IDT3-016 | Genetic analysis of F2 generation of four derived crosses for yield and water use efficiency related traits in groundnut (*Arachis hypogaea* L.)

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The objective of this study is to develop high water use efficient genotypes of groundnut, which thrive well under water-limited conditions. The F2 generation of four crosses, GKVK16×KCG2, GKVK13×KCG2, GKVK6×KCG2 and GKVK16×ICGV91114, were analysed for genetic variability and correlation studies. Yield component traits and SLA exhibited high GCV and PCV whereas SCMR exhibited low GCV and PCV in all the four crosses, indicating the presence of genetic variation for yield traits and SLA. High heritability accompanied with high GAM was recorded for plant height, SLA, pods/plant, pod yield/plant, kernel yield/plant, shelling percent and SMK. This indicates that characters are under additive gene action and selection would be effective in later segregating generations for improvement of these traits. Pods/plant and kernel yield/plant had high positive correlation with pod yield/plant in all the four crosses and also exhibited high positive direct effect on pod yield/plant. High positive correlation with high direct effect indicated true relationship of these characters, and importance should be given to these traits during selection for higher yield. Positive association was found between SCMR and pod yield/plant whereas negative association was found between SLA and pod yield/plant; SLA and SCMR in all the crosses. In segregating generations of all the crosses, adoption of indirect selection based on yield components and WUE related traits, particularly kernel yield/plant, pods/plant, SLA and SCMR rather than direct selection for pod yield/plant will be highly rewarding for developing high-yielding and water-use-efficient groundnut genotypes which are suitable for drought conditions.

IDT3-017 | Fine mapping of the linkage group 2 drought tolerance QTL in pearl millet [*Pennisetum glaucum* (L.) R. Br.]

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Pearl millet is an important cereal crop capable of growing in semi-arid, arid and marginal regions of the world. Drought is a major abiotic constraint affecting pearl millet production globally. Previously identified and validated major linkage group 2 (LG2) drought tolerance (DT) QTL contributing to hybrid grain and stover yield potential to terminal drought stress is being fine mapped. The fine mapping population was generated by crossing two near-isogenic lines (NILs) differing for the LG2 DT QTL. A modified double digest restriction site associated DNA (ddRAD) technique using *Sph*I and *Mlu*CI enzyme combination was employed. A total of 290 out of 6,067 F2 mapping population of the cross (H77/833-2-P10 × ICMR 01029-P10), and parents were genotyped on Illumina HiSeq2500. Out of 52,028 SNPs that were identified from a total of 888.85 million reads at a read depth of 10 in the mapping population, a total of 6,821 SNPs were used for mapping. The genotypic data of these SNPs were used in combination with that of seven SSRs that had known linkage relationship with LG2 DT QTL interval. Linkage map was constructed using QTL IciMapping 4.1 software at a LOD threshold of 3.0. A total of 189 SNPs anchored to seven SSRs were mapped to the LG2 DT QTL. The length of linkage group (LG) was 639.72 cM (Haldane units) with an average inter-marker distance of 6.73 cM. In order to refine the fine mapping process, ddRAD technique is being further employed for genotyping rest of the fine mapping population.