

#044

Genetic variation and QTLs for transpiration efficiency and yield related traits under low rainfall environments in canola

ADDRESS

*Harsh Raman*¹
*Rosy Raman*¹
*Yu Qiu*¹
*Simon Diffey*²
*Lauren Borg*³
*Brett McVittie*¹
*Suzu Rogiers*⁴
*Nawar Shamaya*¹
*Andrew Easton*⁵
*David Tabah*⁵

PLENARY TALKS

1 NSW Department of Primary Industries, Wagga Wagga Agricultural Institute, Pine Gully Road, Wagga Wagga, Australia

2 Apex Biometry, Perth, WA, Australia

3 National Institute for Applied Statistics Research Australia (NIASRA) University of Wollongong, NSW, Australia

ORALS

4 National Wine and Grape Industry Centre, Wagga Wagga, NSW, Australia

5 Advanta Seeds Pty Ltd, Toowoomba, QLD, Australia

POSTERS

WORKSHOPS

Australia is the driest continent of the world, where frequent episodes of drought and heat limit plant development and productivity. Canola is more sensitive to water (drought) stress as compared to cereal crops such as wheat and barley. Identification of canola genotypes with stable yield and genetic loci controlling seed yield across diverse growing environments is essential for canola improvement, especially under water-limited conditions. We evaluated canola accessions (144-150) across seven Australian environments to determine the extent of genetic variation in grain yield (2013-2015). Meta-analysis revealed some accessions of interest, which consistently yield higher as compared to others. To dissect attributes contributing to high seed yield, we determined genetic variation in fractional ground cover, shoot biomass, carbon isotope discrimination (CID), and flowering time and found a trade-off between flowering time and drought avoidance traits. To uncover the genetic basis of high seed yield and related traits, we conducted QTL analysis of two doubled haploid populations derived from Skipton/Ag-Spectrum/Skipton and 06-5101 crosses, which were evaluated across 2-4 years. We identified significant QTLs associated with CID, early vigour, flowering time and seed yield. In order to understand the relationship between transpiration efficiency (TE) and CID, we selected extreme phenotypes of a DH population and evaluated for variation in carbon assimilation, stomatal conductance, intrinsic water use efficiency, and chlorophyll content. Data on relationship between flowering time, grain yield and TE will be presented. Our research provides valuable insights of genetic variation and underlying genetic determinants associated with high yield, and tools for breeding canola especially under low rainfall environments.