

Recent Advances in Sorghum Breeding

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Sorghum (*Sorghum bicolor*(L) has been a vital source of food especially for the people in the Semi-Arid Tropics. Sorghum is emerging as a crop with diverse end-uses such as food, feed, fodder, fiber and fuel which makes it ideal for both subsistence and commercial farming (Hao *et al.*, 2021). It has received increasing attention as a good source of slowly digestible starch (Simnadis *et al.*, 2016) and exclusive bioactive flavonoids (Yang *et al.*, 2015). It has great potential as being sustainable staple food and fodder crop, because of its hardiness and low water requirement. Being more resilient to adverse environmental conditions, sorghum performs well under high temperature and drought conditions and occupies even the marginal fertile area for cultivation. It is the main source of livestock feed and industrial uses in developed countries like USA, Canada and Australia. As a C₄ crop with low input requirements and high net return, sorghum is more resilient to adverse environmental conditions and performs well under water shortage and increasing temperature.

Domestication and Distribution

Sorghum bicolor (L.) Moench is a single cultivated species. It is an annual crop, often branched with many tillers and have thick culms. Sorghum was first domesticated in Africa (Harlan and De Wet, 1971) probably in the Ethiopia Sudan region (Doggett, 1988). Domesticated sorghum has been classified into five basic races: *bicolor*, *guinea*, *caudatum*, *kafir* and *durra* (Harlan and de Wet, 1972) having different geographic origin. Genomic studies have clearly

indicated that the sorghum races are genetically diverse. *Bicolor* is the most primitive race derived from the wild progenitor *S. bicolor* subsp. *verticilliflorum* (Ananda *et al.*, 2020). Kafir is the main source of male sterile genes and is photo insensitive whereas Guinea is photo sensitive; Caudatum is having recent origin and mainly used for beer brewery. Durra is widely used in crop-improvement programs (Cuevas *et al.* 2017). The improved sorghum types were spread by the movement of people and trade routes into India (1500–1000 BC), the Middle East (900–700 BC) and eventually into the Far East (AD 400). Most of the wild types have characteristic phenotypes of profuse tillers, inflorescences with spreading branches, shattering and dark-colored small seeds. Early domestication of sorghum was associated with improvement in seed size and panicle type such as larger, compact ear heads with non-shattering seeds

Sorghum Genetic resources

In Sorghum, immense range of genetic variability is available in Africa where domestication first occurred followed by Asia due to the early introduction of the crop. The existing sorghum germplasm contains four major types such as grain sorghum with high seed yield, forage sorghum with good biomass and regeneration capacity, sweet sorghum with juicy, sugary stems and broom sorghum with long fibrous ear heads (Dahlberg *et al.*, 2011). Weedy sorghum such as Johnson grass and spontaneous sorghum (shatter cane) are widespread in temperate zone. Johnson grass (*S. halepense*), is one of the world's worst weed

which reproduces through both seed and rhizome. Knowledge on wild progenitors of sorghum (*Sorghum bicolor*) helps in exploiting the underutilized gene pool for developing climate-resilient sorghum cultivars. In Sorghum, approximately 2,56,000 germplasm accessions are being conserved Globally. Gene bank at ICRISAT conserves the largest collection of about 42,000 accessions and these accessions are well characterized for various morpho-physiological and agronomic traits (Ashok Kumar *et al.*, 2013). Other institutions include Australian Tropical Crops and Forages Genetic Resources Center which has the largest collection of Australian wild sorghum, National Bureau of Plant Genetic Resources in India with about 20,000 collections (www.nbpgr.ernet.in) and the Institute of Crop Germplasm Resources in China with 16,874 collections (<http://www.icgr.caas.net.cn>).

Breeding programmes

Because of the huge availability of diverse genetic resources, great progress has been made in sorghum breeding in the past decades. Stable, high-yielding sorghum varieties have been recently developed through breeding programmes utilizing sorghum landraces especially with traits such as photoperiod insensitivity, dwarf stemmed suitable for machine harvest, resistance to abiotic and biotic stress. Breeding methods followed for the improvement of sorghum cultures with higher yield quality include selection, hybridization, heterosis breeding, mutation breeding and population improvement. In India, essentially all the sorghum types cultivated are white (including tan-plant types) or red (non tannin grain types), which are used for human food. At present, the emphasis in India is more on breeding improved, dual purpose

(grain and fodder) open pollinated varieties and hybrids.

Modern breeding concepts

Modern breeding approaches are urgently needed to accelerate the breeding for sorghum varieties combined with high genetic yield potential and stress tolerance. Molecular marker techniques enhance breeding efficiency by improving the accuracy of selection process and also by reducing the time required for cultivar development (Hasan *et al.*, 2021). Conventional breeding techniques can be strengthened through modern breeding concepts and technologies such as high throughput, genomic map-based marker – assisted selection and through integrated breeding platforms supported by modern data management system. Because of diverse germplasm collections, its adaptation to harsh environments and value for comparing the genomes of other cereal crops such as rice and maize, sorghum is the main target for plant genomic mapping. Knowledge of the available genetic variation, molecular breeding approaches and genomic selection strategies is required for exploring genetic gain for a range of important traits such as grain yield, biomass production, drought tolerance and stem sugar accumulation.

Sorghum is highly suitable for association mapping due to its self-pollinating mating system and its medium-range patterns of linkage disequilibrium (Hamblin *et al.*, 2005). Genome-wide association studies using high density SNP array technologies for the identification of single-nucleotide polymorphisms (SNPs) and next-generation sequencing (NGS) platforms have opened the way for genomic selection (GS). Next generation sequencing (NGS) provides tools for sequencing the entire genome of species instead of few selected genomic regions and capture single

nucleotide polymorphisms (SNPs) throughout the genome. Genomic selection is a viable tool that predicts the genetic values of individuals using genome-wide markers and permits the use of molecular markers with both major and minor effects in developing the prediction model to predict the phenotypes of untested individuals. In recent years, such techniques have the potential to improve the effectiveness of advance breeding techniques and thereby the accelerate selection gain.

Developing new sorghum varieties tailored with ideal traits is possible through genome-based technologies. Genome sequencing of wild as well as improved sorghum genotypes will provide new genomic variations for sorghum domestication and diversification. Small genome size (730 Mb), simple (10 chromosomes, diploid) and complete genome sequence availability (Paterson *et al.*, 2009) make sorghum an amenable crop for the application of genomics-based approaches. Genomic research in sorghum is further accelerated because of the availability whole genome reference sequence, based on the elite line BTx623 (Paterson *et al.*, 2009).

Future thrust

Based on the breeding objective, precision molecular breeding of sorghum should be carried out; For example, slow digestibility, low cholesterol, antioxidant and other health benefits are the characteristic features of grain sorghum. Increasing the protein content especially lysine and starch (especially amylopectin) are the future thrust area in sorghum breeding. The goal of future breeding is to increase protein (especially lysine) and starch contents and reduce tannins. Although great progress has been made in locating the genetic loci for traits, advanced techniques such as high-throughput sequencing, pan-genomes and epigenomes has to be integrated to identify the

superior alleles and the functional regulation network underlying the complex agronomical traits and the stress resilience of sorghum. An enormous amount of research on molecular markers has been accomplished in the recent past in sorghum, there is still an immense need to develop breeder-friendly high-throughput markers for the important traits for stress tolerance along with nutrient traits like grain iron and zinc concentration.

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