

Plant Genomics

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Breeding of drought tolerant canola: From laboratory to the field

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The production of oilseed rape, a globally important oil crop, is tremendously limited by drought stress. To cope with this issue, the breeding of new cultivars with improved ability to drought stress is of great interest. To this aim, we carried out experiment-1 to establish selection criteria for drought tolerance at different developing stages. The impacts of water deficit established at the germination stage on biological traits of 37 semi-winters rapeseed cultivars was first analyzed. The results proved that osmotic stress induced by 14% polyethylene glycol (PEG-6000) had a substantial impact on seed germination and caused a significant reduction in plant growth and seed vigor. Relative water content was identified as an indicator for early screening of drought tolerance. At the reproductive stage, seed yield, 1000-seed weight, height of the first branch, plant height and number of pods per plant were all markedly reduced under the exceptionally long (>100 d) and severe drought condition (a total of 162 mm precipitation during rapeseed life cycle, 52% reduced). Out of top three two of the tolerant genotypes at the germination stage were also shown to be tolerant based on drought susceptibility index of yield. Path analysis and phenotypic correlation were employed to rank the relative importance of other agronomic traits with regard to seed yield under drought conditions the important contributors to seed yield, in descending order, were as follows: 1000-seed weight, days to maturity, number of pods per plant and plant height. By taking this concept in mind, we have recently bred a new drought-tolerant cultivar (YG85) that can be grown in the drought-prone environments in the Northwest of China. To facilitate the breeding of drought tolerance with the aid of molecular markers, we conduct experiment-2 with a panel of 101 lines, which had previously been analyzed by RNA-Seq. The evaluation of drought tolerance at seedling stage resulted in the identification of 7 drought tolerant lines that could be incorporated into breeding program. The ongoing genome-wide Associative Transcriptomics analysis is expected to bring about the discovery of some candidate genes underlining drought tolerance and the development of functional markers.

Biography

Guangyuan Lu has completed his PhD from Huazhong Agricultural University, China and worked as a Visiting Scholar in John Innes Centre, UK during 2013-2014. He is the Group Leader of 'rapeseed molecular breeding' section, Oil Crops Research Institute, CAAS, a premier crop innovation organization. He has published more than 43 papers in reputed journals and has been serving as a Reviewer of *Molecular Breeding*.

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