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Development of a novel high-throughput assay for root phenotypic traits of canola varieties

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Background:

Poor establishment in canola limits yield potential and worsens the burden of weeds, diseases and pests. Increased seedling root growth has been associated with greater seed yields in canola and proposed as a trait for improved establishment. Primary root length and early shoot vigour have been shown to be correlated in canola, but few studies have been published and the authors are not aware of any in large populations.

Objective:

To develop an efficient and accurate assay with which to determine the phenotypic variation and genetic architecture of seedling root traits in a canola GWAS panel of global and Australian varieties. The population comprises 256 varieties which have dense SNP map information.

Methods:

A germination pouch cultivation system was designed in which three seedlings could be grown for 5 days without nutrients. Seeds from the GWAS panel were sieved for similarity in size and then individually weighed on a fine balance for use as a covariate in analysis. This was done to partition out the maternal influence of seed size on the phenotype.

Each variety was replicated eight times over six batches of 116 pouches containing 348 seeds, with each variety allocated to batch, pouch and pouch position in an optimised design. Each pouch was opened and imaged with a digital camera in a copy stand. The images were processed with the AI tool RootPainter to produce skeletonised images of the seedling root system, which were in turn analysed for root traits with the RhizoVision imaging software for total root length and the number of root tips. The root systems were also dried and weighed for the calculation of specific root length.

Results:

Root traits were analysed with a linear mixed model in which the extraneous effects of the experimental setup (batch, pouch position, etc) were accounted for as a random factor and the effect of seed size was treated as a fixed factor. The effect of variety was treated as a random factor to generate best linear unbiased predictors (BLUPs). Heritability was calculated from the residual variance and the variety variance and/or mean of covariance between the varieties. 18 varieties were identified with significantly higher total root length than the population mean; six varieties were identified with a significantly higher greater number of root tips than the population mean. These traits had a repeatability of 0.63 and 0.54 respectively.

Conclusions:

The study identified variation for seedling root traits that was separate to the influence of seed size. There is an opportunity to explore the genetic architecture of seedling root traits in this study and to associate it with traits identified in other screens with this population and with performance in the field.