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Sorghum Genetic Resources: Conservation and Diversity Assessment for Enhanced Utilization in Sorghum Improvement

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ABSTRACT

World collection of sorghum consists of 235,711 accessions, housed in national and international genebanks, of which, ICRISAT genebank holds 37,949 accessions, predominantly landraces from SAT regions. Biologically, this collection represents all basic and intermediate races, and geographic regions. Core/mini core, genotype-based reference set or in some cases trait-based diversity panels have been developed. These reduced subsets are in demand to discover new sources of variation, dissect population structure and diversity, estimate linkage disequilibria, map marker-trait associations, and mine allelic variations associated with agronomically beneficial traits. More emphasis should also be to discover germplasm with novel seed quality traits imparting health benefits. Few germplasm, such as IS 18758, IS 1054, and IS 33844, have proved to be an excellent source of desirable plant type, high grain yield, good grain quality, resistant to leaf diseases, and used extensively in breeding programs at ICRISAT and elsewhere. New sources such

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as IS 26962 and IS 23680 identified as having high Fe and Zn serve as potential parents for developing improved nutrient dense cultivars. In addition, 34 germplasm lines have been directly released as cultivars in 17 countries. There is a continuous need to identify germplasm lines with multiple resistances to abiotic and biotic stresses and those with novel seed quality traits to develop sorghum cultivars and hybrids adapted to diverse agroclimatic conditions. A better understanding of available genetic resources, genomic tools and resources including sequenced variation in sorghum genome will assist germplasm curators/breeders efficiently conserve and utilize diverse germplasm in sorghum improvement.

Keywords: Genetic resources, sorghum improvement, mini core, abiotic and biotic stresses, population structure and diversity, association mapping

2.1 Introduction

Sorghum [*Sorghum bicolor* (L.) Moench], the 5th most important cereal after maize, rice, wheat, and barley in area, is mostly grown worldwide by the resource-limited farmers in the Semi-Arid Tropics (SAT). Africa and the Americas together contribute 75% (40.74 m t) of the total world sorghum production, while Asia 19.5% (10.59 m t). India and Nigeria are the largest producers, and each contribute ~13% of the world sorghum production (6.9 to 7.0 m t). The average productivity of sorghum varies from 0.28 t ha^{-1} in Niger to 4.4 t ha^{-1} in Argentina (Table 2-1; http://faostat.fao.org, accessed on April 15, 2013). Several factors contribute to such variability in sorghum productivity. Abiotic and biotic stresses, amongst others, contribute maximum to the variation in sorghum production and productivity. Drought, salinity and heat are the major abiotic stresses. The biotic stresses include diseases, pests and viruses. The major diseases affecting sorghum production include grain mold (caused by a complex of several fungal species), downy mildew (*Peronosclerospora sorghi* [Wetson and Uppal (Shaw)]), anthracnose [*Colletotrichum graminicola* (Ces.) GW Wilson], rust (*Puccinia purpurea* Cooke), leaf blight [*Exserohilum turcicum* (Pass.) KJ Leonard & EG Suggs], charcoal rot/stalk rot [*Macrophomina phaseolina* (Tassi) Goid], and several virus diseases, while amongst the pests, shoot fly [*Atherigona soccata* (Rondani)], stem borer [*Chilo partellus* (swinhoe)] and [*Sesamia inferens* (Walker)], midge (*Contarinia sorghicola* Coq.), and head bug (*Calocoris angustatus* Leth) are the major pests of sorghum. These stresses often occur in combinations that cause substantial worldwide losses to sorghum production (House 1985; Sharma 1993; Kumar et al. 2011).

Sorghum is an important grain and feed crop in the SAT regions of Africa and Asia. Beside food and fodder crop, sorghum also provides raw

Table 2-1 Top 15 sorghum producing countries in the world, 2011 (http://faostat.fao.org; accessed on April 15, 2013).

Country	Area (million ha)	Production (million ton)	Grain yield (t ha^{-1})
India	7.38	7.00	0.95
Nigeria	4.89	6.90	1.41
Niger	2.88	0.81	0.28
Ethiopia	2.15	3.96	1.84
Mexico	1.73	6.43	3.72
Mali	1.69	1.19	0.71
Burkina Faso	1.68	1.51	0.90
United States of America	1.59	5.45	3.43
Argentina	1.01	4.46	4.40
United Republic of Tanzania	0.81	0.81	0.99
Cameroon	0.80	1.15	1.44
Chad	0.79	0.65	0.82
Brazil	0.76	1.93	2.55
Mozambique	0.64	0.50	0.79
Australia	0.63	1.93	3.06
World (total)	35.48	54.2	1.53

materials for production of starch, fiber and alcohol, while the sorghum straw is often used for thatching, fencing materials or brooms (Doggett 1988). Sorghum is gluten free; it is thus an attractive alternative food for those who suffer from Celiac disease (Dahlberg et al. 2011). Sorghum grains are also an important source of animal feed in many countries. It is also grown for forage, which can either be fed directly to animals or preserved as hay or silage. Ethanol is the best renewable source, which is produced from various crops like sugarcane, sugar beet molasses, corn starch and sweet sorghum. Sugar, starch and lignocellulose are the raw materials for the production of ethanol, and sweet sorghum is the only plant of which all parts can be used for bioethanol production (Rao et al. 2009).

Plant genetic resources are the basic raw materials for use in crop improvement programs and their use in breeding is one of the most sustainable ways to conserve valuable genetic resources. ICRISAT has a collection of 37,949 sorghum germplasm accessions, including cultivated and wild relatives, from 92 countries. In spite of such a large collection, there has been very limited use of these accessions in breeding mainly due to i) non availability of reliable information on traits of economic

importance that show high genotype x environment interaction, due to lack of accurate and precise large-scale multilocation evaluation of germplasm collections, ii) non availability of information needed by the breeder for genetically diverse, trait-specific and agronomically desirable parents in genebank databases, iii) linkage load of many undesirable genes and assumed risks, iv) restricted access to the germplasm collections due to limited seed quantities particularly of wild relatives and unadapted landraces and regulations governing international exchange, v) enhanced role of non additive genetic variation when diverse exotic germplasm is used by the breeders, vi) lack of robust, cost-effective tools to facilitate the efficient utilization of exotic germplasm in plant breeding programs, and vii) limited exposure to available germplasm and recirculation of the same genotypes already available with the researchers (Duvick 1995; Dwivedi et al. 2009; Upadhyaya et al. 2011). Conservation, characterization, regeneration, diversity assessment, forming representative subsets for enhanced utilization in breeding, and information dissemination with respect to sorghum germplasm have been discussed in this chapter.

2.2 Taxonomy

Sorghum belongs to the family Poaceae, tribe Andropogoneae, subtribe Sorghinae, and genus *Sorghum* Moench (Clayton and Renvoize 1986). The genus *Sorghum* has 25 species, grouped into five taxonomic subgenera or sections: *Eu-Sorghum*, *Chaetosorghum*, *Heterosorghum*, *Para-Sorghum*, and *Stiposorghum*. Section *Eu-Sorghum* contains all domesticated/cultivated sorghum races and varieties as *Sorghum bicolor* subsp. *bicolor*, and few wild and weedy species including *S. halepense* (Johnsons grass) and *S. arundinaceum*, the known progenitor of *S. bicolor*. All the *Sorghum bicolor* subsp. *bicolor* have $2n = 2x = 20$ chromosomes. Cultivated sorghum has five basic races—*bicolor*, *guinea*, *caudatum*, *kafir*, and *durra* and 10 intermediate races—*guinea-bicolor*, *caudatum-bicolor*, *kafir-bicolor*, *durra-bicolor*, *guinea-caudatum*, *guinea-kafir*, *guinea-durra*, *kafir-caudatum*, *durra-caudatum*, and *kafir-durra*, all recognized by observing spikelet/panicle morphology (Harlan and de Wet 1972; Smith and Frederiksen 2000; Dillon et al. 2007; Table 2-2). Sorghum like any other crop also has three genepools: primary (GP 1), secondary (GP 2), and tertiary (GP 3) genepools (Acheampong et al. 1984). The primary genepool consists of *Sorghum bicolor* complex, including a wild diploid, *S. propinquum* (Kunth.) Hitchc. The species in this genepool easily intercross and produce fertile hybrids. The secondary genepool includes *S. halepense* (L.) Pers., a tetraploid perennial with well developed creeping rhizomes. Some of the species in this genepool can be crossed with primary gene pool species to produce fertile hybrids, indicating that gene transfer

Table 2-2 Five basic and ten intermediate races in sorghum (Harlan and de Wet 1972) and their proportion in ICRISAT genebank.

Races	Designation (Alphabetic)	Designation (Numeric)	No of accessions	Percentage of total collection
Basic races				
Bicolor	B	1	1,531	4.08
Guinea	G	2	4,848	12.93
Caudatum	C	3	7,569	20.19
Kafir	K	4	1,314	3.5
Durra	D	5	7,977	21.28
Intermediate races				
Guinea-bicolor	GB	6	340	0.91
Caudatum-bicolor	CB	7	1,925	5.13
Kafir-bicolor	KB	8	146	0.39
Durra-bicolor	DB	9	2,415	6.44
Guinea-caudatum	GC	10	3,941	10.51
Guinea-kafir	GK	11	106	0.28
Guinea-durra	GD	12	218	0.58
Kafir-caudatum	KC	13	417	1.11
Durra-caudatum	DC	14	4,402	11.74
Kafir-durra	KD	15	272	0.73
Un-classified			70	0.19
Total			37,491	

between two gene pools (GP 1 and GP 2) is possible; however, usually difficult to achieve. The species from the section/genera *Parasorghum, Stiposorghum*, *Heterosorghum* and *Chaetosorghum* constitute tertiary genepool as these do not cross readily with primary genepool species. Hybrids produced, if any, are invariably sterile; special techniques are needed to effect gene transfer to the primary genepool species.

2.3 Sorghum Genetic Resources at Genebanks

2.3.1 Assembly, Conservation, Characterization and Regeneration

Assembly: The first step towards assembling a world collection of sorghum germplasm was made by the Indian Agricultural Program of the Rockefeller Foundation (Murty et al. 1967; Rockefeller Foundation 1970), which resulted into 16,138 accessions, collected from major sorghum growing areas in many countries. The accessions were assigned IS (International sorghum) number. Subsequently, the Indian program, All India Coordinated Sorghum Improvement Project (AICSIP), could transfer only 8,961 accessions to ICRISAT, as other accessions lost their seed viability due to lack of proper

storage facilities. Vigorous and sustained efforts were made by ICRISAT to fill the gaps. ICRISAT obtained 3,000 accessions from the duplicate sets maintained at Purdue University, National Seed Storage Laboratory, Fort Collins, USA and from Mayaguez, Puerto Rico (Mengesha and Prasad Rao 1982). In 1974, in accordance with the recommendation of the Advisory Committee on Sorghum and Small Millet Germplasm sponsored by the International Board for Plant Genetic Resources, IBPGR (now Bioversity International), Rome, Italy, ICRISAT has accepted the responsibility to maintain sorghum germplasm and enlarge the world collection. Special efforts were made to collect or assemble germplasm (landraces and wild relatives) from the areas threatened by genetic erosion. During 1975 to 1996, ICRISAT has launched 94 collecting missions and collected 9,011 accessions worldwide. Seventeen countries including India, the USA, Ethiopia, France and Sudan have contributed maximum numbers of germplasm accessions to ICRISAT genebank (Fig. 2-1). About 16% (37,949 accessions from 92 countries) of the world collection of sorghum (235,711 accessions) is conserved in ICRISAT genebank at Patancheru, India (FAO 2010). This collection comprises of 32,578 landrace accessions, 4,814 advanced breeding lines, 99 cultivars, and 458 wild and weedy relatives (Table 2-3), ~80% of these were donated by the developing countries from the SAT. Biologically, the basic races, *durra* represented by 21.21%, *Caudatum* 20.12%, *Guinea* 12.89%, *bicolor* 4.59%, and *kafir* 3.49%. *Durra-caudatum* and *guinea-caudatum*, *durra-bicolor* and *caudatum-bicolor*, and *kafir-caudatum* and *guinea-bicolor*, amongst the intermediate races, were represented by 10.48 to 11.70%, 5.12

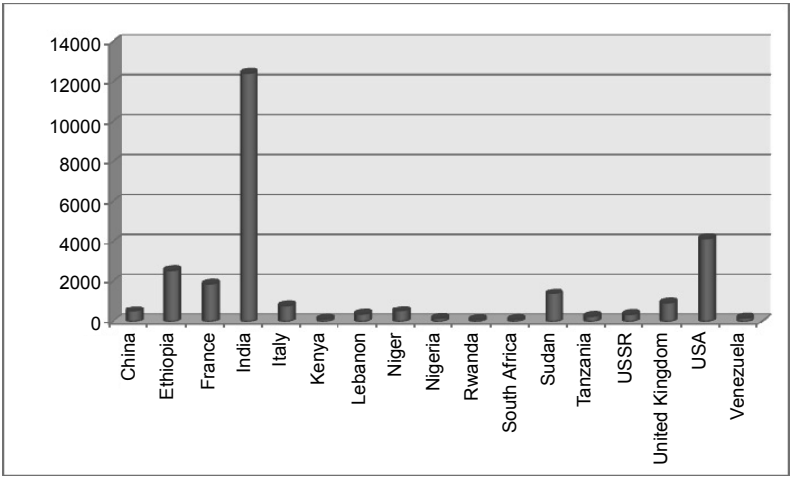

Figure 2-1 Sorghum germplasm accessions received at ICRISAT from different donors (1973–2012).

Table 2-3 Geographical distribution of sorghum germplasm assembled at ICRISAT genebank, Patancheru, India (as on 31st March, 2013).

Region	Landraces	Advanced lines/ cultivars	Wild and weedy relatives	Total
Northern Africa	2,159	396	68	2,623
Southern Africa	1,524	319	39	1,882
Eastern Africa	10,785	508	144	11,437
Western Africa	4,667	281	25	4,973
Middle Africa	3,022	72	51	3,145
South Asia	5,856	1,062	27	6,945
South-East and East Asia	869	137	4	1,010
West Asia	2,246	383	1	2,630
North America	553	1,517	68	2,138
South America	215	4	1	220
Central America	109	57		166
Europe	488	38	7	533
Oceania	47	6	22	75
Unknown	38	133	1	172
Total	**32,578**	**4,913**	**458**	**37,949**

to 4.59%, and 0.90 to 1.11%, respectively. Other intermediate races in the collection were represented ≤0.72% to ≥0.28% (Table 2-2).

Conservation: The germplasm has to be maintained in such a state that there is minimum risk of its loss and can be directly planted in field. *In situ* or *ex situ* are the two forms that the germplasm can be conserved. Conservation of the germplasm in its natural habitat is known as *in situ* conservation, while conserving germplasm away from its natural habitat is *ex situ*, i.e., genebanks. *Ex situ* conservation is easy, cost effective, relatively safe and requires minimum space. For operational purposes, the collections are divided into two forms, i.e., the active and base collections. The active collection is stored under medium term storage condition (4ºC and 20–30% RH), which remains viable for 10–20 years with ≥85% viability. Germplasm categorized in active collection are used for distribution, utilization and multiplication. For each accession, about 400 g of sorghum seed is harvested from post-rainy season multiplication plot, field dried to 8% moisture and stored in screw capped aluminum container. The base collection is kept for long term storage at –20ºC. For this purpose, ~75 g sorghum seed is cleaned and dried to 5–7% moisture content by equilibration with air at 15ºC and

15% RH for approximately 3–4 weeks. The dried seed is vacuum sealed in an aluminum foil pouch and stored after confirming initial germination (>90%). Seed viability is regularly monitored at 5 and 10 years interval in medium and 10–20 in long term storage. Any sample having seed stocks <50 g or seed viability <85% is taken out for regeneration.

Characterization: Highly heritable phenotypic traits are often used for basic characterization as such information is of high interest to users of genetic diversity. Sorghum germplasm collection at ICRISAT has been characterized for morpho-agronomic traits, and evaluated for abiotic and biotic stresses, and for seed quality traits (IBPGR/ICRISAT 1993). However, the proportion of accessions screened to the total collection maintained at ICRISAT genebank varie considerably (Table 2-4). For example, 94–99% of the 37,949 world collection of sorghum has been characterized for most of the morphological descriptors; 42–44% screened for shoot fly, downy mildew, and stem borer; 18–22% to grain mold, leaf blight, rust, and *Striga*; and 10% to anthracnose. For grain quality, 26–29% accessions were evaluated for protein and lysine contents. Clearly, more emphasis should be towards identifying germplasm with improved seed quality traits. This collection has shown immense variability for qualitative traits as well (Table 2-4). Tan plant color is said to be associated with resistance to leaf diseases and grain weathering (Frederiksen and Duncan 1982; Duncan et al. 1991). Only 4.48% of the accessions in the present collection had no pigmentation, while the remaining pigmented. The midrib color in the collection varied from white, dull green, yellow and brown, while the majority of them are of white and dull green types. Brown mid rib is mainly associated with reduced lignin content and higher forage digestibility (Pedersen 1996; Casler et al. 2003). The brown midrib germplasm is also a good source of biofuel, especially for ethanol production. The cellulose in some of the brown mid rib types is associated with low lignin content, it therefore take less energy for conversion to ethanol. The brown midrib color accessions represent only 0.03% of the total collection. Substantial variation has been found for glume and grain colors. However, the variation for grain color is more than that observed for glume color. Grain mold resistance has been found mostly in colored grain sorghums with or without tannin and also in a few white hard grain sorghums (Bandyopadhyay et al. 1988; Audilakshmi et al. 2000, 2005). Sorghum accessions with more glumes coverage, in addition to glume color, are also closely associated with grain mold resistance (Thakur et al. 2008). There were 12% of the accessions in ICRISAT collection whose three fourth portions of the grains are fully covered by the glume, while the grains in 3.66% of the accessions are totally uncovered. However, proportions of accessions with 1/2 and 1/4 coverage of the grains by glumes were much higher. Such diversity in grain color and/or grain coverage by the glumes

Table 2-4 Range variation for different characters in sorghum germplasm characterized at Patancheru, India.

Character	# accessions characterized	Range of variation
Days to 50% flowering (days)	37,482	33–199
Plant height (cm)	37,717	50–655
Peduncle exsertion (cm)	37,453	0–72
Head length (cm)	37,454	2.5–90.0
Head width (cm)	37,454	1–80.0
Grain size (mm)	36,886	0.8–6
100- seed weight (g)	37,384	0.21–9.4
Midrib color	37,681	White (74.46%), dull green (23.85%), yellow (1.66%), brown (0.03%)
Pigmentation	37,686	Pigmented (95.52%), tan (4.48%)
Panicle compactness and shape	37,444	Semi loose stiff branches (33.21%), semi compact elliptic branches (31.31%), loose stiff branches (12.15%), compact elliptic branches (9.93%), loose drooping branches (5.34%), compact oval branches (2.57%), semi compact oval branches (2.09%), very loose drooping branches (1.47%), semi loose drooping branches (1.05), very loose stiff branches (0.88%)
Glume color	37,447	Straw (31.85%), black (26.89%), red (7.38%), purple (6.40%), partly straw and purple (5.70%), partly straw and brown (5.08%), light red (4.80%), brown (4.11%)
Glume covering	37,455	Half grain covered (43.44%), one fourth grain covered (37.11%), three fourth grain covered (12.00%), grain fully covered (3.79%), grain uncovered (3.66%)
Grain color	37,277	Straw (22.72%), white (18.16%), reddish brown (14.80%), light red (12.17%), brown (8.50%), yellow (6.36%), light brown (4.92%), gray (4.89%), chalky white (3.37%), red (2.93%), purple (1.13%), white and red mixed (0.05%), straw and red mixed (0.01%), black (0.003%)
Threshability	35,805	Freely threshable (74.08%), partly threshable (20.80%), Difficult to thresh (5.12%)
Endosperm texture		Partly corneous (37.06%), mostly starchy (33.20%), completely starchy (13.89%), mostly corneous (12.50%), completely corneous (3.35%)
Lustre	37,381	Lustrous (62.49%), Non lustrous (37.51%)
Subcoat (testa)	37,378	Absent (70.70%), present (29.30%)

provides researchers opportunities to increase the level of resistance to grain mold in new cultivars.

Regeneration: Sorghum is predominantly self pollinated species, but with varying degrees of outcrossing (Pedersen et al. 1998; Barnaud et al. 2008). Germplasm accessions are maintained and multiplied by selfing. Individual panicles are covered with well labeled selfing paper bags (LxWxH; 35x10x 5 cm) as soon as heads emerge from flag leaf before anthesis. Heads are kept covered for at least 21 days (i.e., up to dough stage) and then removed, but the bags are tied around the peduncles to identify the selfed plants, to allow the seeds to mature and dry. At harvest, at least seeds from 50 selfed plants are bulked to maintain an accession (Upadhyaya et al. 2008). Wild relatives are also maintained by selfing; however, some wild species do not set seeds, which are maintained as live plant in a field genebank (Stenhouse et al. 1997).

2.3.2 Germplasm Distribution, Utilization, and Impact

Distribution: ICRISAT genebank has been the major source of supplying limited amount of seeds of germplasm worldwide for use in crop improvement programs. The diversity available among the cultivated sorghums and their wild relatives assembled at the genebank is truly amazing. Since 1973, ICRISAT genebank has distributed 261,521 samples of 32,657 sorghum germplasm to 109 countries, with majority of the samples distributed during the 80s and 90s (Fig. 2-2), and India receiving ~50%

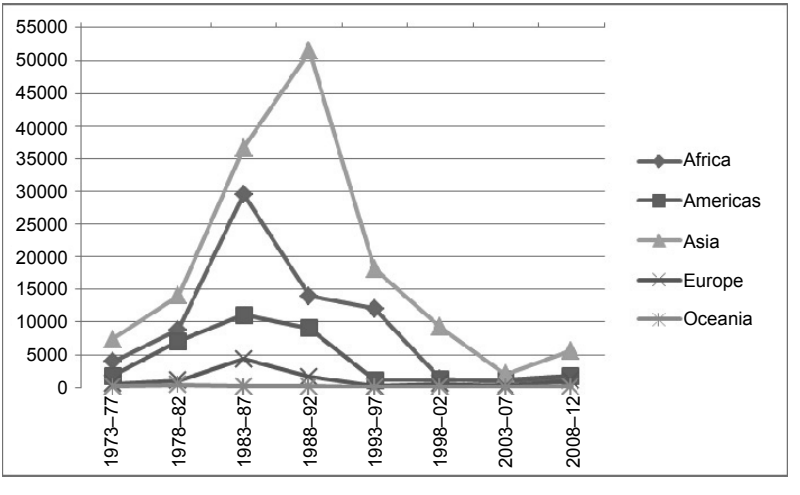

Figure 2-2 Supply of sorghum germplasm to different regions in different periods (1973–2012).

of these samples. Eighty-five percent of 32,657 unique germplasm were landraces/traditional cultivars and 13% were advanced breeding lines. Only 1% of the samples distributed belong to wild species. The most frequently requested accessions were IS 18758, IS 1059 and IS 5604. The former belongs to Zerazera landrace, while the latter two to *durra-bicolor* intermediate race. Other most frequently requested accessions were IS# 2205, 3443, 4776, and 18484; all possessing resistance to major pests and/or diseases. IS 2205 seeds have a good popping quality.

Utilization: Plant genetic resources are the basic raw materials to meet current and future needs of crop improvement programs. Though a wide range of genetic resources are available nationally and internationally. The breeders tend to concentrate only on adapted and improved materials avoiding wild and weedy relatives, and landraces in their crossing program (Nass and Paterniani 2000). Plant breeders are aware of the limitation of working with exotic germplasm. Use of wild and landrace diversity in breeding programs is low either because of lack of knowledge about the genetic worth or the linkage drag associated with transfer of beneficial traits from such germplasm. There is therefore need to discover new sources of variation and assess the pattern of diversity to identify genetically diverse germplasm with beneficial traits to promote utilization of such germplasm in sorghum improvement. At ICRISAT, efforts have been made to diversify the germplasm base to enhance yield levels, and to identify resistance sources to develop new varieties. The major germplasm sources utilized in varietal improvement include temperate lines from the USA, Zerazera lines from Ethiopia and Sudan, and some lines of Indian origin (Vidyabhushanam et al. 1989).

Impact: Thirty-four sorghum germplasm accessions have been directly released as cultivars in 17 countries, with few of these released in more than one country (Table 2-5). For example, IS 18758, a popular *guinea-caudatum* landrace from Ethiopia, has been released as E 35-1 in Burkina Faso and as Gambella 1107 in Burundi. It has proved to be an excellent source of desirable plant type, high grain yield, good grain quality, straw glume color, resistant to leaf diseases and tolerant to grain weathering. It has been extensively used in sorghum breeding programs at ICRISAT and elsewhere in national breeding programs. IS 33844, another *durra* race accession, an excellent maldandi-type with large and lustrous grains and high yield potential, and a selection from it has been released as "Parbhani Moti" for post-rainy season cultivation in Maharashtra, India (Reddy et al. 2006). The *kafir* race in combination with *durra* sorghum from eastern Africa provided the basis of the nuclear cytoplasmic male-sterility system for exploiting hybrid vigor in sorghum. The *Guinea* race from West Africa has provided resistance to grain mold, while the *bicolor* race have contributed to the breeding of forage sorghum (Kameswara Rao et al. 2004).

Table 2-5 List of sorghum germplasm accessions directly released as cultivars for cultivation.

Accession	Country of origin	Year of release	Country of release	Released name
IS 5424	India	1980	Myanmar	Shwe-ni 8
IS 302	China	1980	Myanmar	Shwe-ni 10
IS 9321	South Africa	1990	Mexico	--
IS 9302	South Africa	1980	Ethiopia	ESIP 11
IS 8965	Kenya	1980	Myanmar	Shwe-ni 1
IS 8571	Tanzania	1989	Mozambique	Mamonhe
IS 8193	Uganda	2001	Rwanda	IS 8193
IS 9447	South Africa	1990	Mexico	--
IS 6928	Sudan	1978	India	Moti
IS 9468	South Africa	2000	Mexico	Marvilla NoSOFO430201092
IS 4776	India	1983	India	U P Chari-1
IS 3924	Nigeria		India	Swarna
IS 3923	Zimbabwe	1994	Botswana	Mahube
IS 3693	USA	1989	Swaziland	MRS 94
IS 3541	Sudan		India	CS 3541
IS 2940	USA	1981	Myanmar	Shwe-ni 2
IS 2391	South Africa	1989	Swaziland	MRS 13
IS 8193	Uganda	2001	Kenya	Kari Mtama 2
IS 18758	Ethiopia	1990	Burundi	Gambella 1107
IS 33892	India	1980	India	NTJ 2
IS 33891	India		India	NTJ 1
IS 33844	India	2002	India	Parbhani Moti
IS 29415	Lesotho	2000	Eritrea	Shiketi
IS 25395	Kenya	2001	Rwanda	IS 25395
IS 23520	Ethiopia	1989	Zambia	Sima
IS 9323	South Africa	1984	Ethiopia	ESIP 12
IS 21219	Kenya	2001	Rwanda	IS 21219
IS 21055	Kenya	2008	Kenya	Legio
IS 18758	Ethiopia	1983	Burkina Faso	E-35-1
IS 18484	India	1984	Honduras	Tortillerio 1
IS 15845	Cameroon	1996	India	Paiyur 2
IS 15401	Cameroon	2001	Mali	Soumalemba
IS 13809	South Africa	1990	Mexico	--
IS 13444	Zimbabwe	2000	Sudan	Arous el Rimal
IS 9830	Sudan	1991	Sudan	Mugawim Buda-2
IS 23496	Ethiopia	1995	Tanzania	Pato

2.3.3 Germplasm Restoration

A total of 7,608 sorghum germplasm accessions were restored back to seven countries in Africa, from where these germplasm were originally obtained. The countries include Botswana (362 accessions), Cameroon (1,827 accessions), Ethiopia (1,723 accessions), Kenya (838 accessions), Nigeria (1,436 accessions), Somalia (445 accessions), and Sudan (977 accessions). Additionally, 14,615 sorghum germplasm accessions were restored to India. For safety duplication, over 30,000 sorghum germplasm accessions have also been conserved in the Svalbard Global Seed Vault, Norway.

2.4 Forming Representative Germplasm Sets to Discovering New Sources of Variation

2.4.1 Representative Germplasm Sets

2.4.1.1 Core and Mini Core Collections

Frankel and Brown (1984) suggested that maximum use of germplasm in a crop improvement program is possible if a small collection representing diversity of well characterized accessions is made available to researchers. Frankel (1984) coined the term "core collection" to sample representative variability from the entire collection. Core collection consists of a subset of accessions from the entire collection, capturing most of the species diversity in a given crop. Upadhyaya and Ortiz (2001) postulated the concept of mini core collection, which consists of 10% core collection accessions (or 1% entire collection accessions). Essentially, the passport, characterization and evaluation data of entire germplasm of a given species is used to identify 10% of the accessions to form core collection. This core is further evaluated for morpho-agronomic and seed quality traits to select 10% of the core collection accessions for forming mini core collection. At both stages, standard clustering procedures are used to create groups of similar accessions (Fig. 2-3; Upadhyaya et al. 2009d). Core collection in sorghum consists of 3,475 accessions (Prasada Rao and Ramantha Rao 1995), 2,247 accessions (Grenier et al. 2001) or 3,011 accessions (Dahlberg et al. 2004), while mini core collection 242 accessions (Upadhyaya et al. 2009a). The selected accessions in mini core represent all five basic and 10 intermediate races, as well 10 geographic regions. However, the entire collection as well as both the subsets are dominated by *caudatum*, *durra*, and *guinea*, the basic races, and *caudatum-bicolor* and *guinea-caudatum*, the intermediate races.

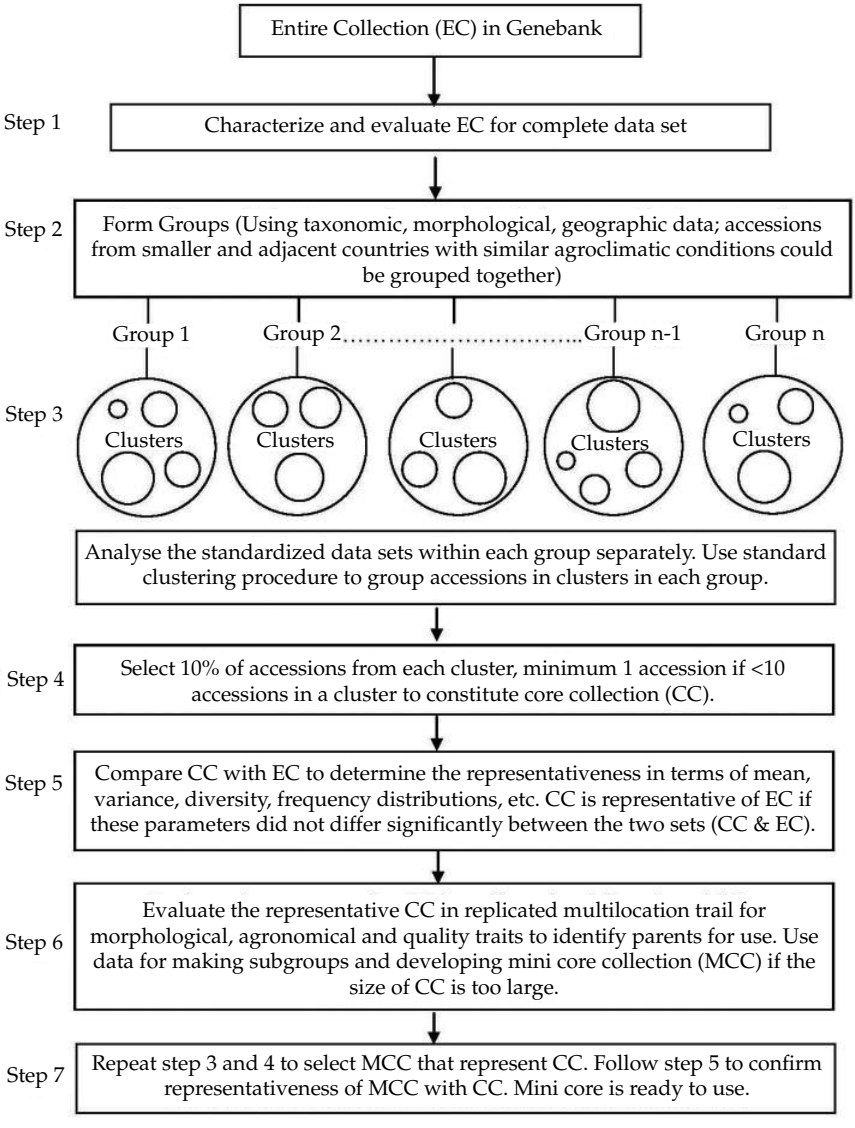

Figure 2-3 Flow diagram for forming core and mini core collections involving entire collection of germplasm of a given crop species.

2.4.1.2 Genotype-based Reference Set

Global Composite Germplasm Collection (GCGC) of sorghum, which consists of 3,367 cultivated and wild accessions, was genotyped with

41 simple sequence repeat (SSR) markers to form a reference set of 383 accessions, which captured 78.3% of the SSR alleles detected in the GCGC, with an average of 14.9 alleles per marker, comparable to allelic richness of the GCGC (783 alleles, 19.2 alleles per marker) (Billot et al. 2013). This reference set includes 332 landraces, 28 breeding lines and 23 wild/weedy accessions. All five basic and 10 intermediate races and accessions from different geographic origins (except South America) were represented in a reference set, which is sufficiently diverse to serve as a panel for linkage disequilibrium mapping, and for detailed characterization of traits of economic importance to plant breeding programs and for the assessment of allelic diversity in genes associated with trait expression (Billot et al. 2013).

2.4.2 Sources of Natural Genetic Variation

2.4.2.1 Abiotic Stresses

Drought: Sorghum reference set and stay-green QTL introgression lines have been evaluated for post-flowering drought tolerance under two moisture regimes—Water Stress (WS) and Well Watered (WW) conditions—during the post-rainy season at Patancheru, India and several accessions with stay-green trait under post-flowering drought stress conditions were identified (Upadhyaya et al. 2009b). A large variation was observed among accessions for water extraction under WS (10.2 kg plant^{-1} to 15.3 kg plant^{-1}) and WW (10.5 kg plant^{-1} to 42.3 kg plant^{-1}) conditions. Several accessions with either high or low water-extraction ability under WS as well as under WW conditions were identified. Transpiration Efficiency (TE) varied between 2.44 kg plant^{-1} to 6.09 kg plant^{-1} water transpired, with a few reference set accessions had higher TE than the highest TE of the stay-green introgression lines. This reference set was also evaluated for drought tolerance in Kenya and Mali, with IS 3963, IS 22287, IS 24009, 452(411)510 and 393(421) 659 in the former and IS 1284 and IS 28389 in the latter were identified as tolerant to drought. IS# 301, 1037, 1045, 2877, 4405, 4663 and 17595 were reported tolerant to drought at seedling emergence stage (Reddy et al. 2004; Kumar et al. 2011), while IS# 824, 1037, 3477, 8370, 10596 and 10701 tolerant to early season drought, IS 1347 and IS 13441 to mid-season drought, and IS# 6928, 12611, 22314 and 22380 to terminal drought (Reddy et al. 2004).

Salinity: Based on two years evaluation and three levels of salinity (5, 10 and 15 dSm^{-1}), Reddy et al. (2008) reported 18 accessions (IS# 164, 237, 707, 1045, 1049, 1052, 1069, 1087, 1178, 1232, 1243, 1261, 1263, 1328, 1366, 1568, 19604 and 29789) tolerant to salinity.

2.4.2.2 Biotic Stresses

Grain mold: Bandyopadhyay et al. (1988) reported 156 of the 7,132 sorghum accessions screened during the period from 1980 to 1985 at Patancheru, India, resistant to grain mold. Four *guinea* race white-grained accessions were also reported resistant to grain mold (Singh et al. 1995). Recently, Sharma et al. (2010) found 50 sorghum mini core accessions resistant to grain mold (≤10% mean disease severity). IS# 602, 608, 3121, and 1212 had zero disease incidence in both years of evaluation. The first three of these accessions belong to race *bicolor* while the latter to *kafir-bicolor*.

Anthracnose: Sharma et al. (2012) reported 13 accessions of the sorghum mini core resistant to anthracnose. The disease score amongst resistant accessions ranged from 2 to 3, while a few accessions from the susceptible group had disease score up to 7.0. Some of the promising accessions include IS# 10302 (*caudatum*), 19153 (*guinea-cadatum*), 20956 (*durra-caudatum*) and 24218 (*guinea*), with a mean disease score ~2.0.

Leaf blight: Resistance to leaf blight include IS# 2906, 18417, 18425, 18758, 19667 and 19669 (Reddy et al. 2004). Twenty-seven sorghum mini core accessions were reported resistant to leaf blight, with most of these accessions in two seasons evaluation under artificial inoculation conditions had mean disease score of 2, while the highly susceptible accessions scored up to 6 (Sharma et al. 2012).

Rust: Resistance to rust include IS# 3413, 13896, 18417, 21454 and 29016 (Reddy et al. 2004). More recently, the greenhouse and field evaluation of sorghum mini core resulted six accessions, IS# 473, 23521, 23684, 24503, 26737 and 33023, resistant to rust, with a mean disease severity of 3.8% (range 0 to 10%), while few highly susceptible accessions had mean rust disease severity of 78% (Sharma et al. 2012).

Downy mildew: Reddy et al. (2004) reported resistance to downy mildew in IS 3547 and IS 20450. Recently, Sharma et al. (2010) reported six sorghum mini core accessions, IS# 23992, 27697, 28449, 28747, 30400 and 31714, resistant to downy mildew, with mean disease <10% in comparison to 88% in susceptible controls (SPV 104 and Bulk Y).

Potyvirus spp.: Sorghum is a host to several virus species of the family Potyviridae, including Maize Dwarf Mosaic Virus (MDMV), sugarcane mosaic virus strain MDB (SCMV-MDV), Johonsongrass mosaic virus (JGMV), sorghum mosaic virus (SrMV), and *Zea* mosaic virus (ZeMV). Of these, MDMV and SCMV-MDB are most often associated with the disease known as maize dwarf mosaic of corn and sorghum (Toler and Bockholt 1969, Toler and Fredericksen 1971). More recently, Seifers et al. (2012) reported IS 7679 and IS 20740 from mini core as a new source of resistance

to several Potyvirus species (MDMV, SCMV-MDB, SrMV, and JGMV-N, and ZeMV), which systematically infect sorghum.

Multiple resistances to diseases: The previously reported multiple diseases resistant sources include IS 2058 and IS 18758 (anthracnose and rust); IS 3547 (grain mold, downy mildew, anthracnose and rust); IS 14332 (grain mold, downy mildew and rust); IS 17141 (grain mold and anthracnose); IS 2333 and IS 14387 (grain mold and downy mildew); and IS# 3413, 14390 and 21454 (grain mold and rust) (Reddy et al. 2008), while more recently, IS 23992 resistant to grain mold and downy mildew (Sharma et al. 2010) and IS# 473, 23521, and 23684 to anthracnose, leaf blight and rust (Sharma et al. 2012) were reported.

Insect pests: Researchers at ICRISAT evaluated substantial number of sorghum germplasm for resistance to insect pest. Resistance to shoot fly have been reported in 40 accessions, with IS# 1054, 1071, 2123, 2195, 2394, 4664, 5484, 18368 and 18551 having stable resistance to shoot fly damage. Seventy-one accessions showed resistance to spotted stem borer, of which, IS 1044, 1853, 2205, 5470, 5604 and 8320 had shown stable resistance to borer. Fifty accessions showed resistance to sorghum midge. IS# 7005, 8891 and 10712 had stable resistance to midge. Thirty-five accessions were reported resistant to sorghum head bug, with IS# 17610, 17618, 17645, 20664 and 20740 highly resistant to head bug (Sharma et al. 2003). Some of the newly identified sources include IS# 1054, 1082, 2134, 2146, 2195, 2205, 2312, 2313, 5604, 18417 and 18551 for shoot fly; IS# 1044, 1151, 2122, 2123, 2205, 2375, 5470, 5480, 5604, 18425, 18432, 18554 and 18577 for stem borer and IS 3443 and IS 18961 for sorghum midge (Reddy et al. 2008).

The available wild relatives of sorghum have been screened for resistance to sorghum shoot fly. Accessions belonging to section *Parasorghum*, *Stiposorghum*, *Heterosorghum* and *Chaetosorghum* have shown resistance to shoot fly, with many of these exhibiting high level of antibiosis to shoot fly, which may be used as an alternate source to shoot fly resistance (Kamala et al. 2009).

Striga: It is the parasitic weed, confined to many crops including sorghum in Africa. Resistance to *Striga* has been reported in IS# 2221, 4202, 5106, 7471, 9830, 9951, 18331(N 13) and 87441 (Framida) (Reddy et al. 2008).

2.4.2.3 Seed Quality Traits

Protein: The protein content amongst the 10,937 sorghum accessions, evaluated at Patancheru, ranged from 2.8 to 21.6%, averaged 8.99%, and IS 9955 being the highest in protein (www.icrisat.org/what-we-do/crops/sorghum/project1/pfirst.asp).

High lysine: Singh and Axtell (1973) reported that IS 11167 and IS 11758 are high lysine sources from Ethiopia. The lysine content amongst 9,918 sorghum accessions, evaluated at Patancheru, ranged from 0.14 to 5.0%, averaged 2.31%, and IS 25792 being the highest in lysine (www.icrisat.org/what-we-do/crops/sorghum/project1/pfirst.asp).

High Iron (Fe) and Zinc (Zn): Sorghum reference set (383 accessions) was evaluated for grain iron (Fe) and zinc (Zn) contents. Seven reference set accessions, IS# 35, 1076, 5720, 15772, 29638, 30335 and 30409, had high grain Fe and Zn under well-watered and post-flowering drought stressed conditions (Upadhyaya et al. 2009b). Likewise, IS# 55, 3283, 3760, 5427 and 5514 from sorghum core collection, evaluated for two seasons, showed high Fe (>50 mg kg^{-1}) and Zn (>37 mg kg^{-1}) content (Kumar et al. 2009). The control cultivars (ICSR 40 and 296B) in this evaluation recorded grain Fe and Zn contents of 39–40 mg kg^{-1} and 23–24 mg kg^{-1}, respectively.

Reddy et al. (2008) detected large variability for Fe (7.77 ppm to 192.3 ppm) and Zn (13.7 ppm to 91.3 ppm) in sorghum core collection (2,262 accessions), which is much higher than that exists among hybrid parents of released/marketed hybrids and popular cultivars. Seventeen of these accessions had Fe >90 ppm (96–192 ppm), while 11 accessions had Zn >58 ppm (58–91 ppm).

Popping: The collection in ICIRSAT contains 36 sorghum accessions with good popping characteristics (Prasada Rao and Murty 1982).

2.4.2.4 Bioenergy

Sweet sorghum is a good source of ethanol. Sweet sorghum germplasm are tall, produce high biomass and accumulate high levels of sugars (10–15%) in the stem. Seventy-six accessions with Brix (sugar) content greater than 16.2% were reported in sorghum collection (ICRISAT 1987), with some of the sweet sorghum accessions such as IS# 2266, 3572, 8157, 9639, 9890, 14970, 15428, 15448, 20963 and 21100 consistently showed high Brix content (Reddy et al. 2008). Likewise, a set of 125 diverse accessions of sweet sorghum are also available in the US sorghum germplasm collection (Murray et al. 2009).

2.5 Assessing Population Structure and Diversity

2.5.1 Phenotypic Diversity for Morpho-agronomic Traits

Sorghum germplasm maintained at ICRISAT showed large variation for most of the morpho-agronomic descriptors (Table 2-4). For example, days to flower 33 to 199 days, plant height 50 to 655 cm, peduncle exsertion 0. to 72 cm, head length 2.5 to 90 cm, head width 1 to 80 cm, grain size 0.8

to 6.0 mm and 100 grain weight 0.21 to 9.4 g. Likewise, panicle compactness and shape were categorized into 10 classes, while glumes color in eight classes, glumes covering in five classes, and grain color in 14 classes.

Stenhouse et al. (1997) reported substantial variation for both the length and strength of the central rachis, primary and secondary branches, and combinations that confer distinct panicle shape and densities. Upadhyaya et al. (2010) reported substantial diversity for four agronomic traits amongst 667 newly acquired sorghum germplasm accessions, representing five basic and eight intermediate races and two wild species. The hierarchical cluster analysis grouped these accessions into three clusters. Cluster 1 consisted of accessions from race *bicolor* and *guinea*, and intermediate races *durra-bicolor* and *guinea-bicolor,* while accessions from three basic races (*caudatum*, *durra*, and *kafir*) and four intermediate races (*durra-cadatum*, *caudatum-bicolor*, *kafir-bicolor*, and *guinea-caudatum*) grouped in cluster III. Wild species (*drummondi* and *helepense*) accessions formed separate cluster II. Further, they identified a number of trait-specific diverse accessions based upon the mean phenotypic diversity index. For example, 104 accessions representing four basic and five intermediate races, flowered significantly earlier than the control, Parbhani Moti. Of these, IS# 6181, 6931, 11992, 12232 and 12313 were earliest to flower thus would serve as sources of extra-early flowering in sorghum improvement programs. Dwarf sorghum is desirable for mechanical harvesting and five such accessions identified were IS# 10924, 12313, 12522, 13362 and 13397. Likewise, the most promising accessions for panicle exsertion were IS# 2533, 11168, 12956, 13356 and 15645, while the best accessions for medium seed weight were IS# 13322, 14927, 14793, 14973 and 15582.

2.5.2 Population Structure and Diversity

Assessment of population structure and diversity in germplasm collection provide an opportunity for efficient conservation, management and utilization of germplasm, and mine allelic variations associated with agronomically beneficial traits. Sorghum GCGC consisting of 3,367 accessions, dominated by landraces (89.5%) was developed. Advanced breeding lines and cultivars represented 8.3%, while wild and weedy relatives only 2%. All five basic and 10 intermediate races of sorghum were represented in GCGC. A massive effort was made to genotype this collection using 41 highly polymorphic SSR markers, mapped across all 10 chromosome pairs in the nuclear genome of *Soghum bicolor*, which detected a total of 783 SSR marker alleles, with an average of 19.2 alleles per marker, and landraces capturing 94% of the allelic variation, while breeding lines and wild/weedy relatives, respectively, possessing 57 and 67% alleles. Accessions from eastern Africa exhibited the largest gene diversity, followed by those

from Central Africa while southern Africa had the lowest allelic diversity. In Asia, accessions from Middle East origins had high genetic diversity than India and East Asia. Thirty-five percent (280 alleles) of 783 alleles were found only in cultivated sorghum while only 5% (40 alleles) in wild/weedy accessions. Further, this study detected 13 groups of variable size, with cultivated sorghum accessions appeared structured according to geographic regions and races within region. The peripheral groups in western Africa, southern Africa and eastern Asia were the most homogeneous and clearly differentiated. There was little correspondence between races (except *kafir*) and marker-based groups. The race *bicolor*, *caudatum*, *durra*, and *guinea* were each dispersed in three or more groups. Wild and weedy accessions were very diverse and scattered among cultivated samples, reinforcing the belief that there exists large gene-flow between the different types (Billot et al. 2013). The inclusion of broad range of germplasm in Billot et al. (2013) investigation resulted in larger allele numbers (19 alleles per locus) and higher diversity parameters than in most previous studies (Grenier et al. 2000; Ghebru et al. 2002; Agrama and Tuinstra 2003; Casa et al. 2005; Folkertsma et al. 2005; Manzelli et al. 2007; Ali et al. 2008; Deu et al. 2008; Shehzad et al. 2009b; Ng' Uni et al. 2011; Han et al. 2011; Mbeyagala et al. 2012; Cuevas and Prom 2013). Ethiopian sorghum collection is reported to be composed of highly genetically diverse germplasm (Cuevas and Prom 2013). Sorghum in Ethiopia is grown under diverse environmental conditions, which includes the eastern and southwestern highlands region, the warmer and mid-elevation terraces of the north, and the hot and dry valleys and lowland savannahs of the south and west region (Stemler et al. 1977). Moreover, Ethiopian farmers amongst themselves exchange seeds to use diversity as a tool to overcome the difficult farming system of the region (McGuire 2002). Both diversity in growing conditions and frequent seed exchange amongst sorghum farmers in Ethiopia may have contributed to increase phenotype and genetic diversity through different selection pressure by nature or farmers (Cuevas and Prom 2013).

Population structure analysis reported here showed different and diverse pattern of groupings. For example, 20 SSRs differentiated 137 Ethiopian accessions into three groups (Cuevas and Prom 2013), while 21 SSRs differentiated 241 sorghum landraces from Uganda into two distinct groups, each with seven subclusters representing agroclimatic zones (Mbeyagala et al. 2012). Likewise, 95 SSRs differentiated 96 sweet sorghum accessions into four groups, which corresponded well with the geographic locations (Wang et al. 2009), 369 markers (Simple Sequence Repeats, SSRs and Single Nucleotide Polymorphism, SNPs) differentiated 125 sweet sorghum accessions into three groups (Murray et al. 2009), or 41 SSRs differentiated 3,367 GCGC accessions into 13 groups (Billot et al. 2013). The reason for such differences in groupings could be either due

to differences in sample size (both in case of marker and the germplasm); the marker system (SSR or SNP) and the marker coverage of the genome; or the nature of variability present in the germplasm collection used in the study. Clearly, using appropriate high throughput assay and marker systems, it is possible to differentiate sorghum germplasm collection into genetically distinct groups, which in some cases paralleled either with racial or geographic diversity. The genetically diverse accessions from such stratification and possessing beneficial traits can be selected for use in breeding programs. The diversity information will also be valuable to promote *ex situ* and *in situ* conservation of germplasm.

2.5.3 Association Mapping

Association or linkage disequilibrium mapping is an alternative to traditional genetic mapping, which uses a population generated from two parents, to map quantitative trait loci (QTL) associated with beneficial traits. It offers increased mapping resolution, reduced research time, and greater allelic variation (Yu and Buckler 2006). It is a powerful tool to fine map QTL but dependent on the structure of linkage disequilibrium of alleles at different loci (Flint-Garcia et al. 2003). More recent studies using genomewide association mapping revealed significant marker-trait association in sorghum, i.e., days to flowering, culm length, number of tillers, number of panicles and panicle length (Shehzad et al. 2009b; Bhosale et al. 2012); kernel weight and tiller number (Upadhyaya et al. 2012a); plant height (Murray et al. 2009; Wang et al. 2012; Upadhyaya et al. 2012b, 2013a); stem sugar (brix) (Murray et al. 2009); anthracnose resistance (Upadhyaya et al. 2013b), rust and grain mold resistance (Upadhyaya et al. 2013c) and maturity (Upadhyaya et al. 2012b, 2013a), with many of these markers co-mapped on the same linkage groups previously reported as harboring QTL or candidate gene associated with anthracnose, rust and grain mold resistance, tillering, plant height and maturity. A study on genomewide patterns of genetic variation revealed that 1,442 genes differentiated sweet and grain sorghum inbreds, with some clearly involved in the starch and sucrose metabolism pathway and the lignin- and coumarine-biosynthesis-associated phenylpropanoid biosynthesis pathway, the candidates of sugar and biofuel production (Zheng et al. 2011). Using genomewide SNP map (971 sorghum accessions characterized at 265,000 SNPs by using genotyping-by-sequencing), Morris et al. (2012) quantified variation in nucleotide diversity, linkage disequilibrium, and recombination rates across the genome. This study provided evidence of selective sweeps around starch metabolism genes in landraces, whereas signature of introgressions around known height and maturity loci in landrace-derived introgression lines. Furthermore, genomewide association mapping reveals several

SNPs associated with total plant height (or height components, i.e., preflag height, which quantifies elongation in the lower portion of the stem, and flag-to-apex length, which quantifies elongation in the upper portion of the stem) and candidate genes for inflorescence architecture, and independent spread of multiple haplotypes carrying alleles for short stature or long inflorescence branches. Such genome-wide map of SNP variation clearly provides a basis for crop improvement through marker-assisted breeding and genomic selection in sorghum.

2.5.4 Diversity Panels to Mine Allelic Variations

A detailed analysis of genetic diversity involving a large collection of germplasm accessions of a given species provide researchers the opportunity to identify a set of trait-based genetically diverse accessions, recently named "diversity research panels" for varied uses in breeding and genomics. The core and mini core collections (Grenier et al. 2001; Upadhyaya et al. 2009c) have been reported which may be used as resources to form diversity panel in sorghum. Casa et al. (2008) were probably the first to develop sorghum diversity panel of 377 US accessions (149 breeding lines and their 228 progenitors), for association mapping, while Shehzad et al. (2009a) and Upadhyaya et al. (2009a) formed other diversity panel consisting of 107 and 242 genetically diverse accessions, respectively. These diversity panels showed significant differences among accessions for all of the traits. More recently, Billot et al. (2013) reported a genotype-based reference set (383 accessions) in sorghum, selected from GCGC consisting of 3,367 accessions that were genotyped using 41 SSRs, which represented the full spectrum of variability present in the GCGC (see Section 2.5.2). The diversity panels discussed here are the ideal resource for identifying new sources of variation, developing mapping populations and mining allelic variations, linkage disequilibrium analysis and association genetics to map markers associated with beneficial traits.

2.6 Outlook

Global warming is significantly impacting crops productivity, especially when more food is needed by a growing population. Sorghum is a C_4 plant and in comparison to other cereals, it is highly tolerant to drought. Sorghum has also been recognized as an emerging bioenergy crop. Nontraditional use of sorghum as a health food is likely to grow as awareness increases about the sorghum grains imparting health benefit to humans and livestock. Cultivated sorghum has a rich diversity of germplasm, housed in national and international genebanks, and categorized into five basic and 10 intermediate races. Germplasm with specific adaptation and resistance

to stresses are being used in breeding programs to develop cultivars and hybrids with wide adaptation. However, there will be an increased demand to new sources of variations associated not only with agronomic traits, including resistance to abiotic and biotic stresses, but also to discover novel traits to make sorghum grains as a source of functional food. Various subsets representing diversity in germplasm collection, housed *ex situ* in genebanks, have been developed in sorghum. There is increasing evidence that researchers are making use of these representative subsets of germplasm, core/mini core, reference set or diversity panels, for identifying new sources of variation for agronomic traits. Assessing population structure and diversity in germplasm collection assist germplasm curators and breeders for efficient conservation, management and utilization of germplasm in crop improvement programs. Today, abundant genetic (germplasm with unique traits) and genomic (SSRs, SNPs, high density genetic maps) resources, and many QTLs/candidate genes associated with agronomic traits are known in sorghum. More importantly, the sorghum genome has been sequenced (Paterson et al. 2009) and resequencing of select germplasm may guide researchers to identify a germplasm with unique allelic variants for use in crop breeding. For example, we now know that 1,442 genes differentiate sweet and grain sorghum, with some of these clearly involved in sucrose metabolism or lignin biosynthesis pathways or association mapping detected significant marker-trait association, with many of these markers, mapped on the same linkage group, previously reported as harboring QTLs for agronomic traits. Clearly, more such studies are needed to enhance the use of genetic and genomic resources in breeding to develop sorghum cultivars/hybrids that withstand adverse impact of climate change and variability and at the same time ensuring that the produce is more nutritious and healthy.

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