's sensitivity to heat stress, research on breeding methodologies to improve heat stress tolerance are warranted. This research utilized a doubled haploid population created from two parents (PB36 and PB56) that differed in their ability to set seed following growth at high temperatures. This experiment was designed to utilize this population as a test case for evaluating the prospects of whole genome prediction. The population was phenotyped using a split plot RCB design at three locations with two planting date treatments. The first planting date occurred earlier in the growing season (control), while the second planting occurred subsequently to shift the flowering period later and expose the genotypes to increased temperatures. The average temperatures during the second planting date were increased by, 1.7, 2.0 and 1.2 C while number of days with maximum temperatures above the critical temperature of 29.5 C increased by, 4, 12 and 3 days during the growing season. The high temperature treatment reduced yield on average by 16.7 %. Given the quantitative nature for the traits collected, the ability to use whole genome prediction was investigated. The prediction accuracies ranged from 0.14 (yield) to 0.66 (thousand kernel weight). Prediction within the high temperature treatment had higher accuracy than within the control treatment for seven of the nine traits demonstrating that phenotyping within a stress environment can provide valuable data for whole genome predictions.