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Development and In-Field Validation of Genomic and Optimal Haploid Value Selection for Disease Resistance, Agronomic, and Seed Quality Traits in Canola

Hans D. Daetwyler
Mulusew Fikere, Denise M. Barbulescu, Michelle M. Malmberg, Fan Shi, Joshua C. O. Koh, Sally Norton, Phillip A. Salisbury, Surya Kant, Pankaj Maharian, Joe Panozzo, German C. Spangenberg, Noel O. I. Cogan

Agriculture Victoria and La Trobe University, Bundoora, Australia

Genomic selection (GS) uses single nucleotide polymorphisms (SNP) genotyped on germplasm that also has field trial data to predict genomic estimated breeding values for lines that have only been genotyped. Optimal Haploid Value (OHV) selection focusses selection on haplotypes and aims to predict lines with the highest potential to produce an elite doubled haploid (DH). A diverse set of B. napus spring and winter lines was compiled. Field trials were carried out across four years. Two blackleg field disease nurseries (Green Lake and Wickliffe, Victoria, Australia) were completed in 2015 on a set of 600 spring and winter lines. Additionally, a subset of 200 spring lines were grown in four agronomic field trials at Horsham (irrigated 2016, 2017), Mininera (rainfed, 2016), and Green Lake (rainfed, 2017). Phenotypes were also collected on 1215 lines in one large blackleg nursery at Wonwondah in 2018. An in-field validation study compared GS and OHV and selected DHs and their original parents were in the 2018 field trial. The following 22 traits were recorded: emergence, survival, internal blackleg infection, vigour, days to flowering, days to maturity, plant height, seed yield, seed moisture content. Seed composition was determined with NIR for seed oil and protein %, total seed glucosinolate, and the main fatty acids.

All lines were genotyped with an in-house transcriptome genotype-by-sequencing (GBS) protocol with up to 98,000 SNP. Genomic best linear unbiased prediction and BayesR GS methods were used. Genomic prediction accuracies were moderate to high for most traits, including yield, survival, and internal infection, but were lower for emergence count. Known blackleg QTL regions explained at most 33% of the genetic variance in survival or internal infection, demonstrating that selecting only on major known blackleg QTL using marker-assisted selection ensures sub-optimal genetic gain. GS and OHV resulted in very similar genetic gain of 12% survival for selected DHs compared to the original parents, and OHV selected DHs were more phenotypically diverse. The top DH line in the field trial was an OHV selected line. Our findings have confirmed previous simulation results and demonstrated that OHV is an effective selection method.