Retrospect and prospect of improving groundnut (*Arachis hypogaea* L.) for drought-prone areas of India

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Groundnut in India is often cultivated with low inputs in marginal lands of arid and semi-arid tropics in around 5.5 million ha, with production of 7 million tonnes and productivity of about 1530 kg/ha. However, productivity is often affected by drought, the frequency and intensity of which is likely to increase in future owing to climate change. Though a few donor lines and released varieties have been claimed to be tolerant to early-, mid-, and end-off season drought, cultivars capable of assured production in limited water availability are still lacking. Success of transferring *mtID*, *DREB,* genes for proline, glycine and betaine pathways to confer drought tolerance and improve the much-needed water-use efficiency has been limited. To cope with drought, identification of ideal plant ideotypes, use of identified QTLs related to drought stress tolerance, and water-use efficiency by genome assisted breeding to introgress the required traits in cultivated background are required. The screening methods currently used in conventional breeding need radical changes to produce drought-tolerant cultivars. To address the issues of reduction in photosynthesis, carbon gain and yield, and enhancement in photorespiration during drought stress, transfer of C4-photosynthetic machinery into C3-groundnut can be considered with enhanced water-use efficiency. Management of nutrient uptake and N-fixation in drought stress, along with use of endophytc microbes could also be part of the strategies to alleviate drought. The availability of genomic and transcriptomic data of wild and cultivated groundnut brightens the possibility of developing drought-tolerant groundnut cultivars in future.

The first high density genotyping 'Axiom_Arachis' 58K SNPs array for genetic studies and molecular breeding in groundnut

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Genome complexity and narrow genetic base are the major problems that hinder achieving accelerated genetic gains in groundnut or peanut, a major source of vegetable oil (48%) and protein (25%). High density genotyping is a must-have genomic resource in a crop for use in several genetic and breeding applications. Availability of genome sequence for both the diploid genome progenitors of cultivated groundnut has provided an opportunity for discovery of structural variations in large-scale including single nucleotide polymorphisms (SNPs), the most abundant DNA sequence variation in the genomes. In this context, we developed a high-density SNP array 'Axiom_*Arachis*' with 58K SNPs with uniform genome coverage. We identified initially a total of 163,782 SNPs that included 118,860 SNPs (58,438 SNPs for A-genome and 60,422 SNPs for B-genome) from 30 tetraploids and 44,922 SNPs (39,937 SNPs for A-genome and 4,985 SNPs for B-genome) from 11 diploids. Finally, a total of 58,233 highly informative SNPs with genome specificity were used for array development. In addition to cultivated groundnuts (*Arachis hypogaea)*, this array has fair representation of other diploids (*A. duranensis, A. stenosperma, A. cardenasii, A. magna* and *A. batizocoi*). Genotyping of the groundnut 'Reference Set' containing 300 genotypes identified 44,424 polymorphic SNPs and genetic diversity analysis provided in-depth insights into the genetic architecture of this material. In summary, this high-density SNP array will accelerate the process of trait dissection and molecular breeding including genomic selection for achieving higher genetic gains in groundnut.