Vilas A. Tonapi · Harvinder Singh Talwar
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Timothy J. Dalton *Editors*

Sorghum in the 21st Century: Food – Fodder – Feed – Fuel for a Rapidly Changing World

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Editors
Vilas A. Tonapi
ICAR-Indian Institute of Millets Research
Hyderabad, Telangana, India

Harvinder Singh Talwar
ICAR-Indian Institute of Millet Research
Hyderabad, Telangana, India

Ashok Kumar Are
International Crops Research Institute for the Semi-Arid Tropics
Patancheru, Telangana, India

B. Venkatesh Bhat
ICAR-Indian Institute of Millets Research
Hyderabad, Telangana, India

Ch. Ravinder Reddy
Formerly, International Crops Research Institute for the Semi-Arid Tropics
Patancheru, Telangana, India

Timothy J. Dalton
Department of Agricultural Economics
Kansas State University
Manhattan, Kansas, USA

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Sorghum Germplasm for Enhanced Productivity and Nutrition

Hari D. Upadhyaya, M. Vetriventhan, Ashok Kumar Are, Vania C. R. Azevedo, and Y. H. Wang

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H. D. Upadhyaya (✉)
University of Georgia, Athens, GA, USA

Department of Agronomy, Kansas State University, Manhattan, KS, USA
e-mail: harideo.upadhyaya@gmail.com

M. Vetriventhan · A. K. Are · V. C. R. Azevedo
International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Telangana, India
e-mail: M.Vetriventhan@cgiar.org; a.ashokkumar@cgiar.org; v.azevedo@cgiar.org

Y. H. Wang
Department of Biology, University of Louisiana at Lafayette, Lafayette, LA, USA
e-mail: yxw9887@louisiana.edu

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Abstract

Sorghum [*Sorghum bicolor* (L.) Moench] is an important crop in the semi-arid tropics and being cultivated in about 110 countries. The rate of genetic gain in sorghum has been slower compared to other field crops, that could be because the crop is grown under marginal environments with limited resources, and often affected by biotic and abiotic stresses, besides other constraints such as poor crop management and low research priority than other cereals. Globally, a large number of sorghum germplasm accessions have been conserved in genebanks, and they are source of genetic variation to potentially raise genetic gain, and have played a key role in improving sorghum productivity. This chapter detailed about major constraints in sorghum production and research domains, germplasm diversity, capturing germplasm diversity in the form of representative subsets, mini core collection as a source of variation for important traits, wild and weedy relatives for sorghum improvement, and enhancing genetic gains. This information could greatly help sorghum researchers in planning and prioritizing traits for enhancing productivity and nutrient density of sorghum cultivars that can deliver genetic gains in the farmers' fields.

Keywords

Sorghum · Germplasm · Genetic gains · Diversity · Genebank · Mini core collection

1 Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is a staple food crop for millions of the poorest and most food-insecure people in the semi-arid tropics. Globally sorghum was cultivated in 44.8 million ha with a production of 63.9 million tons during 2016, largely comes from Africa which contributes about 68% of area and 47% of total global sorghum production; followed by about 13% and 16% area in the Americas and Asia, contribute 36% and 13% to production, respectively. The world sorghum productivity is about 1428 kg ha^{-1} in 2016, which is very low, mainly because sorghum is largely cultivated in marginal lands with limited inputs, often damaged by several insect pests and diseases and abiotic stresses (Upadhyaya and Vetriventhan 2018). The genetically improved hybrids and varieties of sorghum were reported to be less diverse compared to the wild and weedy relatives and landraces (Jordan et al. 1998, 2003; Mace et al. 2013; Murray et al. 2009; Mutegi et al. 2011; Smith et al. 2010). Low diversity of cultivars is mainly because of low use of existing variability in sorghum breeding, for example, post rainy sorghum in India. Such a narrow genetic base of cultivars may result in an increased risk of crop vulnerability, such as crop failure due to insect pests and disease epidemics or unpredictable climatic effects, and leads to low productivity (Upadhyaya and Vetriventhan 2018).

In sorghum, a significant number of germplasm accessions have been conserved globally that could be potentially utilized to enhance quality and productivity of sorghum. Lack of reliable information on traits of economic interest is one of the main reasons for limited use of germplasm, besides other reasons such as restricted access to the germplasm as a result of regulations governing international exchange, the linkage load of many undesirable genes, etc. Efforts have been made to establish germplasm diversity representative subsets and trait-specific sources have been identified in sorghum. Utilization of such diverse trait-specific sources could potentially enhance productivity and quality of sorghum cultivars and increase rate of genetic gains. This chapter details about constraints in sorghum production and research domains, germplasm diversity, capturing germplasm diversity in the form of core/mini core collections, mini core collection as a source for economic important traits, wild and weedy relatives for sorghum improvement, utilization of germplasm in breeding and genetic gains.

2 Constraints in Sorghum Production and Sorghum Research Domains

Sorghum is largely cultivated on marginal soils with limited inputs as compared to major cereals such as wheat, maize, and rice. In addition, sorghum production is affected by many factors leading to significant losses to farmers. Broadly four major production constraints in sorghum can be categorized into biotic, abiotic, crop management, and socio-economic factors, of these biotic and abiotic stresses cause severe crop losses. From a crop management point of view, most of sorghum crop in Africa and to some extent in Asia is under fertilized and grown with limited crop care. Socio-economic constraints especially poor access to agricultural information and inadequate farmer knowledge and training result in limited adoption of improved technologies.

2.1 Biotic Stress

Around 150 insect species attack the sorghum crop throughout its life cycle (Sharma 1993). Among them, sorghum shoot fly (*Atherigona soccata*), stem borers (*Chilo partellus, Busseola fusca, Eldana saccharina*, and *Diatraea* spp.), armyworms (*Mythimna separata, Spodoptera frugiperda*, and *S. exempta*), shoot bug (*Peregrinus maidis*), aphids (*Schizaphis graminum* and *Melanaphis sacchari*), spider mites (Oligonychus spp.), grasshoppers and locusts (*Hieroglyphus*, *Oedaleus*, *Aliopus*, *Schistocerca*, and *Locusta*), sorghum midge (*Stenodiplosis sorghicola*), mirid head bugs (*Calocoris angustatus* and *Eurystylus oldi*), and head caterpillars (*Helicoverpa, Eublemma*, *Cryptoblabes*, *Pyroderces*, and *Nola*) are the major pests worldwide. The damages caused by them have been estimated to be $1089 million in the semi-arid tropics (SAT), $250 million in the United States, and $80 million in Australia (ICRISAT 1992). In India, nearly 32% of sorghum crop is lost due to insect

pests (Borad and Mittal 1983). Sorghum shoot fly, *Atherigona soccata*, is an important pest of sorghum in Asia, Africa, and the Americas. Shoot fly females lay cigar-shaped eggs singly 5–25 days after seedling emergence below the surface of the leaves. After 1–2 days the eggs hatch and the larvae crawls toward the growing tip and feed the growing tip thus resulting in typical dead heart. The dead heart can be pulled out easily. The damaged plants produce side tillers, which may also be attacked leading to reduced yield. The lifecycle of shoot fly is completed in 17–21 days. The shoot fly infestation is high when sorghum plantings are staggered due to irregular rainfall. Shoot fly infestation is normally high in the late sown post-rainy season crop planted in September to October. It is observed that the shoot fly infestation is lower at temperatures above 35 °C and below 18 °C. Spotted stem borer, *Chilo partellus*, also feeds on the growing point resulting in dead heart formation. Stem borer is common in Asia and East and Southern Africa. The stem borer larvae feed on the young whorls of leaf creating elongated holes, and the third instar larvae bores into the stem and continue to feed inside the stem throughout the crop growth. Extensive tunneling of the stem and peduncle leads to drying up of the panicle, production of a partially chaffy panicle or peduncle breakage. Stem borer infestation starts about 20 days after seedling emergence, and dead hearts appear on 30–40 days old-crop. Another important insect is sugarcane aphid, *Melanaphis sacchari,* mostly occurs in Asia, Africa, and the Americas. Aphids colonize under the leaf surface and suck the sap from the leaf which results in stunted plant growth. The damage proceeds from lower to the upper leaves. Their population increases rapidly during the end of rainy season. This aphid also reproduces by parthenogenesis.

Diseases such as downy mildew, grain mold, charcoal rot, anthracnose, leaf blight, and rust are important causing considerable loss to grain and forage sorghum production worldwide. Grain mold, caused by a complex of many fungi, is a major disease on sorghum that causes severe grain losses when the crop harvesting coincides with the rains (Thakur et al. 2006). Damage resulting from early infection includes reduced kernel development; discoloration of grains; colonization and degradation of endosperm; and decreased grain density, germination, and seedling vigor (Sharma et al. 2010). Charcoal rot of sorghum caused by the fungus *Macrophomina phaseolina* is a soil-borne pathogen usually attacks plants with compromised plant immunity caused due to unfavorable growing conditions (Das et al. 2008). Drought stress is the main factor that predisposes sorghum to charcoal rot. In diseased roots and stalks, *M. phaseolina* is often associated with other fungi, suggesting that the disease is of complex etiology. Anthracnose, caused by *Colletotrichum sublineolum* Hann. Kabát et Bub. (syn. *C. graminicola* (Ces.) G.W. Wilson), weakens the plant, severely reducing grain yield and quality (Sharma et al. 2012). Leaf blight, caused by *Exserohilum turcicum* (Pass.) K.J. Leonard & Suggs, is widely distributed and, at times, one of the most damaging foliar pathogen of sorghum**,** causing significant grain losses due to the reduction of the photosynthetic leaf area (Sharma et al. 2012). Rust (*Puccinia purpurea* Cooke) is another foliar disease of sorghum that reduces forage quality and grain yield. It occurs in almost all sorghum-growing areas of the world. Under favorable conditions, rust

development is fast and affects panicle exertion and grain development, resulting in poor grain yield (Sharma et al. 2012). Downy mildew, caused by *Peronosclerospora sorghi*, can cause severe epidemics, resulting in considerable yield losses, and economically important and widespread in many tropical and subtropical regions of the world where sorghum and maize are grown, and its systemic nature of infection, resulting in the death of plants or lack of panicle initiation (Sharma et al. 2010).

Besides insect pests and diseases, in sub-Saharan Africa, Striga is the major biotic constraint which competes with the crop for nutrients thus causing fertility reduction, N deficiency necessitating the use of higher quantity of fertilizer to balance the yield.

2.2 Abiotic Stress

Sorghum is an important crop in semi-arid tropics because of their better adaptability to abiotic stresses, as it is mainly grown in areas of low rainfall and resource-poor agronomic conditions. Owing to its ability to survive in water-limiting conditions, sorghum has majorly been studied for its drought resistance mechanism. The drought response in sorghum differs depending on the occurrence of stress during pre-flowering and post-flowering. Post-flowering drought is a major production constraint in sorghum. Stay-green (non-senescence or delayed senescence) under moisture stress is an important trait in sustaining a positive nitrogen balance in sorghum and for sustaining yield under stress during grain filling (Borrell and Hammer 2000; Sanchez et al. 2002). Efforts were made to identify several genomic regions of sorghum associated with pre- and post-flowering drought tolerance using several donors such as B 35, QL 41, and SC 56 (Sabadin et al. 2012). Researchers at Patancheru selected six candidate QTLs for the stay-green trait from donor B 35, using published results including Stg1, Stg2, Stg3, and Stg4 reported by Subudhi and Nguyen (2000), Sanchez et al. (2002), and Harris et al. (2007) as well as additional QTLs on SBI-01 (StgA) and SBI-02 (StgB), and initiated marker-assisted backcross to transfer these QTLs into a number of genetically diverse, tropically adapted elite sorghum varieties of Asia, Africa and Latin America, having a range of drought tolerance (Hash et al. 2003). Reddy et al. (2014) reported 61 QTL controlling stay-green trait in sorghum. Another donor parent for stay-green, E 36-1, a cultivar of Ethiopian origin, has also been used to map QTLs for the stay-green trait in two RIL (recombinant inbred line) mapping populations from which a total of seven QTLs were identified (Haussmann et al. 2002), with three of them being common to both populations. So, overall, six sources of the stay-green trait (B 35, E 36-1, QL 41, SC 56, SC 283, and SDS 1948-3) have so far been used for the identification of QTLs, and QTLs have been identified on all ten sorghum linkage groups. Recurrent parents included highly senescent rabi adapted durra variety R 16, 2-dwarf tan white-grained caudatum variety ISIAP Dorado, and 2-dwarf tan white-grained sweet-stemmed caudatum sister-line varieties S 35 and ICSV 111. Several of the stay-green QTLs identified have been validated in different backgrounds (Harris et al. 2007; Kassahun et al. 2010; Vadez et al. 2011). The

stay-green QTL Stg1 in sorghum has also shown its capacity to enhance water uptake in senescent S 35 background (Vadez et al. 2011). However, the effect of Stg1 was not visible in R 16 background. This highlights the importance for future research on stay-green to precisely decipher the mechanisms involved, and whether any of these mechanisms is already available in target recipients. In most sorghum improvement programs globally, E 36-1 and B 35 have been extensively used for developing hybrid seed parents (B-lines) and pollen parents (R-lines) and cultivars.

3 Sorghum Research Domains (SRDs)

The sorghum research domains provide scope for better utilization of results and the data obtained for prioritization of the research and facilitating the interaction among the sorghum researchers. The research domains were designed based on different agro-ecologies, which are analogous to current day product profiles. In sorghum, a total of eight research domains have been designed in terms of soil and climatic conditions regardless of national boundaries (Bantilan et al. 2004). These domains are: (1) SRD I: Production of rainy season and dual purpose sorghum with main emphasis on feed and fodder. The constraints to be focused in SRD I are grain mold, shoot fly, head bug, and post-flowering drought tolerance. (2) SRD II: Rainy season dual-purpose sorghum (grain and fodder), and the constraints focused includes stem borer, grain mold, midge, shoot fly, and drought. (3) SRD III: Emphasis is to improve dual purpose and fodder sorghum along with their associated pests and diseases. (4) SRD IV: Emphasis is on forage sorghum and their associated pests and diseases. (5) SRD V: Early-sown post rainy sorghum, (6) SRD VI: Late-sown post rainy sorghum. (7) SRD VII: Irrigated sorghum. (8) SRD VIII: Extreme altitude sorghum.

More recently specific product profiles were developed for sorghum improvement. For example, in Asia program at ICRISAT, there are four product profiles:

Post-rainy season sorghum for food and feed: The estimated area under post rainy sorghum production is 4.0 million ha, focusing on Indian sub-continent, predominantly Maharashtra, Karnataka, Telangana, Andhra Pradesh, and Madhya Pradesh states in India. Must-have traits include high grain yield, white bold globular lustrous grains, with maturity duration of 120–130 days and plant height 2–2.2 m and resistant to shoot fly and charcoal rot, and tolerant to post-flowering drought stress.

Rainy season sorghum for food, feed, and industrial uses (brewing): The estimated area for production is 2.5 million ha. This product profile covers the Indian states of Maharashtra, Rajasthan, Madhya Pradesh, Karnataka, Telangana, Andhra Pradesh, Tamil Nadu, and Gujarat with spillover benefits in other parts of Asia and Africa. High grain yield and stover yield, with maturity duration of 110–120 days, white bold grains for food and feed use, and high starch (>68%) and medium protein (8–10%) for industrial use, and resistant to shoot fly, stem borer and grain mold, are must-have traits.

Sorghum for forage: Targeting Punjab, Haryana, Uttarakhand, Uttar Pradesh, Bihar, Madhya Pradesh, Tamil Nadu, and Gujarat states of India with spillover benefits in countries such as Ethiopia, Eritrea, Kenya, Uganda, Tanzania, Sudan, Zimbabwe, Malawi, Zambia, China, and Thailand. High stalk yield, tan plant, fast growth, high tillering, in vitro organic matter digestibility >52%, plant height 2.2–2.5 m with single cult/multi-cut types and resistant to shoot fly, stem borer, anthracnose and leaf blight, are must-have traits.

Sorghum for biofuel: Across India, with spillover benefits in countries such as Ethiopia, Eritrea, Kenya, Uganda, Tanzania, Sudan, Zimbabwe, Malawi, Zambia, and China. Must-have traits include high fresh stalk yield and high Brix (%), with maturity duration of 120–130 days, plant height over 2.5 m, and resistant to shoot fly and stem borer.

4 Germplasm Diversity

Plant genetic resources (PGR) are conserved under in situ and ex situ conditions. In situ conservations aim to protect, manage, and monitor the selected populations in their natural habitats so that the natural evolutionary process can be maintained and allows new variations to be generated. Conservation of crop wild relatives in natural habitat/genetic reserves and on-farm conservation of landraces are two forms of in situ conservation. On-farm conservation of sorghum landraces is practiced by farmers, and the genetic diversity of on-farm conserved landraces were investigated by several researchers (Abdi et al. 2002; Mutegi et al. 2011; Ngugi and Onyango 2012; Okeno et al. 2012; Rabbi et al. 2010). Due to the evolutionary process, the landraces and wild and weedy relatives continue to evolve and adapt to the prevailing environmental conditions. Because of replacing the traditionally grown landraces with the modern high yielding cultivars resulted in loss of landraces, causing genetic erosion of important genes. Therefore, it is essential to collect and conserve crops' diversity ex situ. Ex situ conservation aims to conserve components of biological diversity outside their natural habitats, such as seed storage, in vitro storage, DNA storage, pollen storage, field genebank, and botanical gardens.

Sorghum germplasm accessions are largely stored as seeds in genebanks under medium (active collection) and/or long-term (base collection) storage conditions. Over 236,000 germplasm accessions of sorghum have been conserved in genebanks globally (Upadhyaya and Vetriventhan 2018). The major genebanks which conserve the largest collection of sorghum germplasm are (1) International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India (>41,000 accessions), (2) Plant Genetic Resources Conservation Unit, USDA-ARS (36,173 acc.), (3) Institute of Crop Science, Chinese Academy of Agricultural Sciences (ICS-CAAS) (18,263 acc.), and (4) ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi (17,466 acc.), together conserve about 47% of total sorghum germplasm collections conserved globally. The ICRISAT genebank conserves a major part of sorghum germplasm conserved globally (about 17%) and supplying

them worldwide for use in crop improvement programs following Standard Material Transfer Agreement (SMTA) (Upadhyaya and Vetriventhan 2018).

4.1 Phenotypic Diversity

Sorghum germplasm accessions conserved globally reported to harbor a large diversity. The ICRISAT genebank conserves over 41,000 germplasm accessions of sorghum originating from 93 countries and representing all five basic races and ten intermediate races of sorghum (http://genebank.icrisat.org/). The ICRISAT sorghum collection shows a large variability for morpho-agronomic traits: mid-rib color (white, dull green, yellow, brown); panicle compactness and shape (very loose stiff branches, very loos drooping branches; loose stiff branches, loose drooping branches, semi-loose drooping branches, semi-loose stiff branches, semi-compact elliptic, semi-compact oval, compact elliptic, and compact oval); glume color (white, straw, yellow, light brown, brown, reddish brown, light red, red, purple, black, grey, partly straw and brown, partly straw and purple); glume covering (grain uncovered, one-fourth grain covered, half grain covered, three-fourth grain covered, grain fully covered, glumes longer than grain); seed color (chalky white, white, straw, yellow, light brown, brown, reddish brown, light red, red, grey, purple, white and red mixed, black, and straw and red mixed); days to 50% flowering varies from 31 to 199 days in rainy and 36–154 days to 50% flowering in post-rainy; plant height from 50 to 655 cm in rainy and 50–580 cm in post-rainy; basal tillers number from 1 to 14; panicle length from 3 to 90 cm; panicle width from 1 to 80 cm; seed size from 0.8 to 6.0 mm; and hundred seed weight from 0.1 to 9.4 g.

Investigation on geographical pattern of trait diversity using sorghum collection conserved at the ICRISAT genebank provided information on specific regions to focus for certain traits. The landraces from India were late flowering, tall and produced stout panicles and larger seeds, while landraces from Pakistan flowered early in both rainy and post-rainy seasons and produced stout panicles. Accessions from Sri Lanka were late flowering and tall in both seasons, produced more basal tillers and stout panicles (Upadhyaya et al. 2016b). The landraces from Ethiopia were early flowering and short plant height, high panicle exertion, panicle width and 100 seed weight; Kenya for high basal tiller number; Sudan for early flowering and tall height in rainy season and larger seeds; and Tanzania for long panicles (Upadhyaya et al. 2017c). The collection from Sierra Leone flowered late in both rainy and post-rainy seasons, produced more basal tillers per plant and longer panicles. The collection from Central African Republic grew significantly short in rainy season and tall in post-rainy season. The collection from Gambia is for panicle exertion and panicle width, Nigeria for seed width, and Cameroon for seed weight (Upadhyaya et al. 2017b).

4.2 Genetic Diversity

The genetic diversity assessment of global sorghum composite collection (3367 accessions) using 41 SSRs (simple sequence repeats) revealed a large diversity, with an average gene diversity of 0.674, and the highest numbers of alleles were detected among the accessions of African origin (Billot et al. 2013). In Africa, Eastern African exhibited the largest gene diversity followed by Central Africa and the lowest was in Southern Africa. In Asia, Middle East origins showed higher gene diversity than India and East Asia. Among races, the race *bicolor* had highest gene diversity (0.669), followed by *guinea* (0.628), *caudatum* (0.626), *durra* (0.600), and least in *kafir* (0.410). The cultivated sorghum structured according to geographic regions and race within the region (Billot et al. 2013). In an another study, Morris et al. (2013) characterized a large number of sorghum germplasm including the U.S. sorghum association panel (Casa et al. 2008), sorghum minicore collection (Upadhyaya et al. 2009), and the sorghum reference set (Billot et al. 2013) through genotyping-by-sequencing (GBS) approach and showed that the sorghum diversity is structured along both morphological types and geographic origin: the *kafir* sorghums that predominate in southern Africa showed the strongest pattern of population subdivision relative to other races; *durra* type sorghums, found in warm semi-arid or warm desert climates of the Horn of Africa, Sahel, Arabian peninsula and west central India, formed a distinct cluster that was further differentiated according to geographic origin; *bicolor* types are not remarkably clustered, except those from China; *Caudatum* types, which are primarily found in tropical savanna climates of central Africa, are diverse and showed only modest clustering according to geographic distribution; *guinea* types, which are widely distributed in tropical savanna climates, show five distinct subgroups, four of which cluster according to their geographic origin (far west Africa, west Africa, eastern Africa, and India), while the fifth guinea subgroup formed a separate cluster along with wild genotypes from western Africa.

5 Capturing Germplasm Diversity

The management and use of germplasm collections in breeding program can be enhanced if a small sample of a few hundred germplasm lines, which represent the entire diversity present in the crop species, were selected. Germplasm subset could possibly benefit breeders by providing a subset of sorghums from different areas of the world that have been carefully described and characterized. Frankel (1984) proposed a "core collection" represents a limited set of accessions (about 10%) derived from an existing germplasm collection, chosen to represent the genetic spectrum in the whole collection. Core collections in some cases are still large in size (over 2000 accessions), restricts effective and precise evaluations for traits of interest. To overcome this, Upadhyaya and Ortiz (2001) developed the concept of mini core collection (10% of core or 1% of entire collection). Following these approaches, core and mini core collections have been established in sorghum.

Core collection in sorghum consists of 3475 accessions (Prasada Rao and Ramanatha Rao 1995), 2247 accessions (Grenier et al. 2001) or 3011 accessions (Dahlberg et al. 2004) while mini core collection consisted of 242 accessions (Upadhyaya et al. 2009).

In addition, under the Generation Challenge Program (GCP), Global Composite Germplasm Collection (GCGC) of sorghum was established, which consists of 3384 accessions (http://www.generationcp.org/issue-59-march-2012/32-research/sorghum/180-sorghum-products). This GCP sorghum GCGC included 280 breeding lines and elite cultivars from public sorghum breeding programs, 68 wild and weedy accessions, and over 3000 landrace accessions from collections held by CIRAD or ICRISAT that were selected either from previously defined core collections (Grenier et al. 2001; Upadhyaya et al. 2009) for resistance to various biotic stresses, and/or for variation in other agronomic and quality traits. Further sorghum GCGC was genotyped with 41 SSR markers and formed a genotype-based reference set of 383 accessions that captured 78.3% of the SSR alleles detected in the sorghum GCGC (Billot et al. 2013).

6 Mini core Collection for Trait Enhancement and for Broadening the Genetic Base of Cultivars

Identification of trait-specific germplasm from large ex situ collection is a key to successfully introgressing new diversity in crop improvement programs (Billot et al. 2013). Greater use of diverse germplasm in sorghum breeding to develop cultivars with broad genetic base will result in sustainable sorghum production. The sorghum mini core collection consisting of 242 accessions originating from 57 countries was established (Upadhyaya et al. 2009) from sorghum core collection (Grenier et al. 2001). The mini core collection represents all the five basic races (caudatum 16.1%, durra 12.4%, guinea 12%, kafir 8.7%, and bicolor 8.3%) and 10 intermediate races (caudatum-bicolor 12.4%; guinea-caudatum 11.2%; durra-caudatum 7.9%; durra-bicolor and kafir-caudatum each 2.9%; kafir-durra 1.7%; guinea-kafir 1.2%; and guinea-bicolor, guinea-durra, and kafir-bicolor each 0.8%) of sorghum. Following the establishment of sorghum mini core collection, researchers have started utilizing it to evaluate and identify germplasm sources' early flowering and high grain yielding (Table 1), for resistant to abiotic stress such as anthracnose, leaf blight, rust, grain mold, downy mildew, charcoal rot (Borphukan 2014; Radwan et al. 2011; Sharma et al. 2010, 2012) and tolerance to abiotic such as drought and low temperature (Kapanigowda et al. 2013; Upadhyaya et al. 2017a) stresses, and also for grain nutritional (Upadhyaya et al. 2016a) and bioenergy traits (Upadhyaya et al. 2014; Wang et al. 2011). Further, utilizing agronomic performance of mini core accession and SNP data, 28 genetically diverse agronomically desirable multiple trait-specific germplasm sources have been identified (Upadhyaya et al. 2019). This multi-trait accessions include IS 23684 (nutrition traits, diseases, insect pests), IS 1212 (earliness, nutrition traits, drought, seedling vigor, diseases), IS 5094 (yield, drought, diseases, insect pests), IS 473 (earliness, diseases), IS 4698 (yield, Brix,

Table 1 Germplasm sources identified in sorghum minicore collection for grain nutritional and bioenergy traits and for biotic and abiotic stress tolerance

Trait	Mini core accession	References
Agronomic traits		
Early maturing	IS 1233, IS 2379, IS 2864, IS 12706, IS 14861, IS 16382, IS 17941, IS 20298, IS 28313 and IS 28849	Upadhyaya et al. (2019)
High grain yield	IS 4698, IS 23590, IS 23891 and IS 28141	Upadhyaya et al. (2019)
Grain nutritional traits		
Fe, 40.3–48.6 mg kg^{-1} seed	IS 16382, IS 23992, IS 28313, IS 28389, IS 28849, IS 20743, IS 21645, IS 21863, IS 28747, IS 30508 and IS 31681	Upadhyaya et al. (2016a)
Zn, 32.2–36.4 mg kg^{-1} seed	IS 30460, IS 602, IS 17980, IS 19859, IS 28451, IS 30466, IS 30536, IS 5301, IS 8774, IS 4951, IS 25249, IS 24139, IS 24175 and IS 24218	Upadhyaya et al. (2016a)
Fe, 40.8–48.9 mg kg^{-1} seed and Zn, 32.8–42.6 mg kg^{-1} seed	IS 1219, IS 1233, IS 30450, IS 30507, IS 1212, IS 27786, IS 30383, IS 31651 and IS 24503	Upadhyaya et al. (2016a)
Protein (12.2–13.8%)	IS 2902, IS 4951, IS 19975, IS 23684, IS 25249, IS 25910, IS 25989, IS 26025 and IS 26046	http://genebank.icrisat.org/
Lysine (3.1–4.3%)	IS 3971, IS 25836 and IS 5386	http://genebank.icrisat.org/
Bioenergy traits		
Stalk sugar content (Brix: 14.0–15.2%)	IS 13294, IS 13549, IS 23216, IS 23684, IS 24139, IS 24939 and IS 24953	Upadhyaya et al. (2014)
Dual purpose (grain and sweet stalk)	IS 1004, IS 4698, IS 23891 and IS 28141	Upadhyaya et al. (2014)
High saccharification yield	IS 2872, IS 27887, IS 19262, IS 3158, IS 7305, IS 33353 and IS 4951	Wang et al. (2011)
Biotic stresses		
Downy mildew	IS 28747, IS 31714, IS 23992, IS 27697, IS 28449, IS 30400; IS 1212, IS 2413, IS 3121, IS 4060, IS 4360, IS 4372, IS 4613, IS 4631, IS 5094, IS 7305, IS 9745, IS 12302, IS 12804, IS 12883, IS 12965, IS 13549, IS 15170, IS 15478, IS 15945, IS 16528, IS 20625, IS 20632, IS 21083, IS 22294, IS 22720, IS 23216, IS 24453, IS 24462, IS 24463, IS 26222, IS 26484, IS 26617, IS 26749, IS 27557, IS 29239, IS 29314, IS 29358, IS 29392, IS 29606, IS 29627, IS 29654, IS 30092, IS 30383, IS 30443, IS 30466, IS 30562 and IS 31557	Sharma et al. (2010), Radwan et al. (2011)
Grain mold	IS 602, IS 603, IS 608, IS 1233, IS 2413, IS 3121, IS 12697, IS 12804, IS 20727, IS 20740, IS 20743, IS 20816, IS 30562,	Sharma et al. (2010)

(continued)

Table 1 (continued)

Trait	Mini core accession	References
	IS 31681, IS 2379, IS 2864, IS 12302, IS 13971, IS 17941, IS 19389, IS 23992, IS 26694, IS 29335, IS 21512, IS 21645, IS 12945, IS 22294, IS 995, IS 2426, IS 12706, IS 16151, IS 24453, IS 26701, IS 29326, IS 30383, IS 30533, IS 30536, IS 20956, IS 29314, IS 30092, IS 10969, IS 23590, IS 29187, IS 29269, IS 473, IS 29304, IS 1212, IS 13893, IS 29241 and IS 29568	
Anthracnose	IS 473, IS 5301, IS 6354, IS 7679, IS 10302, IS 16382, IS 19153, IS 20632, IS 20956, IS 23521, IS 23684, IS 24218 and IS 24939	Sharma et al. (2012)
Leaf blight	IS 473, IS 2382, IS 7131, IS 9108, IS 9177, IS 9745, IS 12937, IS 12945, IS 14861, IS 19445, IS 20743, IS 21083, IS 23521, IS 23644, IS 23684, IS 24175, IS 24503, IS 24939, IS 24953, IS 26694, IS 26749, IS 28614, IS 29187, IS 29233, IS 29714, IS 31557 and IS 33353	Sharma et al. (2012)
Charcoal rot	IS 24463, IS 4515, IS 13549, IS 29582, IS 25301, IS 12735, IS 30533, IS 23514, IS 29950, IS 14010, IS 14090, IS 29358, IS 19859, IS 16528, IS 22986, IS 5094, IS 26046, IS 23590, IS 24503, IS 21512, IS 29269, IS 27697, IS 19676, IS 19389, IS 22294, IS 7250, IS 17941, IS 602, IS 30092, IS 29733, IS 31557, IS 23216, IS 10757, IS 12945, IS 29606, IS 12697, IS 31651, IS 7679, IS 23891, IS 32787, IS 29091, IS 29335, IS 30466, IS 4631, IS 29233, IS 28451, IS 24218, IS 1041, IS 30507, IS 29627 and IS 2379	Kapanigowda et al. (2013), Borphukan (2014)
Rust	IS 473, IS 23521, IS 23684, IS 24503, IS 26737 and IS 33023	Sharma et al. (2012)
Potyvirus spp.	IS 7679 and IS 20740	Seifers et al. (2012)
Shoot fly	IS 2205, IS 4515, IS 4698 and IS 5094	ICRISAT unpublished
Spotted stem borer	IS 4698, IS 5094, IS 1041, IS 18039, IS 19445 and IS 23992	ICRISAT unpublished
Sugarcane aphid	IS 2205, IS 4515, IS 4698, IS 18039, IS 1004, IS 3121, IS 4581, IS 5386, IS 12937, IS 15744, IS 16528, IS 20625, IS 20632, IS 23514, IS 23521, IS 23586, IS 23684, IS 24492, IS 24939, IS 25089, IS 25249, IS 25301, IS 25548, IS 27034, IS 27887, IS 28614, IS 29314, IS 29654, IS 29772, IS 31446, IS 31557 and IS 33023	ICRISAT unpublished

(continued)

Table 1 (continued)

Trait	Mini core accession	References
Abiotic stress		
Drought	IS 14779, IS 23891, IS 31714, IS 4515, IS 5094, IS 9108, IS 15466 and IS 1212	Upadhyaya et al. (2017a), Kapanigowda et al. (2013)
Seedling vigor under low temperature stress	IS 1212, IS 14779, IS 15170, IS 22986, IS 7305 and IS 7310	Upadhyaya et al. (2016c)
Germinability under low temperature stress	IS 602, IS 1233, IS 7305, IS 10302 and IS 20956	Upadhyaya et al. (2016c)

insect pests), and IS 23891 (large seeds, yield, Brix, drought, diseases). These are useful genetic resources that meet breeder's needs to develop agronomically superior sorghum cultivars having desirable combinations of multiple traits and a broad genetic base.

7 Wild and Weedy Relatives for Sorghum Improvement

Wild relatives of crops continue to play a key role in crop improvement and contribute genes for adaptation to various stresses besides yield and quality traits. Kamala et al. (2002, 2009) have reported sorghum wild accessions resistance to downy mildew, stem borer, and shoot fly. Kamala et al. (2002) identified 45 wild accessions comprising 15 species from 4 sections, *Parasorghum*, *Heterosorghum* (*S. laxiflorum* Bailey), *Chaetosorghum* (*S. macrospermum* Garber), and *Stiposorghum* (*S. angustum* S.T. Blake, *S.ecarinatum* Lazarides, *S. extans* Lazarides, *S. intrans* F. Muell. ex Benth., *S. interjectum* Lazarides, *S. stipoideum* (Ewart & Jean White) C. Gardener & C.E. Hubb.) that showed immunity to downy mildew, while cultivated types and wild accessions of section *Sorghum* showed the greatest susceptibility. For shoot fly resistance, 32 accessions belonging to *Parasorghum*, *Stiposorghum*, and *Heterosorghum* that did not suffer any shoot fly damage under field conditions, and under greenhouse condition, the same accessions either showed non-preference for oviposition under no-choice conditions or were preferred for oviposition, but suffered low dead-heart damage (Kamala et al. 2009). For stem borer, accessions of *Heterosorghum* (*Sorghum laxiflorum*), *Parasorghum* (*S. australiense, S. purpureo-sericeum, S. versicolor, S. matarankense, S. timorense, S. brevicallosum* and *S. nitidum*), and *Stiposorghum* (*S. angustum, S. ecarinatum, S. extans, S. intrans, S. interjectum* and *S. stipoideum*) showed very high levels of resistance to stem borer, while *Chaetosorghum* (*S. macrospermum*), four wild races of *S. bicolor* subsp. *verticilliflorum* and *S. halepense* were found to be susceptible (Kamala et al. 2012). Sorghum wild relatives also reported as sources of genes for resistance to sorghum midge (Sharma and Franzmann 2001) and green bug (Duncan et al. 1991).

Striga (also known as witch weed) can destroy a crop with up to a 100% yield loss and over 60% of farmland under cultivation in sub-Saharan Africa is infested with

one or more species of Striga (Ejeta 2007). *Striga* resistance mechanisms such as low germination stimulant production, germination inhibition, and low historical initiation activity have been reported to occur in wild sorghum (Rich et al. 2004). Mbuvi et al. (2017) have identified sorghum wild accessions (WSA 1, WSE 1, and WSA 2) that had significantly higher resistance to *Striga* than the resistant control, N13. Gobena et al. (2017) have identified a gene regulating Striga resistance in sorghum. Mutant alleles at the *LGS1* (*Low Germination Stimulant 1*) locus drastically reduce Striga germination stimulant activity.

Valuable traits such as resistance/tolerance to biotic and abiotic stresses are often present but inaccessible in the wild relatives of cultivated crop species due to strong reproductive barriers that prevent hybridization between them. However, Price et al. (2006) demonstrated the production of hybrids involving cultivated sorghum (*S. bicolor*) with those of species from tertiary genepool (*S. angustum*, *S. nitidum*, and *S. macrospermum*) through use of recessive *iap* allele (dominant allele *Iap* = inhibition of alien pollen) to produce or eliminate the pollen-pistil incompatibilities that prevent hybridization. They used cytoplasmic male-sterile *S. bicolor* plants homozygous for the *iap* allele and three wild species *S. angustum, S. nitidum*, and *S. macrospermum*as pollen parents. The pollen of these three wild species readily germinated and the pollen tubes grew to the base of the *S. bicolor* ovary within 2 h after pollination, and obtained hybrids of *S. bicolor* × *S. macrospermum* by simply germinating the hybrid seed, while *S. bicolor* × *S. angustum* and *S. bicolor* × *S. nitidum* hybrids through embryo rescue followed by in vitro culture techniques.

8 Utilization of Germplasm in Breeding

The role of germplasm in the improvement of sorghum has been well recognized. To enhance the yield, adaptation along with resistance to pests and diseases, utilization of germplasm at ICRISAT and other places have proven to be very useful. One of the immediate uses of germplasm is directly released as cultivar after testing their yield and adaptation. There were many instances where selection from germplasm lines were directly released as cultivars. For example, the ICRISAT genebank supplies a large number of germplasm to researchers worldwide. Since 1974, the ICRISAT genebank has distributed over 268,000 samples of sorghum germplasm accessions to 110 countries. Of the germplasm supplied by ICRISAT genebank, 39 accessions have been directly released as 41 varieties in 18 countries. Two accessions namely IS 8193 and IS 18758 have been released in more than one country (IS 8193 as Kari Mtama 2 and IS 8193 in Kenya and Rwanda, respectively; IS 18758 as E-35-1 and Gambella 1107 in Burkina Faso and Burundi, respectively). IS 18758 is a popular sorghum landrace from Ethiopia, belonging guinea-caudatum race, has excellent grain quality, high grain yield potential, and resistance to leaf disease. IS 33844 is an excellent Maldandi-type sorghum accession, with large and lustrous grains and high yield, and a selection from it has been released as “Parbhani Moti” for post-rainy cultivation in Maharashtra, India.

Some germplasm lines may be promising for one or more important traits but may not have desirable agronomic traits. In such cases, breeders have transferred the trait of interest into the cultivated varieties. In sorghum, germplasm utilization has been primarily focused on agronomically important traits and in some cases resistance to pests and diseases. Earlier utilization of sorghum germplasm was limited to pure line selection within cultivated landrace populations in Africa and India that resulted in improved cultivars. Later, selection within dwarf populations was taken up, followed by exploitation of cytoplasmic male-sterility, which permitted the production of commercial hybrids (Dahlberg et al. 1997). Crossing and/or backcrossing between adapted introductions and local germplasm has been used to derive improved pure-line varieties and parental lines (Prasada Rao et al. 1989). *Zerazera* lines from Ethiopia and Sudan were some of the germplasm sources used in varietal improvement globally (Ashok Kumar 2018).

Selection of highly adaptable sorghum lines from the germplasm sources and further improving them for yield and quality traits are the basic steps followed by any breeding program. This strategy helped ICRISAT to maximize the utilization of germplasm in breeding program and enhance the yield potential significantly. The improved lines developed using these sources are later shared with public and private partners, globally. The ICRISAT germplasm lines have been used for the development of high yielding male sterile lines (CK 60, 172, 2219) and restorers (IS 84, IS 3691, IS 3541) which are eventually used in hybrid development. Genetic diversification of hybrid parents using germplasm lines in breeding program helped in developing heterotic hybrids that improved the yields in farmers' fields. Using the germplasm lines, resistance for different pests and diseases has been transferred such as shoot fly, stem borer resistance, midge resistance, and multiple disease resistance (Reddy et al. 2008; Ashok Kumar 2018). Table 2 shows the number of germplasm lines utilized between 2000 and 2014 in the ICRISAT sorghum breeding program for different traits of interest, indicating greater use of germplasm conserved in the ICRISAT genebank for breeding high yielding, nutrient dense, diseases and insect pest resistance cultivars. However, this number indicates about 2% of the total number of accessions conserved in the ICRISAT genebank have been used, thus there is large scope to introduce novel traits into breeding program to broaden the genetic base of sorghum cultivars.

9 Genetic Gains

In spite of good advances in breeding for improved cultivars, sorghum production has increased only marginally. The on-station and on-farm productivity gap remains a challenge for agricultural scientists and extension specialists to bridge. Most of the times the challenge remains in the delivery of improved cultivars to farmers for lack of effective seed systems. Sometimes genetics also pose challenge for improving the traits of interest, e.g., grain mold resistance and drought tolerance. The recent thrust is on genetic enhancement of sorghum to improve the yield and resistance for different biotic (pests, diseases, and striga) and abiotic (drought, cold, and acidic

Table 2 Germplasm accessions used in the ICRISAT sorghum breeding program

S No	Trait	Year			Total
		2000–2004	2005–2009	2010–2014	
1	Biofortification	–	33	62	95
2	Biomass	–	29	–	29
3	Bold grain	17	–	–	17
4	Bold red grain	7	–	–	7
5	Brown mid rib	3	–	–	3
6	Chimeric	–	–	2	2
7	Grain mold	25	14	22	61
8	Grain yield	99	65	51	215
9	Long panicle	4	–	–	4
10	Pop sorghum	8	–	–	8
11	Rabi adaptation	–	42	–	42
12	Shoot fly	15	30	110	155
13	Sweet stalk	12	71	82	165
14	Waxy	9	–	–	9
	Grand total	199	284	329	812

soil) stresses and enhance genetic diversity to achieve sustainability in sorghum productivity gains. Over years *caudatum* and its intermediate races were exploited in sorghum to increase the grain yields for the rainy/summer adaptations while the *durra* and intermediate races were exploited well for the post-rainy/cold season adaptations. The elite x elite crosses are increasingly made to stabilize the gains and achieve higher yields. Considering the yield plateau in *caudatum* growing regions efforts are underway to diversify the genetic base of the cultivars by bringing in more of *guinea* types into crossing programs. Similarly, *durra* landraces from Ethiopia, Eritrea, and Yemen are increasingly crossed with Indian *durra* landraces for increasing the genetic base of post-rainy sorghums in India. The A_1 cytoplasm is most widely exploited globally in sorghum hybrids development. To diversify the cytoplasmic base, large number of restorer lines were identified on A_2 cytoplasm and heterotic hybrids with higher grain yield, shoot fly and grain mold resistance and high grain Fe and Zn concentration developed (Reddy et al. 2010; Ashok Kumar et al. 2011). More recently, heterotic hybrids with high fertility restoration developed using the A_3 and A_4 cytoplasm for grain yield and high Fe and Zn concentration. The increased genetic gain from these efforts is manifested under good management conditions like rice-fallow sorghum where the yield levels in farmers' fields are more than 8 t ha^{-1} compared to $<$1.5 t ha^{-1} for rainy season sorghum in India while the hybrids used are same in both the adaptations (Ashok Kumar 2018).

Increasing the breeding efficiency is the key component in enhancing the genetic gain. Taking this into consideration, in addition to genetic enhancement for yield and adaptation, various efficient phenotyping techniques are being employed to identify the resistant sources for different biotic and abiotic constraints that can help in developing improved varieties, parents, and hybrids for enhancing the genetic

gains. Over the years, ICRISAT has made considerable progress in developing various screening techniques for various pests and diseases such as shoot fly, stem borer, grain mold (Bandyopadhyay et al. 1988; Thakur et al. 2006), anthracnose (Pande et al. 1994), leaf blight, downy mildew (Pande et al. 1997) and Striga. The strategy of pest/disease management is mainly through host plant resistance (HPR), which is economical, environment-friendly, and technically feasible at farmers' level, although expensive at the research level. Disease management through HPR involves sound knowledge of biology and epidemiology of the disease (Bandyopadhyay et al. 2000). A number of elite lines have been developed for major pest and disease resistance and widely distributed to partners (Reddy et al. 2012). Drought is the major limiting factor in sorghum production. Seedling drought recovery and grain yield under water stress (drought) and optimal conditions for early-stage drought, mid-season drought recovery and stay green, non-lodging are important traits to focus in identifying drought tolerance germplasm. For grain nutritional traits, various methods are being used to measure Fe and Zn concentrations in sorghum, which include simple staining procedures to complex analytical protocols. Prussian blue and diphenyl thiocarbazone-based dithizone (DTZ) is a simple technique which gives rough estimation of Fe and Zn. On the other hand, analytical methods such as atomic absorption spectrometer (AAS), inductively coupled plasma-optical emission spectrometer (ICP-OES), X-ray fluorescence spectrometer (XRF), near-infrared reflectance spectrophotometer (NIRS), elemental distribution maps secondary ion mass spectrometry (NanoSIMS), synchrotron X-ray, fluorescence spectroscopy, and micro- X-ray fluorescence spectroscopy (μ-XRF) gives exact estimation of Fe and Zn in the grain. Among all, XRF is a low-cost, high-throughput method for assessing grain Fe and Zn, and there is good correspondence between ICP-OES and XRF methods for assessing the grain Fe and Zn but ICP is more accurate. So XRF could be used in large-scale screening to identify and discard low Fe and Zn lines, and validate those lines with high Fe and Zn using ICP-OES method. Contamination through soil, dust, metallic, or any other foreign material should be avoided for accurate results.

Information on genetic gain achieved over time is essential to develop effective and efficient breeding strategies and suggest on future direction to facilitate further improvement. Rakshit et al. (2014) analyzed 40 years (1970–2009) of sorghum production data of the top 10 sorghum producing countries (United States, India, Mexico, Nigeria, Sudan, Ethiopia, Australia, Brazil, China, and Burkina Faso) to study the global trends of sorghum area and yield. The study indicated that, globally, sorghum harvested area declined at a linear rate of 154,000 ha year^{-1} over the last four decades. China, India, and the United States, recorded drastic reduction in harvested area. Compared with 1970 baseline, maximum area loss was in China (~89%) followed by the United States (~59%) and India (~56%), while other countries recorded in increase in area under sorghum. Brazil recorded maximum proportional increase in area compared with the 1970 baseline followed by Ethiopia, Sudan, Australia, Mexico, Nigeria, and Burkina Faso in decreasing order. However, global sorghum yield has not changed significantly across years, while decadal analysis showed a nearly 30 kg ha^{-1} year^{-1} increase in yield during the first decade,

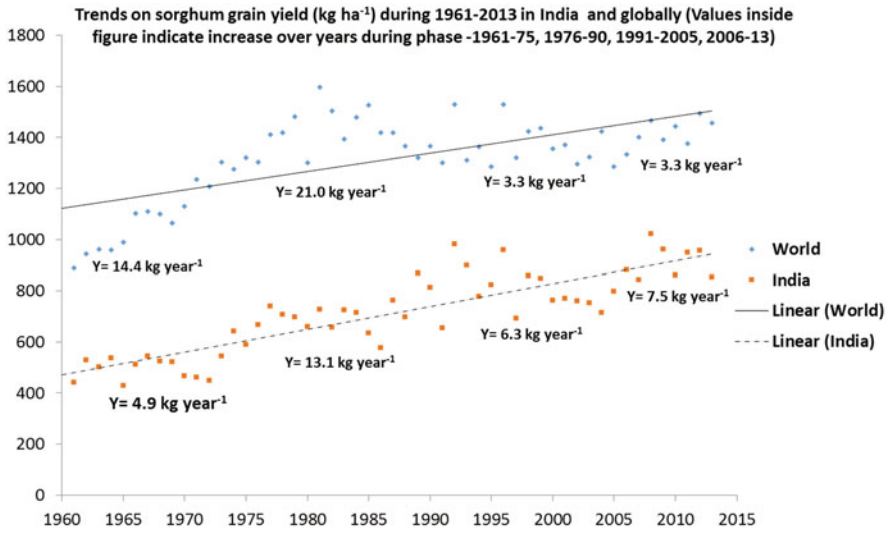

Fig. 1 Sorghum grain yield (kg ha^{-1}) during the last five decades, in India and globally

which was followed by a decline at 12 kg ha^{-1} $year^{-1}$ until 1995, after which there were insignificant changes in yield (Rakshit et al. 2014). Relative to yield level of 1970, sorghum productivity increased annually at 0.96% $year^{-1}$ across the top 10 countries, and China (100.9 kg ha^{-1} $year^{-1}$) and Nigeria (48.6 kg ha^{-1} $year^{-1}$) experienced phenomenal yield gain before reaching a plateau. Adoption of hybrids has contributed significantly to yield gains in countries like China, the United States, Australia, Brazil, and Mexico and to rainy-season sorghum in India, where 85–100% of sorghum acreage in under hybrids (Rakshit et al. 2014).

Precise development of sorghum product profiles, use of elite germplasm with adaptation traits in crossing program, efficient emasculation methods for crossing, used of single seed descent (SSD) in advancing the generations, early generation selection using molecular markers, multi-location testing, assessing the combining ability, use of appropriate designs, electronic data capture and breeding data management systems (BMS), developing standard operating procedures (SOPs) for breeding operations could increase the breeding efficiency. The increased breeding efficiency results in development of superior products in a cost-effective way in shortest possible time. In the last five decades, there is a considerable increase in grain yields in farmers' fields (more than 50% of it is contributed by the use of improved cultivars) globally (Fig. 1). In recent years, the increase in sorghum productivity in India is more than double compared to global increase. The genetic gain here is close to 0.5 per annum.

The ICRISAT sorghum breeding program compared the mean performance of seed parents (B-lines) developed over years for two major traits, grain yield and shoot fly resistance. Five parents were randomly selected at 5-year interval and evaluated them along with a control in a replicated trial. A significant increase in

grain yield in the recently developed parents was observed vis-à-vis parents developed in the last 20 years. There was a considerable yield improvement in B-lines developed during the last decade with a genetic gain of ~3%. Apart from selections, assessing the combining ability of the parents may also play a significant role in improving the genetic gains. Furthermore, increasing the diversity among hybrid parents may also be helpful in improving the genetic gains.

The rate of genetic gain in sorghum has been slower compared to other field crops, that could be because the crop is grown under marginal environments with limited resources, and often affected by biotic and abiotic stresses, besides other constraints such as poor crop management and low research priority than other cereals.

10 Future Direction

Globally a significant number of germplasm accessions have been conserved in genebanks, and they are source of genetic variation to potentially raise genetic gain, and continues to a key role in improving sorghum productivity and nutrition. Major constraints in the use of germplasm are time and resources required to precisely characterize the accessions at large scale. This could be avoided by the use of core and mini core collections, representing the entire diversity of germplasm. Diverse multi-trait-specific mini core germplasm accessions have been identified that would be a potential resource for broadening the genetic base of cultivar and for enhancing quality and productivity. The use of genebank passport data to extract the long-term climate data (e.g., rainfall, temperature, soil pH, frost, etc.) from the collection sites could help in identification new variability that is valuable for sorghum improvement. Sequencing germplasm accessions and genomic selection could fast-track genebank mining and could enable prediction of traits for larger numbers of accessions in the genebanks, and contribute to enhanced genetic gains and broaden the genetic base of cultivars and to enhance productivity and nutrition.

References

Abdi A, Bekele E, Asfaw Z, Teshome A (2002) Patterns of morphological variation of sorghum (Sorghum bicolor L. Moench) landraces in qualitative characters in North Shewa and South Welo, Ethiopia. Hereditas 137:161–172

Ashok Kumar A (2018) Sorghum hybrids development for important traits: progress and way forward. In: Ciampitti I, Prasad V (eds) Sorghum: state of the art and future perspectives. Agronomy monograph 58. © ASA and CSSA, Madison. https://doi.org/10.2134/agronmonogr58.2014.0059

Ashok Kumar A, Reddy BVS, Sharma HC, Hash CT, Rao PS, Ramaiah B, Reddy PS (2011) Recent advances in sorghum genetic enhancement research at ICRISAT. Am J Plant Sci 2:589–600

Bandyopadhyay R, Mughogho LK, Prasada Rao KE (1988) Sources of resistance to sorghum grain molds. Plant Dis 72:504–508

Bandyopadhyay R, Butler DR, Chandrashekar A, Reddy AK, Navi SS (2000) Biology, epidemiology and management of sorghum grain mold. In: Chandrashekar A, Bandyopadhyay R, Hall AJ

(eds) Technical and institutional options for sorghum grain mold management: proceedings of an international consultation, 18−19 May 2000, ICRISAT, Patancheru, India. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, pp 34–71

Bantilan MCS, Deb UK, Gowda CLL, Reddy BVS, Obilana AB, Evenson RE (2004) Sorghum genetic enhancement research process, dissemination and impacts. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, p 320. ISBN: 92-9066-470-3

Billot C, Ramu P, Bouchet S, Chantereau J, Deu M, Gardes L, Noyer J-L, Rami J-F, Rivallan R, Li Y, Lu P, Wang T, Folkertsma RT, Arnaud E, Upadhyaya HD, Glaszmann J-C, Hash CT (2013) Massive sorghum collection genotyped with SSR markers to enhance use of global genetic resources. PLoS One 8:e59714

Borad PK, Mittal VP (1983) Assessment of losses caused by pest complex to sorghum hybrid CSH 5. In: Krishnamurthy Rao BH, Murthy KSRK (eds) Crop losses due to insect pests. Special issue of the Indian Journal of Entomology. Entomological Society of India, Rajendranagar, Hyderabad, pp 271−278

Borphukan B (2014) Evaluation of minicore germplasm of rabi sorghum for charcoal rot resistance and yield component traits, expression analysis of selected R-genes during charcoal rot disease incidence. M.Sc. Dissertation, University of Agricultural Sciences, Dharwad

Borrell AK, Hammer GL (2000) Nitrogen dynamics and the physiological basis of stay-green in Sorghum. Crop Sci 40:1295–1307

Casa AM, Pressoir G, Brown PJ, Mitchell SE, Rooney WL, Tuinstra MR, Franks CD, Kresovich S (2008) Community resources and strategies for association mapping in sorghum. Crop Sci 48:30–40

Dahlberg JA, Hash CT, Kresovich S, Maunder B, Gilbert M (1997) Sorghum and pearl millet genetic resources utilization. In: Proceedings of the international conference on genetic improvement of sorghum and pearl millet, 22−27 September 1996, Lubbock, TX, pp 42–54

Dahlberg JA, Burke JJ, Rosenow DT (2004) Development of a sorghum core collection: refinement and evaluation of a subset from Sudan. Econ Bot 58:556–567

Das IK, Fakrudin B, Arora DK (2008) RAPD cluster analysis and chlorate sensitivity of some Indian isolates of Macrophomina phaseolina from sorghum and their relationships with pathogenicity. Microbiol Res 163:215–224

Duncan RR, Bramel-Cox PJ, Miller FR (1991) Contributions of introduced sorghum germplasm to hybrid development in the USA. Use Plant Introduction in Cultivar Development, Part 1 CSSA Special Publication no. 17:69–102

Ejeta G (2007) Breeding for Striga resistance in sorghum: exploitation of an intricate host-parasite biology. Crop Sci 47(S3):S216–S227

Frankel OH (1984) Genetic perspective of germplasm conservation. In: Arber W, Illmensee K, Peacock WJ, Starlinger P (eds) Genetic manipulations: impact of man and society. Cambridge University Press, Cambridge, pp 161–170

Gobena D, Shimels M, Rich PJ, Ruyter-Spira C, Bouwmeester H, Kanuganti S, Mengiste T, Ejeta G (2017) Mutation in sorghum LOW GERMINATION STIMULANT 1 alters strigolactones and causes Striga resistance. Proc Natl Acad Sci U S A 114:4471–4476

Grenier C, Hamon P, Bramel-Cox PJ (2001) Core collection of sorghum: II. Comparison of three random sampling strategies. Crop Sci 41:241–246

Harris K, Subudhi PK, Borrell A (2007) Sorghum stay green QTL individually reduce post-flowering drought-induced leaf senescence. J Exp Bot 58:327–338

Hash CT, Bhasker Raj AG, Lindup S, Sharma A, Beniwal CR, Folkertsma RT, Mahalakshmi V, Zerbini E, Blümmel M (2003) Opportunities for marker-assisted selection (MAS) to improve the feed quality of crop residues in pearl millet and sorghum. Field Crop Res 84:79–88

Haussmann BIG, Mahalakshmi V, Reddy BVS, Seetharama N, Hash CT, Geiger HH (2002) QTL mapping of stay-green in two sorghum recombinant inbred populations. Theor Appl Genet 106:133–142

ICRISAT (1992) ICRISAT medium-term plan 1994-1998. International Crops Research Institute for the Semi-Arid Tropics, Patancheru

Jordan DR, Tao YZ, Godwin ID, Henzell RG, Cooper M, McIntyre CL (1998) Loss of genetic diversity associated with selection for resistance to sorghum midge in Australian sorghum. Euphytica 102:1–7

Jordan DR, Tao Y, Godwin ID, Henzell RG, Cooper M, McIntyre CL (2003) Prediction of hybrid performance in grain sorghum using RFLP markers. Theor Appl Genet 106:559–567

Kamala V, Singh SD, Bramel PJ, Rao DM (2002) Sources of resistance to downy mildew in wild and weedy sorghums. Crop Sci 42:1357–1360

Kamala V, Sharma HC, Rao DM, Varaprasad KS, Bramel P (2009) Wild relatives of sorghum as sources of resistance to sorghum shoot fly, Atherigona soccata. Plant Breed 128:137–142

Kamala V, Sharma HC, Rao DM, Varaprasad KS, Bramul PJ, Chandra S (2012) Interactions of spotted stem borer Chilo partellus with wild relatives of sorghum. Plant Breed 131(4):511–521

Kapanigowda MH, Perumal R, Djanaguiraman M, Aiken RM, Tesso T, Prasad PV, Little CR (2013) Genotypic variation in sorghum [Sorghum bicolor (L.) Moench] exotic germplasm collections for drought and disease tolerance. Springerplus 2:650

Kassahun B, Bidinger FR, Hash CT, Kuruvinashetti MS (2010) Stay-green expression in early generation sorghum [Sorghum bicolor (L.) Moench] QTL introgression lines. Euphytica 172:351–362

Mace ES, Tai S, Gilding EK, Li Y, Prentis PJ, Bian L, Campbell BC, Hu W, Innes DJ, Han X, Cruickshank A, Dai C, Frère C, Zhang H, Hunt CH, Wang X, Shatte T, Wang M, Su Z, Li J, Lin X, Godwin ID, Jordan DR, Wang J (2013) Whole-genome sequencing reveals untapped genetic potential in Africa's indigenous cereal crop sorghum. Nat Commun 4:2320. https://doi.org/10.1038/ncomms3320

Mbuvi DA, Masiga CW, Kuria E, Masanga J, Wamalwa M, Mohamed A, Odeny DA, Hamza N, Timko MP, Runo S (2017) Novel sources of witchweed (Striga) resistance from wild sorghum accessions. Front Plant Sci 8:116. https://doi.org/10.3389/fpls.2017.00116

Morris GP, Rhodes DH, Brenton Z, Ramu P, Thayil VM, Deshpande S, Hash CT, Acharya C, Mitchell SE, Buckler ES, Yu J, Kresovich S (2013) Dissecting genome-wide association signals for loss-of-function phenotypes in sorghum flavonoid pigmentation traits. G3 (Bethesda) 3:2085–2094

Murray SC, Rooney WL, Hamblin MT, Mitchell SE, Kresovich S (2009) Sweet sorghum genetic diversity and association mapping for Brix and height. Plant Genome J 2:48–62

Mutegi E, Sagnard F, Semagn K, Deu M, Muraya M, Kanyenji B, de Villiers S, Kiambi D, Herselman L, Labuschagne M (2011) Genetic structure and relationships within and between cultivated and wild sorghum (Sorghum bicolor (L.) Moench) in Kenya as revealed by microsatellite markers. Theor Appl Genet 122:989–1004

Ngugi K, Onyango CM (2012) Analysis of the molecular diversity of Kenya sorghum germplasm using microsatellites. J Crop Sci Biotechnol 15:189–194

Okeno JA, Mutegi E, de Villiers S, Wolt JD, Misra MK (2012) Morphological variation in the wild-weedy complex of Sorghum bicolor in situ in western Kenya: preliminary evidence of crop-to-wild gene flow? Int J Plant Sci 173:507–515

Pande S, Thakur RP, Karunakar RI, Bandyopadhyay R, Reddy BVS (1994) Development of screening methods and identification of stable resistance to anthracnose in sorghum. Field Crop Res 38:157–166

Pande S, Bock CH, Bandyopadhyay R, Narayana YD, Reddy BVS, Lenné JM, Jeger MJ (1997) Downy mildew of Sorghum. Information Bulletin no. 51. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, pp 1–35

Prasada Rao KE, Ramanatha Rao V (1995) The use of characterisation data in developing a core collection of sorghum. In: Hodgkin T, Brown AHD, van Hintum TJL, Morales EAV (eds) Core collections of plant genetic resources. Wiley, Chichester, pp 109–116

Prasada Rao KE, Mengesha MH, Reddy VG (1989) International use of sorghum germplasm collection. In: Brown AHD, Frankel OH, Marshall DR, Williams JT (eds) The use of plant genetic resources. Cambridge University Press, Cambridge, pp 150–167

Price HJ, Hodnett GL, Burson BL, Dillon SL, Stelly DM, Rooney WL (2006) Genotype dependent interspecific hybridization of Sorghum bicolor. Crop Sci 46:2617–2622

Rabbi IY, Geiger HH, Haussmann BIG, Kiambi D, Folkertsma R, Parzies HK (2010) Impact of farmers' practices and seed systems on the genetic structure of common sorghum varieties in Kenya and Sudan. Plant Genet Resour Character Util 8:116–126

Radwan GL, Perumal R, Isakeit T, Magill CW, Prom LK, Little CR (2011) Screening exotic sorghum germplasm, hybrids, and elite lines for resistance to a new virulent pathotype (P6) of Peronosclerospora sorghi causing downy mildew. Plant Heal Prog. https://doi.org/10.1094/PHP-2011-0323-01-RS

Rakshit S, Hariprasanna K, Gomashe S, Ganapathy KN, Das IK, Ramana OV, Dhandapani A, Patil JV (2014) Changes in area, yield gains, and yield stability of sorghum in major sorghum-producing countries, 1970 to 2009. Crop Sci 54:1571–1584

Reddy BVS, Kumar AA, Reddy PS, Elangovan M (2008) Sorghum germplasm: diversity and utilization. In: Reddy BVS, Ramesh S, Kumar AA, Gowda CLL (eds) Sorghum improvement in the new millennium. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, pp 153–169

Reddy BVS, Ashok Kumar A, Sanjana Reddy P (2010) Recent advances in sorghum improvement research at ICRISAT. Kasetsart J (Nat Sci) 44:499–506

Reddy BV, Reddy PS, Sadananda AR, Dinakaran E, Ashok Kumar A, Deshpande SP, Srinivasa Rao P, Sharma HC, Sharma R, Krishnamurthy L, Patil JV (2012) Postrainy season sorghum: constraints and breeding approaches. J SAT Agric Res 10(1):1–12

Reddy NRR, Ragimasalawada M, Sabbavarapu MM, Nadoor S, Patil JV (2014) Detection and validation of stay-green QTL in post-rainy sorghum involving widely adapted cultivar, M35-1 and a popular stay-green genotype B35. BMC Genomics 15:909

Rich PJ, Grenier C, Ejeta G (2004) Striga resistance in the wild relatives of sorghum. Crop Sci 44:2221–2229

Sabadin PK, Malosetti M, Boer MP, Tardin FD, Santos FG, Guimarães CT, Gomide RL, Andrade CLT, Albuquerque PEP, Caniato FF, Mollinari M, Margarido GRA, Oliveira BF, Schaffert RE, Garcia AAF, van Eeuwijk FA, Magalhaes JV (2012) Studying the genetic basis of drought tolerance in sorghum by managed stress trials and adjustments for phenological and plant height differences. Theor Appl Genet 124:1389–1402

Sanchez AC, Subudhi PK, Rosenow DT, Nguyen HT (2002) Mapping QTLs associated with drought resistance in sorghum (Sorghum bicolor L. Moench). Plant Mol Biol 48:713–726

Seifers DL, Perumal R, Little CR (2012) New sources of resistance in sorghum (Sorghum bicolor) germplasm are effective against a diverse array of Potyvirus spp. Plant Dis 96:1775–1779

Sharma HC (1993) Host plant resistance to insects in sorghum and its role in integrated pest management. Crop Prot 12:11–34

Sharma HC, Franzmann BA (2001) Host-plant preference and oviposition responses of the sorghum midge, Stenodiplosis sorghicola (Coquillett) (Dipt., Cecidomyiidae) towards wild relatives of sorghum. J Appl Entomol 125:109–114

Sharma R, Rao VP, Upadhyaya HD, Reddy VG, Thakur RP (2010) Resistance to grain mold and downy mildew in a mini-core collection of sorghum sermplasm. Plant Dis 94:439–444

Sharma R, Upadhyaya HD, Manjunatha SV, Rao VP, Thakur RP (2012) Resistance to foliar diseases in a mini-core collection of sorghum germplasm. Plant Dis 96:1629–1633

Smith S, Primomo V, Monk R, Nelson B, Jons E, Porter K (2010) Genetic diversity of widely used U.S. sorghum hybrids 1980-2008. Crop Sci 50:1664–1673

Subudhi PK, Nguyen HT (2000) Linkage group alignment of sorghum RFLP maps using a RIL mapping population. Genome 43:240–249

Thakur RP, Reddy BVS, Indira S, Rao VP, Navi SS, Yang XB , Ramesh S (2006) Sorghum grain mold. Information Bulletin no. 72. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, 32 pp

Upadhyaya D, Ortiz R (2001) A mini core subset for capturing diversity and promoting utilization of chickpea genetic resources in crop improvement. Theor Appl Genet 102:1292–1298

Upadhyaya HD, Vetriventhan M (2018) Ensuring the genetic diversity of sorghum. In: Roony W (ed) Achieving sustainable cultivation of sorghum. Burleigh Dodds Science Publishing Limited, Cambridge, p 546

Upadhyaya HD, Pundir RPS, Dwivedi SL, Gowda CLL, Reddy VG, Singh S (2009) Developing a mini core collection of sorghum for diversified utilization of germplasm. Crop Sci 49:1769–1780

Upadhyaya HD, Dwivedi SL, Ramu P, Singh SK, Singh S (2014) Genetic variability and effect of postflowering drought on stalk sugar content in sorghum mini core collection. Crop Sci 54:2120–2130. https://doi.org/10.2135/cropsci2014.01.0040

Upadhyaya HD, Dwivedi SL, Singh S, Sahrawat KL, Singh SK (2016a) Genetic variation and postflowering drought effects on seed iron and zinc in ICRISAT sorghum mini core collection. Crop Sci 56:374–383

Upadhyaya HD, Reddy KN, Vetriventhan M, Gumma MK, Ahmed MI, Reddy MT, Singh SK (2016b) Status, genetic diversity and gaps in sorghum germplasm from South Asia conserved at ICRISAT genebank. Plant Genet Resour Character Util 15:527–538

Upadhyaya HD, Wang Y-H, Dintyala SV, Dwivedi SL, Prasad PVV, Burrell AM, Klein R, Morris GP, Klein PE (2016c) Association mapping of germinability and seedling vigor in sorghum under controlled low temperature conditions. Genome 59:137–145

Upadhyaya HD, Dwivedi SL, Vetriventhan M, Krishnamurthy L, Singh SK (2017a) Post-flowering drought tolerance using managed stress trials, adjustment to flowering, and mini core collection in sorghum. Crop Sci 57:310–321

Upadhyaya HD, Kothapally NR, Vetriventhan M, Mohammed IA, Gumma MK, Mulinti TR, Singh SK (2017b) Sorghum germplasm from West and Central Africa maintained in the ICRISAT genebank: status, gaps, and diversity. Crop J 5:518–532

Upadhyaya HD, Narsimha RK, Vetriventhan M, Murali KG, Irshad AM, Manyasa E, Reddy MT, Singh SK (2017c) Geographical distribution, diversity and gap analysis of East African sorghum collection conserved at the ICRISAT genebank. Aust J Crop Sci 11:424–437

Upadhyaya HD, Vetriventhan M, Asiri AM, Azevedo VCR, Sharma HC, Sharma R, Sharma SR, Wang YH (2019) Multi-Trait diverse germplasm sources from mini core collection for sorghum improvement. Agriculture 9(6):121

Vadez V, Deshpande SP, Kholova J, Hammer GL, Borrell AK, Talwar HS, Hash CT (2011) Stay green QTL effects on water extraction and transpiration efficiency in a lysimetric system: influence of genetic background. Funct Plant Biol 38:553–566

Wang Y-H, Poudel DD, Hasenstein KH (2011) Identification of SSR markers associated with saccharification yield using pool-based genome-wide association mapping in sorghum. Genome 54:883–889