# PHENOTYPIC ASSESSMENT OF SORGHUM (Sorghum bicolor L. Moench) GERMPLASM REFERENCE SET FOR YIELD AND RELATED TRAITS UNDER POST FLOWERING DROUGHT CONDITIONS.

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# PHENOTYPIC ASSESSMENT OF SORGHUM (Sorghum bicolor L. Moench) GERMPLASM REFERENCE SET FOR YIELD AND RELATED TRAITS UNDER POST FLOWERING DROUGHT CONDITIONS.

Thesis submitted in part fulfillment of the requirements for the award of degree of DOCTOR OF PHILOSOPHY IN PLANT BREEDING AND GENETICS

to the Tamil Nadu Agricultural University, Coimbatore

By K.SEETHARAM, M.Sc., (Ag) (I.D. No. 08-810-006)

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2011

### CERTIFICATE

This is to certify that the thesis entitled "PHENOTYPIC ASSESSMENT OF SORGHUM (Sorghum bicolor L. Moench) GERMPLASM REFERENCE SET FOR YIELD AND RELATED TRAITS UNDER POST FLOWERING DROUGHT CONDITIONS." submitted in part fulfillment of the requirement for the degree of Doctor of Philosophy in Plant Breeding and Genetics to the Tamil Nadu Agricultural University, Coimbatore is a record of *bonafide* research work carried out by Mr. K. SEETHARAM, under my supervision and guidance and that no part of this thesis has been submitted for the award of any other degree, diploma, fellowship or other similar titles and that the work has not been published in part or full in any scientific or popular journal or magazine.

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## ABSTRACT

# PHENOTYPIC ASSESSMENT OF SORGHUM (*Sorghum bicolor* L. Moench) GERMPLASM REFERENCE SET FOR YIELD AND RELATED TRAITS UNDER POST FLOWERING DROUGHT CONDITIONS.

### BY

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#### 2011

Sorghum reference set collection consisting of 384 accessions of five basic races, 10 intermediate races and five wild sub species was evaluated during 2008-09 (E1), 2009-10 (E2) post rainy season at ICRISAT, Patancheru, Andhra Pradesh and during 2009-10 at UAS, Dharwad (E3- Irrigated condition and E4 – Un-irrigated condition) and RARS, Bijapur (E5- Un-irrigated condition). Data on seven qualitative and 11 quantitative traits were recorded to estimate the phenotypic diversity under post flowering drought conditions and to identify the drought tolerant accessions.

The qualitative traits, white mid rib, pigmented plant, black and purple color glume, one fourth glume covered, white, purple, and brown colored seeds occurred in

high frequencies in the sorghum reference set. These traits are useful markers since they are associated with economically important traits such as increased fodder quality, resistance to grain mould, preference in food and beverage industries.

Variance due to genotypes ( $\sigma^2 g$ ) and genotype X environment ( $\sigma^2 g e$ ) interactions were significant for all the 11 quantitative characters and variance due to genotype X drought interaction was significant for panicle exerstion, panicle length, panicle width The seven flowering groups differed significantly for days to 50 per and grain yield. cent flowering and plant height. The basic races and intermediate races as group differed significantly from the wilds for panicle weight, grain yield and 100 seed weight. Grain yield of entire reference set had significant positive correlation with panicle weight, 100 seed weight but had negative correlation with days to 50 per cent flowering, plant height and basal tillers in all the environments. Principal component analysis in entire reference showed that, nine characters in E1, E2 and its pooled and eight characters in E3, E4, E5 and its pooled were important in explaining the variation. Shannon-Weaver diversity (H') index was high for plant height, 100 seed weight, grain yield, panicle weight, SPAD1 and SPAD2 in entire reference set, in all the flowering groups, basic races, intermediate races and wilds. Average phenotypic diversity index was similar in all the environments. On the basis of phenotypic dissimilarity between pair of accessions, ten pairs of most diverse accessions under drought conditions were identified. These accessions could be used in breeding programs for selecting superior lines in segregating population and for the development of mapping population. The hierarchical cluster analysis grouped five basic races, ten intermediate races and five wild sub species into three clusters in E1, E2, E4 and pooled over E1 and E2, two clusters in E3, five clusters in E5 and four cluster in pooled over E3, E4 and E5.

Based on drought tolerance indices such as STI, MP, GMP, SSI, TOL and DTE a total of 65 drought tolerant accessions were indentified representing the entire reference set and seven flowering groups. Twenty nine accessions based on E1, E2 pooled and 22 accessions based on E3, E4 and E5 pooled were identified for high SCMR. Accessions identified based on drought tolerance indices and with high SCMR were predominantly from the race *caudatum* which was early flowering, had shortest plant height, high panicle weight and grain yield. In addition to this, best twenty accessions were identified

for each of the traits, days to 50 per cent flowering, plant height, panicle length, 100 seed weight, panicle weight and high grain yield. These diverse trait specific promising accessions have the potential for their utilization in breeding programs for developing improved sorghum cultivars with a broad genetic base. The information on phenotypic diversity and trait specific accessions provided valuable baseline knowledge for further progress on the selection and breeding for drought tolerance in sorghum.

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# CHAPTER-I INTRODUCTION

Over the past 12000 years, humans have sampled, selected, cultivated, travelled through and colonized new environments, thus inducing a plethora of bottlenecks, drifts and selection (Glemin *et al.*, 2009). Plant breeders have accelerated the whole process by selecting preferred genotypes (Ross-Ibarra *et al.*, 2007 and Gregory *et al.*, 2009). Meanwhile, evolution was progressing, some genomes were being reshuffled and genes occasionally mutated (Glemin *et al.*, 2009). Overall, plant domestication tailored plant development and adaptation to meet the needs of human populations (Gepts, 2004; Doebley, *et al.*, 2006 and Purugganan and Fuller, 2009). Innumerable varieties, races and cultivars of agricultural plants have been developed to support human and animal demand for food, fiber and building materials.

The Poaceae (rice, wheat, maize, pearl millet, sorghum etc.,) are an important global source of dietary protein, carbohydrates and other nutrients (Dillon, 2007). Sorghum [*Sorghum bicolor* (L.) Moench] is a tropical, C<sub>4</sub> plant belonging to the family Poaceae. Sorghum originated in the Northeast quadrant of Africa over 3000 years ago, and slowly dispersed into other parts of Africa eventually spreading into Asia and rest of the world (Harlan and Stemler, 1976; Mann *et al.*, 1983). High level of diversity was reported in sorghums from Ethiopia (Ayana and Bekele, 2000), the primary center of origin, and from India (Appa Rao *et al.*, 1996) and China (Li and Li, 1997).

The genus Sorghum has 25 recognized species that have been taxonomically classified into five subgenera or sections: *Eusorghum, Chaetosorghum, Heterosorghum, Parasorghum* and *Stiposorghum* (Garber, 1950). Section *Eusorghum* includes cultivated sorghum, *Sorghum bicolor* and its subspecies *drummondii* and *arundinaceum* and the wild species *S.almum* Parodi, *S. propinquum* (Kunth) Hitch. and *S. halepense* (L.) Pers. (de wet, 1978). Harlan and de Wet (1972) classified cultivated sorghum into 15 races. These include five primary races (bicolor, caudatum, durra, guinea, and kafir), and 10 intermediate races originating from possible combinations among the five primary races.

Sorghum ranks 5<sup>th</sup> in the world in terms of area (43.74 million ha) after wheat (225.43 million ha), rice (161.42 million ha), maize (159.53 million ha) and barely (54.12 million ha), and in production (62.10 million tons) after maize (817.11 million tons),

wheat (681.92 million tons), rice (678.69 million tons) and barely (150.27 million tons) (FAO, 2009; verified www.fao.org on January, 2011). In India it ranks 5<sup>th</sup> in area (7.7 million ha) after rice (44.1 million ha), wheat (28.4 million ha), pearl millet (10.5 million ha) and maize (8.4 million ha) and in production (7.24 million tons), after rice (131.27 million tons), wheat (80.68 million tons), maize (17.3 million tons) and pearl millet (8.59 million tons).

Sorghum grain is nutritionally superior to rice because of its high mineral and fiber content. Starch (60-75%) is the main component of sorghum grain, followed by proteins (7-15%), non-starch polysaccharides (2-7%) and fat (1.5-6.0%). The average energetic value of whole sorghum grain flour is 356 kcal/100g (Dicko *et al.*, 2006). Sorghum is a good source of vitamins, notably the B vitamins (thiamin, riboflavin, pyridoxine and niacin) and the liposoluble vitamins A, D, E and K. Sorghum is reported to be a good source of more than 20 minerals among which it is rich in phosphorus, potassium, magnesium, iron and zinc (Glew *et al.*, 1997; Anglani, 1998).

Sorghum is a predominant food crop of the world's poorest and most insecure people of semiarid tropical (SAT) regions of south Asia and Africa. These regions are characterized with high temperature, high evaporate demand, unreliable and irregular rainfall, soils of low fertility and soils of low water holding capacity, that make the production of other major cereals difficult (Rayan and Spencer, 2001 and Kassahun *et al*, 2009). Unique property of sorghum grain makes it well suited to prepare various food items such as porridge, unleavened bread, cookies, cakes, couscous and malted beverages, etc. It is also an important animal (swine, poultry and cattle) feed used in countries like U.S., Mexico, South America and Australia. More recently, sweet sorghum has emerged as a crop for production of ethanol (biofuel) in Brazil, India, which is becoming popular in many Asian countries (Rao *et al.*, 2004). So sorghum, as a food, feed and biofuel with excellent drought resistance compared to other cereals, is considered as a "failsafe crop" (Burke, 2010).

Sorghum is often planted in marginal environments with little inputs of water or fertilizers. Sorghum yields are affected adversely by various abiotic stresses that limit its yield potential (Burke *et al.*, 2010). Unlike in the other parts of the world, sorghum is

grown in both rainy and post rainy seasons in India. The rainy season sorghum grain is mostly used as poultry/animal feed because the grains are often infected with grain mold. The post rainy sorghum is grown mainly in peninsular India on residual moisture and produces high quality grain for human consumption and stover for animal feed. The post rainy sorghum production environment is characterized by increasing moisture stress as the season progresses. Frequent dry spell with varying intensities, periods and timing are cause for low productivity of sorghum in India during rainy and post rainy seasons (Patil, 2007). Though yield levels are relatively low, because of its relative drought tolerance, it is an excellent crop for dry regions and areas with uncertain and scanty rainfall (Chimmad and Kamatar, 2003).

Two distinct drought stress response have been identified in sorghum (Rosenow and Clark, 1981, Rosenow *et al.*, 1983): a pre-flowering drought response that occur prior to anthesis and a post-flowering drought response that is observed when water limitation occurs during the grain filling stage. Symptoms of pre-flowering drought stress susceptibility include leaf rolling, uncharacteristic leaf erectness, leaf bleaching, leaf tip and margin burn, delayed flowering, poor panicle exerstion, panicle blasting and floret abortion and reduced panicle size. Tolerance to pre-flowering drought stress is indicated by the alternative condition in each instance (Rosenow *et al.*, 1983).

Symptoms of post flowering drought stress susceptibility include pre mature plant (leaf and stem) death or plant senescence, stalk collapse and lodging, stalk rot (charcoal rot, *Macrophomina phaseolina*) and reduction in seed size. The best characterized form of drought tolerance during post flowering stage of crop growth is the so called non-senescence or "stay green" trait, which is the ability to resist premature plant senescence (retain green leaf area), resist lodging and fill grain normally. When water is limited during the grain filling period, sorghum genotypes possessing this trait maintain photosynthetically active leaf area better than genotypes that do not possess this trait (Rosenow *et al.*, 1983; McBee, 1983; Borrell *et al.*, 2000). Drought stress during the post flowering stage needs serious consideration because of its impact on yield and yield related traits (Subudhi, *et al.*, 2000).

The devastating effects of drought stress on crop can be overcome by exploiting genetic variation for drought tolerance in the available genetic resource (Sari-Gorla *et al.*,

1999). The primary sources of such genetic resources are landraces, weedy, and wild relatives of crop plants (Prasadrao *et al.*, 1989; Harlan, 1992). Identification of drought tolerant germplasm and genetic enhancement of sorghum for drought tolerant is a cost effective approach to further increase its productivity, stabilized production and contribute to food security in the SAT regions. This requires characterization and multilocation evaluation of available genetic resource, especially in the context of rapidly changing climate which will enhance the identification of new gene combination for drought tolerance and utilization of the available diversity in the sorghum improvement programme.

Sorghum genetic resources are conserved at many centers around the world. The major organizations/countries which maintain sorghum genetic resources are the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India, The National Plant Germplasm System (NPGS) in USA, Ethiopia, Sudan, South Africa, India and China. At present, ICRISAT is a major repository for world sorghum germplasm with a total of 37,943 accessions from 92 countries. The wealth of germplasm is accessible worldwide for use in crop improvement programme, but the collections are barely tapped by the breeders (less than 1%) (Upadhyaya et al., 2006a). Large holdings in genebanks and the non-availability of data on traits of economic importance restricted breeders and caused them to repeatedly use their own working collections in crop breeding (Upadhyaya et al., 2009). To facilitate the use of large collection, Frankel (1984) proposed sampling of the collection to a manageable sample or 'core collection'. A core collection contains a subset of accessions (10% of entire collection) from entire collection that captures most of available diversity of species (Brown, 1989). The germplasm collections held by most International Agricultural Research Centre (IARCs) gene banks are very large in size and hence the size of the core collection again restricts its proper evaluation and use by breeders. To overcome this, Upadhayaya and Oritz (2001) postulated the mini core collection concept (10% of accessions from core or 1% of accessions from entire collection). Following the above strategies, ICRISAT has developed sorghum core (3575 accessions, Prasadarao and Ramanatharao 1995; 2247 accessions, Grenier et al., 2001) and mini core collection (242 accessions; Upadhyaya *et al.*, 2009) capturing over 80% of variability in the entire collections.

Genome analysis tools provide access to thousands of polymorphism, thus considerably broadening our capacity to monitor genetic diversity (Glaszmann *et al.*, 2010). The molecular characterization provides information related to rare alleles from cultivated and wild accessions for allele mining (Upadhyaya *et al.*, 2010d). ICRISAT in collaboration with Generation Challenge Programme, CIRAD, France, and CAAS, China has developed the composite collections of sorghum, (3,367 accessions) from the world collection (33,100 accessions) and molecularly profiled using 41 SSR markers and a reference set of 384 accessions was developed, which represents 78 per cent (615 of the 789 alleles) of the SSR markers allelic diversity. This reference set could be used for extensive genotyping with additional SSR markers and for phenotyping for biotic and abiotic stress and for agronomic traits. The reduced size of germplasm collections (core, mini core and reference set) had provided ample opportunities to the breeders for their efficient and economic multi-environment evaluation.

In light of the above facts, the present investigation was carried out with following objectives:

- 1. Phenotypic assessment of sorghum reference set germplasm under post flowering drought condition.
- 2. To estimate the extent of variability, heritability and genetic advance for various traits associated with drought tolerance.
- 3. Identification of sources for post flowering drought tolerance and for yield traits.
- 4. To study the diversity in the reference set for various traits of economic importance.

#### **REVIEW OF LITERATURE**

Sorghum is a major staple food and fodder crop grown worldwide, with an annual average production of 64.72 million tones (FAOSTAT, 2009). Sorghum is known under a variety of names: great millet and guinea corn in West Africa, kafir corn in South Africa, durra in Sudan, mtama in eastern Africa, jowar in India and kaoliang in China. In the United States it is usually referred to as milo or milo-maize.

Sorghum crop is tolerant to many biotic and abiotic stresses and is often grown in more marginal cropping areas. In developing countries it tends to be a staple food and forage of the poor. In developed countries it is used primarily as an animal feed. Sorghum is often preferentially grown in irrigated and rain fed situations as it is better adapted to water limited environments than other cereal crops. Therefore, they are often referred to as "coarse grain" or "poor people's crops".

#### 2.1 Origin, evolution and distribution

The origin and culture of sorghum is not clear as other crops. The domestication of sorghum has its origins in Ethiopia and surrounding countries, commencing around 4000–3000BC. De wet *et al.* (1970) suggested that sorghum had diverse origin and probably arise from *Sorghum verticilliflorum*. *S. arundinaceum* is a grass of tropical forests and *S. aethiopucum* and *S. virgatum* are found in the desert regions. These habitats are outside the major sorghum areas and probably contributed less to its domestication. *S. verticilliflorum* has tremendous variation and usually found in the areas where sorghum is cultivated. Snowden (1936) and Porteres (1951) suggested that races *durra, guinea*, and *caffra* are closely allied and may have arisen from *S. aethiopicum*, *S. arundinaceum* and *S. veticilliflorum* respectively.

It is difficult to determine when and where domestication occurred (de Wet *et al.*, 1970). Anthropological evidence suggests that hunter-gatherers consumed sorghum as early as 8000BC (Smith and Frederiksen, 2000). Numerous varieties of sorghum were created through the practice of disruptive selection, whereby selection for more than one level of a particular character within a population occurs (Doggett, 1970). This results from a balance of farmer selection for cultivated traits and natural selection for wild

characteristics, generating both improved sorghum types, wild types and intermediate types. These improved sorghum types were spread *via* the movement of people and trade routes into other regions of Africa, India (approx. 1500–1000 BC), the Middle East (approx. 900–700 BC) and eventually into the Far East (approx. AD 400). Distribution suggests that *S. bicolor* was probably introduced into China from India about the third century A.D. The presence of durra types in Korea and adjacent Chinese provinces suggests that it may have been introduced there *via* silk routes from Asia Minor. Sorghum is relatively new to the Americas since it was first introduced into the United States in 1857 and was extensively used in the early 1990s for syrup (Doggett, 1965).

#### 2.2 Taxonomy

Initial domestication of sorghum would have focused primarily on converting wild types with small, shattering (dehiscent) seed to improved types with larger, nonshattering seed. Disruptive selection resulted in sorghum types with vastly different characteristics in height, inflorescence type and end use (food, fodder, fibre, building materials, etc).

In 1753 Linnaeus described three species of cultivated sorghum: *Holcus sorghum*, *Holcus saccaratus* and *Holcus tricolor* in the book, Species platarum. In 1794, Moench distinguished the genus *Sorghum* from the genus *Holcus* and in 1805 Person suggested the name *Sorghum vulgare* for *Holcus sorghum* (L.). In 1961 Clayton proposed the name *Sorghum bicolor* (L.) Moench as the correct name for cultivated sorghum and this is currently being used.

Over time, sorghum has been described and redescribed by numerous taxonomists and is now described under the family Poaceae, tribe Andropogoneae, subtribe Sorghinae and genus *Sorghum* Moench (Clayton and Renvoize, 1986).

The classification of sorghum by Snowden (1936) is detailed and complete. Other classifications proposed since those times have been modifications or adaptations of the Snowden system. Harlan and de Wet (1972) published a simplified classification of sorghum which has been checked against 10,000 head samples.

The genus *Sorghum* is separated into five taxonomic subgenera or sections: *Eu-Sorghum, Chaetosorghum, Heterosorghum, Para-Sorghum* and *Stiposorghum* (Garber, 1950). Section *Eu-Sorghum* contains all domesticated/cultivated sorghum races and varieties as *Sorghum bicolor* subsp. *bicolor* as well as the wild and weed species *S. halepense* (L.) Pers. (Johnsons grass), *S. propinquum* (Kunth) Hitchc, *S. almum* Parodi, *S. drummondii* (Steud.) Millsp. & Chase, and *S. arundinaceum* (Desv.) Stapf. (Harlan and de Wet, 1971; Doggett, 1988). All *S. bicolor* subsp. *bicolor* have 2n = 2x = 20 chromosomes, and are described as annual, with thick culms up to 5m in height, often branched with many tillers. They have been classified into five basic races: *bicolor, guinea, caudatum, kafir* and *durra, caudatum-bicolor, kafir-bicolor, durra-bicolor kafir-caudatum, durra-caudatum,* and *kafir-durra* (Harlan and de Wet, 1972). These 15 races of cultivated sorghum are recognizable based on spikelet/panicle morphology as described below

#### 2.2.1 Bicolor

Grain elongate, sometime slightly obovate, nearly symmetrical dorso-ventrally; glumes clasping the grain which may be completely covered or exposed as much as <sup>1</sup>/<sub>4</sub> of its length at the tip; spikelets persistent. This race is considered to be the most closely related to the wild sorghums of all the cultivated races.

#### 2.2.2 Guinea

The spikelets of the guineas are derived and specialized and there is nothing resembling them in the wild forms. Grain is flattened dorso-ventrally, sub-lenticular in outline, twisting at maturity 90 degrees between gaping involute glumes that are nearly as long to longer than the grain.

#### 2.2.3 Caudatum

Grain markedly asymmetrical, the side next to the lower glume flat or even somewhat concave, the opposite side rounded and bulging; the persistent style often at the tip of a beak pointing toward the lower glume; glumes  $\frac{1}{2}$  of the length of the grain or less. Agronomically, it is one of the most important race of all and the intermediate races involving it are also important.

### 2.2.4 Kafir

Grain approximately symmetrical, more or less spherical, not twisting, glumes clasping and variable in length

#### 2.2.5 Durra

Grain rounded obviate, wedge shaped at the base and broadest slightly above the middle; the glumes very wide, the tip of a different texture from the base and often with a transverse crease across the middle. Durra race are drought resistance or at least drought evading and can be grown in the driest regions where sorghum cultivaton is possible.

### 2.2.6 Intermediate races

The intermediate races will have the combination of two races. Races that are half guinea have grains that twist somewhat, but not as completely as in the true guinea. Races that are half caudatum have grains that are turtle-backed, but not as extreme as in the true caudatum. Races that are half durra have grains broadly rounded above, but less conspicuously obovate than pure durra and the transverse crease may or may not be present. Races that are half kafir are appropriately modified in the direction of kafir and the half bicolor races are modified in the direction of bicolor.

### 2.3 Nutritional quality and uses of sorghum

Sorghum grain is nutritionally superior to fine cereals like rice because of its high mineral and fiber content. Starch (60-75%) is the main component of sorghum grain, followed by proteins (7-15%), non-starch polysaccharides (2-7%) and fat (1.5-6%). Sorghum has a macromolecular composition similar to that of maize and wheat (BSTID-NRC, 1996). However, sorghum contains resistant starch, which impairs its digestibility, notably for infants (FAO, 1995). This resistance is desired in other applications to fight human obesity and to feed diabetic people (Awika and Rooney, 2004).

The non-starch polysaccharides (NSP) in sorghum grain are essentially constituted of arabinoxylans and other  $\beta$ -glucans representing 55 per cent and 40 per cent

of the total NSP. Arabinoxylans, being one of the major NSP present in sorghum cell walls, play an important role in the processing of sorghum for baking and brewing (Hatfield *et al.*, 1999).

The fat in sorghum grain is rich in polyunsaturated fatty acids (Glew *et al.*, 1997). The fatty acid composition of sorghum fat (linoleic acid 49%, oleic 31%, palmitic 14%, linolenic 2.7%, stearic 2.1%, etc.) is similar in content to that of corn fat but it is more unsaturated (FAO, 1995).

Sorghum proteins have been divided into albumins, globulins, kafirins (aqueous alcohol-soluble prolamins), cross-linked kafirins and glutelins. The nutritional quality of sorghum proteins is poor because these kafirins are protease resistant. The protein digestibility of sorghum may decrease upon cooking, but pre-fermentation may increase the digestibility. The low digestibility is due to protein-protein, protein-carbohydrate, protein-(poly) phenol and carbohydrate-(poly) phenol interactions (Taylor and Taylor, 2002).

The average energetic value of whole sorghum grain flour is 356 kcal/100g (Dicko *et al.*, 2006). Sorghum is a good source of vitamins, notably the B vitamins (thiamin, riboflavin, pyridoxine and niacin.), and the liposoluble vitamins A, D, E and K. Sorghum is reported to be a good source of more than 20 minerals among which it is rich in phosphorus, potassium, magnesium, iron and zinc (Glew *et al.*, 1997; Anglani, 1998).

In many parts of the world sorghum has traditionally been used in food products and various food items, porridge, unleavened bread, cookies, cakes, couscous and malted beverages are made from this versatile grain. Traditional food preparation of sorghum is quite varied. Boiled sorghum is one of the simplest uses and small, corneous grains are normally desired for this type of food product. The whole grain may be ground into flour or decorticated before grinding to produce either a fine particle product or flour, which is then used in various traditional foods. Sorghum has unique properties that make it well suited for food uses. Some sorghum varieties are rich in antioxidants and all sorghum varieties are gluten-free, an attractive alternative for wheat allergy sufferers.

Sorghum is also an important animal feed used in countries like the U.S., Mexico, South America and Australia. Good-quality sorghums are available with a nutritional feeding value that is equivalent to that of corn. Sorghum can be processed to further improve its feed value and techniques such as grinding, crushing, steaming, steam flaking, popping and extruding have all been used to enhance the grain for feeding. The products are then fed to beef and dairy cattle, laying hens and poultry, pigs, and in pet foods (http://www.grains.org/sorghum).

#### 2.4 Drought and its effect on sorghum grain yield

Drought is recognized as a condition where the water requirement of the plants, at different crop growth stages, exceeds the available water by more than 50 per cent in the root zone because of inadequate precipitations leading to reduction in crop growth and economic yield.

Sorghum is a predominant food and fodder crop grown in semi-arid tropical regions of South Asia and the Sahelian-sudanian zone of Africa that characterized by high temperature, high radiation, high evaporate demand, unreliable and irregular rainfall, soils of low fertility and low water holding capacity (Reddy, 2009). Sorghum is often planted in marginal environments with little input of water or fertilizers. Sorghum production is affected by range of abiotic yield constrains *viz.*, drought, temperature, and nutritional stress (Burke *et al.*, 2010). Among these, drought will likely be the primary yield constrain throughout the semi-arid tropics.

Unlike in the other parts of the world, sorghum is grown in both rainy and post rainy season in India. The post rainy sorghum is grown mainly in peninsular India following the rainy season, on residual moisture, in a unique production environment which is characterized by increasing moisture stress as the season progresses. Frequent dry spell with varying intensities, periods and timing are cause for low productivity of sorghum in India during rainy and post rainy seasons (Patil, 2007). Though yield levels are relatively low, because of its relative drought tolerance, it is an excellent crop for dry regions and areas with uncertain and scanty rainfall (Chimmad and Kamatar, 2003).

Two distinct drought stress response have been identified in sorghum (Rosenow and Clark, 1981, Rosenow *et al.*, 1983): a pre-flowering drought response that occur prior to anthesis and a post-flowering drought response that is observed when water limitation occurs during the grain filling stage. Symptoms of pre-flowering drought stress susceptibility include: leaf rolling; un-characteristics leaf erectness; leaf bleaching; leaf

top and margin burn; delayed flowering; poor panicle exsertion; panicle blasting, floret abortion and reduced panicle size.

Symptoms of post flowering drought susceptibility include premature plant (leaf and stem) death, stalk collapse and lodging, stalk rot and sometimes significant reduction in seed size, particularly at the base of the panicle.

Pre- or post-flowering drought can have dramatic effects on the agronomics of crop production. Water deficits tend to shift the source-sink relation out of balance in one or other way. Lee and Tollenaar, (2007) reported that the excess source capacity leads to purpling of leaf, sheath and stalk tissue during grain filling stage. Drought can also reduces the leaf area development, leaf size and leaf dry matter accumulation, lowering resource capture and leading to lower canopy photosynthesis.

In sorghum water stress during floral induction and inflorescence development will lead to a delay in flowering or even complete inhibition (Winkel *et al.*, 1997 and Wopereis *et al.*, 1996). Under pre flowering drought stress panicle initiation will be delayed by 2-25 days and flowering can be delayed up to 59 days.

Stress during flowering and anthesis leads to failure of fertilization because of impairment of pollen and ovule function. Drought can inhibit pollen development and cause sterility, reduced seed number and reduced grain filling duration there by reducing seed weight (Prasad *et al.*, 2008).

Prasad *et al.* (2008) reported that drought occurring after flowering had little effect on seed filling rate, but shorten seed filling duration, leading to smaller seed size and less yield. Seed size is largely dependent on photosynthesis reserves that can be mobilized in the plant. Drought events during the grain filling stage can cause major reduction in yield by reducing starch accumulation as result of limited assimilate partitioning to the developing grain (Blum, 1998) or by direct effects on process of grain growth (Yang *et al.*, 2004). Water stress during grain filling period reduces photosynthesis, induces early senescence and shortens the grain filling period, which is more affected by water stress than grain filling rate (Altenbach *et al.*, 2003 and Borras *et al.*, 2003). Grain filling is closely related to senescence and utilization of stem reserves (Barnabas *et al.*, 2008). Van Herwaarden *et al.* (1998) reported that under stress, stem reserves mobilization can account for as much as 75-100 per cent of grain yield.

#### 2.4.1 Post flowering drought tolerance in sorghum

Drought tolerance is the stability of crop yield under a specific target drought stress environment, resulting from the operation of drought tolerance mechanism.

The mechanisms of drought tolerance can be described as escape, avoidance tolerance (Levitt, 1972; Blum, 1979; Ludlow, 1993). Early maturity is a well known drought escape mechanism through which the crop completes its life cycle before the onset of sever moisture deficit and often associated with the reduced yield potential. Avoidance is ability of the plant to maintain a relatively higher level of hydration *i.e.*, maintenance of higher turgor or leaf water potential under conditions of soil or atmospheric moisture stress. Ability of the genotype to yield reasonably high in specified drought stress environment is considered as drought tolerance.

Sorghum, being a  $C_4$  plant better adapted to the stress environment especially soil moisture stress than maize. As such sorghum is the logical crop to support the poor of the world, 25 per cent of whom are expected to experience the sever water scarcity by 2025 (Ryan and Spener, 2001).

Although drought stress can occur any time during the crop cycle, post flowering drought is more damaging to the productivity of the crop than stress at the vegetative or pre-flowering stages (Mahalakshmi and Bidinger *et al.*, 1985). Several physiological traits viz., heat tolerance, desiccation tolerance, osmotic adjustment, rooting depth and epicuticular wax are available for drought tolerant breeding. Though technologies exist for evaluating these traits, little use has been made of them in breeding programme. The best characterized form of drought tolerance during the post-flowering crop growth referred to as non-senescence or "stay green" trait.

Thomas and smart (1993), reported four distinct stay green types (Type A, B, C, D). In type 'A' stay greens senescence is initiated late but then proceeds at normal rate. Type 'B' stay greens initiate senescence on schedule, but thereafter senesce comparatively slowly. Type C stay greens retain green leaf area almost indefinitely, but measures of physiological function such as photosynthetic capacity show that senescence is proceeding normally beneath the cosmetic surface of retained pigmentation. Type D stay green are acquired by artificial means such as boiling, drying or freezing in order to maintain green leaf color. Type A and B are functionally stay green and they may arise after alteration of genes involved, respectively in the timing of the initiation of senescence and the regulation of its rate of progress. Since these stay green types continue to photosynthesis for longer than normal, they are expected to show a higher yield in crops for which carbohydrate is a major component of harvest. The stay green trait in sorghum is genetically and physiologically complex, both in expression and function, and classified as mixture of both Type A and type B. Genotype possessing the stay green trait maintains a greater leaf area during grain filling and extends photosynthesis in upper canopy leaves after physiological grain maturity under post-flowering drought compared to their senescent counterparts (Rosenow *et al.*, 1977). The stay green sorghum accumulate more soluble sugars in stems than do senescent counterparts, both during and after grain filling (Duncan *et al.*, 1981; McBee *et al.*, 1983).

The stay green trait has been used to improve lodging resistance under terminal drought with a positive association of stay green and grain yield under water limited environments (Henzell *et al.*, 1992; Henezell and Hare, 1996). Douglas (1996) have shown that sorghum hybrids with stay green trait have a significant yield advantage when water is limited during the grain fill period, with rate of leaf senescence negatively correlated (r=0.55) with grain dry mass.

Delayed leaf senescence (stay green) in sorghum had been associated with improved grain yield, particularly in environments with inadequate available water during grain filling to support potential transpiration (Borell *et al.*, 2000). Borell and Hammer (2000) reported a strong association between leaf nitrogen content at anthesis and grain yield under stress and that this strong association could be used to screen genotypes for drought tolerance.

The amount of yield reduction depends not only on the timing of stress, but also on the severity of the stress. In a study by Mahalakshmi and Bidingar (2002) a set of 72 non-senescent (stay green) sorghum genotypes was evaluated for post flowering leaf senescence to identify superior sources of stay green. The heritability estimates of the per cent Green Leaf Area (GLA) were high and similar to heritability of days to flowering and GLA at flowering. There was a negative relationship between per cent GLA at 45 DAF and grain yield. This reduced leaf senescence rate ultimately resulted in higher percent GLA at maturity in the late flowering genotypes, despite the fact that senescence began at an early development with different time of flowering under severe stress must be done with care.

Genetic analysis of stay green in sorghum by Tunistra *et al.* (1997) indicated that stay green was controlled by a single dominant factor with some epistatic interactions. The work of different groups has led to a better understanding of the inheritance of stay green to the mapping of QTLs associated with the post flowering drought tolerance in sorghum (Tunistra *et al.*, 1998; Crasta *et al.*, 1999; Tao *et al.*, 2000; Xu *et al.*, 2000; Subudhi *et al* 2000; Kebede *et al.*, 2001; Sanchez *et al.*, 2002 and Haussmann *et al.*, 2002) and identification of markers linked to these QTLs (Harris *et al.*, 2007).

Reddy *et al.* (2007) reported significant genotypic difference for agronomic and stay green traits among 146 sorghum germplasm accessions. Significant year to year differences were observed for stay green score, time to 50 per cent flowering, plant height and plant agronomic score. Genotypes x year interactions were also highly significant for all the traits except plant height. Correlation coefficients revealed that the genotypes with early flowering produced more grain yield (significantly negative correlation). The stay green trait was not associated significantly with any other observed agronomic trait.

Visual ratings of the stay green trait are useful to breeders, they are quick and easy to perform and less expensive than quantitative measurements of stay green. Ratings of visual leaf score for stay green have been used to select drought tolerant sorghum lines (Xu *et al.*, 2000). However personal biases and differences in ratings among scientists can serve as limitations (Borrell *et al.*, 2000). In the last decade, use of hand held chlorophyll meters (SPAD) has increased dramatically. Chlorophyll meters are relatively inexpensive and can acquire readings in rapid succession without damaging the plant. Readings are logged by exploiting the optical properties of leaves based on the reflectance and absorbance of radiation by chlorophyll. Recent studies in wheat and maize have shown that chlorophyll content readings under heat stress are closely correlated with chlorophyll a fluorescence (Ristic *et al.*, 2008). Talwar *et al.* (2009) examined relationship of chlorophyll concentration by using SPAD chlorophyll meter reading (SCMR) with yield components in sorghum lines grown under irrigated and un-irrigated water regimes imposed during post flowering growth period. The SPAD chlorophyll meter reading was significantly related with plant height, total dry matter, panicle weight and grain yield but no relation was observed with days to flowering. Under un-irrigated condition there was reduction on SCMR, total dry matter, panicle weight and grain yield. The drought sensitivity was calculated as sum change in total dry matter, panicle dry weight and grain yield under non-irrigated water regimes over the irrigated water regime during post flowering growth. The strong association between drought sensitivity index and percent change in SCMR indicated that the selection based on SCMR will have 42-67 per cent probability to select the genotypes with higher total dry matter and grain yield respectively.

Bruke *et al.* (2010) reported a novel method of stay green assay. Based on this assay stay green trait could be indentified in the well watered sorghum line. In this assay the yield of quantum efficiency (Fv/Fm) was determined at the start of experiment and after the samples were challenged for 30 min in 40°C followed by a recovery at 25°C. In their study there was clear separation between senescent line (low Fv/Fm) and stay green line (high Fv/Fm) at the boot stage. The ability of this assay to detect these differences in well watered sorghum removes a major road block in breeding for the stay green trait.

Breeding for resistance to drought without losing the yield potential is complicated by the lack of fast, reproducible screening techniques and the inability to routinely create defined and repeatable water stress conditions where large populations can be evaluated efficiently (Ramirez and Kelly, 1998). Loss of yield is the main concern of plant breeders and they hence emphasize on yield performance under moisture stress conditions. But variation in yield potential could arise from factors related to adaptation rather than to drought tolerance *per se*. Thus, drought indices which provide a measure of drought based on loss of yield under drought-conditions in comparison to normal conditions have been used for screening drought-tolerant genotypes (Mitra, 2001). These indices are either based on drought resistance or susceptibility of genotypes (Fernandez, 1992).

Drought resistance is defined by Hall (1993) as the relative yield of a genotype compared to other genotypes subjected to the same drought stress. Drought susceptibility of

a genotype is often measured as a function of the reduction in yield under drought stress (Blum, 1988) whilst the values are confounded with differential yield potential of genotypes (Ramirez and Kelly, 1998). Rosielle and Hamblin (1981) defined stress tolerance (TOL) as the differences in yield between the stress (Ys) and non-stress (Yp) environments and mean productivity (MP) as the average yield of Ys and Yp. Fischer and Maurer (1978) proposed a stress susceptibility index (SSI) of the cultivar. Fernandez (1992) defined a new advanced index (STI= stress tolerance index), which can be used to identify genotypes that produce high yield under both stress and non-stress conditions. Other yield based estimates of drought resistance are geometric mean (GM), mean productivity (MP) and TOL. The geometric mean is often used by breeders interested in relative performance since drought stress can vary in severity in field environment over years (Ramirez and Kelly, 1998).

The optimal selection criterion should distinguish genotypes express uniform superiority in both stress and non-stress environments from the genotypes that are favorable only in one environment. Among the stress tolerance indicators, a larger value of TOL and SSI represent relatively more sensitivity to stress, thus a smaller value of TOL and SSI are favored. Selection based on these two criteria favors genotypes with low yield potential under non-stress conditions and high yield under stress conditions. On the other hand, selection based on STI and GMP will be resulted in genotypes with higher stress tolerance and yield potential will be selected (Fernandez, 1992).

Superior genetic resources with improved tolerance to post flowering drought and with good yield potential under stress and non stress conditions are required to reduce the yield loss due to water deficit. The primary sources of genes for the various biotic and abiotic stresses are present in landraces, weedy, and wild relatives of crop plants (Prasadrao *et al.*, 1989; Harlan, 1992). Utilization of these sources for the crop improvement is inevitable.

#### 2.5 Germplasm utilization

Germplasm is the total gene pool of a species consisting of land races, advanced breeding lines, popular cultivars and weedy relatives. These are the most valuable, essential and basic raw material for crop improvement programmes to meet the demand of increasing population (Upadhyaya *et al*, 2010d). Vavilo (1926) was the first to realize

the essential need for a broader genetic base for crop improvement and organized extensive germplasm collections of various crops from their centre of origin and distribution for conservation.

In the wake of new agricultural development in the early 1970s the loss of traditional cultivars and land races seemed to be the most urgent problem. In addition, change in dietary habits, natural calamities, land and crop conversion, introduction of exotic crops; environmental pollution etc., have further aggravated the situation (Upadhyaya *et al.*, 2010d). The vulnerability of genetically uniform modern varieties, which are planted to large areas, to new pests, diseases, climatic conditions and changes in the market needs is widely acknowledged. The diverse land races, exotics and wild relatives hold a wealth of genes/alleles, which, if included on breeding programmes can help to raise the yield ceilings as well as enhance stress resistance level of agronomically superior cultivar.

To address this, network of international centers was executed from early 1980s to enhance the collection, conservation, evaluation and documentation of the crop genetic resources (Plucknett *et al.*, 1987). According to the World Information and Early Warning System (WIEWS) on Plant Genetic Resources for Food and Agriculture (PGRFA) (http://apps3.fao.org/wiews/wiews.jsp), more than 5,000,000 accessions of germplasm resources are held in world collections.

Over 7.4 million *ex-situ* germplasm accessions are conserved in ~1750 gene banks globally of which ~11% are in the gene bank of CGIAR institutions. ICRISAT has one of the largest collections bank in the CGIAR system, holding 119,739 accessions of its mandate crops from 144 countries. A large number of germplasm lines are distributed by the gene bank for use in crop improvement programme, but crop improvement scientists are using a very small proportion of these large germplasm collections. Low use of germplasm has been reported in ground nut (Upadhyaya *et al.*, 2010d), chickpea (Upadhyaya *et al.*, 2006b), legumes (Kumar *et al.*, 2004), maize (Cantrell *et al.*, 1996), spring barely (Vellve, 1992) and wheat (Dalrymple, 1986). Large holdings in genebanks and the non-availability of data on traits of economic importance restricted breeders and caused them to repeatedly use their own working collections in crop breeding (Upadhyaya *et al.*, 2009). The extent of variation in the large resources and their
accessibility to biologist and breeders are essential factors affecting their utilization (Zhang *et al.*, 2011). Selecting a few lines from the vast pools of germplasm is like searching for a needle in a haystack. Core collection ( $\sim$ 10% of entire collection), representing over 70 per cent of the genetic variation present in the entire collection with 95 per cent certainty (Brown, 1989), has been suggested as a gate way to enhanced utilization of diverse germplasm in crop breeding programs.

Core collections based on phenotypic characterization data have been developed for crops such as pearl millet (Bhattacharjee *et al.*, 2007), Sorghum (Rao and Rao, 1995; Grenier *et al.*, 2001), quinoa (Ortiz *et al.*, 1998), finger miller (Upadhyaya *et al.*, 2006d), foxtail millet (Upadhyaya et al., 2008) Caribbean maize (Taba *et al.*, 1998) and USDA rice (Yan *et al.*, 2007). Establishment of core collections had proven to be a favored approach to facilitate efficient exploration of novel variation from genetic resources (Ellis *et al.*, 1998; Holbrook *et al.*, 2000; Malvar *et al.*, 2004).

The germplasm collections held by most International Agricultural Research Centre (IARCs) gene banks are very large in size and hence the size of the core collection again restricts its proper evaluation and use by breeders. To overcome this, Upadhayaya and Oritz (2001) postulated the mini core collection concept (10% of accessions from core). Following this strategy mini core collections have been developed in chickpea (Upadhyaya and Ortiz, 2001), groundnut (Upadhyaya *et al.*, 2002), pigeonpea (Upadhyaya *et al.*, 2006c), sorghum (Upadhyaya *et al.*, 2009), pearl millet (Upadhyaya *et al.*, 2010a), finger millet (Upadhyaya *et al.*, 2010e) and foxtail millet (Upadhyaya *et al.*, 2010b). The reduced size of mini core collections had provided ample opportunities to the breeders for their efficient and economic multi-environment evaluation, which has lead to the identification of several new sources of variation for different traits for utilization in crop improvement programs.

An extensive characterization of plant genetic resources provides an opportunity for structural dissection to mine the allelic variations, and identify diverse accessions for crop improvement. These mini core collections were used for molecular characterization to analyze genetic diversity at DNA level and to select distinct parents with maximizing diversity. The molecular characterization provides information related to rare alleles from cultivated and wild species accessions which could be used to select specific accessions for allele mining. ICRISAT in collaboration with generation challenge program (GCP) and partners such as ICARDA, Syria; CIRAD, France; EMBRAPA, Brazil and CAAS, China has developed the composite collections of sorghum, pearl millet, chickpea, pigeonpea, groundnut, finger millet and foxtail millet.

In sorghum, Rao and Rao (1995) were first to develop core collection of 3475 accessions. Subsequently, Grenier *et al* (2001) used three sampling procedures constant, logarithmic and proportional to establish three subsets of the core collection each possessing 2247 accessions. A mini core sub set (242 accessions) in sorghum is established by Upadhyaya *et al.* (2009) after evaluating the core sub set (2247) for 11 qualitative and 10 quantitative traits. Composite collection (3,367 accessions) from the world collection (33,100 accessions) was developed, molecularly profiled and a reference set (384 accessions) was proposed, which represents 78 per cent (615 of the 789 alleles) of the SSR markers allelic diversity.

The value of germplasm is realized only when characterized for morphoagronomic traits to unearth new gene combination for use in crop improvement programs (Upadhyaya *et al.*, 2010c). The identification of such germplasm requires characterization and evaluation, especially in the context of rapidly changing climate, which will enhance the utilization of the available diversity in the sorghum improvement programme. The genetic variation in crop plants has been narrowed during domestication due to continuous selection pressure for particular traits like high yield or disease resistance. It is therefore important to study the genetic composition of the germplasm of existing cultivars with their ancestors and related species for comparison. Such studies help to find new and useful genes, and also provide information about the phylogenetic relationship. Maintenance and exploitation of germplasm and understanding the genetic relationships among the genotypes is also possible with such analysis.

# 2.6 Phenotypic diversity studies

Genetic improvement mainly depends upon the amount of genetic variability present in the population. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for breeding programme. The utility of multivariate analysis for measuring the degree of divergence between biological populations and for assessing the relative contribution of different characters to the total divergence has been established by several workers. Hence, estimation of the genetic diversity among genotypes is of immense importance for planning the future hybridization programme.

Upadhyaya *et al.* (2010c) assessed the phenotypic diversity and agronomic performance of 667 newly acquired sorghum germplasm accessions, representing five basic races, eight intermediate races and two wild species, originating from 34 countries. They were evaluated for seven qualitative and eight quantitative traits. Large variability was observed among the accessions. Trait specific accessions for early flowering, short plant height, medium panicle exerstion and medium sized seeds have be identified. The hierarchical cluster analysis grouped five races, six intermediate race and two wild species into three clusters. The races *bicolor* and *guinea* and intermediate races *durra-bicolor* grouped together in cluster I. The wild species grouped in cluster II. The three basic races: *Caudatum, kafir* and *durra* and four intermediate races: *Dura-caudatum, caudatum-bicolor, kafir-bicolor* and *guinea-caudatum* grouped together in the cluster III.

An experiment was conducted by Punitha *et al.*, (2010) to assess the pattern of morphological variations through metroglyph technique in 63 local land races of sorghum collected from different parts of Tamil Nadu. Genetic variability was calculated for grain yield/plant, fodder yield/plant, grain size, 1000 grain weight and ear head compactness. All the accessions were grouped into eight distinct groups. Group II was the largest comprising 25 accessions followed by group V having 13 accessions with moderate yield and fodder yield. Group VI and Group VII had 3 accessions in each group, they have high and medium yield respectively. The germplasm lines of group III, VI, VII and V could be utilized in future breeding programme for achieving higher grain yield and fodder yield.

Mini core (10% of the core or 1% of entire) collection of sorghum was developed from the existing core collection by Upadhyaya *et al.*, (2009). The sorghum core collection was evaluated for 11 qualitative and 10 quantitative traits in augmented design using three controls in the 2004-2005 post rainy season. The hierarchical clustering of data using phenotypic distance resulted in 21 clusters. Number of accessions in each cluster ranged from 27 to 279. The Shannon weaver diversity index (H') for the mini core collection was  $0.460\pm0.085$  for qualitative and  $0.587\pm0.018$  for quantitative traits, which is comparable with H' of core collection ( $0.453\pm0.085$  for qualitative traits and  $0.596\pm0.016$  for quantitative traits).

Sorghum land races from two districts of Zimbabwe were studied to ascertain the genetic relationship among germplasm from different areas (Mujaju and Chakauya, 2008). Forty seven landraces from Nyanga North and Tsholalsho were assessed using 24 agro-morphological characters. Genetic similarities were calculated and genetic relationship between accessions was analyzed by PCA and cluster analysis. The land races were grouped into six clusters according to the geographical location of collection, suggesting environmental adaptation. This leads to the suggestion that varieties and the processes associated with variety development are essentially consequences of adaptation of population to their agro-ecological conditions aided by utility value to the farmer. The study suggest that optimization of on farm conservation strategy for this germplasm should primarily focus on high diversity areas and perhaps recognize those traits envisaged to be of importance by farmer for varietal identification.

Geleta *et al.* (2006), estimated genetic diversity among 45 sorghum germplasm accessions. AFLP, SSR and morphological character were used to estimate the genetic diversity, since comparison of the different methods of the estimation of genetic diversity is important to evaluate their utility as a tool in germplasm conservation and plant breeding. The average pair wise genetic distance estimates were 0.57 (morphological trait), 0.62 (AFLPs) and 0.60 (SSRs). The Shannon-Weaver diversity index was higher for morphological traits (0.678) than AFLPs (0.487) and SSR (0.539). Clustering based on morphological data analysis produced three major clusters and among which the cluster III had the largest number of accessions from different locations. Dendrogram resulting from the cluster analysis of morphological, AFLPs, SSRs and combined data revealed that except morphological traits that failed to distinguish between two accessions, all the other dendrogram clearly discriminated the 45 sorghum accessions. The PCA plots obtained with the three data sets also showed clustering similar to that of the dendrogram.

The genetic and agro-morphological variability of 45 sorghum germplasm were analyzed using 16 SSR markers and evaluated under natural drought condition in three environments. Significant differences were detected among the genotypes for all traits measured under stress condition, which included: days to flowering, plant height, grain yield/plant, growth rate, biomass, 1000 grain weight and harvest index. The dendrogram generated from the UPGMA cluster analysis shows two main clusters differentiated in nine significant sub-clusters. The results suggest that the dendrogram based on the estimated genetic similarity reflects pedigree and varietal relationships. The overall mean genetic diversity in this study was 0.67. All the high yielding genotypes were more or less clustered together in the first main cluster across two sub-groups, while the early genotypes were clustered together in the second main cluster (Assar *et al.*, 2004).

In a study by Mahalakshmi and Bidinger (2002) a set of 72 non-senescent (stay green) sorghum genotypes was evaluated for post flowering leaf senescence to identify superior sources of stay green. The classification of genotype was done based on the type and level of expression of stay green across the two years. Clustering was done based on per cent GLA at 15, 30 and 45 days after flowering in each of the years. The clustering procedure was truncated and five groups retained 74 per cent of the original variation in these traits. Cluster I and II represented the stay green genotype types, whereas cluster IV and V contained the most senescent genotypes.

#### 2.7 Genetics of yield and its components

New genotypes are often collected and evaluated for economically important characters in order to identify genetic stock with desirable genes for use in crop improvement. In addition to inter relationship between characters, path analysis of yield and yield component characters and genetic divergence were also studied. The quality and quantity of yield is influenced by characters under genetic control and environmental conditions. The genetic facts are inferred from phenotypic observations, which are the results of interactions of genotype and the environment. The important findings relevant to the present study are reviewed under the following headings:

- 2.7.1 Variability, heritability and genetic advance
- 2.7.2 Correlation studies

# 2.7.1 Variability, heritability and genetic advance

Traits	PCV (%)	GCV (%)	$H^2$	GA	AUTHORS'
Days to 50 per cent flowering	High	High	High	-	Bello <i>et al.</i> , 2007; Aba <i>et al.</i> , 2001; Totok, 1997; William <i>et al.</i> , 1987; Basu, 1981 and Eckebil <i>et al.</i> , 1977.
	Medium	Medium	High	High	Vedansh <i>et al.</i> , 2010; Sandeep <i>et al.</i> , 2009; Singh <i>et al.</i> , 2006; Singh <i>et al.</i> , 2005; Rajguru <i>et al.</i> , 2005; Kishore and singh, 2005. Chaudhary <i>et al.</i> , 2001; Raut <i>et al.</i> , 1994; Potdukhe <i>et al.</i> , 1993.
	Low	Low	High	Medium	Chavan <i>et al.</i> , 2010; Godbharle <i>et al.</i> , 2010; Kjein and Rosenow, 1984; Mallinath <i>et al.</i> , 2004; Sindhe <i>et al.</i> , 1979 and Prabhakar, 2003.
	High	High	High	-	Bello <i>et al.</i> , 2007; Godbharle <i>et al.</i> , 2010; Sharma <i>et al.</i> , 2006 and Nimbalkar <i>et al.</i> , 1988.
Plant Height	Medium	Medium	High	High	Vedansh <i>et al.</i> , 2010; Godbharle <i>et al.</i> , 2010; Sandeep <i>et al.</i> , 2009; Singh <i>et al.</i> , 2006; Singh <i>et al.</i> , 2005; Rajguru <i>et al.</i> , 2005; Umakanth <i>et al.</i> , 2004; Aba, 2001; Totok, 1997; Sankarapandian <i>et al.</i> , 1986; William <i>et al.</i> , 1986; Basu, 1981 and Eckebil <i>et al.</i> , 1977.

Traits	PCV (%)	GCV (%)	H <sup>2</sup>	GA	AUTHORS'
Panicle Length	High	High	High	-	Bello <i>et al.</i> , 2007; Aba, 2001; Totok, 1997; William <i>et al.</i> , 1987; Basu, 1981 and Eckebil <i>et al.</i> , 1977.
	Medium	Medium	High	High	Godbharle <i>et al.</i> , 2010; Sandeep <i>et al.</i> , 2009; Sharma <i>et al.</i> , 2006; Chaudhary <i>et al.</i> , 2001; Sankarapandian <i>et al</i> 1996 and Nimbalkar <i>et al.</i> , 1988
Panicle width	Medium	Medium	High	Low	Chavan <i>et al.</i> , 2010; Vedansh <i>et al.</i> , 2010; Singh <i>et al.</i> , 2006; Singh <i>et al.</i> , 2005.
	High	High	High	Low	Chavan <i>et al.</i> , 2010; Tiwari <i>et al.</i> , 2003; Bapat and Shinde, 1980.
Panicle weight	High	High	Medium	-	Bello <i>et al.</i> , 2007; Aba, 2001; Totok, 1997; William <i>et al.</i> , 1987; Basu, 1981 and Eckebil <i>et al.</i> , 1977.
	Medium	Medium	High	High	Sandeep <i>et al.</i> , 2009; Rajguru <i>et al.</i> , 2005
	Medium	Medium	High	Medium	Godbharle <i>et al.</i> , 2010; Nimbalkar <i>et al.</i> , 1988; Sharma <i>et al.</i> , 2006.
	High	High	High	High	Sandeep <i>et al.</i> , 2009; Chaudhary <i>et al.</i> , 2001; Sankarapandian <i>et al</i> 1996; Cheralu and Rao, 1989; Kumar and Singh, 1986.

Traits	PCV (%)	GCV (%)	H <sup>2</sup>	GA	AUTHORS'
Panicle exerstion	Medium	Medium	High	High	Sandeep <i>et al.</i> , 2009; Umakantha <i>et al.</i> , 2004; Cheralu and Rao, 1989; Kumar and Singh, 1986.
Test weight	High	High	Low	-	Bello <i>et al.</i> , 2007; Bello <i>et al.</i> , 2001 and William <i>et al.</i> , 1987.
Grain Yield	High	High	High	High	Chavan et al 2010; Sandeep et al., 2009; Sharma et al., 2006; Tiwari et al., 2003; Chaudhary et al., 2001; Sankarapandian et al 1996; Kumar and singh, 1986.

# **2.7.2 Correlation studies**

Yield is the end product of many complex component characters, which singly or jointly influence the yield. Yield does not possess gene for *per se* as such. It is the interaction of phenotype for mutual adjustment and manifestation of its component characters. Therefore, selection of genotype based on yield alone is likely to be ineffective. The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its components (Breese and Hayward, 1972).

The studies on association of various yield components with grain yield in sorghum are reviewed here under:-

Troit	Correlat	tion with yield	Anthons?
Iran	Direction	Significance	Authors
Days to 50 per cent flowering	Positive	Significant	Elangovan <i>et al.</i> , 2007; Jadhav <i>et al.</i> , 1994; Veerabadhiran <i>et al.</i> , 1994; Patel <i>et al.</i> ,1980; Crook and Casady, 1974; Sindagi <i>et al.</i> , 1970; Liang <i>et al.</i> , 1969.

T <b>:</b> 4	Correla	tion with yield	
Irait	Direction	Significance	Autnors
	Negative	Significant	Upadhyaya <i>et al.</i> , 2009; Ezeaku <i>et al.</i> , 2006; Muppidathi <i>et al.</i> , 1999; Rao, 1981; Gupta and Dhilon, 1974; Gupta <i>et al.</i> , 1968.
		Non-significant	Prakash <i>et al.</i> , 2010; Godbharle <i>et al.</i> , 2010; Moyer <i>et al.</i> , 2003; Sanderson <i>et al.</i> , 1993; Nimbalkar <i>et al.</i> , 1988.
Plant height	Positive	Significant	Prakash <i>et al.</i> , 2010; Elangovan <i>et al.</i> , 2007; Desai <i>et al.</i> , 1999; Setimala <i>et al.</i> , 1998; Taurchi and Rezai, 1997; Patil <i>et al.</i> , 1995; Patdukhe <i>et al.</i> , 1994; Nimbalkar <i>et al.</i> , 1988; Thombre and Patil, 1985;
	Positive	Non-significant	Bucheyeki <i>et al.</i> , 2009; Setimela <i>et al.</i> , 1998; Yang and Yang, 1995; Bakheit, 1990.
	Negative	Non-significant	Patel <i>et al.</i> , 1980; Crook and Casady, 1974; Pokle <i>et al.</i> , 1973.
Panicle Length	Positive	Significant	Elangovan <i>et al.</i> , 2007; Tiwari <i>et al.</i> , 2003; Iyanar <i>et al.</i> , 2001; Jeyaprakash <i>et al.</i> , 1997; Taurchi and Rezai, 1997; Patil <i>et al.</i> , 1995.
	Positive	Non-significant	Godbharle et al., 2010; Bucheyeki et al., 2009.
Daniala width	Positive	Significant	Elangovan <i>et al.</i> , 2007;
Panicle width	Positive	Non-significant	Godbharle et al., 2010
Panicle weight	Positive	Significant	Bucheyeki <i>et al.</i> , 2009; Veerbadhiran <i>et al.</i> , 1994; Iyanar <i>et al.</i> , 2001; Jeyaprakash <i>et al.</i> , 1997; Pawar and Jadhav, 1995; Potdukhe <i>et al.</i> , 1994; Geremew and Gebeyhu, 1993.

Trait	Correlation with yield		A	
ารสน	Direction	Significance	Authors	
	Positive	Non-significant	Yang and Yang, 1995; Mannujan <i>et al.</i> , 1991	
100 seed weight	Positive Positive	Significant Non-significant	Warkad <i>et al.</i> , 2010; Elangovan <i>et al.</i> , 2007; Mahammad, 2000; Taurchi and Rezai, 1997; Godbharle <i>et al.</i> , 2010; Bucheyeki <i>et al.</i> , 2009; Bakheit, 1990; Giriraj and Goud, 1983	
Basal tillers	Positive Negative	Significant Non-significant	Prakash <i>et al.</i> , 2010 Bucheyeki <i>et al</i> ., 2009	

Reviews on inter-relationship between characters other than grain yield are presented below

Traits	Associated traits	Direction	Author
Days to 50 per	Plant height, ear head length, ear head width, 100 grain weight.	Positive	Prakash <i>et al.</i> , 2010; Warkad <i>et al.</i> , 2010; Elangovan <i>et al.</i> , 2007; Ayana and Bekele, 2000.
cent nowering	Panicle exerstion, basal tillers, Panicle weight.	Negative	Upadhyaya <i>et al.</i> , 2009; Ezeaku and Mohammed, 2006 and Ayana and Bekele, 2000.
Plant height	Panicle exerstion, panicle length, panicle width, 100 seed weight.	Positive	Godbharle <i>et al.</i> , 2010; Upadhyaya <i>et al.</i> , 2009; Elangovan, 2007; Ezeaku and mohammed, 2006; Ayana and Bekele, 2000; Okonkwo and Onoenyi, 1998.
Paniela avaration	Panicle length, plant height,	Positive	Upadhyaya <i>et al.</i> , 2009; Ayana and Bekele, 2000
	Days to 50 per cent flowering,	Negative	Upadhyaya <i>et al.</i> , 2009; Ayana and Bekele, 2000

Traits	Associated traits	Direction	Author
	panicle width.		
Panicle length	Days to 50 per cent flowering, plant height, panicle width, panicle weight.	Positive	Upadhyaya <i>et al.</i> , 2009; Bucheyeki <i>et al.</i> , 2009; Elangovan <i>et al.</i> , 2007; Ayana and Bekele, 2000.
	100 seed weight, panicle weight.	Negative	Upadhyaya <i>et al.</i> , 2009; Ezeaku and mohammed, 2006.
Panicle width	Days to 50 per cent flowering, plant height, panicle length, panicle weight.	Positive	Upadhyaya <i>et al.</i> , 2009; Bucheyeki, 2009; Elangovan, 2007; Ayana and Bekele, 2000.
	100 seed weight, panicle exerstion.	Negative	Godbharle <i>et al.</i> , 2010; Upadhyaya <i>et al.</i> , 2009; Elangovan <i>et al.</i> , 2007; Ayana and Bekele, 2000.
100 good moiste	Plant height, panicle length, panicle exerstion, panicle weight.	Positive	Upadhyaya <i>et al.</i> , 2009; Elangovan <i>et al.</i> , 2007; Ezeaku and Mohammed, 2006; Ayana and Bekele, 2000; Veerbadhiran <i>et al.</i> , 1994.
Too seed weight	Days to 50 percent flowering, panicle weight, basal tillers.	Negative	Upadhyaya <i>et al.</i> , 2009
Basal tillers	Days to 50% flowering, 100 seed weight,	Negative	Upadhyaya <i>et al.</i> , 2009; Bucheyeki <i>et al.</i> , 2009.

The study of relationships among quantitative traits is important for assessing the feasibility of joint selection of two or more traits and hence for evaluating the effect of selection for secondary traits on genetic gain for the primary trait under consideration. A positive genetic correlation between two desirable traits makes the job of the plant breeder easy for improving both traits simultaneously. Even the lack of correlation is useful for the joint improvement of the two traits. On the other hand, a negative correlation between two desirable traits impedes or makes it impossible to achieve a significant improvement in both traits.

#### **CHAPTER III**

# **MATERIALS AND METHODES**

Sorghum, the world's fifth most important cereal crop, is grown throughout the arid and semi-arid tropics. Drought is a major constrain that result in significant yield losses due to reduced grain size, premature plant death and increased disease susceptibility. The present investigation was undertaken for phenotypic assessment of sorghum reference set under drought condition.

#### 3.1 Material

Materials used for the present investigation was sorghum reference set consist of 384 accessions, and representing the germplasm diversity (**Appendix 1**). This reference set was selected using data on 41 SSR markers from a composite collection consisting of 3,367 accessions. The reference set represents the five basic races [*Bicolor* 37 accessions (9.64%), *Caudatum* 76 accessions (19.79%), *Durra* 40 accessions (10.42%), *Guinea* 66 accessions (17.19%) and *Kafir* 26 accessions (6.77%)], 10 intermediate races [*Caudatum-Bicolor* 29 accessions (7.55%), *Durra-Bicolor* 8 accessions (2.08%), *Durra-Caudatum* 25 accessions (6.51%), *Guinea-Bicolor* 1 accession (0.26%), *Guinea-Caudatum* 45 accessions (11.72%), *Guinea-Durra* 3 accessions (0.78%), *Guinea-Kafir* 1 accession (0.26%), *Kafir-Bicolor* 1 accession (0.26%), *Kafir-Caudatum* 2 accessions (0.52%) and *Kafir-Durra* 1 accession (1.04%), *Drummondii* 10 accessions (2.60%), *Verticilliflorum* 6 accessions (1.56%) and *Virgatum* 1 accession (0.26%)] (**Table.1).** Three control cultivars *viz.*, IS 18758, IS 33844 and IS 2205, two early maturing and one late maturing were included in the evaluation.

#### 3.2 Multilocation Evaluation of sorghum reference set

The sorghum reference set was evaluated during 2008-09 (E1) and 2009-10 (E2) post rainy season at International Crops Research Institute for Semi Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh (18° N latitude, 78° E longitude and 545m above MSL); 2009-10 at University of Agricultural Sciences, Dharwad, Karnataka in irrigated (E3) and un-irrigated (E4) conditions (15°27'N latitude, 75°05'E longitude and

701m above MSL) and at the Regional Agricultural Research Station, Bijapur, Karnataka in un-irrigated (E5) condition (16°50'N latitude, 75°47'E longitude and 609m above MSL) along with three checks viz., IS 2205, IS 18758 and IS 33844 as common to all the environments. IS 18758 is an early maturing, dwarf, high yielding cultivar, resistance to leaf diseases and belong to an intermediate race *Guinea-caudatum*. IS 33844 is an early maturing, tall, maldandi type, high yielding cultivar belong to the race *durra* and suitable for post rainy season. IS 2205 is a late maturing, medium-tall, high yielding cultivar, resistant to shoot fly belong to the intermediate race *Durra-bicolor*. Agro climatic conditions of the environments during the crop period are given in the **Table.2**.

Before undertaking the multilocation evaluation, the 384 accessions were characterized for days to flowering in 2007-08 post rainy season at ICRISAT. The data were used to classify the accessions into seven groups with similar phenology. (Table.3).

Group	Days to 50% flowering	No. of genotypes
Group I (G1)	54-68 days	36
Group II (G2)	69-82 days	114
Group III (G3)	83-96 days	124
Group IV (G4)	97-110 days	51
Group V (G5)	111-124 days	38
Group VI (G6)	125-138 days	13
Group VII (G7)	139-149 days	8
Total		384

Table.3. Classification of sorghum reference set into seven groups based on days to50 per cent flowering.

Each group of accessions together with the three controls was evaluated separately in split plot design with three replications. Drought stressed and non-stressed (irrigated) moisture regimes were considered as main plots and genotypes within the moisture regime were considered as the sub plots. The drought stress was imposed by withholding irrigation from 31 days after sowing (DAS) in G1, 46 DAS in G2, 60 DAS in

G3, 74 DAS in G4, 88 DAS in G5, 102 DAS in G6 and 115 DAS in G7. Once the stress was imposed, drought stressed did not receive any further irrigation. The non-stressed plots continued to receive irrigation through crop maturity.

At Dharwad and Bijapur, the experiment was conducted in an augmented design with one of the three control cultivars (IS 2205, IS 18758 and IS 33844) repeated after every ten test entries. Irrigation in these environments was withheld once 50 per cent of the plots reached 50 per cent of flag leaf emergence. In all five environments each accessions was raised in two rows of 4m length. The row to row spacing was 0.75m and between plants was 10cm so as to accommodate 41 plants per row.

#### 3.3 Observations Recorded:

Observations on seven qualitative and 11 quantitative traits were recorded according to the sorghum descriptor (IBPGR and ICRISAT, 1993). Qualitative traits measured were plant pigmentation, mid rib color, presence of nodal tillers, grain cover, glume cover, grain color and thresability. Quantitative traits measured were days to 50 per cent flowering, plant height, basal tillers, panicle exerstion, panicle length, panicle width, panicle weight, SCMR (SPAD chlorophyll meter reading) at flowering, SCMR at 30 days after flowering, hundred seed weight and grain yield. The data on all the seven qualitative traits and days to 50% flowering, panicle weight and grain yield were converted into Kg ha<sup>-1</sup>. Data for the remaining quantitative traits were recorded on five representative plants from each plot. The mean over the five plants were used for statistical analysis. The details of the qualitative and quantitative data recorded are given in the **Tables 4 and 5**.

S. No.	Qualitative trait	Description
1	Plant pigmentation (PP)	Pigmented (P)
		Tanned (T)
2	Mid rib color (MRC)	Dull (D)
		White (W)
		Yellow (Y)
3	Presence of Nodal tillers (NT)	Presence (P)
		Absence (A)
4	Glume Cover (GLCOV)	25% of grain covered (1)
		50% of grain covered (3)
		75% of grain covered (5)
		Grain fully covered (7)
		Glume longer than grain (9)
5	Glume Color (GCL)	Brown (B)
		Black (BL)
		Light brown (LB)
		Light red (LR)
		Purple (P)
		Partly straw and purple (PSP)
		Partly straw and Brown (PSB)
		Red (R)
		Reddish brown (RB)
		Straw (S)
		White (W)
		Yellow (Y)
6	Grain Color (GCL)	Brown (B)
		Chalky white (CW)
		Grey (G)
		Light Brown (LB)
		Light red (LR)
		Purple (P)
		Red (R)
		Reddish brown (RB)

Table 4. Details of qualitative traits recorded

S. No.	Qualitative trait	Description
		Straw (S)
		White (W)
		Yellow (Y)
7	Thresability (THR)	Fully Threshable (FT)
		Partially Threshable (PT)
		Difficult to thrash (DT)

# Table 5. Details of quantitative traits recorded

S.No.	Quantitative trait	Description
1.	Days to 50% flowering (DF)	The number of days taken from mean emergence date of the field to the date when 50% of the plants in the plot started flowering.
2.	Plant Height (cm) (PH)	Height of five randomly selected plants in each row was measured in centimeters from the base of the plant to the tip of the panicle at maturity stage.
3.	Basal Tillers (BT)	Number of tillers at the ground level.
4.	Panicle Exerstion (cm) (EXE)	Length from the flag leaf to the base of the panicle in centimeters.
5.	Panicle length (cm) (PL)	Length from the base of the panicle to the tip in centimeters.
6	Panicle Width (cm) (PW)	Width in natural position at the widest part of the ear in centimeters.
7.	Panicle weight (Kg ha <sup>-1</sup> ) (PWT)	Weight of the panicles harvested in a plot and converted for $Kg^{-1}ha$
8	SCMR (SPAD chlorophyll meter reading) at Flowering (SPAD1)	SPAD chlorophyll meter reading was recorded in third leaf from the top using SAPD Konica minlota® chlorophyll meter at the time of flowering. In each leaf, reading was taken at three places (Base, middle and tip of the leaf).
9.	SCMR (SPAD chlorophyll meter reading) at 30 Days after flowering (SPAD2)	SPAD chlorophyll meter reading was recorded in the third leaf from the top using SAPD Konica minlota® chlorophyll meter on 30 days after flowering. In each leaf, reading was taken at three places (Base, middle and tip of the leaf).

S.No.	Quantitative trait	Description
10.	Hundred seed weight (g) (HSW). (Not recorded in E1)	100 well filled grains were picked from the produce of plant at random and weighed in grams.
11.	Grain Yield (Kg ha <sup>-</sup> ) (YLD)	Weight of the grains in a plot and converted for Kg <sup>-1</sup> ha.

# **3.4 Statistical Analysis**

In E1and E2 the analysis of variance was done for the 11 quantitative traits recorded in entire set and for the each flowering group in individual season and pooled over seasons using Genstat 12 software (http://www.genstat.co.uk). Variance components due to genotype ( $\delta^2$ g) and genotype x environment influence ( $\delta^2$ ge) were estimated by utilizing the respective mean sum of squares from the variance table.

#### Source of variation **Degrees of freedom** Mean sum of squares Replication r-1 Drought (Main plot factor) d-1 (*r*-1) (*d*-1) Error (a) Genotype (Sub plot factor) M1 g-1 Genotype X Drought (d-1)(g-1)M2 Error (b) d (r-1) (g-1)

# Analysis of variance for split plot design

# Pooled Analysis of variance for split plot design

Source of variation	Degrees of freedom	Mean sum of squares
Replication	r-1	
Drought (Main plot factor)	d-1	
Genotype (Sub plot factor)	g-1	M1
Year	<i>y-1</i>	

Source of variation	Degrees of freedom	Mean sum of squares
Genotype X Drought	(d-1) (g-1)	M2
Drought X Year	(d-1)	
Genotype X Drought X Year	(g-1) (d-1) (y-1)	M3
Error (b)	(r-1) (gdy-1)	

Where,

r = Number of replication, d = Number of main plot factor, g = Number of genotypes, y = Number of years, M1 = Mean sum of squares of genotypes, M2 = Mean sum of squares of Genotype X Drought interaction, M3 = Mean sum of squares of Genotype X Drought X Year interaction.

In E3, E4and E5 the 11 quantitative traits were analyzed for individual environment using Residual Maximum Likelihood (REML) (Paterson and Thompson, 1971) considering genotypes as random using Genstat version12. The pooled analysis of E3, E4 and E5 was performed by considering genotypes as random and environment as fixed. Significance of environment was tested using Wald statistics and the Best Liner Unbiased Predictors (BLUP) were obtained.

# 3.4.1 Comparison of means and variances

Mean, range and variances were calculated for the entire set, flowering groups (E1 and E2 alone), individual races, intermediate races and wilds and as group (basic races, intermediate race and wilds) in individual environment and pooled over environments. The means were compared based on Newman-Keuls test (Newman, 1939; Keuls, 1952) and the homogeneity of variances were tested by the Levene's (1960) test using SAS/SAST2 ® 9.2.

# 3.4.1 Phenotypic and Genotypic coefficient of variation

The genotypic and phenotypic coefficient of variation were estimated by the formula given by Burton (1952) and expressed in percentage.

Phenotypic coefficient of variation (%)

$$PCV = - x \ 100$$

General mean

Genotypic coefficient of variation (%)

(Genotypic variance)  $\frac{1}{2}$ 

GCV = \_\_\_\_\_ x 100

General mean

The estimates of PCV and GCV were categorized on the scale given below (Sivasubramanian and Menon, 1973)

Low:less than 10 per centModerate:11 - 20 per centHigh:more than 20 per cent

# 3.4.2 Heritability

Heritability in broad sense was calculated according to Lush (1940) and expressed in percentage.

Heritability in broad sense (h<sup>2</sup>) = 
$$-\frac{\sigma_{g}^{2}}{\sigma_{p}^{2}}$$

Where,

 $\sigma_{g}^{2}$  = Genotypic variance

 $\sigma_p^2$  = Phenotypic variance

The range of heritability was categorized as

Low	0 - 30 per cent
Medium	31 - 60 per cent
High	61 per cent and above according to Johnson et al.,(1955)

# 3.4.3 Genetic advance

The genetic advance was worked out based on the formula given by Johnson *et al*, (1955).

a) Genetic advance (GA) = 
$$\sigma_g^2 - x K$$
  
 $(\sigma_p^2)^{\frac{1}{2}}$ 

Where,

 $\sigma_{g}^{2}$  = Genotypic variance,  $\sigma_{p}^{2}$  = Phenotypic variance, K = 2.06 (selection differential at 5 per cent selection intensity)

b) GA as per cent of mean = 
$$GA$$
  
Grand mean Grand mean

The range of genetic advance as per cent of mean was classified into low (1-10 per cent), medium (11-20 per cent) and high (21 per cent and above) as suggested by Johnson *et al.* (1955).

#### **3.4.4 Correlation analysis**

Phenotypic correlations between yield and its component traits and among themselves were calculated for entire set, each flowering group ( $E_1$  and  $E_2$  alone), races, intermediate races and wilds as group in individual environment and pooled over environments. Only those correlations which are greater than 0.500 or smaller than - 0.500 were considered as useful as at least 25 per cent of the variation in one trait is predicted by the other (Upadhyaya *et al.*, 2010c).

#### 3.4.5 The Shannon-Weaver diversity index (H')

The Shannon-Weaver diversity index (H') (Shannon and Weaver, 1949) for the seven qualitative and 11 quantitative traits was calculated for entire set, seven flowering groups ( $E_1$  and  $E_2$ ), individual races, intermediate races and wilds and as a group (basic races, intermediate race and wilds) in all the environments using Genstat 12.

Shannon Index was calculated by the formula:

$$H_i = -\sum_{i=1}^k p_i \ln p_i$$

Where,

k = number of categories,

p<sub>i</sub>= proportion of accessions in the i<sup>th</sup> category

A high Shannon index indicates an even distribution of the categories among a trait.

# 3.4.6 Principal component analysis (PCA)

Principal component analysis based on 11 quantitative traits for individual environment and pooled data were performed to find out relative importance of different traits in explaining the variation in sorghum reference set. The observations for each trait were standardized by subtracting mean from each observation, and subsequently dividing by its standard deviation. This resulted in standardized values for each trait with average of 0 and standard deviation of 1 or less. These standardized values were used to perform principal component analysis. A hierarchical cluster analysis for individual environment separately and for pooled data was performed using scores of the first three principal components (PCs) following Ward (1963).

# 3.4.7 Phenotypic Diversity

Gower's (1971) dissimilarity matrix was calculated using 11 quantitative traits for each flowering group and for entire set in individual environment separately and for pooled data using GenStat version 12. Most dissimilar and least dissimilar accessions were identified in sorghum reference set based on dissimilarity matrix.

# 3.4.8 Identification of drought tolerant accessions

# 3.4.8.1 Identification of drought tolerant accessions based on drought tolerance indices

Selection of genotypes that are tolerant to the drought stress was the main objective of the study. In order to select the drought tolerant accessions several selection

criteria have been proposed (Fischer and Maurer, 1978; Rosielle and Hamblin, 1981). The selection criteria were worked out based on the formulas given below.

# 1. Stress susceptibility index (SSI)

SSI= [1-(Ys/Yp)]/SI (Fischer and Maurer, 1978)

SI is the stress intensity =  $1-(Y\overline{s}/Y\overline{p})$ 

The SI ranges between 0 and 1 and larger the value of SI the more sever is the stress intensity. The smaller the value of SSI, the greater is the stress tolerance. Selection based on SSI favor genotypes with high yield under stress condition.

# 2. Stress tolerance Index (STI)

 $STI = (Yp x Ys)/(Yp)^2$  (Fernandez, 1992)

The higher the value of STI for a genotype the higher its stress tolerance and yield potential.

# 3. Mean productivity (MP)

MP = (Ys + Yp)/2 (Rosielle and Hamblin, 1981)

This index favors the genotypes with higher yield and lower stress tolerance. Selection based on MP generally increase the average performance in both stress and non-stress environments.

# 4. Geometric mean productivity (GMP)

GMP=  $\sqrt{(Ys \times Yp)}$  (Fernandez, 1992)

Selections based on GMP favor genotypes which express uniform superiority in both the stress and non-stress environment.

#### 5. Tolerance (TOL)

 $TOL = [(Yp-Ys)/Yp] \times 100$  (Rosielle and Hamblin, 1981)

A lower value of the TOL represents relatively more tolerance to stress.

### 6. Drought tolerance efficiency (DTE)

 $DTE = (Ys/Yp) \times 100$  (Fischer and Wood, 1981)

Higher the value of DTE represents higher the drought tolerance of the genotype. Where,

- Yp = Potential yield of a given genotype in a non-stress environment.
- Ys = Yield of a given genotype in stress environment
- $Y\overline{p}$  = Mean yield of the genotypes in non-stress environment
- $Y\overline{s}$  = Mean yield of the genotypes in stress environment

Selection based on a combination of indices may provide a more useful criterion for selecting drought tolerant accessions. The correlation coefficient between attributes provides only the degree of overall linear association between any two attributes. A better approach than correlation is the biplot analysis. The biplot analysis plots accessions and the drought tolerance indices along with the yield under irrigated and un-irrigated condition and illustrates the relationship between them in the same graph. To display the accessions by drought tolerant indices in biplot, principal component analysis was carried out and inter-relationship between the drought tolerant indices were identified. To select the drought tolerant accessions, clustering of accessions was done based on the first two principal components using Ward (1963) method. Means were worked out for yield and all the drought tolerant indices in each cluster. The accessions of the cluster with high mean for yield and the drought tolerance indices were selected as the drought tolerant accessions with high yield potential under stress and non-stress condition.

# 3.4.8.2 Identification of accessions with high SCMR (SPAD chlorophyll meter reading)

SPAD chlorophyll meter reading was recorded on third leaf from the top using SAPD Konica minlota® chlorophyll meter at the time of flowering and 30 days after flowering in the same leaf. In each leaf, reading was taken at three places *viz.*, Base, middle and tip of the leaf. The observations were recorded in both irrigated and un-irrigated condition. Accessions having high SCMR at flowering and 30 days after flowering under both irrigated and un-irrigated condition were selected as the high SCMR accessions.

# CHAPTER IV EXPERIMENTAL RESULTS

The present study was aimed at the phenotypic assessment of sorghum reference set for yield and related traits under post flowering drought conditions and to identify the drought tolerant accessions. Sorghum reference set of 384 accessions along with three control cultivars was evaluated under five environments for seven qualitative and 11 quantitative traits.

Sorghum reference set consisted of accessions belonging to five basic races, ten intermediate races and five wild sub species (Appendix 1). Among races, the race *caudatum* was predominant (76 accessions) followed by *Durra* (41 accessions) and *Guinea* (37 accessions). Among the intermediate races, *Guinea-caudatum* (37 accessions), *Caudatum-bicolor* (29 accessions) and *Durra-caudatum* (25 accessions) were predominant. In case of wild sub species major contribution was by sub species *Drummondii* (10 accessions) followed by *Verticilliflorum* (6 accessions) and *Arundinaceum* (4 accessions) (Table 1 and Fig 1). The highest number of accessions were from Sudan (36 accessions) followed by United States of America (32 accessions), India (31 accessions), Cameroon (27 accessions) and South Africa (25 accessions) (Fig 2). Seven qualitative and 11 quantitative characters recorded in the present study exhibited large variability.

# **4.1. QUALITATIVE TRAITS**

The frequency distribution of different phenotypic classes of qualitative characters were calculated in per cent for entire reference set, flowering groups, basic races, intermediate races and wild sub species (Table 6a, 6b).

#### 4.1.1. Mid rib color

Observations on mid rib color was recorded at flag leaf stage on the main stem. Mid rib color was recorded in three classes: dull, white and yellow. Among the three classes white mid rib color was more prevalent in entire reference set (76.3%), basic races (78.4%), intermediate races (71.6%) wilds (78.3%) and among the seven flowering groups (G1-69.4%, G2-74.6%, G3-75.0%, G4-82.3%, G5-78.9%, G6-84.6%, G7-87.5%) (Table 6a).

The predominance of white mid rib color was followed by dull mid rib color (entire-21.9%, races-20.0%, intermediate races-26.7% and wilds-13.0%). The occurrence of yellow mid rib was rare with the frequency of 1.8 per cent in entire reference set, 1.6 per cent in the basic races, 1.7 per cent in intermediate races and 8.7 per cent in wilds. In flowering group, yellow mid rib had highest per cent (3.9%) of accessions in G4 followed by the G1 (2.8%) and G5 (2.6%) (Fig. 3)

Among races 86.4 per cent of *bicolor* accessions had white mid rib followed by *guinea* (78.8%) and *durra* (77.5%). Among the intermediate races 87.5 per cent of *durra-bicolor* accessions had white mid rib followed by *durra-caudatum* (81.0%) and *caudatum-bicolor* (79.3%). All the accessions of sub species *Arundinaceum*, *Drummondii*, *Virgatum* and 33 per cent of *Verticilliflorum* had white mid rib color. The frequency of dull mid rib color was high among the basic races *kafir* (23.0%), *durra* (22.5%) and *caudatum* (22.4%), whereas in intermediate races it was high in *kafir-caudatum* (50.0%) followed by *guinea-caudatum* (35.7%) and *guinea-durra* (33.3%). The yellow mid rib color occurred in *bicolor* (2.7%), *caudatum* (3.9%), *guinea* (1.5%), *guinea-caudatum* (2.2%) and *Verticilliflorum* (33.3%) (Table. 6b).

#### 4.1.2. Plant pigmentation

Plant pigmentation is an important seedling characteristic, which is associated with grain quality and reaction to pest and diseases (Axtell *et al.*, 1982). This trait was recorded in two classes: Tan and pigmented on the main stem. Pigmented stem dominated in the entire reference set (94.8%), basic races (96.0%), intermediate races (92.2%) and wilds (95.6%). Among the seven flowering group, all the accessions of G4, G5, G6, G7 and 91.7 per cent of G1, 93.9 per cent of G2 and 92.0 per cent of G3 had pigmented plant type (Table 6a and Fig. 4). Among the five basic races, the percentage of pigmented accessions ranged between 94.6 (*bicolor*) and 97.5 (*durra*). All the accessions of *durra-bicolor* and *guinea-durra* and 96.5 per cent of *caudatum-bicolor*, 96.0 per cent of *durra-caudatum* and 86.7 per cent of *guinea-caudatum* in intermediate races had pigmented plant type (Table 6b)

In entire reference set 5.2 per cent of accessions had tanned plants whereas in flowering group, G1 had 8.3 per cent, G2 had 6.4 per cent and G3 had 8.1 per cent of tanned plants (Table 6a). Tanned plants occurred at the range between 2.5 per cent (*durra*) and 5.5 per cent (*guinea*) among the races. In intermediate races tanned plants were present only in *caudatum-bicolor* (5.4%), *durra-caudatum* (4.0%), *guinea-caudatum* (13.3%) and *kafir*-

*bicolor* (100%). All the accessions from Sudan, India, USA, Cameroon and South Africa had pigmented plants (Table 6b).

#### 4.1.3. Nodal Tillers

In entire reference set, 88.3 per cent of accessions were with nodal tillers. In flowering groups the presence of nodal tillers ranged from 80.7 per cent (G2) to 100 per cent (G6 and G7) (Table 6a and Fig. 5). More than 80.0 per cent of the accessions of all basic races, all flowering groups had nodal tillers. Nodal tillers were present in all the accessions belonging to *Arundinaceum* and *Verticilliflorum*. The nodal tillers were absent in 11.7 per cent of the accessions of entire reference set, 9.0 per cent of the accessions of basic races, 17.2 per cent of the accessions of intermediate races and 13.0 per cent of the accessions of wild subspecies (Table 6b).

# 4.1.4. Glume color

Glume color was classified into 12 classes of which black and purple were dominant in the entire reference set (34.4%, 30.2%) as well as among races (32.6%, 33.5%) and intermediate races (35.3%, 29.2%). In flowering groups the accessions with black colored glume ranged between 29.4 per cent (G4) and 53.8 per cent (G6) and purple colored glume ranged between 7.7 per cent (G6) and 44.7 per cent (G5). These were followed by accession with red (8.3 to 13.7%), partly straw brown (2.6 to 15.4%), brown (2.6 to 12.5%), reddish brown (1.7 to 12.5%) and light red (2.6 to 8.3%) glumes (Table 6a and Fig 6).

A large proportion of the accessions of races *bicolor* (45.9%), *caudatum* (42.1%), and *guinea* (30.3%) and intermediate races *caudatum-bicolor* (41.4%), *durra-caudatum* (36.0%), *guinea-caudatum* (40.0%) and 50 per cent of all wilds except *verticilliflorum* had black colored glumes. Accessions with purple color glume were prevalent in the races *kafir* (73.1%), *durra* (47.5%), *guinea* (33.3%), *durra-caudatum* (48.0%) and *caudatum-bicolor* (24.1%) (Table 6b).

The predominance of black and purple glumes was followed by red and brown color glumes among the five basic races. The accessions of wilds had the higher frequency of black and light brown glumes. The accessions with straw color glume were found only in *guinea* (1.5%), *arundinaceum* (20.0%), yellow color glume only in *verticilliflorum* (16.7%) and with white colored glumes only in *Drummondii* (25.0%). In the entire reference set, 66.7

per cent of the accessions belong to India and they had purple color glumes followed by the accession belonging to South Africa (48.0%) and Sudan (33.3%) (Table 6b).

#### 4.1.5. Glume covering

Glume covering indicates the amount of grain covered by the glumes at maturity and the accessions were classified into five classes. In entire reference set, a large proportion of the accessions had one fourth glume covered (44.0%) followed by half (36.2%), three fourth (10.7%) and fully glume covered (7.3%). The same trend was observed among the flowering group. In flowering group accessions with one fourth glume covered ranged between 37.2 percent (G2) and 62.5 per cent (G7) and accessions with half glume covered ranged from 7.7 per cent (G6) to 41.1 per cent (G3). Accessions with larger glumes occurred in very less frequency, the highest being in G1 (8.3%) followed by G6 (7.7%), G5 (2.6%), G2 (0.9%) and G3 (0.8%) (Table 6a and Fig 6).

Among the races, most of the accessions of *guinea* (93.9%) and *caudatum* (43.0%) had one fourth glume cover followed by 84.6 per cent of *kafir* accessions had half glume covered and 70.3 per cent of *bicolor* accessions had fully glume covered.

Among the intermediate races all the accessions of *guinea-bicolor*, *guinea-kafir*, *kafir-durra*, 72.0 per cent of *durra-caudatum*, 62.5 per cent of *durra-bicolor* and 51.7 per cent of *caudatum-bicolor* had half glume covered. The intermediate races *caudatum-bicolor* (34.5%), *durra-bicolor* (25.0%), *durra-caudatum* (4.0%) and all the accessions of *kafir-bicolor* had three fourth glume covered (Table 6b).

In wilds, 39.1 per cent of the total accessions had three fourth glume covered in which the major contribution was by subspecies *Drummondii* (70.0%). The glume larger than grain was occurred in the wild species *viz.*, *Aethiopicum, Arundinaceum* and *Verticilliflorum* (Table 6b).

#### 4.1.6. Grain color

Grain color showed high variability and was recorded in 11 classes in the reference set. White (19.0%) and purple color (19.0%) grains were most common in the entire reference set followed by brown (15.4%), reddish brown (14.6%) and light red color grains (11.2%). The yellow (2.3%) and red (2.1%) colored grain occurred in less frequencies in the entire reference set (Table 6a and Plate 1). Similar trend was found among the accessions of the flowering groups. All the flowering groups were dominated by white color grains which had the frequency ranged between 14.0 per cent (G2) and 29.4 per cent (G4) followed by purple [7.7% (G6) to 21.8% (G3)] and brown [7.8% (G4) to 37.5% (G7)].

The trends in basic races, intermediate races and wilds were varying between them. The basic races were dominated by white (22.4%) grains followed by purple (18.8%), light red (13.5%) and brown (15.9%). In the intermediate races purple (22.4%) color was prevalent followed by reddish brown (21.5%) and white (14.7%). In case of wilds most of the accessions had brown colored grains (30.4%) followed by straw (21.7%) and chalky white (17.4%) (Table 6a).

Among the individual basic races, the accessions with white and purple colored grains were more prevalent in *guinea* (73.1% and 46.1%) and *durra* (32.5% and 30.0%). The predominance of white and purple was followed by brown and light red. All the classes of grain color were present in *guinea-caudatum* and most of the classes were present in *caudatum-bicolor* and *durra-caudatum* accessions. The other intermediate races represented only few grain color, this was mainly due to the less number of accessions in them (Table 6b).

# 4.1.7. Threshability

Threshability is an important evolutionary and agronomic trait. The trait was recorded in three classes. In entire reference set 63.0 per cent of the accessions, in races 66.5 per cent of the accessions and in intermediate races 66.4 per cent of the accessions, were fully threshable followed by partly threshable accessions (Entire reference set: 22.4%, Basic races: 20.4% and Intermediate races: 28.4%) (Table 6a and Fig 7). The same trend was found among the flowering groups which ranged from 52.6 per cent (G2) to 72.5 per cent (G4). In case of wilds most of the accessions (65.2%) were difficult to thresh followed by fully (17.4%) and partly threshable (17.4%) (Table 6a).

In individual basic races, *bicolor* had 67.6 per cent of accessions that were difficult to thrash whereas most of the accessions of other races were fully threshable (*caudatum* 75.0%, *durra* 55.0%, *guinea* 80.3% and *kafir* 88.5%). In intermediate races all the accessions of *guinea-bicolor*, 84.0 per cent of *durra-caudatum*, 80.0 per cent of *guinea caudatum*, 96.3 per cent of *durra-bicolor* and 66.7 per cent of *guinea- durra* were fully threshable. All the accessions of *Aethiopicum*, *Verticilliflorum*, 80.0 per cent of *Drummondii* and 75.0 per cent of *Arundinaceum* were difficult to thrash (Table 6b).

#### **4.1.8.** Shannon-Weaver diversity index (H')

The Shannon-weaver diversity index (H') was calculated to compare phenotypic diversity for the seven qualitative characters in the entire reference set, flowering groups, basic races, intermediate races and wilds. Intermediate races: *caudatum-kafir, durra-kafir, bicolor-kafir, guinea-kafir, durra-guinea, guinea-bicolor* and wilds: *Arundinaceum, Aethiopicum, Virgatum* and *Verticilliflorum* were not used in the analysis as they are represented by less than five accessions.

The mean H' was highest for grain color and lowest for plant pigmentation in entire reference set (highest H'= 0.93, lowest H' = 0.09) among the flowering group (highest H'= 0.86, lowest H' = 0.07) and among the basic races, intermediate races and wilds as group (highest H' = 0.83, lowest H' = 0.07) (Tables 7a, 7b and Fig. 8a). The H' values averaged over the seven flowering group ranged from  $0.07\pm0.021$  for plant pigmentation to  $0.86\pm0.040$  for grain color. In flowering groups, H' averaged over traits was high in G1 ( $0.47\pm0.124$ ), G2 ( $0.47\pm0.115$ ) and G3 ( $0.45\pm0.118$ ) for all the qualitative characters. The accessions in the G7 were least diverse ( $0.32\pm0.091$ ) for all the qualitative traits (Table 7a).

Accessions of the basic race *bicolor* (0.92) had the highest H' for grain color and the lowest for plant pigmentation in the intermediate race *durra-bicolor* (0.0) (Table 7b and Fig. 8b). The race *bicolor* (0.39 $\pm$ 0.121) and *caudatum* (0.39 $\pm$ 0.113) had the highest H' pooled across the traits and the race *kafir* had the least pooled H' (0.27 $\pm$ 0.089). In intermediate races the highest H' pooled across the traits was found in *guinea-caudatum* (0.43 $\pm$ 0.123) and the lowest was for *durra-bicolor* (0.32 $\pm$ 0.109).

#### **4.2. QUANTITATIVE CHARACTERS**

#### 4.2.1. Analysis of variance and REML analysis

The data on the eleven quantitative traits were analyzed for individual environment separately (Tables 8a to 8c) and for different flowering group in E1 (Tables 9a to 9g), E2 (Tables 10a to 10g) and pooled over both the environments (Tables 11a to 11g). The variance due to genotype was found to be significant for all the characters. Variance due to genotype x drought interaction was significant for panicle exsertion, panicle width, panicle weight and yield in entire reference set and in all flowering group. Variance due to Genotype x drought x year interaction was significant for all the characters in entire

reference set and the characters such as panicle exsertion, panicle width, panicle weight, yield and SPAD2 in all the flowering groups. The characters days to 50 per cent flowering (G1, G2 and G6); plant height (G2, G3, G5 and G6); panicle length (G3, G4, G5, and G6); basal tillers (G1) and SPAD1 (all the flowering groups) showed non-significant genotype x drought x year interaction.

REML analysis for E3, E4 and E5 indicated that the variance due to genotypes were significant for all the characters. The pooled analysis over the three environments (E3, E4, and E5) indicated that variance due to  $\sigma^2 g$  and genotype x environment interaction ( $\sigma^2 ge$ ) was significant for all the characters (Table 12). Wald's statistics was highly significant for all the traits indicating that all the environments were different and appropriate to differentiate the reference set accessions.

# **4.2.2. VARIABILITY PARAMETERS**

The variability parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense  $(h_b^2)$ , and genetic advance as per cent of mean (GA) were estimated for entire reference set in all the environment (Tables 13 and 14).

High PCV and GCV was found for plant height (E1, E2 and pooled over E1 and E2), panicle exsertion, panicle length, panicle width, hundred seed weight, basal tillers, panicle weight, and grain yield in all the individual environments and in pooled over E1 and E2 (Fig. 9a and 9b). These characters were found to have high PCV and moderate GCV in pooled over E3, E4 and E5.

Moderate PCV and GCV was found for the characters days to 50 per cent flowering (E1, E2 and pooled over E1, E2), plant height (E3, E4, E5 and pooled) and SPAD 2 (E5). In pooled over E3, E4 and E5 the characters days to 50 per cent flowering, SPAD1, SPAD2 showed low PCV and GCV (Table 13).

The characters days to 50 per cent flowering (E1, E2, E5 and pooled over E1 and E2), plant height (E1, E2, E3 and pooled over E1 and E2), panicle exsertion, panicle length, panicle width, basal tillers, hundred seed weight, panicle weight and grain yield had high heritability and high genetic advance in all the environments and pooled over E1 and E2 where as in pooled over E3, E4, E5 these characters had moderate heritability and high genetic advance (Table 14 and Fig. 9c).

High heritability and moderate genetic advance was found for the characters days to 50 per cent flowering (E3), plant height (pooled over E3, E4, and E5) and SPAD1 (E1). The characters SPAD1 in E3 and SPAD2 in E4 and pooled over E3, E4, E5 showed low heritability and low genetic advance (Table 14 and Fig. 9d).

# 4.3. MEAN AND RANGE

The means and range for all the 11 quantitative traits for entire reference set, seven flowering groups, individual basic races, intermediate races, wild subspecies and as group were given in the Tables 15a-d, 16a-d, 17a-g, 18a-g and 19a-g respectively. The means were tested using Newman-Keul's test for all the environments.

#### 4.3.1. Days to 50 per cent flowering

The days to 50 per cent flowering for the entire reference set ranged from 38.0 to 125.5 days after sowing (DAS) in E1, 46.5 to 126.8 DAS in E2, 42.5 to 123.4 DAS in pooled over E1 and E2, 51.4 to 80.7 DAS in E3, 50.9 to 77.7 DAS in E4, 48.8 to 92.6 DAS in E5 and 52.6 to 81.1 DAS in pooled over E3, E4 and E5 (Table 15a) Among environments highest range of days to 50 per cent flowering was found in E1 followed by E2 and pooled over E1 and E2.

The highest mean days to 50 per cent flowering was found in E2 (74.9 DAS) followed by pooled over E1 and E2 (72.2 DAS), E1 (70.8 DAS) and E5 (67.4 DAS) (Table 16a and Fig. 10). The mean days to 50 per cent flowering in E2 was significantly greater than the mean of all the other environments and pooled over environments.

The maximum range of days to 50 per cent flowering was observed for the flowering group G7 in E1 (72 to 125.5 DAS), E2 (69.2 to 126.8 DAS) and pooled over E1 and E2 (72.0 to 123.4 DAS) (Tables 15b-d). The highest mean value was found for G6 in E1 (100.9 $\pm$ 7.11 DAS), G7 in E2 (81.1 $\pm$ 2.71 DAS) and pooled over E1 and E2 (90.3 $\pm$ 5.03 DAS). The mean days to 50 per cent flowering of all the flowering group differed significantly from one another in pooled over E1 and E2 (Tables 16b-d).

In basic races, intermediate races and wilds as group the highest range was found in basic races in all the environments except in E1 in which the wilds as group showed the highest range. Intermediate races differ significantly from the races and wilds as group in E1 and pooled over E1 and E2 (Tables 19a-g). The highest range of days to 50 per cent flowering was found in the accessions of race *guinea* in E1 (63.0 to 121.5 DAS), pooled

over E1 and E2 (58.5 to 123.4 DAS), E3 (51.5 to 80.0 DAS), E5 (51.5 to 90.7 DAS) and pooled over E3,E4 E5 (55.4 to 81.1 DAS) where as in E2 and E4 the maximum range was found in *Drummondii* (52.7 to 92.3 DAS) and *bicolor* (51.9 to 75.2 DAS) respectively (Tables 17a-g).

#### 4.3.2. Plant height (cm)

The plant height of entire reference set ranged from 82.2 to 383.5 cm in E1, 84.2 to 340.1 cm in E2, 84.2 to 361.8 cm in pooled over E1 and E2, 89.1 to 342.3 cm in E3, 93.5 to 270.3 cm in E4, 103.6 to 269.7 cm in E5 and 114.9 to 284.8 cm in pooled over E3, E4 and E5 (Table 15a). Among the environments the range of E1 was found to be high. The mean plant height was similar in E2 (232.2 cm), E4 (231.1cm) and E3 (230.1cm). The mean plant height in E2, E3 and E4 was significantly greater than the mean plant height of E1, pooled over E1, E2 and pooled over E3 E4 E5 (Table 16a and Fig. 10).

Among the flowering groups the G5 had the highest range of plant height in E1 (94.0 to 374.2 cm) and in pooled over E1 and E2 (105.7 to 348.2 cm), whereas in E2 the highest range was found in G4 (133.4 to 340.1 cm) (Tables 15b-d). In E1 mean plant height of G6 (291.2 cm) was significantly greater than other flowering group. The mean value of plant height in group 1, 2, 3 and 4 in E1 and E2 showed a significant difference between them in the increasing order. The shortest plant height was observed for G1 in E1 (187.8 cm), E2 (186.9 cm) and pooled over E1 and E2 (188.6 cm) (Tables 16b-d).

The highest mean plant height was found in *Arundinaceum* in E1 (287.1 cm) followed by *virgatum* in E2 (270.7 cm) (Tables 18a-g). The mean plant height of basic race and intermediate races as group differ significantly from the wilds as group in E2, E5 and pooled over E1 and E2 (Tables 19a-g).

#### 4.3.3. Panicle exsertion (cm)

The panicle exsertion of the entire reference set ranged from 0.9 to 47.0 cm in E1. 0.6 to 38.3 cm in E2, 1.9 to 42.6 cm in pooled over E1 and E2, 0.4 to 61.6 cm in E3, 0.2 to 42.1 cm in E4, 0.3 to 40.9 cm in E5 and 1.4 to 39.2 cm in pooled over E3, E4 and E5 (Table 15a). Among the environments the widest range was found in E3 (0.4 to 61.6 cm) followed by E1 (0.9 to 47.0 cm), E4 (0.2 to 42.3 cm) and E5 (0.3 to 40.9 cm). The mean panicle exsertion was similar in E2 (18.0 cm) and in pooled over E1 and E2 (17.8 cm). The mean

panicle exsertion of E2 and pooled over E1 and E2 differs significantly from other environments (Table 16a and Fig. 10).

Among the flowering group the maximum range of panicle exsertion was found in G1 (E1= 1.0 cm to 47.0 cm, E2= 4.4 cm to 38.3 cm and pooled= 3.8 cm to 42.6 cm) and the minimum range of panicle exsertion was found in G6 (E1= 6.0 cm to 23.4 cm, E2= 7.7 cm to 28.5 cm and pooled= 7.7 cm to 25.5 cm) (Tables 15b-d and 16b-d).

The widest range of panicle exsertion was found in the accessions of race *caudatum* in E1 (1.7 to 36.2 cm), E2 (2.4 to 38.1cm) and pooled over E1 and E2 (2.1 to 37.4 cm). In other environments the maximum range was found in the race *bicolor* (E3= 0.4 to 61.6 cm, E4= 0.2 to 41.8 cm, E5= 0.3 to 40.9 cm and pooled over E3, E4 and E5 = 3.9 to 39.2 cm) and the minimum range was found in *Aethiopicum* (E3= 18.7 to 28.9 cm, E4= 12 to 21.8 cm, E5= 16.9 to 33.1 and pooled over E3, E4 and E5= 19.2 to 21.3 cm) (Tables 17a-g and 18a-g). There are no significant differences in the mean values among the individual races, intermediate races and wilds (Tables 19a-g).

#### 4.3.4. Panicle length (cm)

The panicle length of the entire reference set ranged from 6.2 to 48.6 cm in E1, 7.4 and 44.8 cm in E2 and 6.8 to 45.2 cm in pooled over E1 and E2, 7.5 to 60.6 cm in E3, 8.7 to 51.3 cm in E4, 7.6 to 44.2 cm in E5 and 10.8 to 48.3 cm in pooled over E3, E4 and E5 (Table 15a) Among the environments the widest range was found in E3 followed by E4 and E1 (Table 16a and Fig. 10). The mean panicle length among environments did not have any significant differences between them.

In E1, the widest range of panicle length was found in G2 (8.8 cm to 48.6 cm) with overall mean of  $21.5\pm1.8$  cm, whereas in E2 and pooled over E1 and E2 the maximum range was found in G3 (E2= 7.4 to 44.8 cm and pooled= 6.8 to 45.2 cm) (Tables 15b-d). In E1, E2 and pooled over E1 and E2 the highest mean value was found in G4 (E1- 26.0 cm, E2 – 25.2 cm and in pooled 25.6 cm) (Table 16b-d).

The accessions of race *bicolor* had the maximum range in E1 (13.6 to 48.6 cm), E2 (13.1 to 44.8 cm) and pooled over E1 and E2 (13.4 to 45.2 cm), *caudatum-bicolor* in E3 (9.8 to 60.6 cm), E4 (10.0 to 51.3 cm), pooled over E3, E4, E5 (11.9 to 48.3 cm) and *caudatum* in E5 (10.1 to 36.3 cm) (Table 17a-g). The basic races and intermediate races as a group

differed significantly from the wilds as a group in E1, E2 and pooled over E1 and E2 (Tables 19a-g).

#### 4.3.5. Panicle width (cm)

The panicle width of entire reference set ranged from 3.2 to 27.4 cm in E1, 3.6 to 18.3 cm in E2, 3.4 to 19.7 cm in pooled over E1 and E2, 1.4 to 49.2 cm in E3, 0.7 to 36.1 cm in E4, 1.4 to 22.7 cm in E5 and 3.1 to 24.2 cm in pooled over E3, E4 and E5 (Table 15a). The widest range of panicle width was found in E3 followed by E4 and E5. Among the environments mean panicle width was similar in E2 (7.6 cm), pooled over E1 and E2 (7.3 cm). (Table 16a)

In E1 and pooled over E1 and E2 the highest range of panicle width among the flowering groups was found in G3 (E1= 4.2 to 27.4 cm, pooled over E1 and E2 = 4.3 to 19.7 cm). In E2 the maximum range was found in G4 (4.5 to 18.3 cm) (Table 15b-d).

Among the basic races, intermediate races and wilds the widest range of panicle width was observed in the *caudatum-bicolor* in E3 (2.7 to 49.2 cm) followed by *bicolor* (3.5 to 36.1 cm) in E4 (Tables 17a-g). The mean panicle width of the race *bicolor* was significantly greater than other basic races in E1, E2, E5 and pooled over E1 and E2 (Tables 18a-g). The wilds as a group had significantly higher panicle width than races and intermediate races in E1, E2, E5 and in pooled over E1and E2 (Tables 19a-g).

#### 4.3.6. Basal tillers

Number of basal tillers in the entire reference set ranged from 1.0 to 9.0 in E1, 1.7 to 9.0 in E2, 1.5 to 8.7 in pooled over E1 and E2, 0.0 to 9.6 in E3, 0.3 to 9.1 in E4, 0.5 to 7.5 in E5 and 1.0 to 6.7 in pooled over E3, E4 and E5 (Table 15a). Among all the environments the maximum range was found in E3 (0.0 to 9.6) and the minimum range was found in pooled over E3, E4 and E5 (1.0 to 6.7). The means of individual environments do not have any significant difference between them (Table 16a and Fig. 10).

In flowering groups of E1, E2 and pooled over E1 and E2 the maximum range was found in G2 (E1= 1 to 8.5, E2= 1.8 to 9 and pooled= 1.5 to 8.7) (Tables 15b-d). The means of individual flowering group do not differ significantly between environments (Tables 16b-d).

The widest range of basal tillers was found in the accessions of races *caudatum* in E3 (0.0 to 9.6), E5 (1.3 to 5.6) and pooled over E3, E4 and E5 (1.2 to 6.7). In other

environments the widest range was found in the accessions of race *bicolor* in E1 (1.3 to 7.0), *kafir* in E2 (1.8 to 7.7), *guinea* in pooled over E1, E2 (1.8 to 6.7) and in E4 (0.8 to 9.1) (Tables 17a-g). The mean basal tiller of race *bicolor* and *guinea* was significantly higher than the other races in E1, E2 and pooled over E1 and E2. The mean basal tillers of wilds as group differed significantly from basic races and intermediate races as group in all the environments except in E3 and E4 (Table 19a-g).

## 4.3.7. Hundred Seed weight (g)

The hundred seed weight for the entire reference set ranged from 0.3 to 5.1 g in E2, 0.6 to 5.2 g in E3, 0.5 to 4.3 g in E4, 0.6 to 4.9 g in E5 and 1.1 to 3.7 g in pooled over E3, E4 and E5 (Table 15a). Among all the environments the highest mean hundred seed weight was found in E2 ( $2.6\pm0.27$  g) (Table 16a). The mean hundred seed weight of E2 and E3 differed significantly from other environments. Among the flowering groups the maximum range was found in G2 (0.3 to 5.1 g) with the grand mean of 2.6 g (Tables 15c and 16c).

In E2, race *caudatum* had the maximum range (1.1 to 5.1 g) with mean of 2.8 g. In other environments the maximum range was found in the race *bicolor* (E3= 0.7 to 5.2 g, E4= 1.0 to 4.0 g, and pooled= 1.4 to 3.7 g) (Tables 17a-g) with the mean value of 2.44 g in E3, 2.2 g in E4, 1.7 g in E5and 2.1 g in pooled over E3, E4 and E5 (Table 18a-g). In basic races, intermediate races and wilds as group the mean hundred seed weight differed significantly from each other in E1 and E5 where as in pooled over E3, E4 and E5 the wilds differed significantly from the races and intermediate races (Table 19a-g).

# 4.3.8. Panicle weight (kg ha<sup>-1</sup>)

The panicle weight of entire reference set ranged from 286 to 5517 kg ha<sup>-1</sup> with the mean of 2820 kg ha<sup>-1</sup> in E1, 387 kg ha<sup>-1</sup> to 3313 kg ha<sup>-1</sup> with the average of 2542 kg ha<sup>-1</sup> in E2 and 422 to 4243 kg ha<sup>-1</sup> with mean of 2687 kg ha<sup>-1</sup> in pooled over E1 and E2. In other environments the panicle weight ranged from 484 to 3980 kg ha<sup>-1</sup> in E3, 581 to 3060 kg ha<sup>-1</sup> in E4, 809 to 3498 kg ha<sup>-1</sup> in E5, 866 to 3001 kg ha<sup>-1</sup> in pooled over E3, E4 and E5. Among the environments E1 had the widest range and highest mean for panicle weight (Tables 15a and 16a, Fig. 10).

Among the flowering groups G2 had the highest range of panicle weight in E1 (286 to 4990 kg ha<sup>-1</sup>), in E2 (444 to 3313 kg ha<sup>-1</sup>) and in pooled over E1 and E2 (568 to 3667 kg ha<sup>-1</sup>) showed the widest range of panicle weight. There were no significant differences
between the flowering groups in E1, E2 and pooled over E1 and E2 (Tables 15b-d and 16b-d).

The race *caudatum* in E1 (1326 to 5517 kg ha<sup>-1</sup>), E3 (524 to 3148 kg ha<sup>-1</sup>) and E4 (1120 to 3060 kg ha<sup>-1</sup>), race *bicolor* in E5 (1355 to 3498 kg ha<sup>-1</sup>) and the intermediate race *guinea- caudatum* (1215 to 3313 kg ha<sup>-1</sup>) in E2 and pooled over E1 and E2 (620 to 3945 kg ha<sup>-1</sup>) had the widest range of panicle weight (Tables 17a-g). The mean panicle weight of the races and intermediate races as group differed significantly from the wilds group in all the environments and pooled over environments (Table 19a-g).

## 4.3.9. Grain yield (Kg ha<sup>-1</sup>)

The grain yield of entire reference set ranged from 187 to 3817 kg ha<sup>-1</sup> in E1, 224 to 2504 kg ha<sup>-1</sup> in E2 and 301 kg ha<sup>-1</sup> to 3140 kg ha<sup>-1</sup> in pooled over E1 and E2. In other environments the grain yield ranged from 458 to 3148 kg ha<sup>-1</sup> in E3, 293 to 2638 kg ha<sup>-1</sup> in E4, 396 to 3312 kg ha<sup>-1</sup> in E5 and 761 to 2361 kg ha<sup>-1</sup> in pooled over E3, E4 and E5 (Table 15a). Among all the environments the highest mean grain yield found in E1 (2090 kg ha<sup>-1</sup>) followed by pooled over E1, E2 (1844 kg ha<sup>-1</sup>) (Table 16a and Fig. 10).

In the flowering groups G4 had the highest mean grain yield  $(2195 \pm 247.9 \text{ kg ha}^{-1})$  in E1, whereas G3 had highest grain yield  $(1291\pm147.7 \text{ kg ha}^{-1})$  in E2 and in pooled over E1 and E2  $(1719\pm215.9 \text{ kg ha}^{-1})$ . There are no significant differences between the flowering groups in either environments and pooled over both environments (Table 16b-d).

The widest range of grain yield was found in the accessions of race *guinea* in E1 (377 to 3291 kg ha<sup>-1</sup>) and E4 (293 to 2298 kg ha<sup>-1</sup>), *caudatum* in E3 (324 to 3148 kg ha<sup>-1</sup>), E5 (999 to 2754 kg ha<sup>-1</sup>) and in pooled over E3, E4 and E5 (1142 to 2210 kg ha<sup>-1</sup>). In E2 (321 to 2504 kg ha<sup>-1</sup>) and pooled over E1 and E2 (479 to 3140 kg ha<sup>-1</sup>) the widest range was found in the accessions of intermediate race *guinea-caudatum* (Tables 17a-g). In all the environments the races and intermediate races as group differ significantly from the wilds (Tables 19a-g).

## 4.3.10. SCMR at the time of flowering (SPAD1)

The SPAD1 of entire set ranged from 34.2 to 62.6 in E1, 35.4 to 61.2 in E2, 35.0 to 61.3 in pooled over E1 and E2, 33.4 to 59.3 in E3, 41.3 to 56.1 in E4, 32.9 to 59.2 in E5 and 37.6 to 55.8 in pooled over E3, E4 and E5 (Table 15a). Among the environments the widest range was found in E1 (3.2 to 62.6) followed by E2 (35.4 to 61.2) and pooled over E1 and

E2 (35 to 61.3). The highest mean SPAD1 was found in E4 (50.1) followed by pooled over E3, E4, E5 (49.8) and E5 (48.6) (Table 16a).

Among the flowering groups the widest range was found in G2 (39.3 to 62.6) in E1, G3 (35.4 to 58.2) in E2 and G4 (36.2 to 58.9) in pooled over E1 and E2 (Table 15 b-d). The G1 (51.6 $\pm$ 2.50) in E1, G2 in E2 (51.1 $\pm$ 3.20) and in pooled over E1 and E2 (51.1 $\pm$ 2.90) had the highest mean SPAD1 (Table 16b-d). The intermediate race *kafir-caudatum* had the highest mean for SPAD1 in all the environments except in E3 and E5 in which the *guinea-caudatum* had the highest mean SPAD1. The basic races and intermediate races as groups differed significantly from the wilds in all the environments.

#### 4.3.11. SCMR at 30 days after flowering (SPAD2)

The SPAD2 of the entire reference set ranged from 21.1 to 53.2 in E1, 6.8 to 51.5 in E2, 17.2 to 50.3 in pooled over E1 and E2, 27.5 to 52.2 in E3, 33.5 to 47.7 in E4, 15.9 to 56.1 in E5 and 31.1 to 47.8 in pooled over E3, E4 and E5. Among all the environments the widest range and highest mean was found in E5 followed by E2 and pooled over E1 and E2 (Table 15a). The highest mean SPAD2 was found in pooled over E3, E4 and E5 (42.7) followed by E4 (41.9), E5 (41.7) and E3 (40.7) (Table 16a). Among the flowering group, G2 (21.3 to 51.9) in E1, G3 in E2 (13.3 to 49.4) and in pooled over E1 and E2 (17.2 to 49.3) had the widest range for SPAD2 (Table 15b-d) .Among the flowering groups the highest mean SPAD2 was found in G7 (35.1 $\pm$ 3.42) in E1, G1 in E2 (37.5 $\pm$ 3.41) and pooled over E1 and E2 (35.7 $\pm$ 3.49) (Tables 16b-d). The race *kafir* had the highest SPAD2 than other basic races in the all the environments (Table 18a-g). Races, intermediate races and wilds as groups did not differ significantly from each other in all the environments (Tables 19a-g).

#### **4.4 VARIANCES**

Variances were calculated for entire reference set, flowering groups, individual basic races, intermediate races, wild types and as group in all the environments. The homogeneity of variance was tested using Levene's test.

Variances of entire reference set between the environments were heterogeneous for all the eleven quantitative characters (Table 20). Within the flowering group (Tables 21a-c) of E1, E2 and pooled over E1 and E2 variances were homogenous for panicle exsertion, panicle length, panicle width, basal tillers, hundred seed weight, panicle weight and grain yield per plot. The variances in all the flowering group were significantly different for the characters days to 50 per cent flowering (E1, E2 and pooled over E1 and E2), plant height, SPAD1 (E1 and pooled over E1 and E2) and SAPD2 (E2).

The variances among individual races, intermediate races and wilds are given in Tables 22a-g. Variances among basic races were homogeneous for days to 50 per cent flowering, plant height, hundred seed weight, panicle weight, grain yield, SPAD1 and SPAD2 in all the individual environments and pooled.

Variances of races, intermediate races and wilds as group were homogeneous for days to 50 per cent flowering (except E1), plant height, panicle exsertion, grain yield, SPAD1 and SPAD2 in E1, E2 and pooled over E1 and E2. The characters panicle length, panicle width and basal tillers in E1, E2 and pooled over E1 and E2 were found to be heterogeneous. In E3, E4, E5 and in pooled over E3, E4 and E5 all the characters were found to have homogenous variance between races, intermediate races and wilds as group. The wild types as group had highest variance for days to 50 per cent flowering, panicle width and basal tillers followed by intermediate races for panicle exsertion, grain yield per plot and races for panicle length in E1, E2 and pooled over E1 and E2.

#### **4.5. CORRELATION STUDIES**

The correlation analysis was carried out for the entire reference set, each of the seven flowering groups and for five races, ten intermediate races and five wild sub species as groups in all the environments.

## 4.5.1. Correlation study for entire reference set

In entire reference set any correlation with 382 degrees of freedom with a value of more than 0.100 will be significant at P=0.05 and greater than 0.120 will be significant at P=0.01. The correlation coefficients which are greater than 0.500 or smaller than -0.500 are considered as the useful correlation, as at least 25 per cent of the variation in one trait is predicted by the other (Upadhyaya *et al.*, 2010). The entire reference set had 55 correlations in each environment. Of this 55 correlations (in each environment) 6 in E1, 4 in E2, 8 in pooled over E1 and E2, 2 each in E3, E4, E5 and pooled over E3, E4 and E5 were found to

be useful correlations. The details of the correlation for entire reference set were given in the table 23a.

## 4.5.1.1. Correlation between grain yield and other component traits

The grain yield per plot had significant negative correlation with days to 50 per cent flowering, plant height, panicle exsertion, panicle length, panicle width, and basal tillers in E1, E2 and pooled over E1 and E2. Grain yield per plot had highly significant positive correlation with the panicle weight in all environments and with hundred seed weight in E4 and pooled over E3, E4, E5 (Table 23a). Basal tillers in E1(r= -0.590) and in pooled over E1and E2 (r= -0.587) and panicle weight in all the environments (E1-r=0.940, E2- r= 0.781, pooled over E1 and E2- r=0.928, E3-r=0.924, E4-r=0.919, E5-r=0.793 and pooled over E3, E4 and E5- r=0.734) had useful correlations with grain yield per plot (Table 23b).

## 4.5.1.2. Inter correlation among the yield component traits

## 4.5.1.2.1. Plant height

Plant height had significant positive correlation with days to 50 per cent flowering in all the environments and pooled (Table 23a). The useful correlation between the plant height and days to 50 percent flowering was found in E1 (r=0.593), E2 (r=0.513) and in pooled over E1 and E2 (r=0.562) (Table 23b).

## 4.5.1.2.2. Panicle exsertion

Panicle exsertion had highly significant negative correlation with days to 50 per cent flowering and positive correlation with plant height in all the individual environments and pooled (Table 23a).

## 4.5.1.2.3. Panicle length

Panicle length had significant positive correlation with days to 50 per cent flowering, plant height, panicle exsertion in the individual environments and pooled (Table 23a).

## 4.5.1.2.4. Panicle width

Panicle width had significant positive correlation with days to 50 per cent flowering only in E1. Plant height and panicle length had significant positive correlation with panicle width in the individual environments and pooled. In E3 panicle width had significant

negative correlation with panicle exsertion whereas in E5 it had positive correlation (Table 23a).

The useful correlation between panicle width and panicle length was exhibited in E1 (r=0.710), pooled over E1 and E2 (r=0.630), E3 (r=0.633), E4 (r=0.513) and pooled over E3, E4 and E5 (r=0.602) (Table 23b).

## 4.5.1.2.5. Basal tillers

The number of basal tillers had significant negative correlation with days to 50 per cent flowering in E3 and in pooled over E3, E4 and E5. It had significant positive correlation with plant height (in E1, E4, E5 and pooled over E1, E2), panicle exsertion (in all environments and pooled), panicle length and panicle width (in E1, E2, E5 and pooled over E1 and E2) (Table 23a).

## 4.5.1.2.6. Hundred seed weight

Hundred seed weight had a significant negative correlation with days to 50 per cent flowering (in all environments), plant height (in E3, E5 and pooled over E3, E4, E5) panicle length (in all the environments), panicle width (in E2, E4, E5 and pooled over E3, E4, E5) and basal tillers (in E1, E5 and pooled over E3, E4, E5) (Table 23a).

## 4.5.1.2.7. Panicle weight

Panicle weight had significant negative correlation with days to 50 per cent flowering (E1), plant height, panicle exsertion, panicle length, panicle width, basal tillers in E1, E2 and pooled over E1 and E2. In E2, E4 and pooled over E3, E4 and E5 panicle weight had significant positive correlation with hundred seed weight (Table 23a).

The useful correlation between panicle weight and basal tillers was found in E1 (r=-0.607), E2 (r=-0.533) and pooled over E1 and E2 (r=-0.630) (Table 23b).

## 4.5.1.2.8. SCMR at the time of flowering (SPAD1)

SPAD1 had significant negative correlation with days to 50 per cent flowering, plant height, panicle length, panicle width, basal tillers and positive correlation with hundred seed weight, panicle weight and yield in E1, E2 and in polled over E1 and E2. In E3, SPAD1 had significant positive correlation with hundred seed weight (Table 23a).

In E1 and in pooled over E1 and E2 SPAD1 had useful correlation with days to 50 per cent flowering (E1 r= -0.596, pooled over E1 and E2 r= -0.537) and plant height (E1 r= -0.560, pooled over E1 and E2 r= -0.554) (Table 23b).

#### 4.5.1.2.9. SCMR 30 days after flowering (SPAD2)

The SPAD2 in entire reference set had significant negative correlation with plant height and positive correlation with SPAD1 in E1, E2 and pooled over E1 and E2. Panicle width and hundred seed weight had positive correlation where as the basal tillers had negative correlation with SPAD2 in E2. In all the environments SPAD2 had significant positive correlation with SAPD1 (Table 23a)

SPAD2 had useful correlation with SPAD1 in E2 (r= 0.649) and in pooled over E1 and E2 (r= 0.710) (Table 23b).

#### 4.5.2. Correlation study in flowering groups of E1 and E2.

The correlation analysis was carried out for each flowering group in E1, E2 and pooled over E1 and E2. The results of the analysis are given in Tables 24a-c.

The significant positive correlation in the flowering groups ranged from 6 (G6) to 28 (G4) in E1 (Table 24a), 13 (G6) to 35 (G3) in E2 (Table 24b) and 8 (G7) to 31 (G3) in pooled over E1 and E2 (Table 24c). Among these significant correlations, E1 had 61 (total of all flowering group), E2 had 41 and pooled over E1 and E2 had 59 useful correlations. The flowering group G6 had highest number of useful correlation in E1 (18), E2 (13) and pooled over E1 and E2 (16) (Tables 24a-c).

## 4.5.3. Correlation study for races, intermediate races and wilds as group

Correlation analysis was carried for races, intermediate races and wilds as group in all the environments. The correlation coefficients are given in the Tables 25a-g. The correlation analysis of races as group had 33 correlations each in E1 and pooled over E1 and E2, 38 correlations in E2, 14 correlations in E3, 16 correlations each in E4 and E5 and 24 correlations in pooled over E3, E4 and E5 were found to be significant either at p=0.05 or p=0.01. Out of these significant correlations, eight correlations each in E1 and pooled over E3 and E5 and E2 and E2, 4 correlations in E2, 2 correlations each in E3 and pooled over E3, E4 and E5 and E5

and one correlation in E4 and E5 were found to have useful correlation (0.05> r <-0.05) (Table 25a-g).

The correlation analysis of intermediate races as group showed 25 correlations in E1 and E2, 27 correlations in pooled over E1 and E2, 13 correlations in E3, 17 correlations in E4, 11 correlations in E5 and 15 correlations in pooled over E3, E4 and E5 were found to be significant either at p=0.05 or p=0.01 (Tables 25a-g). In these significant correlations, one correlation in E1, 5 correlations in pooled over E1 and E2, 2 correlations each in E3, E4, pooled over E3, E4 and E5 and one correlation in E5 were considered useful.

In case of wild types as a group 10 in E1, 12 in E2, 18 in pooled over E1 and E2, 8 in E3, 6 in E4, 5 in E5 and 4 in pooled over E3, E4 and E5 were significant correlations. Of these, 8 correlations in E1, 6 correlations in E2, 10 correlations in pooled over E1 and E2, 3 correlations in E3, 2 two correlations in E4, 1 correlation in E5 and 3 correlation in pooled over E3, E4 and E5 were considered useful (Table 25 a-g).

Over all, the correlation analysis based on the races, intermediate races and wild types as separate groups showed that the correlation between panicle weight and grain yield and between panicle width and panicle length were found to be useful correlation in all the environments and in all the groups (Table 25a-g).

## 4.6. SHANNON-WEAVER'S DIVERSITY INDEX (H')

The Shannon-weaver's (H') diversity index was calculated to compare phenotypic diversity for the 11 quantitative characters among entire reference set, flowering groups, races, intermediate races and wilds. Intermediate races: *caudatum-kafir, durra-kafir, bicolor-kafir, guinea-kafir, durra-guinea, guinea-bicolor* and in wilds: *Arundinaceum, Aethiopicum, Virgatum and Verticilliflorum* were not used in the analysis as they were represented by less than five accessions.

The H' of entire reference set is given in the Table 26. In E2 and pooled over E1 and E2 the highest H' value was found for grain yield (E2 – 0.64 and pooled -0.63) and the lowest for panicle width (0.52) in E1 and for basal tillers in E2 (0.46) and pooled over E1 and E2 (0.49). The highest H' value was observed for SPAD1 and SPAD2 in E3 (0.64), SPAD1 and basal tillers in E4 (0.63) and for SPAD1 and panicle weight in pooled over E3, E4 and E5 (0.63) whereas in the E5 the highest H' value was found for panicle length,

panicle weight and SPAD2 (0.63). The lowest H' value in E3 (0.47), E4 (0.46), E5 (0.55) and pooled over E3, E4 and E5 (0.48) was found for panicle width. The H' value averaged over the environments ranged from  $0.50\pm0.021$  (panicle width) to  $0.62\pm0.020$  (hundred seed weight) (Table 26).

The H' values averaged over the flowering groups was highest for grain yield  $(0.58\pm0.028)$  in E1, E2  $(0.59\pm0.015)$  and for SPAD1  $(0.59\pm0.015)$  in pooled across E1 and E2. Accessions of G3 (in E1:  $0.58\pm0.023$ , E2:  $0.60\pm0.011$  and pooled over E1 and E2:  $0.59\pm0.015$ ) were found to be highly diverse and the accessions of G7 (E1:  $0.41\pm0.021$ , E2:  $0.46\pm0.040$ , pooled:  $0.46\pm0.017$ ) had lowest H' (Table 27a-c).

The H' value averaged over races, intermediate races and wilds ranged from  $0.47\pm0.043$  (panicle width) to  $0.57\pm0.014$  (panicle weight) in E1;  $0.44\pm0.045$  (basal tillers) to  $0.57\pm0.017$  (SPAD1) in E2 and  $0.53\pm0.013$  (basal tillers) to  $0.58\pm0.011$  (SPAD 2) in pooled across E1 and E2. The H' value ranged from  $0.38\pm0.053$  (panicle width) to  $0.57\pm0.019$  (SPAD2) in E3;  $0.44\pm0.051$  (panicle width) to  $0.57\pm0.014$  (Hundred seed weight) in E4;  $0.41\pm0.043$  (panicle width) to  $0.59\pm0.010$  (plant height) in E5 and  $0.51\pm0.025$  (panicle width) to  $0.57\pm0.011$  (SPAD1) in pooled over E3, E4 and E5.

The lowest H' averaged over the traits was found in the intermediate race *durra-bicolor* in E1 (0.44 $\pm$ 0.034), E2 (0.45 $\pm$ 0.025), E4 (0.47 $\pm$ 0.020) and pooled over E1 and E2 (0.44 $\pm$ 0.024), *caudatum-bicolor* in E3 (0.46 $\pm$ 0.036) and wild subspecies *Drummondii* (0.48 $\pm$ 0.014) in pooled over E3, E4 and E5 (Table 28a to 28g).

## 4.7. PHENOTYPIC DIVERSITY INDEX

The grouping of similar genotypes depends on the dissimilarity among them, which can be determined by the phenotypic diversity index. The average diversity index in the entire reference set was 0.24. The minimum diversity index in the entire reference set (0.00) was observed between IS 29472 and IS 29407 and the maximum diversity (0.54) was observed between IS 36563 and IS 31533. Among the flowering groups, the average diversity index was highest in the G7 (0.30) followed by G1 and G6 (0.28) and the lowest was found in G4 and G5 (0.24). The range of phenotypic diversity was highest in G1 (0.03 to 0.63) and lowest was in G6 (0.10 to 0.47) and it was similar in G3 (0.01- 0.57) and G4 (0.01-0.57).

When compared within each flowering group between accessions, maximum phenotypic diversity was observed between IS 33844 and IS 18821 in G1 (0.63); between IS 13848 and IS 13 in G2 (0.54); between IS 41724 and IS 35 in G3 (0.57); between IS 14206 and IS 9527 in G4 (0.57); between IS 24786 and IS 14216 in G5 (0.48); between IS 27855 and IS 18758 in G6 (0.47) and between IS 18829 and IS 18758 in G7 (0.56). Lowest phenotypic diversity index was observed between IS 28849 and IS 28740 in G1 (0.03); between IS 29472 and IS 29407 in G2 (0.00); between IS 13827 and IS 8685 in G3 (0.01); between IS 26554 and IS 26457 in G4 (0.01); between IS 14414 and IS 4963 in G5 (0.03); between IS 27390 and IS 6828 in G6 (0.10) and between IS 33844 and IS 18758 (0.10) in G7 (Table 29a). The five least similar (most diverse) and five most similar (least diverse) accessions are given in the Table 30a.

Environment wise mean phenotypic diversity index was almost similar in the E3, E4, E5 and pooled over E3, E4 and E5 (0.22 to 0.23). The range of diversity index was highest in the E4 (0.01to 0.52) and it was similar in E3, E5 and pooled over E3, E4 and E5 (0.01 to 0.50) (Table 29b). Maximum phenotypic diversity index was observed between IS 41724 and IS 2678 in E3 (0.50); between IS 41(52)500 and IS 13 in E4 (0.52); between IS 18821 and IS 903 in E5 (0.50) and between IS 41 (52) 500 and IS 13 in pooled over E3, E4 and E5 (0.00); between IS 41 (52) 500 and IS 13 in pooled over E3, E4 and E5 (0.50). The minimum diversity index was between IS 23100 and IS 13827 in E3 (0.00); between IS 26457 and IS 25077 in E4 (0.01); between IS 22506 and IS 22291 in E5 (0.01) and between SSM 215 and IS 24139 in pooled (0.00) (Table 30b).

#### **4.8. PRINCIPAL COMPONENT ANALYSIS**

#### 4.8.1. Principal component analysis for entire sorghum reference set

The principal component analysis (PCA) of entire reference set was carried out using data for individual environment and pooled over environments. The percentage of variation explained by the first five PCs and the vector loadings for each character and PC are given in the Table 31.

The percentage of variation explained by the first five PCs was 88.50 in E1, 79.15 in E2, 87.91 in pooled over E1 and E2, 70.39 in E3, 69.95 in E4, 64.85 in E5 and 71.73 in pooled over E3, E4 and E5. The PCA reduced the original 11 characters into 9 characters in E1, E2 and pooled over E1 and E2 and into 8 characters in E3, E4, E5 and pooled over E3, E4 and E5. The PC1 explained 34.42 per cent variation in E1, 30.15 per cent in E2, 35.20

per cent in pooled over E1 and E2, 18.19 per cent in E3, 20.05 per cent in E4, 19.27 per cent in E5 and 22.23 in pooled over E3, E4 and E5.

The egien values for the PC1 were 3.4 (E1), 3.3 (E2), 3.5 (pooled over E1, E2), 2.0 (E3), 2.2 (E4), 2.1 (E5) 2.5 (pooled over E3, E4 and E5). The PC1 separates the accessions on 3 traits in E1 (panicle width, panicle weight and yield), E2 (basal tillers, panicle weight and yield) and on 4 characters in pooled over E1 and E2 (basal tillers, panicle weight, yield and SPAD1). In E3, E5 and pooled over E3, E4 and E5, PC1 separates the accessions on 2 characters viz., panicle weight and grain yield per plot whereas in E4 accessions were separated based on panicle length and width.

Considering the analysis of entire reference set in individual environment and pooled, the characters such as days to 50 per cent flowering, panicle exsertion, panicle length, basal tillers, panicle weight, grain yield and SPAD1 occurred at least four times in first five PCs indicating their importance for characterization of sorghum reference set.

The scatter plots of first two PCs based on pooled data over E1, E2 and E3, E4 and E5 for 11 quantitative traits are shown in Figure 11a and 11b. In the scatter plot based on pooled data over E1 and E2, PC1 explained 55.9 per cent and PC2 explained 23.0 per cent variation of the total variation. The accessions of wild types *Arundinaceum, Drummondii, Virgatum and verticilliflorum* and the accessions of the races bicolor and guinea were grouped together and they were clearly separated from other races and intermediate races in E1 and E2 pooled data. In the scatter plot of the pooled data over E3, E4 and E5, PC1 explained 30.0 per cent and PC2 explained 26.0 per cent of the total variation. The accessions of all the five basic races, five intermediate races and the wild type *Arundinaceum* were grouped together. The other intermediate races and the wild subspecies grouped separately.

# 4.8.2. Principal component analysis for individual flowering groups of sorghum reference set in E1 and E2.

PCA was carried out for each flowering group (G1 to G7) in E1, E2 and pooled over E1 and E2, separately (Table 32a-c). In E1 the percentage of variation explained by the first three PCs was 73.79 per cent in G1, 71.50 per cent in G2, 71.62 per cent in G3, 74.13 per cent in G4, 71.42 per cent in G5, 80.54 per cent in G6 and 85.62 per cent in G7 (Table 32a). In E2, the percentage of variation explained by first three PC was 60.84 (G1), 60.74 (G2),

65.56 (G3), 67.41 (G4), 66.11(G5), 75.67 (G6) and 83.18 (G7) percent (Table 32b). In pooled over E1and E2 the percentage of variation explained by first three PCs was 68.4 (G1), 72.4 (G2), 71.8 (G3), 75.3 (G4), 69.8 (G5), 82.0 (G6) and 87.4 (G7) per cent (Table 32c).

The variation explained by the first PC ranged from 29.83 (G2) to 48.54 (G6) in E1, 23.91 (G2) to 49.28 (G7) in E2 and 30.5 (G2) to 46.6 (G7) in pooled over E1 and E2. The eigen value of the first PC ranged from 3 (G2) to 4.9 (G6) in E1, 2.63 (G2) to 5.42 (G7) in E2 and 3.1 (G2) to 4.7 (G7) in pooled over E1 and E2.

In E1, PC1 separates the accessions on three characters in G1 (Days to 50% flowering, basal tillers, panicle weight), G2 and G5 (Basal tillers, panicle weight and grain yield per plot); on four traits in G3 (Panicle length, basal tillers, yield and panicle weight), G4 (panicle width, basal tillers, panicle weight and yield) and G7 (plant height, panicle length, panicle width and yield) and on five characters in G6 (Plant height, panicle length, panicle width, panicle weight and grain yield per plot). In E2 and pooled over E1 and E2, PC1 separates the accessions on 3 characters in G1 (Basal tillers, panicle weight and grain yield per plot) and G2 (E2-Basal tiller, panicle length and panicle width, pooled over E1 and E2- Basal tiller, panicle weight and grain yield per plot); four characters in G3 (panicle length, basal tillers, panicle weight and grain yield per plot), G4 (panicle width, basal tillers, panicle weight and grain yield per plot), G5 (E2- Basal tillers, hundred seed weight, panicle weight and grain yield per plot, pooled over E1 and E2 - panicle width, panicle weight and grain yield per plot) and G6 (E2- Panicle width, panicle weight, grain yield, panicle length, in Pooled over E1 and E2- panicle width, panicle weight, plant height and grain yield per plot) and on five characters in G7 (E2 - Panicle length, basal tillers, panicle weight, hundred seed weight and grain yield per plot, in pooled over E1 and E2 - Panicle length, basal tillers, panicle weight, hundred seed weight and plant height).

Considering the analysis of individual flowering groups in E1, E2 and pooled over E1, E2, the characters such as days to 50 per cent flowering (E1), panicle length, panicle width, basal tillers, panicle weight, grain yield, SPAD1 and SPAD2 occurred at least five times in first three PC indicating their importance for characterization of sorghum reference set accessions.

# 4.8.3. Principal component analysis for races, intermediate races and wilds as group of sorghum reference set.

The results of PCA in E1, E2 and pooled over E1 and E2 revealed the importance of first 3 PCs in explaining the variation in races, intermediate races and wild types as group, where as in E3, E4, E5 and pooled E3, E4, E5 first four PCs were found important in explaining the variability (Table 33).

The percentage of total variation explained by three PCs for races as group in E1, E2 and pooled over E1 and E2 and by four PCs in E3, E4 and pooled over E3, E4 and E5 were 67.3 in E1, 61.9 in E2, 70.4 in pooled over E1 and E2, 60.7 in E3, 59.9 in E4, 55.5 in E5 and 61.3 in pooled over E3, E4, E5. In intermediate races as group the percentage of total variation explained by the first three (E1, E2 and Pooled over E1 and E2) and four (E3, E4 and pooled over E3, E4 and E5) PCs were 69.3 in E1, 59.6 in E2, 71.3 in pooled over E1 and E2, 62.0 in E3 and E4, 56.2 in E5 and 63.5 in pooled over E3, E4 and E5. The percentage of variation explained by the wild type as group was 73.6 in E1, 65.4 in E2, 76.1 in pooled over E1 and E2, 76.0 in E3, 73.5 in E4, 67.4 in E5 and 71.9 in pooled over E3, E4 and E5.

The PC1 which is important component accounted for the variation of races as group ranged between 17.4 per cent in E5 and 34.7 in pooled over E1 and E2. In intermediate races the variation explained by the first PC1 ranged from 17.1 in E5 and 31.6 in pooled over E1 and E2, whereas for wild type as group it ranged from 21.9 (E5) to 36.6 (pooled over E1 and E2).

The eigen values of races as group ranged from 1.9 (E5) to 3.5 (pooled over E1 and E2), for intermediate race as group it ranged between 1.9 (E5) to 3.2 (pooled over E1 and E2) and for wild type as group the eigen value ranged from 2.4 to 3.7 (pooled over E1 and E2).

In races as group the PC1 separates the accessions on three traits in E1 (plant height, panicle weight and pot grain yield), E2 (basal tillers, panicle weight, grain yield per plot), pooled over E1 and E2 (panicle weight, grain yield per plot and SPAD1) and on two traits in E3 (panicle length and panicle width), E4 (panicle weight and grain yield per plot), E5 (plant height and panicle length) and pooled over E3, E4 and E5 (panicle weight and grain yield). In intermediate races as group PC1 separates the accessions on three traits in E1, E2 (basal

tillers, panicle weight, grain yield) and in pooled over E1 and E2 (Basal tillers, panicle weight and SPAD1), two traits in E3 (panicle length, panicle width), E4 (plant height and panicle length), E5 (panicle weight and grain yield) and pooled over E3, E4 and E5 (panicle length and panicle width). The wilds as group separates the accessions on three traits in E1, E2 (Days to 50% flowering, plant height and panicle length), E3 (Panicle weight, grain yield per plot and plant height), E4 (panicle weight, grain yield, panicle length), on four traits in pooled over E1 and E2 (plant height, panicle length, panicle width and panicle weight) and on two traits in E5 (panicle weight and hundred seed weight) and pooled over E3, E4 and E5 (plant height and hundred seed weight) and pooled over E3, E4 and E5 (plant height and hundred seed weight) and pooled over E3, E4 and E5 (plant height and hundred seed weight) and pooled over E3, E4 and E5 (plant height and per plot).

Considering the analysis of races, intermediate races and wilds as group, seven character *viz.*, days to 50 per cent flowering, plant height, panicle length, panicle width, panicle weight, grain yield and SPAD1 occurred at least ten times in first three PC indicating their importance for characterization of sorghum reference set accessions.

## **4.9. CLUSTERING**

The hierarchical cluster analysis was conducted for the entire reference set in all the environments using the method of Ward (1963) on the scores of first three PCs.

In E1 the entire reference set was grouped into three clusters. Cluster I consists of all the wild types (13 accessions) except *Drummondii*. In cluster II the races *bicolor*, *guinea* and intermediate races *caudatum-bicolor*, *durra-caudatum* and *kafir-bicolor* grouped together (168 accessions). The remaining races (*caudatum*, *durra and kafir*) and intermediate races (*durra-bicolor*, *guinea bicolor*, *guinea-caudatum*, *guinea-durra*, *kafir-durra*, *guinea-kafir and kafir-caudatum*) grouped in the cluster III (203accessions) (Fig. 12a).

In E2 the accessions of entire reference set was grouped into three clusters. The cluster I grouped with all the wild type along with the races *bicolor* and *guinea* (155 accessions). The remaining races and intermediate races were grouped in the cluster II (174 accessions) and cluster III (55 accessions) (Fig. 12b).

In pooled over E1 and E2 the entire reference set was grouped into three clusters. The wilds *Arundinaceum*, *Drummondii*, *Verticilliflorum* and *Virgatum* along with the races *bicolor* and *guinea* grouped in the cluster I (124 accessions). In cluster II the races *caudatum*, *durra* and the intermediate races *durra-bicolor*, *guinea-bicolor*, *guinea-durra*, *guinea-caudatum* and *kafir-durra* grouped together (177 accessions). The race *kafir* and the remaining intermediate races (*caudatum-bicolor*, *durra-caudatum*, *kafir-bicolor*, *kafir-caudatum*) grouped together in cluster III (84 accessions) (Fig. 12c).

In E3 the entire reference set was grouped into two clusters. The intermediate races *guinea-kafir, guinea-bicolor* and the wilds *Aethiopicum* and *Virgatum* are grouped in cluster I (13 accessions). All the basic races, intermediate races, except *guinea-bicolor* and *guinea-kafir* and wild types except *Aethiopicum* and *Virgatum* grouped together in the cluster II (372 accessions). The cluster II was divided into two sub-clusters (cluster IIa and IIb). The cluster IIa (134 accessions) grouped the accession of *guinea, kafir, caudatum-bicolor, kafir-caudatum, Drummondii* and *Verticilliflorum*. In cluster IIb the remaining races and the intermediate races *durra-bicolor, durra-caudatum, durra-guinea, guinea caudatum* and the wild *Arundinaceum* grouped together which comprising of 237 accessions (Fig. 12d).

In E4 the entire reference set was grouped into three clusters. The cluster I (11 accessions) had two wilds (*Arundinaceum* and *Virgatum*) and one intermediate race (*guinea-kafir*), where as the cluster II (3 accessions) had two wilds *Aethiopicum* and *Verticilliflorum*. All the races and the remaining intermediate races grouped in the cluster III (361 accessions) (Fig. 12e).

The entire reference set in the E5 was grouped into 5 clusters. The wilds except *drummondii* were grouped in the cluster I and cluster II. The cluster III (365 accessiosn) comprises all the basic races, five intermediate races and one wild type. The remaining intermediate races were grouped in cluster IV (3 accessions) (*kafir-caudatum, guinea-kafir*) and cluster V (13 accessions) (*kafir-durra, guinea-durra, guinea-bicolor*) (Fig. 12f).

In pooled over E3, E4 and E5 the accessions were grouped into four clusters. The cluster I consisted of all the basic races (245 accessions) and the intermediate races (113 accessions) *durra-caudatum*, *guinea-caudatum*, *guinea-durra*, *durra-bicolor*, *caudatum-bicolor*, *kafir-durra* and *guinea-bicolor* and the wild types *Drummondii* (10 accessions) and *Virgatum* (6 accessions). The wilds *Aethiopicum*, *Arundinaceum* and *Verticilliflorum* and the intermediate race *guinea-kafir* are grouped in the cluster III (8 accessions). The cluster IV consisted of intermediate race *kafir-bicolor* and *kafir-caudatum* (2 accessions).

## 4.10. IDENTIFICATION OF TRAIT SPECIFIC ACCESSIONS

## 4.10.1. Identification of drought tolerant genotypes based on drought tolerance indices

The drought tolerance indices such as Stress Tolerance Index (STI), Mean Productivity (MP), Geometric Mean Productivity (GMP), Stress Susceptible Index (SSI), Per cent tolerance (TOL) in yield and drought tolerance efficiency (DTE) were worked out from yield under irrigated condition (Yp) and yield under drought stressed conditions (Ys) from the pooled data of entire reference set and each flowering group.

In order to select the genotypes based on the combination of indices, PCA was carried out for assessing the relationship between all of the indices. The PCA for entire reference set and each flowering group revealed that the first PC explained 61.2 per cent (entire reference set), 63.6 per cent (G1), 59.6 per cent (G2), 72.9 per cent (G3), 65.3 per cent (G4), 60.5 per cent (G5), 72.8 per cent (G6) and 60.3 per cent (G7) of variations with Yp, Ys, STI, MP, and GMP. Thus the first dimension is yield potential and drought tolerance and it separates the drought tolerant accessions with good yield potential under drought stress and non-stress conditions. The second PCs explained 38.0 (entire reference set), 35.5 (G1), 39.8 (G2), 26.2 (G3), 33.9 (G4), 38.9 (G5), 26.5 (G6) and 38.8 (G7) per cent of variations with SSI, TOL, and DTE (Table 34). The second component is stress tolerant dimension and it separates the stress tolerant accessions from the non-stress tolerant accessions.

Based on the scores of first two PCs cluster analysis was carried out for entire reference set and in each flowering group. The genotypes in G1, G5, G6 and G7 were grouped in to 3 clusters and the genotypes of entire reference set and the flowering groups G2, G3 and G4 were grouped into five clusters.

The accessions of cluster 1 in G1 (13 accessions), G5 (17 accessions), G6 (4 accessions), G7 (4 accessions) and the accessions of cluster 3 (35 accessions) in G2, accessions of cluster 4 in G3 (34 accessions), G4 (10 accessions) and entire reference set (118 accessions) were found to have high mean for Yp, Ys, STI, MP, GMP, DTE and low SSI and TOL (Table 35). The accessions selected from these clusters will perform well in both drought stress and non-stress condition with good yield potential.

Thirty five drought tolerant accessions were selected from the entire reference set represents three races (15 *Caudatum*, 7 *Durra*, and 5 *Kafir*) and three intermediate races (1

each of c*audatum-bicolor* and *durra-bicolor*, 6 *guinea-caudatum*) and seventy five accessions were selected from the flowering groups represents all the five races (1 *bicolor*, 27 *caudatum*, 7 *durra*, 4 *guinea* and 10 *kafir*) and three intermediate races (4 *caudatum-bicolor*, 1 *durra-caudatum* and 13 *guinea-caudatum*).

In entire reference set 35 accessions *viz.*, IS 23574, SSM19, IS 16125, IS 23601, IS 929, SSM 215, IS 15466, IS 5106, IS 33261, IS 24786, IS 6351, IS 33423, IS 102(111)525, IS 12110, IS 26833, IS 30898, IS 5622, IS 8882, IS 21991, IS 22239, IS 31179, IS 22632, IS 2730, IS 29872, IS 13845, SSM1592, IS 23048, IS 22334, IS 11026, IS 15443, IS 14963, IS 15428, IS 29911, IS 19418 and IS 22294, were identified with high mean for STI, GMP, MP, DTE and low mean for SSI, TOL. The mean grain yield of these accessions was 2669 kg ha<sup>-1</sup> under irrigated conditions and 2281 kg ha<sup>-1</sup> under un-irrigated conditions which is higher than the control cultivars IS2205 (Irrigated - 1952 kg ha<sup>-1</sup>, Un-irrigated-1844 kg ha<sup>-1</sup>), IS18758 (Irrigated - 2438 kg ha<sup>-1</sup>). The mean productivity (2475 kg ha<sup>-1</sup>) and geometric mean (2459 kg/ha<sup>-1</sup>) of the selected accessions were 11 per cent higher than the control cultivar IS 18758 (MP- 2244 kg/ha<sup>-1</sup>, GMP- 2235 kg/ha<sup>-1</sup>), 30 per cent higher than IS 2205 (MP- 1898 kg/ha<sup>-1</sup>, GMP- 1897 kg/ha<sup>-1</sup>) and 13 per cent higher than IS 33844 (MP- 2180 kg/ha<sup>-1</sup>, GMP- 2171 kg/ha<sup>-1</sup>). The average drought tolerance indices of the selected accessions were 1.6 (STI), 0.79 (SSI), 11.46 per cent (TOL), 88 per cent (DTE).

In G1, six accessions were selected *viz.*, IS 14963, IS 15752, IS 2848, IS 30335, IS 36563 and IS 36633. The yield of these accessions ranged from 1824 kg ha<sup>-1</sup> to 2945 kg ha<sup>-1</sup> under irrigated conditions and 1450 kg ha<sup>-1</sup> to 1774 kg ha<sup>-1</sup> under un-irrigated conditions with a mean productivity of 1994 kg ha<sup>-1</sup>. The mean SSI (0.82) and TOL (27.25) of selected accessions were lower than mean of the three control cultivars (SSI-1.0, TOL-33.5).

In G2, 9 accessions IS 15428, SSM1102, IS 22996, IS 16044, IS 3583, IS 30469 (453(486)512), IS 15443, IS 10978 and IS 3073 were selected. The yield of these selected accessions ranged between 2094 kg ha<sup>-1</sup> and 2687 kg ha<sup>-1</sup> under irrigated condition with the mean of 2402 kg/ha<sup>-1</sup> and it ranged between 1747 kg ha<sup>-1</sup> and 2029 kg ha<sup>-1</sup> under unirrigated conditions with mean of 1865 kg/ha<sup>-1</sup>. The mean drought tolerance indices of the selected accessions were 1.51 (STI), 2133 kg ha<sup>-1</sup> (MP), 2115 kg ha<sup>-1</sup> (GMP) and 1.26 (SSI)

and they were almost equal to the mean of three control cultivars (STI-1.67, MP-2230, GMP-2221 and SSI-1.0).

In G3 the following accessions (28 genotypes) IS 22334, SSM215, IS 33261, IS 20762, IS 23048, IS 22330, IS 31179, IS 102(111)525, IS 13845, IS 20842, IS 30898, SSM19, IS 10234, IS 19053, IS 8882, IS 16125, IS 9911, IS 6351, IS 5867, IS 23601, IS 2730, IS 33423, IS 19016, IS 23574, IS 21991, IS 26833, IS 5106 and SSM1592 were selected for their drought tolerance. Grain yield of these accessions ranged from 2109 kg ha<sup>-1</sup> to 3244 kg ha<sup>-1</sup> under irrigated conditions with the mean of 2651 kg ha<sup>-1</sup> and 1853 kg ha<sup>-1</sup> to 3083 kg ha<sup>-1</sup> under un-irrigated conditions with the mean of 2228 kg ha<sup>-1</sup>. The mean grain yield of the selected accessions was higher than the two control cultivars both in irrigated (IS 2205-2002 kg ha<sup>-1</sup>, IS 33844-1957 kg ha<sup>-1</sup>) and un-irrigated (IS 2205-1894 kg ha<sup>-1</sup>, IS 33844- 1781 kg ha<sup>-1</sup>) conditions. The MP (2439 kg/ha<sup>-1</sup>) and GMP (2424 kg/ha<sup>-1</sup>) of the selected accessions were 25 per cent higher than the IS 2205 (MP- 1948 kg/ha<sup>-1</sup> and GMP- 1947 kg/ha<sup>-1</sup>) and 30 per cent higher than IS 33844 (MP- 1869 kg/ha<sup>-1</sup> and GMP-1866 kg/ha<sup>-1</sup>). The mean drought tolerance indices of the selected accessions were 1.8 (STI), 1.4 (SSI), 15.2 (TOL) and 84.7 (DTE). The drought tolerance index, STI of the selected accessions was greater than the three checks IS2205 (STI-1.15), IS 18758 (STI -1.99) and IS 33844 (STI-1.05).

In G4 ten accessions, IS 15466, IS 29872, IS 13791, IS 13926, IS 22287, IS 19418, IS 29911, IS 22239, IS 22632 and IS 11026 were selected. The grain yield of the selected accessions ranged from 2155 kg ha<sup>-1</sup> to 3083 kg ha<sup>-1</sup> under irrigated conditions with a mean of 2402 kg ha<sup>-1</sup> and it ranged from 1778 kg ha<sup>-1</sup> to 2392 kg ha<sup>-1</sup> with the mean of 2176 kg ha<sup>-1</sup> under un-irrigated conditions. The grain yield per plot of the selected accessions were greater than the control cultivars both in irrigated (IS 2205-1971 kg ha<sup>-1</sup>, IS 18758- 2500 kg ha<sup>-1</sup>, IS 33844- 1928 kg ha<sup>-1</sup>) and un-irrigated conditions (IS 2205- 1859 kg ha<sup>-1</sup>, IS 18758- 2592 kg ha<sup>-1</sup>, IS 33844- 1745 kg ha<sup>-1</sup>). The drought tolerance index STI (1.7) of selected accessions were higher than the control cultivars IS 2205 (STI-1.19) and IS 33844 (STI-1.10). The mean MP (2289 kg/ha<sup>-1</sup>) and GMP (2282 kg/ha<sup>-1</sup>) of the selected accessions were 24 per cent higher than 18 2205 (MP- 1915 kg/ha<sup>-1</sup> and GMP- 1914 kg/ha<sup>-1</sup>).

In G5 the following accessions were selected IS 20792, IS 3685, IS 11119, IS 21891, IS 22294, IS 6745, IS 27891, IS 14735 and IS 32986. The grain yield per plot of the selected accessions ranged from 1434 kg ha<sup>-1</sup> to 2235 kg ha<sup>-1</sup> with the mean of 1739 kg/ha<sup>-1</sup> under irrigated conditions and 1563 kg ha<sup>-1</sup> to 2274 kg ha<sup>-1</sup> with the mean of 1711 kg/ha<sup>-1</sup> under un-irrigated conditions. The mean grain yield of the accessions were greater than the control cultivar IS 2205 under irrigated (1567 kg/ha<sup>-1</sup>) and un-irrigated conditions (1507 kg/ha<sup>-1</sup>). The mean MP (1725 kg /ha<sup>-1</sup>) and GMP (1724 kg/ha<sup>-1</sup>) of the selected accessions were 12 per cent higher than the control cultivar IS 2205 (MP- 1537 kg/ha<sup>-1</sup> and GMP- 1536 kg/ha<sup>-1</sup>).

In G6 and G7 a total of three genotypes were selected viz., IS 29691, IS 24713 (G6) and IS 32454 (G7). The mean grain yield of these genotypes under irrigated and unirrigated conditions was 1991 kg ha<sup>-1</sup> under irrigated conditions and 1760 kg ha<sup>-1</sup> under unirrigated conditions with the mean productivity of 1875 kg ha-1 which were on par with the mean grain yield of control cultivars under irrigated (2163 kg ha<sup>-1</sup>) and un-irrigated condition (1743 kg ha<sup>-1</sup>). The mean drought tolerance indices of the selected accessions were 1.57 (STI), 0.46 (SSI), 11.44 (TOL) and 88.58 (DTE).

## 4.10.2 Identification of accessions with high SCMR reading

SCMR was recorded at two stages of crop growth i.e. at the time of flowering and 30 days after flowering in both irrigated and un-irrigated conditions. The accessions with high SCMR (at both stages) in irrigated and un-irrigated condition were selected from the entire reference set and from each flowering group based on the E1 and E2 pooled and E3, E4 and E5 pooled.

#### 4.10.2.1 Identification of accessions with high SCMR in flowering groups

A total of 77 accessions were identified for high SCMR lines representing all the seven flowering groups based on the SCMR value at both stage in irrigated and un-irrigated conditions. The selected accessions represented five basic races (6 *bicolor*, 17 *caudatum*, 5 *durra*, 13 *guinea* and 20 *kafir*) from 21 countries and six intermediate races (5 *caudatum bicolor*, 1 *durra-bicolor*, 2 *durra-caudatum*, 13 *guinea-caudatum*, 1 *kafir-bicolor* and 1 *kafir-caudatum*) from 10 countries.

In G1, eight accessions IS 2848, IS 3511, IS 7958, IS 9883, IS 19262, IS 20749, IS2963 and IS30317 were identified with high SCMR at both the stage in irrigated and unirrigated conditions. The mean value of SCMR at flowering (SPAD1) under irrigated was 55.0 and under un-irrigated conditions it was 54.1 and the SCMR at 30 days after flowering (SAPD2) was 44.7 in irrigated condition and 36.7 in un-irrigated condition. The SCMR of the selected accessions at both the stages under irrigated and un-irrigated condition were higher than the control cultivars IS 2205 (SPAD1- 45.9 (irrigated), 41.7 (Un-irrigated), SPAD2- 41.3 (irrigated), 24.0 (Un-irrigated)), IS 18758 (SPAD1- 47.0 (irrigated), 47.0 (Un-irrigated), SPAD2- 39.5 (irrigated), 34.7 (Un-irrigated)), IS 33844 (SPAD1- 47.8 (irrigated), 46.1 (Un-irrigated), SPAD2- 36.2 (irrigated), 23.0 (Un-irrigated)).

In G2 the following 21 accessions were identified for high SCMR *viz.*, IS 303, IS 2367, IS 2398, IS 2807, IS 3672, IS 6973, IS 14276, IS 20710, IS 20727, IS 20743, IS 22325, IS 24009, IS 29375, IS 29407, IS 29409, IS 29472, IS 29496, IS 29569, IS 29876, IS 393(411)659 and IS 452(484)510. The mean SPAD1 of these accessions were 55.9 in irrigated condition and 56.9 in un-irrigated condition and SPAD2 was 40.9 in irrigated and 40.7 in un-irrigated condition. The SPAD1 and SPAD2 of the selected accessions under both the conditions were greater than the control cultivars IS 2205 (SPAD1 irrigated -42.8, Un-irrigated -44.0 and SPAD2 irrigated- 32.1, Un-irrigated- 27.5), IS 18758 (SPAD1 irrigated -49.3, Un-irrigated – 49.2 and SPAD2 irrigated-30.5, Un-irrigated- 25.0) and IS 33844 (SPAD1 irrigated – 43.1, Un-irrigated – 42.5 and SPAD2 irrigated- 30.2, Un-irrigated-23.0). In irrigated and un-irrigated conditions the mean grain yield of these high SCMR lines were 1918 kg ha<sup>-1</sup> and 1525 kg ha<sup>-1</sup> respectively.

In G3, 25 accessions IS 2902, IS 5106, IS 8882, IS 12169, IS 13845, IS 13989, IS 15478, IS 16396, IS 17593, IS 19016, IS 19041, IS 19053, IS 20016, IS 20762, IS 22334, IS 24481, IS 27490, IS 29870, IS 31202, IS 33261, IS 102(111)525, IS 447(471)496, SSM12, SSM1267 and SSM19 were identified for high SCMR. The mean SPAD1 of these accessions in irrigated condition was 53.0 and in un-irrigated condition it was 51.6 and SAPD2 was 40.4 in irrigated and 38.6 in un-irrigated condition. The SPAD1 and SPAD2 of the selected accessions under irrigated and un-irrigated condition were greater than the control cultivars IS 2205 (SPAD1 irrigated – 43.7, Un-irrigated –41.4 and SPAD2 irrigated-35.1, Un-irrigated-27.7), IS 18758 (SPAD1 irrigated -47.0, Un-irrigated – 45.0 and SPAD2 irrigated – 42.5 and SPAD2 irrigated-32.8, Un-irrigated-19.5). Selected accessions had a mean grain yield of 2248 kg ha<sup>-1</sup> in irrigated and 1964 kg ha<sup>-1</sup> in un-irrigated condition which were equal

to the mean yield of the three control cultivars (irrigated -2209 kg ha<sup>-1</sup>, Un-irrigated -2054 kg ha<sup>-1</sup>).

Twelve accessions with high SCMR were identified in G4 viz., IS 9468, IS 9527, IS 10882, IS 13791, IS 13926, IS 15466, IS 22239, IS 22287, IS 22632, IS 29310, IS 29872 and IS 29966. The selected accessions had mean SPAD1 of 51.4 in irrigated and 54.8 in unirrigated condition and the SPAD2 was 40.7 in irrigated and 34.1 in un-irrigated condition. These selected accessions had SPAD readings higher than the control cultivars IS 2205 (SPAD1 irrigated – 41.8, Un-irrigated –46.0 and SPAD2 irrigated- 34.23, Un-irrigated-31.82), IS 8758 (SPAD1 irrigated -37.2, Un-irrigated – 48.2 and SPAD2 irrigated- 22.76, Un-irrigated- 23.7) and IS 33844 (SPAD1 irrigated – 42.1, Un-irrigated – 48.7 and SPAD2 irrigated- 27.87, Un-irrigated- 27.31). The mean grain yield of these high SCMR lines was 2306 kg ha<sup>-1</sup> under irrigated conditions and 1903 kg ha<sup>-1</sup> under un-irrigated conditions which were higher than the control cultivars IS 2205 (Irrigated- 1971 kg ha<sup>-1</sup>, Un-irrigated – 1859 kg ha<sup>-1</sup>) and IS 33844 (Irrigated – 1928 kg ha<sup>-1</sup>, Un-irrigated - 1745 kg ha<sup>-1</sup>).

In G5 eight accessions were identified with high SCMR at both the stages in irrigated and un-irrigated condition. The accessions identified were, IS 3685, IS 9303, IS 12110, IS 20792, IS 22294, IS 24786, IS 32986 and SSM205. These accessions had mean SPAD1 of 43.5 in irrigated and 53.8 in un-irrigated condition and the SPAD2 was 35.3 in irrigated and 38.0 in un-irrigated condition. These selected accessions had high SCMR than the three control cultivars IS 2205 (SPAD1 irrigated – 35.2, Un-irrigated –46.6 and SPAD2 irrigated- 32.5, Un-irrigated- 37.8), IS 18758 (SPAD1 irrigated -34.9, Un-irrigated – 46.5 and SPAD2 irrigated- 25.3, Un-irrigated- 30.9) and IS 33844 (SPAD1 irrigated – 38.0, Un-irrigated – 49.5 and SPAD2 irrigated- 28.3, Un-irrigated- 31.3). The mean yield of selected accessions (irrigated – 2007 kg ha<sup>-1</sup>, un-irrigated- 1830 kg ha<sup>-1</sup>) was equal to the mean yield of the control cultivars (Irrigated- 1941 kg ha<sup>-1</sup>, Un-irrigated – 1965 kg ha<sup>-1</sup>).

Four accessions each in G6 (IS 6828, IS 23254, IS 23777, IS 31195) and G7 (IS 3957, IS 18835, IS 25077, IS 32454) were identified as the high SCMR lines. The mean SCMR of the accessions of G6 (SPAD1 – 42.5 (irrigated), 46.3 (Un-irrigated), SPAD2 – 31.7 (irrigated), 34.0 (Un-irrigated)) and G7 (SPAD1 – 45.7 (irrigated), 46.0 (Un-irrigated), SPAD2 – 32.5 (irrigated), 33.3 (Un-irrigated)) were higher than the mean SCMR of the

control cultivars (SPAD1 -39.4 (irrigated), 39.2 (un-irrigated), SPAD2 – 26.5 (irrigated), 26.2 (un-irrigated).

#### 4.10.2.2 Identification of high SCMR lines in entire reference set

In entire reference set 29 accessions with high SCMR based on pooled data of E1 and E2, 22 accessions based on pooled data of E3, E4 and E5 were identified. The accessions identified were belong to five races in pooled over E1 and E2 (2 *bicolor*, 6 *caudatum*, 1 *durra*, 1 *guinea* and 14 *kafir*) and pooled over E3, E4 and E5 (1 *bicolor*, 9 *caudatum*, 2 *durra*, 1 *guinea* and 1 *kafir*) and three intermediate races in pooled over E1 and E2 (2 *caudatum-bicolor*, 2 *guinea-caudatum* and 1 *durra-caudatum*), four intermediate races in pooled over E3, E4 and E5 (1 *durra-caudatum*, 5 *guinea-caudatum*, 1 *kafir-caudatum* and 1 *kafir-durra*).

The identified accessions in pooled over E1 and E2 were IS 2902, IS 3147, IS 8882, IS 9468, IS 9527, IS 9911, IS 12169, IS 13845, IS 13926, IS 19041, IS 19053, IS 20710, IS 22287, IS 22325, IS 22334, IS 22986, IS 24481, IS 29375, IS 29407, IS 29409, IS 29472, IS 29496, IS 29569, IS 29606, IS 29872, IS 31202, IS 36563, SSM12 and SSM1267. The SCMR at flowering (SPAD1) of the identified accessions ranged from 50.2 to 61.3 with the mean value of 55.0 under irrigated condition and it ranged from 48.8 to 60.1 with the mean of 54.6 under un-irrigated condition. The SCMR at 30 days after flowering (SPAD2) ranged from 34.7 to 51.6 with the mean value of 42.1 under irrigated condition and it ranged from 25.6 to 47.7 with the mean of 37.0 under un-irrigated condition. The SCMR of the selected accessions were higher than the checks IS 2205 (SPAD1- 40.9 (irrigated), 43.4 (Un-irrigated), SPAD2 – 33.7 (irrigated), 29.5 (un-irrigated), 1S 18758 (SPAD1- 41.4 (irrigated), 44.6 (un-irrigated) SPAD2- 27.6 (irrigated), 27.3 (un-irrigated)) and IS 33844 (SPAD1- 42.4 (irrigated), 44.5 (un-irrigated), SPAD2- 29.9 (irrigated), 25.3 (irrigated)).

In pooled over E3, E4 and E5, 22 accessions IS 1127, IS 2262, IS 2416, IS 3583, IS 4112, IS 14963, IS 15478, IS 16044, IS 17593, IS 20713, IS 20792, IS 22239, IS 22325, IS 22506, IS 22909, IS 23601, IS 31202, IS 33173, IS 41(52)500, SSM1049, SSM1123 and SSM547 were identified with high SCMR at both stages. The SCMR at flowering ranged from 54.7 to 49.4 and SCMR at 30 days after flowering ranged from 46.5 to 42.5. The mean values of SCMR at flowering (51.1) and SCMR at 30 days after flowering (44.2) were significantly higher than the mean of the checks (SPAD1 – 47.9 and SPAD2 –

37.2). The grain yield of the identified accessions ranged between 2121 kg ha<sup>-1</sup> and 1695 kg ha<sup>-1</sup> with a mean of 1865 kg ha<sup>-1</sup> which is equal to the mean of checks (1895 kg ha<sup>-1</sup>).

#### 4.10.3 Identification of other trait specific accessions.

In the entire reference set twenty best accessions specific to each quantitative trait were indentified considering pooled data over E1 and E2 and over E3, E4 and E5, separately.

## Accessions for early flowering

IS 18821, IS 31861, IS 31852, IS 18879, IS 28740, IS 18919, IS 3511, IS 36633, IS 32050, IS 30538, IS 28849, IS 28645, IS 3507, IS 32234, IS 9883, SSM1057, IS 14535, SSM1102, IS 27599 and IS 2848 were identified as the early flowering accessions in E1 and E2 pooled. The flowering of the selected accessions ranged from 42.5 to 59.8 days with mean of 55.4 days and these accessions flowered earlier than the checks IS 2250 (82.8 days), IS18758 (72.7 days) and IS 33844 (82.5 days). In E3, E4 and E5 pooled the early flowering accessions were, IS 1127, IS 2156, IS 2848, IS 3511, IS 3583, IS 4963, IS 6973, IS 7463, IS 9586, IS 9597, IS 18919, IS 19262, IS 20205, IS 22325, IS 23988, IS 26833, IS 29375, IS 29876, IS 32454, IS 33173. Flowering of the selected accessions ranged from 52.6 to 57.6 days with mean of 55.7 days which were earlier than the flowering of checks IS 2205 (69.3 days), IS 18758 (64.7 days) and IS33844 (73.5 days). The accessions IS 2848, IS 3511, IS 18919 were found to be early flowering in all the five environments.

## Accessions for plant height

The following accessions IS 393(411)659, IS 13848, IS 24009, IS 14276, IS 19466, IS 452(484)510, IS 41724, IS 2807, SSM1267, IS 651(902)656, IS 19262, IS 36563, IS 29876, IS 20700, IS 13452, IS 3511, IS 19026, IS 64(75)511, IS 3583 and IS 3073 were dwarf in pooled over E1 and E2. The height of the selected accessions ranged from 84.2 to 139.3 cm with mean of 118.4 cm and these accessions were shorter than the shortest check IS18758 (154.5 cm). The six most dwarf accessions were IS 393(411)659, IS 13848, IS 24009, IS 14276, IS 19466 and IS 452(484)510 (84.2 to 108.5 cm).

In pooled analysis over E3, E4 and E5 the accessions, IS 19262, IS 14276, IS 18821, IS 7463, IS 25207, IS 18919, IS 64(75)511, IS 16186, IS 3511, IS 303, IS 3443, SSM501, IS

19053, IS 28645, IS 25442, IS 14-1(16)480, IS 12110, IS 30335, IS 31123, IS 18868 were found to be medium in height. Height of the selected accessions ranged from 114.5 to 169.78 cm with mean of 156.0 cm which were shorter than the check IS 18758 (171.7 cm). The accessions IS 4276, IS 19262, IS 3511 and IS 64(75)511 were found to be the shortest accessions in all the five environments.

## Accessions for panicle exsertion

In pooled analysis over E1 and E2 the following accessions IS 18879, IS 6723, IS 26788, IS 23992, IS 14735, SSM1284, IS 27490, IS 20016, IS 20387, IS 27287, IS 23988, IS 8218, IS 14351, IS 23948, IS 32050, IS 15752, IS 4112 and IS 6154 were identified with panicle exsertion longer than the checks IS 2250 (11.0 cm), IS 18758 (6.6 cm) and IS 33844 (8.3 cm). The panicle exsertion of the selected accessions ranged from 30.0 cm to 42.6 cm with the mean of 33.3 cm. Among the selected accessions IS 18879, IS 6723, IS 26788, IS 23992 and IS 14735 were found to have panicle exsertion >35 cm. In pooled over E3, E4 and E5 the accessions IS 12169, IS 23254, IS 31693, IS 14298, IS 2730, IS 25301, IS 23988, IS 13452, IS 27287, IS 14571, SSM1267, IS 23992, IS 14449, IS 21891, IS 6723, IS 29872, IS 8882, IS 23903, IS 6973 and IS 20205 were identified to have panicle exsertion longer than the checks IS 2205 (8.1 cm), IS 18758 (5.4 cm) and IS 33844 (11.2 cm). The panicle exsertion of the selected accessions ranged from 24.7 cm to 39.2 cm with mean of 28.5 cm. The accessions IS 6723, IS 23992, IS 27287 were found to have long panicle exsertion in all the environments.

#### Accessions for panicle length

In pooled over E1 and E2, SSM1049, IS 13, IS 12804, IS 30538, IS 35, IS 3780, IS 18813, IS 20097, IS 14414, IS 27587, IS 24503, IS 13113, IS 7889, IS 6745, IS 18829, IS 11026, IS 24887, IS 3905, IS 25733 and IS 30417 were identified with panicle length longer than the checks IS 2250 (14.6 cm), IS 18758 (16.1 cm) and IS 33844 (13.9 cm). The panicle length of the selected accessions ranged from 35.3 cm to 45.2 cm with the mean of 38.6 cm. In pooled over E3, E4 and E5, IS 12169, IS 23254, IS 31693, IS 14298, IS 2730, IS 25301, IS 23988, IS 13452, IS 27287, IS 14571,SSM 1267, IS 23992, IS 14449, IS 21891, IS 6723, IS 29872, IS 8882, IS 23903, IS 6973 and IS 20205 were identified to have panicle exsertion longer than the checks IS 2205 (8.1 cm), IS 18758 (5.4 cm) and IS 33844 (11.2 cm). The panicle exsertion of the selected accessions ranged from 24.7 cm to 39.2 cm with the mean

of 31.8 cm. The accessions IS 6723, IS 23992, IS 27287 were found to have long panicle exsertion in all the environments.

#### Accessions for hundred seed weight

IS 33173, IS 17593, IS 22632, IS 7314, IS 32087, IS 24940, IS 30748, IS 16186, IS 24713, IS 7722, IS 14963, IS 20842, IS 16396, IS 23053, IS 20205, IS 28991, IS 10876, IS 10978, SSM29 and IS 19132 were identified with hundred seed weight greater than the control cultivars IS 2250 (2.2 g), IS 18758 (3.9 g) and IS 33844 (2.9 g). The hundred seed weight of the selected accessions ranged from 4.0 g to 5.1 g with the mean of 4.3 g. In pooled over E3, E4 and E5, IS 41(52)500, IS 29569, IS 20782, IS 30335, IS 16044, IS 33178, IS 22334, IS 31861, IS 8283, IS 9597, IS 6723, IS 18879, IS 36633, SS M19, IS 15466, IS 22074, IS 22040, IS 22632, IS 27287 and IS 7463 were identified to have hundred seed weight higher than the control cultivars IS 2205 (2.40 g), IS 18758 (3.0 g) and IS 33844 (2.5 g). The hundred seed weight of the selected accession IS 22632 was found to have high hundred seed weight in all the environments.

## Accessions for Panicle weight

In pooled over E1 and E2 IS 33261, IS 23574, IS 24786, IS 16125, IS 23601, IS 403(418)662, IS 929, SSM215, IS 5622, IS 102(111)525, IS 15443, SSM19, IS 12110, IS 15466, IS 16044, IS 31179, IS 5106, IS 22334, IS 6351and IS 5867 were identified with panicle weight higher than the checks IS 2250 (2619 kg ha<sup>-1</sup>), IS 18758 (3215 kg ha<sup>-1</sup>) and IS 33844 (2855 kg ha<sup>-1</sup>). The panicle weight of the selected accessions ranged from 3279 kg ha<sup>-1</sup> to 4243 kg ha<sup>-1</sup> with the mean of 3563 kg ha<sup>-1</sup>. The mean panicle weight of the selected accessions was 36 per cent higher than the control cultivar IS 2205, 11 per cent higher than IS 18758 and 25 per cent higher than IS 33844. In pooled over E3, E4 and E5 the accessions IS 11827, IS 19041, IS 2848, IS 31852, IS 21124, IS 22609, IS 2263, IS 22986, IS 20697, IS 22074, IS 13848, IS 25596, IS 31202, IS 19418, IS 8218, IS 22330, IS 452(484)510, IS 358 and SSM1049, were identified to have panicle weight higher than the control cultivars IS 2205 (1898 kg ha<sup>-1</sup>) and IS 33844 (2855 kg ha<sup>-1</sup>). The panicle weight of the selected accessions ranged from 1979 kg ha<sup>-1</sup> to 3140 kg ha<sup>-1</sup>. The mean panicle weight of the selected accessions (2332 kg ha<sup>-1</sup>) was 23.0 per cent higher than the control cultivar IS 2205.

## Accessions for Grain yield

In pooled over E1 and E2 the following accessions IS 23574, SSM19, IS 16125, IS 23601, SSM215, IS 929, IS 15466, IS 33261, IS 5106, IS 24786, IS 102(111)525, IS 6351, IS 12110, IS 33423, IS 30898, IS 26833, IS 8882, IS 5622, IS 31179 and IS 21991 were identified with grain yield higher than the checks IS 2250 (2356 kg ha<sup>-1</sup>), IS 18758 (2265 kg ha<sup>-1</sup>) and IS 33844 (2155 kg ha<sup>-1</sup>). The grain yield the selected accessions ranged from 2780 kg ha<sup>-1</sup> to 3001 kg ha<sup>-1</sup>. The mean grain yield (2586 kg ha<sup>-1</sup>) of the selected accessions was 9.0 per cent higher than the control cultivar IS 2205, 14 per cent higher than IS 18758 and 20 per cent higher than IS 33844. In pooled over E3, E4 and E5 the accessions IS 11827. IS 7314, IS 15466, IS 26554, IS 16173, IS 26815, IS 13848, IS 16125, IS 25596, IS 3583, IS 31852, IS 22074, IS 11119, SSM547, SSM1049, IS 36563, IS 12110, IS 4726 and IS 20697 were identified to have grain yield higher than the checks IS 2205 (1791 kg ha<sup>-1</sup>), IS 18758 (1718 kg ha<sup>-1</sup>) and IS 33844 (2178 kg ha<sup>-1</sup>). The grain yield of the selected accessions ranged from 1774 kg ha<sup>-1</sup> to 2361 kg ha<sup>-1</sup>. The mean grain yield of the selected accession (2133 kg ha<sup>-1</sup>) was 19 per cent higher than the control cultivar IS 2205 and 24 per cent higher than IS 18758. The accessions IS 16125, IS 15466 and IS 12110 were found to have high grain yield in all the environments.

## **CHAPTER V**

## DISCUSSION

Sorghum [*Sorghum bicolor* (L.) Moench] is the world's fifth most important cereal crop after wheat, rice, maize and barely (FAO, 2009; verified www.fao.org on January, 2011) in terms of area and production. It is the staple food for more than 500 million people in more than 30 countries (Reddy, 2010). Sorghum is indigenous to Africa, where it is grown in the semiarid zone, spread over a large belt from Senegal to Ethiopia, bordering the Sahara desert in the north, the equatorial forest in the south and extending southwards through the drier parts of eastern and southern Africa (Upadhyaya, 2009).

Drought is one of the major limiting factors of agriculture and considered as the most important cause of yield reduction in crops (Sari-Gorla, 1999). Although sorghum is well known for its versality of adaptation in the adverse agro-climatic conditions, its productivity is affected greatly by unpredictable drought and other stress factors (Stone *et al.*, 2001). Two distinct types of drought stress responses related to pre-flowering and post-flowering stages have been identified and described in sorghum (Rosenow *et al.*, 1996). These two drought responses directly affect the panicle size, grain number and yield. The most damaging drought stress is one that occurs during the post flowering stage of the crop growth (Kassahun *et al.*, 2009).

Genetic enhancement of sorghum for drought tolerance is cost effective approach to further increase its productivity, stabilize production and contribute to food security (Reddy *et al.*, 2009). Plant genetic resources are the most valuable and essential basic raw material for the genetic enhancement of crops.

In sorghum, a composite collection (3,367 accessions) from the world collection (33,100 accessions) was developed, molecularly profiled using 41 SSR markers and a reference set (384 accessions) was identified, which represents 78 per cent (615 of the 789 alleles) of the SSR markers allelic diversity. In present study, the phenotypic assessment of sorghum reference set for yield and related traits under post flowering drought conditions was carried out. The results obtained are discussed below.

## **5.1. QUALITATIVE CHARACTERS**

The characterization of the sorghum reference set for seven qualitative characters revealed large variation in the entire reference set as well as among the seven flowering groups, five basic races, ten intermediate races and five wild sub species. Morphological characters with distinct phenotypic expressions can be used for indirect selection if found associated with useful traits (Reddy *et al.*, 2008).

In the present study, accessions with white mid rib color and pigmented plants were found to be more prevalent in entire reference set, flowering groups, basic races, intermediate races and wild types. The accessions with white mid rib were mainly from India and accessions with pigmented plants mainly from the Sudan. Accessions with pigmented plants have been reported to be less susceptible to *Fusarium spp* than the accessions with tanned plants (Funnel and Pederson, 2006).

The present study showed considerable variation for glume color, glume cover and grain color. These qualitative characteristics were found to have high Shannon-Weaver diversity index (H') in the entire reference set, flowering groups, individual races, intermediate races and wild types. The H' of these characters were similar to the H' of sorghum core (Gernier, 2001) and mini core collections (Upadhyaya, 2009) and this indicated that the diversity of these qualitative characters represents the entire sorghum collection.

The accessions with black and purple color glume were found in higher frequency in the entire set and flowering groups. The race *bicolor, caudatum, guinea* and intermediate races *caudatum- bicolor, guinea-caudatum* and *durra-caudatum* were found to have most of the accessions with black color glume and most of the accessions of race *kafir* had purple colored glumes. All the basic races were found to have one fourth glume cover whereas in intermediate races and wilds most of the accessions had half glume cover and three fourth glume cover respectively. Similar results were reported by Upadhyaya *et al.* (2010c) in 667 newly acquired sorghum accessions.

The traits darker glume color (r = -0.75) and glume cover (r = -0.50) were strongly associated with mould resistance (Audhilakshmi *et al.*, 1999). This association indicates that these traits either play a role in determination of grain mould resistance or

linked to the genes that control grain mould. (Audhilakshmi *et al.*, 1999 and Reddy *et al.*, 2005). In sorghum reference set a total of 162 accessions with dark colored glume (12 brown, 64 black, 17 purple colored glume accessions) and with glume coverage >50 per cent were present. These accessions with the combination of darker glume and high glume coverage can be used in the mould resistance breeding.

Sorghum grain color and quality are important characteristics in baking and livestock feed industry. White grain is more desirable for human and animal consumption. The entire reference set was represented by 11 grain colors among which the white, purple and brown color were found to be predominant. White colored grains are preferred for food because they give desired color to food and while red and brown grains are preferred by brewing industries in African countries for making beers (Demuyakor and Ohta, 1993).

The qualitative characters under study were reported useful as markers since they are associated with one or the other economically important traits such as increased fodder quality with mid rib color (Porter *et al.*, 1978), resistance to grain mould infection with darker, closed glumes and open panicles (Thakur *et al.*, 2008 and Murthy *et al.*, 2000), preference in food and beverage industries with colored grains, immunity to fungal diseases with tanned plants (Melake-Berhen *et al.*, 1996). Further, these qualitative characters were more important from the point of identification of cultivar which is much needed in the present era of plant variety protection (Teshome *et al.*, 1997 and Roy *et al.*, 2004).

## **5.2. QUANTITATIVE CHARACTERS**

In the present investigation the data on 11 quantitative characters were recorded in all the environments. The results of the study are discussed under the following subheadings

- 1. Analysis of variance and REML analysis
- 2. Genetic variability, heritability in broad sense and genetic advance
- 3. Mean performance of sorghum reference set
- 4. Correlation studies
- 5. Phenotypic diversity of sorghum reference set
- 6. Identification of trait specific accessions

## 5.2.1. Analysis of variance and REML analysis

The analysis of variance in E1, E2 and REML analysis in E3, E4 and E5 showed that the variance due to genotype was significant for all the eleven quantitative characters. Interaction effects of genotypes with drought in E1 and E2 were found to be significant for most characters like panicle exerstion, panicle length, panicle weight and grain yield. This indicates that the genotypes under study were genetically diverse. The pooled analysis over the environments indicated that variance due to genotype and genotype x environment interactions was significant for all the characters indicating differential response of genotypes to environments. Wald's statistics was significant for all the traits indicating that the environments E3, E4 and E5 were different and appropriate to differentiate the reference set accessions.

## 5.2.2. Genetic variability, heritability in broad sense and genetic advance

Effectiveness of selection depends on the magnitude of genetic variability in a particular character. It is necessary to study variability in respect of quantitative characters with reference to genetic parameters such as genotypic variance, phenotypic variance, heritability and genetic advance. The absolute values of phenotypic and genotypic variances cannot be used for comparing the magnitude of variability for different characters since the mean and units of measurement of the characters may be different. Hence, the coefficients of variation expressed in percentage at phenotypic and genotypic levels have been used to compare the variability observed among the different characters.

In the present study, the extent of variability available in 384 accessions was studied, and the scope of selection through heritability and genetic advance estimates was analyzed and interpreted. The genotypes exhibited considerable amount of variability for all the characters studied. Narrow difference between phenotypic and genotypic coefficient of variation were observed for all the characters indicating that the expressions of these characters were genetic which can be exploited in breeding programs.

High PCV and GCV were found for plant height (E1, E2 and pooled over E1 and E2), panicle exerstion, panicle length, panicle width, hundred seed weight, basal tillers, panicle weight and grain yield in all the environments. Similar results were obtained for plant height (Godbharle *et al.*, 2010; Bello *et al.*, 2007; Sharma *et al.*, 2006; and

Nimbalkar *et al.*, 1988), panicle length (Bello *et al.*, 2007; Aba, 2001; Tako, 1997; William *et al.*,1987; Basu, 1981 and Eckebil *et al.*, 1977), panicle width (Chavan *et al.*, 2010; Tiwari *et al.*, 2003; Bapat and Shinde, 1980), hundred seed weight (Bello *et al.*, 2007 and William *et al.*, 1987), panicle weight (Bello *et al.*, 2007; Aba, 2001, Tako, 1997, William *et al.*, 1987; Basu *et al.*, 1981 and Eckebil, 1977) and grain yield (Chavan *et al.*, 2010, Sandeep *et al.*, 2009; Sharma *et al.*, 2006; Tiwari *et al.*, 2003; Chaudary *et al.*, 2001; Sankaranpandian *et al.*, 1996 and Kumar and Singh, 1986).

Moderate PCV and GCV was found for days to 50 per cent flowering (E1, E2 and pooled over E1, E2), plant height (E3, E4, E5 and pooled) and SPAD 2 (E5). Similar results were reported for days to 50 per cent flowering and plant height (Vedansh *et al.*, 2010; Snadeep *et al.*, 2009; Singh *et al.*, 2006, Singh *et al.*, 2005; Rajguru *et al.*, 2005; Ksihore and Singh, 2005; Chaudhary *et al.*, 2001, Raut *et al.*, 1994 and Potdukhe *et al.*, 1993). In pooled analysis over E3, E4 and E5 the characters days to 50 per cent flowering, SPAD1, SPAD2 showed low PCV and GCV. The low PCV and GCV of days to 50 per cent flowering was also reported by Chavan *et al.* (2010), Godharle *et al.* (2010), Kjein and Rosenow (1984), Mallinath *et al.* (2004), Sindhe *et al.* (1979) and Prabhakar (2003).

High heritability coupled with high genetic advance was observed for days to 50 per cent flowering (E1, E2, E5 and pooled over E1 and E2), plant height (E1, E2, E3 and pooled over E1 and E2), panicle exerstion, panicle length, panicle width, basal tillers, hundred seed weight, panicle weight and grain yield in all the environments and pooled over E1 and E2, where as in E3, E4, and E5 these characters had moderate heritability and high genetic advance. The high and moderate heritability of these characters may be due to the effect of environment. The characters with high genetic advance can be improved with simple selection. High heritability and moderate genetic advance was also found for days to 50 per cent flowering (E3), plant height (pooled over E3, E4, and E5) and SPAD1 (E1), and hence recombination breeding would favor for improvement of this traits. These findings are in line with Vedansh *et al.* (2010), Sandeep *et al.* (2009); Singh *et al.* (2005); Rajguru *et al* (2005); Chaudhary *et al.* (2001) and Raut *et al.* (1994).

#### 5.2.3 MEAN PERFORMANCE OF THE SORGHUM REFERENCE SET

The mean performance of sorghum reference set in all the environments were significantly different indicating adequacy of these environments in differentiating the genotypes.

The mean days to 50 per cent flowering, plant height, panicle exerstion, panicle width, panicle weight, grain yield, SPAD1 and SPAD2 differed significantly in E1 and E2. In E4 and E5 the characters such as plant height, panicle exerstion, panicle length, hundred seed weight, panicle weight and grain yield had low mean values when compared to other environments and the mean values of E5 were lower than the E4. Both E4 and E5 were un-irrigated and hence had low values for these traits. Drought events during the grain filling period can cause major reduction in yield by reducing starch accumulation as a result of limited assimilate partitioning to the developing grain (Blum, 1998) or by direct effects on processes of grain growth (Yang *et al.*, 2004).The reduction in yield and its related traits under drought conditions have been reported by Khizzah *et al.*, 1995, Assar *et al.*, 2004, Golabadi, *et al.*, 2006 and Groene, 2008.

The mean performance of seven flowering groups (G1 to G7) differed significantly for days to 50 per cent flowering and plant height in all the environments. The accessions of G1 were early flowering and dwarf to medium in plant height, G3 and G4 were medium flowering and medium to tall in plant height whereas the accessions in G5, G6 and G7 were late flowering and with tall plants. There was positive correlation between days to 50 percent flowering and plant height in all the flowering groups in all the environments, indicating that with increase in days to 50 per cent flowering plant height also increased.

Among the flowering groups, G3 was found more promising for important agronomic characteristics such as panicle weight, grain yield and SPAD2. G3 had accessions with higher panicle weight, plot yield and SPAD2 and was dominated by the accessions from race *caudatum*. The race *caudatum* is one of the most important races agronomically and the plants are generally medium to tall in stature with high yielding capacity (Smith and Fredersen, 2000 and Mann *et al.*, 1983). The grain yield of G6 and

G7 were lower than the G3. This is because the accessions of G6 and G7 were tall and late flowering, these traits negatively correlated with grain yield. Similar results were reported by Mutava et al. (2011) by assessing 300 sorghum accessions.

The basic races and intermediate races as group differed significantly for panicle weight, grain yield and hundred seed weight from the wilds as group in all the environments. The mean values of these characters of basic races and intermediate races as group were greater than the wilds as group, as the wild types were poor yielders and have open and lax panicle and grain smaller in number.

The race *guinea* differed significantly from other basic races for days to 50 per cent flowering, panicle exerstion, panicle length and basal tillers. The accessions of race *caudatum* were early flowering and had shortest plant height, but had highest panicle weight and grain yield. The accessions of race *bicolor* recorded high panicle length and panicle width but it had low panicle weight and grain yield. This concurs well with the race characteristics as described by Mann *et al.* (1983) and also in line with the findings of Mutava et al. (2011).

Among the intermediate races, *durra-caudatum* accessions were early flowering, dwarf and had long panicle exerstion and panicle length and *guinea- caudatum* accessions had high panicle weight and grain yield. Accessions of the *Aethiopicum* were found to be early flowering and had highest SPAD2. The accessions of *verticilliflorum* flowered late and were tall and had high number of basal tillers but with low panicle weight and grain yield. Accessions of *Drummondii* had high panicle weight and grain yield.

Variances of entire reference set between the environments were heterogeneous for all the quantitative characters. The variances of all the flowering group were significantly different for days to 50 per cent flowering, grain yield (E1, E2 and pooled over E1 and E2), plant height, SPAD1 (E1 and pooled over E1 and E2) and SAPD2 (E2). Within the flowering groups the variances were homogenous for panicle exerstion, panicle length, panicle width, basal tillers, hundred seed weight, panicle weight and grain yield.

Variances within individual basic races, intermediate races and wilds as groups were homogeneous for days to 50 per cent flowering, plant height, hundred seed weight,

panicle weight, grain yield, SPAD1 and SPAD2 in all the environments and in pooled. The variances between the basic races, intermediate races and wilds as group were significantly different for the characters panicle length, panicle width and basal tillers in E1, E2 and pooled over E1 and E2. In other environments all the characters were found to have homogenous variance between the groups of races, intermediate races and wilds. The homogeneity of these characters shows that they were less influenced by the environments and so they can be used for germplasm characterization.

Over all, the results indicated the presence of large genotypic variability in the sorghum reference set for the quantitative characters and thus there is a considerable scope for identifying useful germplasm in this collection.

## **5.2.4. CORRELATION STUDIES**

Grain yield is a dependent trait, which is influenced by many independent traits. Studies on the correlation of traits and their association with yield are important, as they are helpful in selecting desirable yield contributing traits. Correlation analysis was carried in entire reference set, races, intermediate races and wilds as group in all the environments and for each flowering group in E1, E2 and pooled over E1 and E2. The results obtained are discussed below.

Grain yield had highly significant positive correlation with the panicle weight, and hundred seed weight and negatively correlated with days to 50 per cent flowering, plant height, panicle exerstion, panicle length, panicle width, and basal tillers in all the environments. Similar results were reported for days to 50 per cent flowering, plant height, panicle exerstion (Muppidathi *et al.*, 1999, Ezeaku *et al.*, 2006 and Upadhyaya *et al.*, 2009), panicle weight (Geremew and Gebeyhu, 1993; Potdukhe *et al.*, 1994; Jeyaprakash *et al.*, 1997; Iyanar, 2001; Bucheyeki *et al.*, 2009) and hundred seed weight (Taurchi and Rezai, 1997; Elangovan *et al.*, 2007; and Warkad *et al.*, 2010).

The useful correlation (-0.500> r > 0.500) found in the entire reference set was 6 in E1, 4 in E2, 8 in pooled over E1 and E2, 2 each in E3, E4, E5 and pooled over E3, E4 and E5. Among these useful correlations, the trait basal tillers in E1 (r= -0.590) and in pooled

over E1and E2 (r= -0.587) and panicle weight in all the environments (E1: r =0.940, E2: r = 0.781, pooled over E1 and E2: r=0.928, E3:0.924, E4:0.919, E5:0.793 and pooled over E3, E4 and E5: r=0.734) had consistent useful correlations with grain yield.

In correlation study among the flowering groups, G1 had 17; G2 had 12; G3 had 18; G4 had 30; G5 had 20; G6 had 35; G7 had 25 useful correlations. Among these useful correlations, the positive correlation (r > 0.500) between panicle width and panicle length, grain yield and panicle weight, SPAD1 and SPAD2 and negative correlation (r < 0.500) between plot yield and basal tillers were found to have consistent correlation at least in five flowering groups in E1, E2 and pooled over E1 and E2.

The correlation analysis of basic races, intermediate races and wilds as group in all the environments had 26, 18 and 22 useful correlations (sum of all the environments). Of these useful correlations, positive correlation between panicle width and panicle length, grain yield and panicle weight occurred consistently in all the three groups and in all the environments.

In all the environments, the correlation between panicle width and panicle length, grain yield and panicle weight, grain yield and basal tillers occurred consistently in entire reference set, all flowering groups, basic races, intermediate and wilds as group. Similar association was also reported by Jeyaprakash (1997), Ayana and Bekele (2000), Iyanar (2001), Elangovan (2007), Bucheyeki *et al.* (2009) and Upadhyaya *et al.* (2009). Thus these attributes should be considered while making effective selections for higher grain yield and this information would also help in optimizing the data recording by taking observations on a few related traits in the preliminary trails involving a large number of germplasm accessions.

## 5.2.5. PHENOTYPIC DIVERSITY OF SORGHUM REFERENCE SET

The methods of assessing the phenotypic diversity are useful for characterization, evaluation and classification of plant genetic resources when a large number of accessions are to be assessed for several characters of agronomic and physiological importance (Peeters and Martinelli, 1989). The information generated can be useful for identifying groups of accessions that have desirable characters for crossing, for planning efficient germplasm collecting expeditions, for revealing the patterns of variation in germplasm collections and for investigating some aspects of crop evolution (Brown, 1991; Perry and McIntosh, 1991; Souza and Sorrels, 1991). The usefulness of multivariate methods for handling morphological variation in germplasm collections have been demonstrated in many crops like barley (*Hordeum vulgare* L.) (Cross, 1992); finger millet (*Eleusine coracana* (L.) Gaertn.) (Hussaini *et al.*, 1977); maize (*Zea mays*L.) (Alika *et al.*, 1993), oat (*Avena sativa* L. and *A.byzantina* C. Koch) (Souza and Sorrells, 1991); rice (*Oryza sativa* L.) (Kanwal *et al.*, 1983); sorghum (Prasadarao and Ramanatha Rao, 1995); tef (*Eragrostis tef* (Zucc.) Trotter) (Bekele, 1996); wheat (*Triticum spp.*) (Damania *et al.*, 1996; Pecetti *et al.*, 1992; Elings, 1991; Bekele, 1984).

#### 5.2.5.1. Shannon diversity index

The Shannon-Weaver diversity index (H') is one of the most widely used diversity index (Magurran, 1988). It is used to estimate the diversity from phenotypic descriptors among germplasm collections (Singh *et al.*, 1998; Ayana and Bekele, 1999; Balakrishnan *et al.*, 2000; Dong *et al.*, 2001; Pecetti and Piano, 2002, Upadhyaya *et al.*, 2009). In the present study the H' was calculated to compare the phenotypic diversity for all the characters among the entire reference set, flowering groups, races, intermediate races and wild types. A low H' indicates extremely unbalanced frequency classes for an individual trait and lack of genetic diversity in the trait. The diversity values would be variable among traits and among the groups. So the extent of diversity within the group depends upon the trait under consideration (Upadhyaya *et al.*, 2007).

The average H' of entire reference set across the quantitative characters was similar for all the environments. In entire reference set, grain yield (E1, E2 and pooled over E1 and E2), SPAD1 (E3, E4 and pooled over E3, E4 and E5) and panicle length (E5) had highest H'. The average H' for the sorghum reference set ( $0.60\pm0.013$ ) was comparable to the sorghum core collection ( $0.60\pm0.016$ ) (Gernier, 2001) and mini core collection ( $0.60\pm0.018$ ) (Upadhyaya *et al.*, 2009) and this indicated that the reference set represents the entire collection. The accessions of G3 were highly divers whereas the accessions in G7 were least diverse. The accessions from race *guinea* had the highest H' averaged over the traits in E1 and pooled over E3, E4 and E5, whereas in E2, E3 and pooled over E1 and E2 *caudatum* had the highest H'.

In all the environments, plant height, hundred seed weight, grain yield, panicle weight, SPAD1 and SPAD2 were found to have highest H' in entire reference set, flowering groups, races, intermediate races and wild types.

#### **5.2.5.2.** Phenotypic diversity index

The grouping of similar genotypes depends on the dissimilarity among them, which can be determined by the phenotypic diversity index. The average diversity index in the entire reference set was 0.24. The most diverse pair of accessions in the reference set was IS 36563 (*caudatum*) from Niger and IS 31533 (*verticilliflorum*) from Brundi in E1 and E2 pooled, IS 41724 (*guinea-caudatum*) from ICRISAT and IS 2678 (*caudatum-bicolor*) from Uganda in E3, IS 18821 (*Aethiopicum*) from Egypt and IS 9303 (*Kafir*) from south Africa in E4 and IS 41(52)500 (*guinea-caudatum*) from ICRISAT and IS 13 (*bicolor*) from USA in E5 and pooled over E3, E4 and E5. The diverse accessions in E1 and E2 were from basic race and wild type, in E3 accessions were from intermediate races and in E4 the accessions belonged to intermediate race and basic race. However all these diverse accessions had different geographical origin. This shows that the highly diverse accessions should be selected on the basis of diversity and not on the basis of geographic origin or races (Upadhyaya *et al.*, 2010c).

In the flowering groups diverse pair of accessions were IS 33844 (*Durra*) and IS 18821 (*Aethiopicum*) in G1, IS 13848 (*Caudatum*) and IS 13 (*Bicolor*) in G2, IS 41724 (*Guinea-caudatum*) and IS 35 (*Bicolor*) in G3, IS 14206 (*Bicolor*) and IS 9527 (*Kafir*) in G4, IS 24786 (*Durra-bicolor*) and IS 14216 (*Arundinaceum*) in G5, IS 27855 (*Bicolor*) and IS 18758 (*Guinea-caudatum*) in G6, IS 18829 (*Arundinaceum*) and IS 18758 (*guinea-caudatum*) in G7. In each flowering group one of the diverse accessions is either from the race *bicolor* or from the wild sub species *Aethiopicum* and *Arundinaceum*. The other accession is from basic races or intermediate races. *Bicolor* is a primitive type and it would be useful to involve the accessions belong to this races in hybridization program to see the extent of segregation for different characters (Upadhyaya *et al.*, 2010c). Similar to the present study high level of phenotypic diversity was also reported by Ayana and Bekele (2000), Appa Rao *et al.* (1996) and by Li and Li (1997).
Exploitation of these widely diverse accessions would help in the development of mapping population to identify QTLs and use in breeding programs to study the segregating generation and selection of superior lines. As the diversity between parents increases, the dominance and epistatic variations have significant role in the inheritance of quantitative characters (Halward and Wynne, 1991). This would have implication in choosing appropriate selection strategy for quantitative characters (Upadhyaya and Nigam, 1999). The use of these diverse accessions in the sorghum improvement programs would help the breeders to develop cultivars with broad genetic base.

#### 5.2.5.4. Principal component analysis

Principal Component Analysis (PCA) was done to convert a set of observations of possibly correlated variables into a set of values of uncorrelated variables called principal components (PC). The PCA was carried out in the entire reference set, each flowering group (E1 and E2), races, intermediate races and wilds as group in all the environments.

The first five principal components in entire reference set and three principal components in flowering groups, races, intermediate races and wilds as group explained more than 60 per cent of variation in all the environments. The PCA in entire reference set reduced the 11 quantitative characters into 9 characters in E1, E2 and pooled over E1 and E2 and into 8 characters in E3, E4, E5 and pooled over E3, E4 and E5. In each flowering group of E1, E2 and pooled over E1 and E2 and in the races, intermediate races and wilds as group in all the environments the 11 characters were reduced into 7 characters.

The characters such as days to 50 per cent flowering, panicle length, panicle weight, grain yield and SPAD1 occurred in all the principal components in entire reference set, all flowering groups, races, intermediate races and wild type in all the environments. This indicates that these characters can be considered as important for the characterization of sorghum reference set accessions.

#### 5.2.5.5. Clustering

The hierarchical cluster analysis was conducted for the entire reference set in all the environments using the method of ward (1963) on the first three PC scores.

All the races, intermediate races, and wilds were grouped into three clusters in E1, E2, E4 and pooled over E1 and E2, two clusters in E3, five cluster in E5 and four cluster in pooled over E3, E4 and E5. The wild types *Aethiopicum, Arundinaceum, Verticilliflorum and Virgatum* were grouped together in all the environments. The wild types are so closely related morphologically and ecologically (de Wet, 1978) and are considered to be well defined ecotypes (de Wet, 1970 and Dogget, 1988) and were therefore grouped together. The subspecies *Drummondii* and the race *bicolor* were grouped together in all the environments. This is because the race *bicolor* is a primitive and heterogeneous type and always closely related to wild sorghum (de Wet, 1978). In all the environments there was no separate clustering of races and intermediate races. The race *Durra* and its intermediate race and the race *caudatum* and its intermediate races were found to group together in all the environments. This pattern of clustering may be due to sharing of common alleles of caudatum and its intermediates races with durra and its intermediate races (Brown *et al.*, 2011; Preumal *et al.*, 2007; Kimber, 2007).

## 5.2.6. IDENTIFICATION OF TRAIT SPECIFIC ACCESSIONS

Crop genetic resources will be the main contributing factor in the future progress and developing sustainable solution to basic crop constrains or enhancing productivity (Upadhyaya, *et al.*, 2007). The use of genetic resources in the breeding programs have been mainly as sources of resistance to pests and diseases or as sources of male sterility, short stature or any such character with simple inheritance. There have been fewer efforts for identifying germplasm lines for increasing yield potential than for pest resistance and nutritional qualities because such traits are highly environmental interactive and require multi environment testing to accurately characterize them. In ICRISAT several germplasm lines are identified for tolerance to biotic and abiotic stresses, for agronomic and nutritional characters (Upadhyaya, 2010d). In the present study drought tolerant accessions were identified based on drought tolerance index and SPAD chlorophyll meter reading (SCMR) and accessions specific to various characters.

# 5.2.6.1. Identification of drought tolerant accessions based on drought tolerance indices.

In arid and semi arid regions drought is a potential major constrain to plant production, which affects the crop mainly during the grain filling period. Breeding for drought tolerance is complicated by the lack of fast, reproducible screening techniques (Ramirez and Kelly, 1998). Loss of yield is the main concern of plant breeders and they hence emphasize on yield performance under moisture stress conditions. But variation in yield potential could arise from factors related to adaptation rather than to drought tolerance *per se.* Thus drought indices which provide a measure of drought based on loss of yield under drought conditions in comparison to normal conditions have been used for screening drought tolerant genotypes (Mitra, 2001). Selection based on the drought tolerant indices will distinguish the genotypes that are favorable only in one environment.

In the present study, based on the drought tolerance indices *viz.*, STI, MP, GMP, SSI, TOL and DTE, a total of 35 drought tolerant accessions with good yield potential representing entire reference set and 65 accessions from the seven flowering groups were selected. In entire reference set the maximum of the accessions selected belong to the race *Caudatum* from Cameroon, Ethiopia, Kenya, Sudan and Uganda where as in flowering group the maximum of the accessions belong to the race *caudatum* and intermediate races *guinea-caudatum* from 20 countries.

The accessions selected in entire reference were found to be of medium flowering (60 - 87 days) with medium to tall in height (158 - 324 cm), low to medium panicle exerstion (5-27 cm) and panicle length (9-35 cm). In flowering groups, the accessions of G1 were with medium plant height, panicle exerstion and panicle length, G2, G3 and G4 were with medium to tall in height, low to medium panicle exerstion and panicle length, G5, G6 and G7 were with tall plant height, medium panicle exerstion and panicle length. The mean panicle weights, grain yield, SCMR at both the stages in entire reference set and flowering group were higher than the check cultivars.

#### 5.2.6.2. Identification of drought tolerant accessions based on SCMR

Senescence is normally characterized by chlorophyll loss and progressive decline in photosynthetic capacity (Thomas and Howarth, 2000; Borrell *et al.*, 2000). Early onset of senescence affects assimilation and grain filling in crop plants. The rate of senescence determines the maintenance of quality flowers, fruits and vegetables. Therefore any defence mechanism that postpones the onset of senescence and keeps leaves green will benefit the crop. Tolerance of senescence in the advent of post flowering drought stress is known as the stay green trait (Xu *et al.*, 2000).

The stay green is visually scored at or soon after physiological grain maturity. Visual rating of stay green trait is easy and quick with some limitations such as individual biases and difference in rating among the observers (Rosenow, 1994). An alternate to visual scoring is the SPAD chlorophyll meter reading (SCMR), which has been used to quantify the chlorophyll concentration, leaf nitrogen and leaf photosynthesis in various crops. The SPAD chlorophyll meter reading can provide a useful tool to screen large breeding populations for improved photosynthetic capacity under water deficit conditions. The importance of this trait for drought screening was reported in sorghum (Xu *et al.*, 2000, Talwar *et al.*, 2009, Bruke *et al.*, 2010), maize (Gentinetta *et al* 1986 and Rajcan and Tollenaar, 1999), chickpea (Kashiwagi *et al.*, 2010), groundnut (Boontang *et al.*, 2010) and sugarcane (Jangpromma *et al.*, 2010) etc.

In the present study, in entire reference set 29 accessions with high SCMR based on pooled data of E1 and E2, 22 accessions based on pooled data of E3, E4 and E5, and 77 accessions representing the seven flowering groups were identified. The accessions identified in entire reference set belonged to five races (2 *bicolor*, 6 *caudatum*, 1 *durra*, 1 *guinea* and 14 *kafir*) and three intermediate races (2 *caudatum-bicolor*, 2 *guineacaudatum* and 1 *durra-caudatum*) in pooled over E1 and E2 whereas in pooled over E3, E4 and E5 the selected accessions belong to five basic races (1 *bicolor*, 9 *caudatum*, 2 *durra*, 1 *guinea* and 1 *kafir*) and four intermediate races (1 *durra-caudatum*, 5 *guineacaudatum*, 1 *kafir-caudatum* and 1 *kafir-durra*). The selected accessions from flowering group represents five basic races (6 *bicolor*, 17 *caudatum*, 5 *durra*, 13 *guinea* and 20 *kafir*) from 21 countries and six intermediate races (5 *caudatum bicolor*, 1 *durra-bicolor*, 2 *durra-caudatum*, 13 *guinea-caudatum*, 1 *kafir-bicolor* and 1 *kafir- caudatum*) from 10 countries.

The accessions identified were found to be medium in flowering with medium to tall in plant height, low to medium panicle exerstion, medium panicle length. The mean plot yield, SCMR at flowering and SCMR at 30 days after flowering of identified accessions were higher than the checks.

The accessions identified based on the drought tolerance indices and with SCMR reading are dominated with the race *caudatum* and by the intermediate race *guinea*caudatum. The race *caudatum* had greater agronomic value (Dogget, 1988), better adaptation to harsh conditions (Stemler et al., 1975) and a wide range of response to changes in photoperiod (Grenier, 2000). Vadez et al. (2011) evaluated 149 accessions of sorghum reference set using lysimetric system under terminal drought stress and fully irrigated conditions and reported that race *caudatum* and intermediate races *caudatum*guinea were had highest transpiration efficiency. Over all in entire reference set the accessions IS 8882 (Caudatum, Unganda), IS 13845 (Kafir, South Africa), IS 22334 (Kafir, Botswana), IS 29872 (Kafir, Zimbabwe) were found to have high drought tolerance indices and high SCMR. All these accessions were from Sub Shararian African region. In flowering groups the following accessions were identified with high drought tolerance indices and high SCMR values: G1- IS2848 (Caudatum, South Africa), G2- IS 29569 (Kafir, Lesotho), IS 102(111)525, (Guinea-caudatum, ICRISAT), IS 13845 (Kafir, South Africa), IS 19016 (Caudatum, Sudan), IS 19053 (Guinea-caudatum, Sudan), IS 20762 (Guinea-caudatum, USA), IS 22334 (kafir, Botswana), IS 33261 (Caudatum, Cameroon), IS 5106 (Durra, India), IS 8882 (Caudatum, Uganda), G4- IS 9468 (Kafir, South Africa), IS 15466 (Caudatum, Cameroon), IS 13791 (Kafir, South Africa), IS 13926 (Kafir, South Africa), IS 22287 (Kafir, Botswana), IS 22239 (Kafir, Botswana), IS 22632 (Durra, Cameroon), G5- IS 3685 (Caudatum, USA), IS 32986 (Guinea -Tanzania), IS 22294 (Kafir, Botswana), IS 20792 (Guinea-caudatum, USA) and G7 – IS 32454 (Guinea, India).

Accessions with good drought tolerant indices and with high SCMR would be more desirable for the drought tolerant breeding program. Since the accessions with good drought tolerant indices will have good yield potential in both stress and non-stress environment and the accessions with high SCMR at both the stages (During flowering and 30 days after flowering) is the indication of stay green nature which is a important characteristic of post flowering drought tolerance and it reduces the yield loss by preventing lodging and stalk rot.

#### 5.2.6.2. Identification of other trait specific accessions

In the entire reference set best 20 accessions were identified for days to 50 percent flowering, plant height, panicle length, hundred seed weight, panicle weight and grain yield were identified. IS 18821, IS 31861, IS 31852, IS 7463, IS 18919 and IS 3511 were early flowering in all the environments indicating that these accessions could be source of genes for developing early maturing variety.

Dwarf sorghum is desirable for the mechanical harvesting and in reference set four accessions IS 13848, IS 4276, IS 24009 and IS 41724 were found to be dwarf in all the environments (>100 cm) and hence these accessions can be used as the source for dwarf plants. Similarly three accessions (IS 15466, IS 16125 and IS 12110) for higher grain yield, three accessions for high SCMR at flowering (IS 29375, IS 303 and IS 3926) and five accession for high SCMR at 30 days after flowering (IS 29569, IS 20782, IS 30335, IS 6044 and IS 33178) were identified. Extensive evaluation of these accessions in different locations may be useful to assess the stability of the identified trait specific accessions.

#### SUMMARY

Drought is one of the major limiting factors of agriculture and most important cause of yield reduction in crops (Sari-Gorla, 1999). Although sorghum is well known for its versality of adaptation in the adverse agro-climatic conditions, its productivity is affected greatly by unpredictable drought and other stress factors (Stone *et al.*, 2001). Pre-flowering and post-flowering drought will directly affect the panicle size, grain number and yield. The most damaging drought stress is one that occurs during the post flowering stage of the crop growth (Kassahun *et al.*, 2009). Genetic enhancement of sorghum for drought tolerance is cost effective approach to increase its productivity, stabilize production and contribute to food security (Reddy *et al.*, 2009).

Plant genetic resources are the most valuable and essential basic raw material for the genetic enhancement of crops. A large gap exists between availability and actual utilization of the materials. To overcome the size related problems the concepts of core collection (Frankel, 1984) (10% of entire collection) and mini core collection (Upadhyaya and Ortiz, 2001) (1% of entire collection) were developed which helped in utilization of the genetic variation in the germplasm, without losing diversity. The composite collections for various crops were developed from entire collection under the Generation Challenging Programme.

Sorghum composite collection (3,367 accessions) from the world collection (33,100 accessions) was developed, molecularly profiled using 41 SSR markers and a reference set of 384 accessions was identified, which represents 78 per cent (615 of the 789 alleles) of the SSR markers allelic diversity. The sorghum reference set of 384 accessions was evaluated during 2008-09 post rainy (E1), 2009-10 post rainy (E2) at ICRISAT, Patancheru, Andhra Pradesh and during 2009-10 under irrigated (E3) and unirrigated conditions (E4) at UAS, Dharwad, Karnataka and only under un-irrigated condition at ARRS, Bijapur, Karnataka. In E1 and E2 the experiment was conducted in split plot design and in E3, E4 and E5 the experiment was conducted in augmented design. Data was recorded for seven qualitative (Mid rib color, Plant pigmentation, Presence of nodal tillers, Glume color, Glume cover, Grain color and Thresability) and eleven quantitative characters (days to 50 per cent flowering, plant height, panicle length, panicle width, basal tillers, hundred seed weight, panicle weight, grain yield, SCMR at flowering and SCMR at 30 days after flowering).

### The results obtained are summarized below.

- The qualitative traits such as white mid rib, pigmented plants, black and purple color glume, one fourth glume cover, white, purple and brown colored seeds were predominant in reference set.
- The analysis of variance in E1, E2 and REML analysis in E3, E4 and E5 showed that the variance due to genotype, genotype x drought and genotype x environments was significant for all the quantitative characters in sorghum reference set. This indicated that the accessions of reference set were genetically diverse. Wald's statistics was highly significant for all the traits indicating that E3, E4 and E5 were different and appropriate to differentiate the reference set accessions.
- Narrow difference between phenotypic and genotypic co-efficient of variation were observed for all the characters indicating the relative importance of genetic component in expressions of these characters which can be exploited in breeding programs.
- High heritability coupled with high genetic advance was observed for the days to 50 per cent flowering (E1, E2, E5 and pooled over E1 and E2), plant height (E1, E2, E3 and pooled over E1 and E2), panicle exerstion, panicle length, panicle width, basal tillers, hundred seed weight, panicle weight and grain yield in individual environments and pooled over E1 and E2, where as in pooled over E3, E4, and E5 these characters had moderate heritability and high genetic advance.
- E1 showed significantly greater mean values than E2 for panicle weight, plot grain yield, SPAD1 and SPAD2.
- The seven flowering groups (G1 to G7) differed significantly for days to 50 per cent flowering and plant height in all the environments. Among the flowering groups, the accessions of G3 were found more promising for important agronomic character such as panicle weight, grain yield and SPAD2.

- The basic races and intermediate races as group differed significantly from the wilds as group for panicle weight, grain yield and hundred seed weight in all the environments. Within the individual intermediate races and wilds differences were not significant for any of the characters.
- Accessions of the race *guinea*, had mean values greater than other basic races for days to 50 per cent flowering, panicle exerstion, panicle length and basal tillers. The accessions of race *caudatum*, intermediate race *durra-caudatum* and wild *Aethiopicum* were early flowering, had shortest plant height, highest panicle weight and grain yield
- Variances in entire reference set between the environments were heterogeneous for all the quantitative characters. The variances in all the flowering group were significantly different for days to 50 per cent flowering, grain yield (E1, E2 and pooled over E1 and E2), plant height, SPAD1 (E1 and pooled over E1 and E2) and SAPD2 (E2).
- The variances of the races, intermediate races and wilds as group were significantly different for panicle length, panicle width and basal tillers in E1, E2 and pooled over E1 and E2. In other environments variances for all the characters were homogenous between races, intermediate races and wilds as group.
- Grain yield had highly significant positive correlation with the panicle weight, and 100 seed weight. Grain yield was negatively correlated with days to 50 per cent flowering, plant height, panicle exerstion, panicle length, panicle width and basal tillers.
- In all the environments positive correlation between panicle width and panicle length, grain yield and panicle weight, grain yield and basal tillers occurred consistently in entire reference set, all flowering groups, races, intermediate and wilds as group. Thus these attributes should be considered while making effective selections for higher grain yield
- The Shannon Weaver diversity index (H') of entire reference set across the quantitative characters was similar for all the environments. In entire reference set the

highest diversity index was found for grain yield (E1, E2 and pooled over E1 and E2), SPAD1 (E3, E4 and pooled over E3, E4 and E5) and panicle length (E5). The diversity index of flowering group increases from the G1 to G5 and then it decrease in the G6 and G7 in E1, E2 and pooled over E1 and E2. The average H' of races across the quantitative characters was higher than the average H' of intermediate races and wild types.

- Plant height, 100 seed weight, plot grain yield, panicle weight, SPAD1 and SPAD2 were found to have highest H' in entire reference set, all flowering groups, races, intermediate races and wild types.
- The most diverse pairs of accessions in the reference set were IS 36563 (*caudatum*) and IS 31533 (*verticilliflorum*) in pooled over E1 and E2, IS 41724 (*guinea-caudatum*) and IS 2678 (*caudatum-bicolor*) in E3, IS 18821 (*Aethiopicum*) and IS 9303 (*Kafir*) in E4 and IS 41(52)500 (*guinea-caudatum*) and IS 13 (*bicolor*) in E5 and pooled over E3, E4 and E5.
- The first five principal components in entire reference set and three principal components in flowering groups, races, intermediate races and wilds as group explained more than 60 per cent of variation in all the environments.
- The principal component analysis in entire reference set reduced the 11 quantitative characters into 9 characters in E1, E2 and pooled over E1 and E2 and into 8 characters in E3, E4, E5 and pooled over E3, E4 and E5. In flowering group, races, intermediate races and wilds as group in all the environments the 11 characters were reduced into 7 characters.
- Days to 50 per cent flowering, panicle length, panicle weight, grain yield and SPAD1 occurred in all the principal components in entire reference set, flowering groups, races, intermediate races and wild type in all the environments. This indicates that these characters can be considered as important for the characterization of sorghum reference set accessions.

- Races, intermediate races, and wilds were grouped into three clusters in E1, E2, E4 and pooled over E1 and E2, two clusters in E3, five clusters in E5 and four cluster in pooled over E3, E4 and E5.
- The wild types *Aethiopicum, Arundinaceum, Verticilliflorum and Virgatum* are grouped together in E1, E2 pooled over E1 and E2, E5 and polled over E3, E4 and E5. The accessions basic race *bicolor* and the accessions of wild sub species *Drummondii* were cluster together in all the environments.
- Based on the drought tolerance indices viz., STI, MP, GP, SSI, TOL and DTE, a total of 35 drought tolerant accessions representing entire reference set and in addition 30 drought tolerant accessions representing seven flowering groups were identified.
- In entire reference set the maximum of the accessions identified for drought tolerance belong to the race *Caudatum* from Cameroon, Ethiopia, Kenya, Sudan and Uganda where as in flowering group the maximum of the accessions belong to the race *caudatum* and intermediate races *guinea-caudatum* from 20 countries.
- In entire reference set 29 accessions with high SCMR based on pooled data of E1 and E2, 22 accessions based on pooled data of E3, E4 and E5 and 77 accessions representing the seven flowering groups were identified.
- The accessions identified based on the drought tolerance indices and with SCMR reading are dominated with the race *caudatum* and by the intermediate race of *guinea-caudatum*.
- Over all in entire reference set the accessions IS8882, IS13845, IS22334 and IS29872 were found to have high drought tolerant indices and high SCMR in all the environments.
- In flowering groups the following accessions were identified with high drought tolerant indices and high SCMR values: G1- IS2848, G2- IS29569, IS102(111)525, IS13845, IS19016, IS19053, IS20762, IS22334, IS33261, IS5106, IS8882, G4-IS9468, IS15466, IS13791, IS13926, IS22287, IS 22239, IS22632, G5- IS3685, IS32986, IS22294, IS20792, G7 IS32454.

• In the entire reference set best 20 accessions were identified for each of the traits, days to 50 percent flowering, plant height, panicle length, hundred seed weight, panicle weight and plot grain yield.

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Accession	Race	Origin	Accession	Race	Origin
IS 13	Bicolor	USA	IS 3885	Guinea	Mali
IS 35	Bicolor	USA	IS 3905	Guinea	Mali
IS 303	Kafir-bicolor	China	IS 3957	Guinea	Nepal
IS 602	Bicolor	USA	IS 3971	Durra	India
IS 929	Durra	Sudan	IS 4027	Bicolor	India
IS 1127	Durra-caudatum	India	IS 4035	Durra-bicolor	India
IS 1398	Durra	Sudan	IS 4112	Caudatum	India
IS 2156	Bicolor	Nigeria	IS 4285	Durra	India
IS 2179	Bicolor	India	IS 4726	Durra	India
IS 2221	Guinea-kafir	USA	IS 4776	Durra	India
IS 2262	Kafir-caudatum	Sudan	IS 4821	Durra	India
IS 2263	Durra	Sudan	IS 4963	Guinea	India
IS 2367	Caudatum-bicolor	Nigeria	IS 5106	Durra	India
IS 2398	Kafir	South Africa	IS 5622	Durra	India
IS 2416	Kafir-durra	South Africa	IS 5720	Durra-bicolor	India
IS 2430	Guinea	Nigeria	IS 5867	Durra-caudatum	India
IS 2678	Caudatum-bicolor	Uganda	IS 5910	Guinea	India
IS 2730	Caudatum	Uganda	IS 5972	Durra	India
IS 2787	Caudatum	Kenya	IS 6118	Durra-caudatum	India
IS 2807	Caudatum	Zimbabwe	IS 6154	Durra	India
IS 2814	Caudatum	Zimbabwe	IS 6193	Guinea	India
IS 2834	Guinea	Zimbabwe	IS 6351	Durra	India
IS 2848	Caudatum	South Africa	IS 6413	Durra	India
IS 2873	Caudatum	Egypt	IS 6718	Guinea	Burkina Faso
IS 2902	Caudatum-bicolor	Nigeria	IS 6723	Caudatum	Burkina Faso
IS 3073	Caudatum	Sudan	IS 6745	Guinea	Burkina Faso
IS 3121	Bicolor	Kenya	IS 6828	Guinea	Burkina Faso
IS 3147	Caudatum-bicolor	South Africa	IS 6928	Guinea-caudatum	Sudan
IS 3421	Guinea	India	IS 6973	Caudatum	Sudan
IS 3443	Guinea-caudatum	Sudan	IS 7125	Caudatum	Somalia
IS 3450	Bicolor	Sudan	IS 7277	Caudatum-bicolor	Nigeria
IS 3507	Caudatum	Sudan	IS 7314	Caudatum	Nigeria
IS 3511	Kafir-caudatum	Sudan	IS 7463	Durra-caudatum	Nigeria
IS 3583	Caudatum	Sudan	IS 7722	Durra-caudatum	Nigeria
IS 3672	Caudatum	USA	IS 7861	Guinea	Nigeria
IS 3675	Guinea-durra	USA	IS 7889	Guinea	Nigeria
IS 3685	Caudatum	USA	IS 7958	Guinea	Nigeria
IS 3771	Caudatum-bicolor	Korea	IS 8218	Durra-bicolor	Uganda
IS 3780	Bicolor	China	IS 8283	Caudatum	Uganda
IS 8347	Guinea	Pakistan	IS 13989	Kafir	South Africa
IS 8348	Durra	Pakistan	IS 14206	Bicolor	Australia

Appendix 1. List of sorghum reference set accessions with their race and origin.

# Appendix 1 Contd...

Accession	Race	Origin	Accession	Race	Origin
IS 8685	Caudatum	Sudan	IS 14216	Arundinaceum	Angola
IS 8882	Caudatum	Uganda	IS 14259	Verticilliflorum	Angola
IS 9168	Bicolor	Kenya	IS 14276	Caudatum	South Africa
IS 9303	Kafir	South Africa	IS 14298	Bicolor	South Africa
IS 9468	Kafir	South Africa	IS 14317	Guinea	Swaziland
IS 9527	Kafir	South Africa	IS 14331	Guinea	South Africa
IS 9586	Caudatum	Niger	IS 14351	Guinea	Malawi
IS 9597	Guinea	Niger	IS 14414	Guinea	Malawi
IS 9713	Durra-caudatum	Sudan	IS 14446	Guinea-caudatum	Sudan
IS 9830	Caudatum	Sudan	IS 14449	Bicolor	Sudan
IS 9883	Caudatum	Sudan	IS 14478	Drummondii	Sudan
IS 9911	Caudatum	Sudan	IS 14535	Guinea-caudatum	Kenya
IS 10234	Guinea-caudatum	Central Africa	IS 14556	Guinea-caudatum	Ethiopia
IS 10801	Guinea-caudatum	Tchad	IS 14571	Verticilliflorum	Kenya
IS 10876	Guinea-caudatum	Nigeria	IS 14735	Caudatum-bicolor	Ethiopia
IS 10882	Guinea-caudatum	Nigeria	IS 14830	Caudatum	Cameroon
IS 10897	Drummondii	India	IS 14963	Caudatum	Cameroon
IS 10971	Durra-bicolor	USA	IS 15428	Caudatum	Cameroon
IS 10978	Durra	USA	IS 15443	Caudatum	Cameroon
IS 11026	Durra	Ethiopia	IS 15466	Caudatum	Cameroon
IS 11119	Caudatum	Ethiopia	IS 15478	Guinea-caudatum	Cameroon
IS 11374	Caudatum-bicolor	Ethiopia	IS 15526	Caudatum	Cameroon
IS 11758	Durra	Ethiopia	IS 15752	Caudatum	Cameroon
IS 11827	Durra	Ethiopia	IS 16044	Caudatum	Cameroon
IS 12110	Caudatum	Ethiopia	IS 16125	Caudatum	Cameroon
IS 12169	Bicolor	Ethiopia	IS 16173	Caudatum	Cameroon
IS 12447	Durra-caudatum	Sudan	IS 16186	Caudatum	Cameroon
IS 12531	Bicolor	Ethiopia	IS 16396	Guinea	Cameroon
IS 12804	Bicolor	Turkey	IS 16545	Caudatum	Cameroon
IS 12931	Guinea	China	IS 17593	Durra	Yemen
IS 13113	Bicolor	India	IS 18551	Durra-bicolor	Ethiopia
IS 13452	Guinea-caudatum	Zimbabwe	IS 18698	Caudatum	USA
IS 13791	Kafir	South Africa	IS 18800	Verticilliflorum	South Africa
IS 13827	Caudatum	South Africa	IS 18813	Virgatum	Egypt
IS 13845	Kafir	South Africa	IS 18821	Aethiopicum	Egypt
IS 13848	Caudatum	South Africa	IS 18829	Arundinaceum	Tanzania
IS 13926	Kafir	South Africa	IS 18835	Drummondii	USA
IS 18868	Verticilliflorum	USA	IS 20792	Guinea-caudatum	USA
IS 18874	Verticilliflorum	USA	IS 20842	Caudatum	USA
IS 18876	Arundinaceum	Benin	IS 21124	Caudatum	Kenya
IS 18879	Arundinaceum	USA	IS 21126	Drummondii	Kenya
IS 18919	Drummondii	Sudan	IS 21401	Drummondii	Malawi
## Appendix 1 Contd...

Accession	Race	Origin	Accession	Race	Origin
IS 18922	Drummondii	Sudan	IS 21425	Guinea	Malawi
IS 19016	Caudatum	Sudan	IS 21519	Guinea	Malawi
IS 19026	Caudatum	Sudan	IS 21622	Guinea	Malawi
IS 19041	Caudatum	Sudan	IS 21691	Drummondii	Niger
IS 19053	Guinea-caudatum	Sudan	IS 21849	Guinea	Sirra leone
IS 19132	Guinea-caudatum	Sudan	IS 21854	Drummondii	Burkina Faso
IS 19262	Guinea-caudatum	Sudan	IS 21891	Caudatum	USA
IS 19418	Caudatum	Ethiopia	IS 21991	Durra	India
IS 19453	Durra	Botswana	IS 22040	Durra	India
IS 19455	Guinea	Botswana	IS 22074	Durra	India
IS 19466	Guinea	Sri Lanka	IS 22239	Kafir	Botswana
IS 19685	Guinea	India	IS 22282	Bicolor	Botswana
IS 19847	Durra-caudatum	India	IS 22287	Kafir	Botswana
IS 19953	Guinea	Senegal	IS 22291	Guinea	Botswana
IS 20016	Guinea	Senegal	IS 22294	Kafir	Botswana
IS 20064	Guinea	Senegal	IS 22325	Guinea	Botswana
IS 20097	Guinea	Senegal	IS 22330	Durra	Botswana
IS 20205	Durra	Niger	IS 22332	Kafir	Botswana
IS 20351	Durra	Niger	IS 22334	Kafir	Botswana
IS 20387	Durra-caudatum	Niger	IS 22506	Caudatum	Sudan
IS 20665	Caudatum-bicolor	USA	IS 22609	Caudatum	Sri Lanka
IS 20681	Kafir	USA	IS 22632	Durra	Cameroon
IS 20697	Caudatum	USA	IS 22909	Durra	Sudan
IS 20700	Guinea-caudatum	USA	IS 22986	Caudatum	Sudan
IS 20709	Caudatum	USA	IS 22996	Guinea-caudatum	Sudan
IS 20710	Bicolor	USA	IS 23048	Caudatum	Sudan
IS 20713	Guinea-caudatum	USA	IS 23053	Caudatum	Sudan
IS 20724	Bicolor	USA	IS 23100	Guinea	Tanzania
IS 20727	Bicolor	USA	IS 23142	Durra	Tanzania
IS 20743	Bicolor	USA	IS 23166	Drummondii	Tanzania
IS 20749	Bicolor	USA	IS 23178	Bicolor	Zambia
IS 20762	Guinea-caudatum	USA	IS 23254	Bicolor	Zambia
IS 20763	Caudatum-bicolor	USA	IS 23574	Guinea-caudatum	Ethiopia
IS 20782	Bicolor	USA	IS 23601	Guinea-caudatum	Ethiopia
IS 23645	Guinea	Gambia	IS 27146	Durra	Zimbabwe
IS 23666	Guinea	Gambia	IS 27164	Kafir	Zimbabwe
IS 23669	Guinea	Gambia	IS 27287	Guinea	Burkina Faso
IS 23777	Guinea	Malawi	IS 27390	Guinea	Burkina Faso
IS 23903	Caudatum-bicolor	Yemen	IS 27490	Guinea	Burkina Faso
IS 23948	Caudatum-bicolor	Yemen	IS 27587	Aethiopicum	Cameroon
IS 23988	Durra-caudatum	Yemen	IS 27599	Guinea-caudatum	Cameroon
IS 23992	Caudatum	Yemen	IS 27791	Durra-bicolor	Germany

## Appendix 1 Contd...

Accession	Race	Origin	Accession	Race	Origin
IS 24009	Caudatum	USA	IS 27855	Bicolor	South Africa
IS 24072	Guinea	Tanzania	IS 27891	Caudatum-bicolor	South Africa
IS 24083	Guinea	Tanzania	IS 28332	Durra-caudatum	Yemen
IS 24139	Guinea	Tanzania	IS 28389	Durra-caudatum	Yemen
IS 24481	Kafir	South Africa	IS 28409	Durra	Yemen
IS 24503	Kafir	South Africa	IS 28645	Durra-caudatum	Yemen
IS 24713	Bicolor	Nigeria	IS 28740	Durra-caudatum	Yemen
IS 24786	Durra-bicolor	Nigeria	IS 28849	Durra-caudatum	Yemen
IS 24887	Guinea-caudatum	Nigeria	IS 28991	Guinea-caudatum	Yemen
IS 24913	Guinea-bicolor	Zambia	IS 29233	Kafir	Swaziland
IS 24939	Bicolor	Zambia	IS 29310	Guinea-caudatum	Swaziland
IS 24940	Guinea-durra	Zambia	IS 29375	Guinea-caudatum	Lesotho
IS 24953	Guinea-caudatum	Zambia	IS 29407	Kafir	Lesotho
IS 25055	Guinea	Ghana	IS 29409	Kafir	Lesotho
IS 25077	Guinea	Ghana	IS 29472	Kafir	Lesotho
IS 25207	Bicolor	Ethiopia	IS 29496	Kafir	Lesotho
IS 25301	Durra-bicolor	Ethiopia	IS 29569	Kafir	Lesotho
IS 25442	Caudatum	Kenya	IS 29606	Kafir	South Africa
IS 25596	Caudatum	Rwanda	IS 29638	Caudatum-bicolor	China
IS 25702	Caudatum-bicolor	Mali	IS 29691	Guinea	Zimbabwe
IS 25733	Guinea	Mali	IS 29870	Durra-caudatum	Zimbabwe
IS 25836	Durra	Mali	IS 29872	Kafir	Zimbabwe
IS 25910	Guinea	Mali	IS 29876	Guinea-caudatum	Zimbabwe
IS 26041	Guinea	Mali	IS 29911	Caudatum	Zimbabwe
IS 26110	Guinea	Mali	IS 29966	Kafir	Zimbabwe
IS 26457	Guinea	Benin	IS 30175	Guinea	Zimbabwe
IS 26554	Guinea	Benin	IS 30207	Guinea-caudatum	Zimbabwe
IS 26731	Bicolor	South Africa	IS 30317	Caudatum-bicolor	China
IS 26788	Durra-caudatum	South Africa	IS 30335	Caudatum-bicolor	China
IS 26815	Caudatum	Yemen	IS 30352	Caudatum-bicolor	China
IS 26833	Caudatum	Sudan	IS 30385	Caudatum-bicolor	China
IS 30400	Caudatum-bicolor	China	IS 41724	Guinea-caudatum	ICRISAT
IS 30405	Caudatum-bicolor	China	IS 102 (111) 525	Guinea-caudatum	ICRISAT
IS 30409	Caudatum-bicolor	China	IS 14-1 (16) 480	Durra	ICRISAT
IS 30417	Caudatum-bicolor	China	IS 30469 (453 (486) 512)	Guinea-caudatum	Ethiopia
IS 30436	Caudatum-bicolor	China	IS 393 (411) 659	Caudatum-bicolor	ICRISAT
IS 30441	Caudatum	China	IS 403 (418) 662	Guinea-caudatum	ICRISAT
IS 30443	Caudatum-bicolor	China	IS 41 (52) 500	Guinea-caudatum	ICRISAT
IS 30451	Caudatum-bicolor	China	IS 447 (471) 496	Guinea-caudatum	ICRISAT
IS 30503	Bicolor	Korea	IS 452 (484) 510	Durra	ICRISAT
IS 30538	Bicolor	Korea	IS 62 (73) 5 09	Guinea-durra	ICRISAT
IS 30619	Caudatum	Cameroon	IS 64 (75) 511	Guinea-caudatum	ICRISAT

# Appendix 1 Contd...

Accession	Race	Origin	Accession	Race	Origin
IS 30748	Durra-caudatum	Cameroon	IS 651 (902) 656	Guinea-caudatum	ICRISAT
IS 30898	Guinea-caudatum	Uganda	SSM 1046	Guinea-caudatum	Senegal
IS 31123	Guinea-caudatum	Uganda	SSM 1049	Bicolor	Senegal
IS 31179	Caudatum	Uganda	SSM 1057	Guinea	Senegal
IS 31195	Guinea-caudatum	Uganda	SSM 1102	Guinea-caudatum	Tchad
IS 31202	Caudatum	Uganda	SSM 1123	Caudatum	Niger
IS 31299	Caudatum	Uganda	SSM 12	Durra	Cameroon
IS 31533	Verticilliflorum	Burundi	SSM 1267	Durra-caudatum	Cameroon
IS 31559	Caudatum	Burundi	SSM 1284	Bicolor	Congo
IS 31681	Bicolor	Algeria	SSM 1370	Bicolor	South Africa
IS 31693	Caudatum-bicolor	Algeria	SSM 1592	Caudatum-bicolor	Tchad
IS 31852	Durra-caudatum	Yemen	SSM 19	Guinea-caudatum	Cameroon
IS 31861	Durra-caudatum	Yemen	SSM 205	Guinea	Burkina Faso
IS 32050	Durra	Yemen	SSM 215	Guinea-caudatum	Ethiopia
IS 32087	Durra-caudatum	Yemen	SSM 249	Guinea	Burkina Faso
IS 32092	Durra-caudatum	Yemen	SSM 275	Guinea	Burkina Faso
IS 32234	Durra-caudatum	Yemen	SSM 276	Guinea	Burkina Faso
IS 32454	Guinea	India	SSM 29	Durra	Cameroon
IS 32569	Durra	Somalia	SSM 379	Guinea	Mali
IS 32986	Guinea	Tanzania	SSM 501	Guinea-caudatum	Niger
IS 33173	Caudatum	Cameroon	SSM 505	Guinea	Niger
IS 33178	Durra	Cameroon	SSM 547	Caudatum	Niger
IS 33209	Durra-caudatum	Cameroon	CONTROL CULTIVAR	S	
IS 33261	Caudatum	Cameroon	IS 2205	Durra-bicolor	India
IS 33353	Caudatum	Kenya	IS 18758	Guinea-caudatum	Ethiopia
IS 33423	Caudatum	Kenya	IS 33844	Durra	India
IS 36563	Caudatum	Niger			
IS 36633	Caudatum	ICRISAT			

		Temp	erature	Rainfall	Relative
Location	Season / date	Min (°C)	Max (°C)	(mm)	Humidity (%)
International Crops Research	Post rainy				
Institute for semi arid tropics, Patancheru, Andhra Pradesh	(October, 2009 to April, 2010)	19.50	32.64	461.59	82.83
University of Agricultural Sciences, Dharwad, Karnataka	Post rainy (November, 2009 to April, 2010)	14.0	32.13	81.3	80.1
Regional Agricultural Research Station, Bijapur, Karnataka	Post rainy (November, 2009 to April, 2010)	20.3	33.4	73.5	70.3

# Table 2. Meteorological details of evaluated locations of sorghum reference set

Countries         B         C         D         C         KB         DB         DC         GB         GC         GB         GC         KB         KC         KD         KD         KD         KD         SU         SU <ths< th=""></ths<>
Algeria       1       -       -       1       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       1       -       -       -       1       -       -       -       -       -       -       -       -       1       -       -       1       -       -       1       -       -       1       -       -       1       -       -       1       -       -       1       -       -       1       -       -       1       -       1       -       -       1       1       1       1       1       1       1 </th
Angola       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       1       1       1       -       -       -       1       -       -       -       1       1       -       -       -       1       -       -       -       1       1       1       1       -       -       -       -       -       -       1       1       -       -       1       1       1       -       -       1       -       -       -       1       1       1       -       -       1       1       1       1       1       1       1       1       1       1       1
Australia       1       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       1       -       -       -       -       -       -       -       -       -       -       1       -       -       -       -       -       -       -       -       1       1       -       1       -       -       -       -       -       -       -       1       -       -       1       -       -       -       1       1       -       -       1       1       1       -       1       1       1       1       1       1       1       1       1
Benin       -       -       2       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       1       -       -       -       1       -       -       -       -       -       -       -       -       1       -       1       -       1       -       1       -       -       1       -       -       1       -       1       -       1       -       1       -       -       1       -       1       -       -       1       -       -       1       -       -       1       -       -       1       1       -       -       1       1       1       -       -       1       1       1
Botswana       1       -       2       3       5       -       -       -       -       -       -       -       -       -       -       -       11         Burkina       -       1       -       10       -       -       -       -       -       -       -       -       -       -       -       12         Burundi       -       15       4       1       -       -       -       -       -       -       -       -       -       2       2         Cameroon       -       15       4       1       -       -       -       -       -       -       -       -       2       -       -       -       2       -       -       -       -       -       -       1       -       -       -       1       -       -       1       -       -       1       -       -       1       -       -       1       -       -       1       2       2       2       2       1       -       -       -       1       1       2       2       1       1       2       2       1       1       2
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$
Burundi-12Cameroon-15413-31-27Central11-27Central11-Africa11-1-1211Congo111Egypt-111Brinpia333225113Gambia1113Gambia1113Gambia2
Cameroon       -       15       4       1       -       -       3       -       3       -       -       -       -       -       1       -       -       -       1       -       -       -       -       1       -       -       -       -       1       -       1       -       -       -       1       -       1       -       1       -       1       -       1       -       1       -       1       -       1       -       1       -       1       -       1       -       1       -       1       -       1       -       1       1       -       1       -       -       -       -       -       -       1       1       -       -       1       1       -       -       1       1       -       -       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1
Central       Africa       -       -       -       1       -       -       -       -       -       1       -       -       -       1       -       1       -       -       1       -       1       -       -       1       -       1       -       1       -       1       -       1       -       -       1       -       -       -       1       -       -       1       1       -       1       1       1       1       1       1       1       -       1       -       -       -       1       -       -       -       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1 <t< td=""></t<>
China       1       1       -       1       -       12       -       -       -       1       -       -       -       -       1       -       -       -       -       1       -       -       -       -       1       -       -       -       -       1       -       -       -       1       1       3       3       3       -       -       1       1       3       3       3       3       3       -       -       2       2       -       -       5       -       -       -       -       -       1       1       3       3       3       -       -       2       2       -       -       5       -       -       -       -       -       1       1       3       3       3       -       -       -       -       -       -       -       1       3       3       3       -       -       -       -       -       -       -       -       3       3       -       -       1       -       -       3       3       -       -       1       -       -       -       1       -       -
Congo       1       -       -       -       -       -       -       -       -       -       -       -       -       1       3         Egypt       -       1       -       -       2       2       -       -       -       -       -       -       -       1       1       3         Ethiopia       3       3       3       -       2       2       -       -       5       -       -       -       -       1       1       3         Gambia       -       -       3       -       -       2       2       -       -       5       -       -       -       -       1       3         Gambia       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       3       3       3       -       -       1       -       -       -       -       -       1       3       3       3       -       -       1       -       -       1       1       -       1       1       1       1       1       1
Egypt       -       1       -       -       -       -       -       -       -       -       1       1       1       3         Ethiopia       3       3       3       -       -       2       2       -       -       5       -       -       -       -       -       1       1       1       3         Gambia       -       -       -       1       -       -       -       -       -       -       -       18         Gambia       -       -       -       -       -       -       -       -       -       3         Germany       -       -       -       -       -       -       -       -       -       -       1       -       -       1       -       -       1       -       -       -       -       -       -       -       1       -       -       1       1       -       -       1       1       -       -       1       1       -       -       1       1       -       -       1       1       -       1       1       1       1       1       1       1
Ethiopia       3       3       3       3       -       -       2       2       -       -       5       -       -       -       -       -       18         Gambia       -       -       -       -       -       -       -       -       -       -       -       -       3         Germany       -       -       -       -       -       -       -       -       -       -       -       -       -       3         Germany       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       1       -       -       -       1       -       -       1       -       -       1       -       -       -       1       -       -       1       -       -       1       1       -       -       1       1       -       -       1       -       -       1       1       -       1       1       -       -       1       1       1       1
Gambia       -       -       3       -       -       -       -       -       -       3         Germany       -       -       -       1       -       -       -       -       -       -       3         Ghana       -       -       2       -       -       -       -       -       -       -       -       -       1         Ghana       -       -       2       -       -       -       -       -       -       -       -       -       1       1         Ghana       -       -       2       -       -       1       -       -       -       -       -       -       2       1       1       1       1       1       1       1       1       1       -       -       1       -       -       1       1       1       1       1       1       1       1       1       1       -       1       1       -       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1
Germany       -       -       -       -       1       -       -       -       -       -       -       -       -       -       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1 </td
Ghana       -       -       2       -       -       -       -       -       -       -       -       -       2         ICRISAT       -       1       2       -       -       1       -       -       7       -       1       -       -       -       -       2         India       3       1       14       6       -       -       2       4       -       -       -       -       -       1       -       -       12         India       3       1       14       6       -       -       2       4       -       -       -       -       -       1       1       -       -       12         India       3       1       14       6       -       -       2       4       -       -       -       -       1       1       -       -       131         Kenya       2       5       -       -       1       -       -       -       -       -       10       -       -       31         Lesotho       -       -       -       -       -       -       -       -
ICRISAT       -       1       2       -       -       1       -       -       1       -       -       -       -       -       -       -       1       1       -       -       1       1       -       -       -       1       1       -       -       -       -       -       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1 </td
India       3       1       14       6       -       -       2       4       -       -       -       -       -       -       -       1       -       -       31         Kenya       2       5       -       -       -       -       1       -       -       1       1       -       -       31         Kenya       2       5       -       -       -       -       1       -       -       1       1       -       -       31         Kenya       2       5       -       -       -       1       -       -       1       1       -       -       10         Korea       2       -       -       -       1       -       -       -       -       -       -       31         Lesotho       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       33         Lesotho       -       -       1       -       -       -       -       -       -       -       -       -       1       -       -
India       2       5       -       -       -       1       -       -       1       1       -       -       10         Kenya       2       5       -       -       -       1       -       -       1       1       -       -       10         Korea       2       -       -       -       1       -       -       -       -       1       1       -       -       10         Korea       2       -       -       -       1       -       -       -       -       -       -       10         Korea       2       -       -       5       -       -       -       -       -       -       -       -       3         Lesotho       -       -       -       -       1       -       -       -       -       -       -       6         Mali       -       -       1       -       -       -       -       -       -       -       -       9         Nepal       -       -       1       1       -       -       -       -       1       1       -       1
Koriya       2       -       -       1       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       1       -       -       -
Korea       2       -       -       -       -       1       -       -       -       -       -       6         Lesotho       -       -       -       1       -       -       -       -       -       -       -       6         Malawi       -       -       -       6       -       -       -       -       -       -       -       -       -       6       -       -       -       -       -       -       -       -       -       -       6       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       -       6       -       -       -       -       -       -       -       -       -       -       -       -       7       9       Nepal       -       -       -       -       -       -       -       -       -       -       -       -       1       -       -       -       -       1       1       -       -       -       -       -       1       1       -       -       - </td
Lesonio       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I       I </td
Malawi       -       -       1       -       -       -       -       -       -       -       -       9         Mali       -       -       1       7       -       1       -       -       -       -       -       9         Nepal       -       -       1       -       -       -       -       -       -       9         Niger       -       4       2       2       -       -       1       1       -       -       -       1       1         Nigeria       2       1       -       4       -       3       1       2       -       3       -       -       -       -       1       1         Nigeria       2       1       -       4       -       3       1       2       -       3       -       -       -       -       1       1       1       -       -       -       -       1       1       1       -       -       -       -       1       1       1       1       1       -       -       -       -       -       1       1       1       1       1
Nepal       -       -       1       -       -       -       -       -       1       1         Niger       -       4       2       2       -       -       1       1       -       -       -       1       1         Nigeria       2       1       -       4       -       3       1       2       -       -       -       1       1         Nigeria       2       1       -       4       -       3       1       2       -       3       -       -       -       -       16         Delaister       -       -       1       1       -       -       -       -       16
Niger       -       4       2       2       -       -       1       1       -       -       -       1       1         Nigeria       2       1       -       4       -       3       1       2       -       -       -       1       1         Nigeria       2       1       -       4       -       3       1       2       -       3       -       -       -       -       16         Delvister       -       -       1       1       -       -       -       -       16       -       -       16
Nigeria $2 1 - 4 - 3 1 2 - 3 16$
$\mathbf{R}_{\mathbf{W}}$
Seneral $1 - 5 7$
Somalia $-1$ $1$ $-1$ $-1$ $-1$ $-1$ $-1$ $-1$
South Africa $4 \ 4 \ - \ 1 \ 11 \ 2 \ - \ 1 \ - \ - \ - \ 25$
South Anda $\cdot$
Sudan 2 16 4 2 - 7 2 3 $36$
Swaziland $  1$ $1$ $  1$ $    3$
Tanzania 1 5 8
Tchad 1 2 3
Turkey 1 1
Uganda - 6 1 1 3 11
USA 9 8 1 - 1 2 1 4 1 1 1 2 1 32
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Table 1. Geographical and race wise distribution of sorghum reference set

B-Bicolor, C-Caudatum, D-Durra, G-Guinea, K-Kafir, Sae-Aethiopicum, , Sar-Arundinaceum, sd-Drummondii, SV-Verticilliflorum ,Svr-Virgatum

							F	lowering	Group		
Character	Entire reference set	Races	Intermediate races	Wild types	Gl	G2	G3	G4	G5	G6	G7
No. of accessions	384	245	116	23	36	114	124	51	38	13	8
Mid rib color											
Dull	21.9	20.0	26.7	13.0	27.8	24.6	23.4	13.7	18.4	15.4	12.5
White	76.3	78.4	71.6	78.3	69.4	74.6	75.0	82.3	78.9	84.6	87.5
Yellow	1.8	1.6	1.7	8.7	2.8	0.9	1.6	3.9	2.6	0.0	0.0
Plant pigmentation											
Pigmented	94.8	96.0	92.2	95.6	91.7	93.9	92.0	100.0	100.0	100.0	100.0
Tanned	5.2	4.1	7.8	4.3	8.3	6.4	8.1	0.0	0.0	0.0	0.0
Nodal tillers											
Presence	88.3	91.0	82.8	87.0	91.7	80.7	87.1	94.1	97.4	100.0	100.0
Absence	11.7	9.0	17.2	13.0	8.3	19.3	12.9	5.9	2.6	0.0	0.0
Glume color											
Brown	5.2	5.3	5.2	4.3	0.0	7.9	5.6	3.9	2.6	0.0	12.5
Black	34.4	32.6	35.3	47.8	33.3	35.1	30.6	29.4	42.1	53.8	50.0
Light Brown	1.3	2.4	3.4	20.8	8.3	3.5	4.0	7.8	0.0	0.0	0.0
Light Red	1.0	4.9	7.8	0.0	8.3	5.3	4.8	0.0	2.6	7.7	0.0
Purple	30.2	33.5	29.3	0.0	22.2	30.7	29.8	31.4	44.7	7.7	25.0
Partly straw brown	4.9	6.1	3.4	0.0	8.3	2.6	5.6	3.9	5.3	15.4	0.0
Partly straw purple	3.9	2.9	6.9	0.0	2.8	7.0	2.4	5.9	0.0	0.0	0.0
Red	8.1	9.4	5.2	8.7	8.3	6.1	11.3	13.7	0.0	0.0	0.0
Reddish Brown	3.4	3.7	3.4	0.0	5.6	1.7	4.0	2.0	2.6	7.7	12.5
Straw	0.5	0.4	0.0	4.3	2.8	0.0	1.6	0.0	0.0	7.7	0.0
White	0.5	0.0	0.0	8.7	0.0	0.0	0.8	2.0	0.0	0.0	0.0
Yellow	0.3	0.0	0.0	4.3	0.0	0.0	0.8	0.0	0.0	0.0	0.0
Glume covering											
One fourth of grain covered	44.0	51.0	32.8	26.1	38.9	37.2	43.5	52.4	47.4	61.5	62.5
Half of grain covered	36.2	31.0	51.7	13.0	38.9	36.0	41.1	33.3	36.8	7.7	12.5
Three fourth of grain covered	10.7	7.3	12.1	39.1	5.6	14.9	8.1	9.8	13.2	15.4	25.0
Grain Fully covered	7.3	10.6	1.7	0.0	8.3	10.5	6.4	3.9	0.0	0.0	0.0
Glume larger than grain	1.8	0.0	1.7	21.7	8.3	0.9	0.8	0.0	2.6	7.7	0.0

 Table 6a. Frequency distribution of qualitative characters in entire reference set, races, intermediate races, wild types and flowering groups of reference set.

Table 6a Contd...

							Fl	owering	Group		
Character	Entire reference set	Races	Intermediate races	Wild types	G1	G2	G3	G4	G5	G6	G7
Grain Color											
Brown	15.4	15.9	11.2	30.4	19.4	16.7	15.3	7.8	10.5	23.1	37.5
Chalky white	4.7	4.1	3.4	17.4	5.6	8.8	2.4	2.0	5.3	0.0	0.0
Grey	3.6	2.4	6.0	4.3	2.8	4.4	4.0	2.0	5.3	0.0	0.0
Light Brown	4.9	5.3	4.3	4.3	8.3	8.8	2.4	3.9	0.0	0.0	0.0
Light red	11.2	13.5	8.6	0.0	16.7	8.8	11.3	13.7	10.5	15.4	0.0
Purple	19.0	18.8	22.4	4.3	13.9	20.2	21.8	19.6	18.4	7.7	0.0
Red	2.1	2.0	1.7	4.3	22.2	1.7	1.6	2.0	0.0	0.0	0.0
Reddish Brown	14.6	3.7	21.5	8.7	5.6	14.9	14.5	11.8	13.2	7.7	0.0
Straw	3.1	1.6	2.6	21.7	5.6	1.7	1.6	3.9	5.3	7.7	12.5
White	19.0	22.4	14.7	4.3	0.0	14.0	20.2	29.4	26.3	23.1	25.0
Yellow	2.3	2.0	3.4	0.0	0.0	0.0	4.0	3.9	5.3	0.0	0.0
Threshability											
Difficult to thresh	14.6	13.5	6.9	65.2	16.7	21.9	8.9	9.8	10.5	23.1	25.0
Fully Threshable	63.0	66.5	66.4	17.4	61.1	52.6	68.5	72.5	65.8	61.5	62.5
Partly Threshable	22.4	20.4	28.4	17.4	22.2	25.4	22.6	17.6	23.7	15.4	12.5

			Races							Interm	ediate ra	nces				Wild types						
	В	С	D	G	K	СВ	DB	DC	GB	GC	GD	GK	KB	KC	KD	Sae	Sar	sd	SV	SVr		
No. of accessions	37	76	40	66	26	29	8	25	1	45	3	1	1	2	1	2	4	10	6	1		
Mid rib color																						
Dull	10.8	22.4	22.5	19.7	23.0	20.7	12.5	20.0	0.0	35.7	33.3	100.0	0.0	50.0	100.0	50.0	0.0	0.0	33.3	0.0		
White	86.4	73.7	77.5	78.8	77.0	79.3	87.5	80.0	100.0	62.2	66.6	0.0	100.0	50.0	0.0	50.0	100.0	100.0	33.3	100.0		
Yellow	2.7	3.9	0.0	1.5	0.0	0.0	0.0	0.0	0.0	2.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	33.3	0.0		
Plant pigmentation																						
Pigmented	94.6	96.0	97.5	95.4	96.1	96.5	100.0	96.0	100.0	86.7	100.0	100.0	0.0	100.0	100.0	50.0	100.0	100.0	100.0	100.0		
Tanned	5.4	3.9	2.5	5.5	3.8	5.4	0.0	4.0	0.0	13.3	0.0	0.0	100.0	0.0	0.0	50.0	0.0	0.0	0.0	0.0		
Nodal tillers																						
Presence	91.9	83.8	95.0	92.4	92.3	79.3	100.0	88.0	100.0	77.8	100.0	100.0	100.0	50.0	100.0	50.0	100.0	90.0	100	83.3		
Absence	8.1	13.1	5.0	7.6	7.7	20.7	0.0	12.0	0.0	22.2	0.0	0.0	0.0	50.0	0.0	50.0	0.0	10.0	0.0	6.7		
Glume color																						
Brown	8.1	3.9	7.5	6.1	0.0	3.4	0.0	8.0	0.0	4.4	33.3	0.0	0.0	0.0	0.0	0.0	0.0	10.0	0.0	0.0		
Black	45.9	42.1	17.5	30.3	15.4	41.4	0.0	36.0	0.0	40.0	0.0	0.0	0.0	100.0	0.0	50.0	50.0	50.0	50.0	0.0		
Light Brown	13.5	0.0	0.0	1.5	0.0	0.0	4.0	0.0	0.0	6.7	0.0	0.0	0.0	0.0	0.0	50.0	25.0	10.0	0.0	100.0		
Light Red	0.0	3.9	5.0	6.1	0.0	6.9	0.0	0.0	0.0	13.3	33.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		
Light straw brown	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	16.67	0.0		
Purple	8.1	25.0	47.5	33.3	73.1	24.1	20.0	48.0	0.0	15.6	33.3	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0		
Partly straw brown	8.1	3.9	10.0	6.1	3.8	3.4	8.0	0.0	0.0	2.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		
Partly straw purple	2.7	1.3	7.5	3.0	0.0	10.3	0.0	4.0	0.0	8.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		

Table 6b. Frequency distribution of qualitative characters in individual races, intermediate races and wilds of sorghum reference set.

			Races						]	Interm	ediate ra	ices					١	Wild typ	es	
	В	С	D	G	K	CB	DB	DC	GB	GC	GD	GK	KB	KC	KD	Sae	Sar	sd	SV	SVr
Red	13.5	13.2	5.0	7.6	3.8	3.4	0.0	4.0	100.0	6.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	10.0	16.67	0.0
Reddish Brown	0.0	6.6	0.0	4.5	3.8	6.9	0.0	0.0	0.0	2.2	100.0	0.0	0.0	0.0	0.0	0.0	0.0	Tał	ole 6b C	ontd
Straw	0.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	20.0	0.0	0.0	0.0
White	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	25.0	0.0	0.0
Yellow	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	16.6	0.0
Glume covering																				
One fourth of grain covered	0.0	43.0	7.9	93.9	19.2	3.4	0.0	24.0	0.0	60.0	66.7	0.0	0.0	100.0	0.0	50.0	0.0	30.0	16.6	100
Half of grain covered	0.0	22.8	19.7	4.5	84.6	51.7	62.5	72.0	100.0	40.0	33.0	100.0	0.0	0.0	100.0	0.0	25.0	0.0	33.3	0.0
Three fourth of grain covered	29.7	0.9	3.9	1.5	0.0	34.5	25.0	4.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	25.0	70.0	16.6	0.0
Grain Fully covered	70.3	0.0	0.0	0.0	0.0	3.4	25.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Glume larger than grain	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	50.0	50.0	0.0	33.3	0.0
Grain Color																				
Brown	18.9	13.2	10.0	53.8	15.4	10.3	0.0	12.0	0.0	15.6	0.0	0.0	0.0	0.0	0.0	0.0	33.3	30.0	50.0	0.0
Chalky white	2.7	10.5	0.0	3.8	0.0	6.9	0.0	4.0	0.0	2.2	0.0	0.0	0.0	0.0	0.0	50.0	0.0	10.0	16.6	0.0
Grey	2.7	2.3	0.0	11.5	0.0	3.4	0.0	12.0	0.0	6.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	10.0	0.0	0.0
Light Brown	8.1	5.3	7.5	7.7	3.8	3.4	0.0	4.0	0.0	4.4	0.0	0.0	100.0	0.0	0.0	0.0	0.0	10.0	0.0	0.0
Light red	13.5	15.8	10.0	23.1	23.1	3.4	12.5	16.0	0.0	8.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	10.0	0.0	0.0
Purple	5.4	17.1	30.0	46.1	26.9	17.2	0.0	24.0	0.0	26.7	66.7	0.0	0.0	50.0		0.0	0.0	0.0	0.0	0.0
Red	5.4	1.3	0.0	7.7	0.0	3.4	0.0	0.0	0.0	2.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	16.6	0.0
Reddish Brown	21.6	13.2	10.0	19.2	7.7	48.3	62.5	12.0	0.0	6.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	20.0	0.0	0.0
Straw	0.0	2.6	0.0	7.7	0.0	0.0	0.0	0.0	0.0	6.7	0.0	0.0	0.0	0.0	0.0	50.0	66.7		16.6	100.0

			Races							Interme	ediate ra	ices					١	Vild typ	es	
	В	С	D	G	К	СВ	DB	DC	GB	GC	GD	GK	KB	KC	KD	Sae	Sar	sd	SV	SVr
White	10.8	18.4	32.5	73.1	19.2	3.4	12.5	12.0	100.0	15.6	33.3	100.0	0.0	50.0	100.0	0.0	0.0	10.0	0.0	0.0
Yellow	10.8	0.0	0.0	0.0	3.8	0.0	12.5	4.0	0.0	4.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Thresability																				
Difficult to thrash	67.6	3.9	5.0	4.5	0.0	17.2	0.0	0.0	0.0	2.2	33.3	0.0	100.0	0.0	0.0	100.0	75.0	80.0	16.6	100.
Fully Threshable	18.9	75.0	55.0	80.3	88.5	37.9	6.2	84.0	100.0	80.0	66.7	0.0	0.0	0.0	0.0	0.0	25.0	10.0	33.3	0.0
Partly Threshable	13.5	21.0	40.0	15.1	11.5	44.8	3.7	16.0	0.0	17.8	0.0	100.0	0.0	100.0	100.0	0.0	0.0	10.0	50.0	0.0

B-Bicolor, C-Caudatum, D-Durra, G-Guinea, K-Kafir, Sae-Aethiopicum, Sar-Arundinaceum, sd-Drummondii, SV-Verticilliflorum, Svr-Virgatum

	Group 1	Group2	Group 3	Group 4	Group 5	Group 6	Group 7	Entire set	
	(36) <sup>a</sup>	(114)	(124)	(51)	(38)	(13)	(8)	(384)	Mean±SE
РР	0.12	0.09	0.12	0.00	0.00	0.00	0.13	0.09	$0.07 \pm 0.021$
NT	0.12	0.21	0.16	0.09	0.05	0.00	0.00	0.15	$0.10 \pm 0.028$
MRB	0.30	0.26	0.28	0.23	0.25	0.16	0.13	0.26	$0.23 \pm 0.020$
GLCL	0.85	0.79	0.84	0.82	0.58	0.71	0.64	0.83	$0.76 \pm 0.036$
GLCOV	0.58	0.56	0.50	0.46	0.47	0.49	0.37	0.54	$0.50 \pm 0.023$
GRC	0.92	0.91	0.89	0.90	0.87	0.84	0.58	0.93	$0.86 \pm 0.040$
THR	0.40	0.44	0.35	0.33	0.37	0.40	0.39	0.39	$0.39 \pm 0.012$
Mean±SE	$0.47 \pm 0.124$	0.47±0.115	0.45±0.118	$0.41 \pm 0.131$	0.37±0.116	0.37±0.126	$0.32{\pm}0.091$	0.46±0.124	$0.41 \pm 0.118$

Table 7a Shannon Weaver diversity index (H') of qualitative characters in different flowering groups and entire sorghum reference set.

<sup>a</sup> Numbers within parenthesis indicate number of accessions in each flowering group

Table 7b Shannon-Weaver diversity index (H) for qualitative characters in different races, intermediate races and wilds of sorghum reference set.

			<b>Basic Races</b>				Intermed	iate Races		Wild	
	B (37) <sup>a</sup>	C (76)	D (47)	G (66)	K (26)	CB (29)	DB (15)	DC (25)	GC (52)	Sd (10)	Mean±SE
РР	0.09	0.07	0.04	0.08	0.07	0.06	0.00	0.07	0.17	0.00	0.07±0.015
NT	0.12	0.17	0.08	0.12	0.12	0.22	0.00	0.16	0.22	0.14	0.13±0.021
MRB	0.20	0.28	0.21	0.25	0.24	0.23	0.27	0.22	0.31	0.00	$0.22 \pm 0.027$
GLCL	0.74	0.69	0.77	0.78	0.39	0.72	0.51	0.51	0.85	0.59	$0.66 \pm 0.047$
GLCOV	0.26	0.31	0.41	0.11	0.19	0.49	0.37	0.31	0.28	0.26	$0.30\pm0.034$
GRC	0.92	0.90	0.75	0.84	0.76	0.72	0.82	0.89	0.94	0.79	0.83±0.025
THR	0.37	0.29	0.35	0.26	0.15	0.45	0.28	0.19	0.23	0.28	0.28±0.027
Mean±SE	0.39±0.121	0.39±0.113	0.37±0.112	0.35±0.122	$0.27 \pm 0.089$	$0.41 \pm 0.096$	$0.32 \pm 0.109$	$0.34{\pm}0.106$	0.43±0.123	0.30±0.113	$0.36 \pm 0.028$

<sup>a</sup> Numbers within parenthesis indicate number of accessions in each race, intermediate race and wild .

B-Bicolor, C-Caudatum, D-Durra, G-Guinea, K-Kafir, sd-Drummondii

PP- Plant pigmentation, NT- Nodal tillers, MRB- Mid rib color. GLCL- Glume color, GLCOV- Glume covering, GRC- Grain color, THR- Thresability

		Mean sum of squares												
Source	DF	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2			
Rep	2	7.4	921.4	14.4	22.7	20.2	0.7	2290000	902400	99.8	105.8			
Drought	1	166.7	14933.8	1980.3	68.6	26.7	0.01	59210000	60690000	987.3	12346.6			
Residual	2	14.0	1631	11.7	21.3	17.6	2.5	5321	31920	64.7	7.0			
Genotype	386	866.3**	16516.9**	341.7**	323.2**	70.1**	6.6**	5182000**	3290000**	167.4**	180.3**			
Drought. Genotype	386	19.7**	276.9**	18.3**	7.4**	9.7**	0.9**	636900**	424900**	26.3**	67.9**			
Residual	1544	10.9	156.1	5.2	3.9	1.8	0.2	133000	69580	9.5	21.2			
Total	2321													
CV%		4.2	5.4	12.7	8.5	17.0	17.8	13.1	13.4	6.3	14.1			

Table 8a. Analysis of variance of entire sorghum reference set evaluated during 2008/09 (E1) at ICRISAT, Patancheru, India.

Table -8b. Analysis of variance of entire sorghum reference set evaluated during 2009/10 (E2) at ICRISAT, Patancheru, India.

0	DE					Mear	sum of s	quares				
Source	D.F	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Rep	2	25.0	3757.3	44.6	82.9	16.7	0.1	0.05	338945	39524	410.4	
Drought	1	382.4	1764.4	1277.2	334.4	42.6	2.2	4.8	14095912	12642629	2056.6	
Residual	2	9.7	280.9	11.3	46.6	5.8	0.0	0.07	15089	36398	285.1	
Genotype	386	416.3**	10636.9**	305.6**	255.6**	26.0**	4.9**	4.2**	2070318**	1146169	130.5**	
Drought. Genotype	386	5.4**	217.6**	19.5**	5.6**	6.4**	0.3**	0.2**	271364**	193612	37.2**	
Residual	1544	4.0	1690.7	4.9	4.2	0.9	0.2	0.04	49796	24674	12.7	
Total	2321											
CV%		2.9	6.0	11.3	9.1	12.4	15.1	8.1	13.3	13.7	7.3	

Table 8c. Analysis of variance of entire sorghum reference pooled over E1 and E2.

	DE					Mean su	im of squar	res			
Source	D.F.	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	8.7	1209.9	6.0	89.8	18.0	0.5	2090000	568900	245.0	238.0
Genotype	386	1120.6**	25971.2**	608.2**	560.0**	75.5**	10.5**	5979000**	3397000**	265.4**	314.4**
Drought. Genotype	386	12.6**	317.0**	22.0**	6.7**	7.8**	0.6**	468500**	334500**	48.0**	107.1**
Residual	1544	7.6	199.0	5.2	4.4	1.3	0.2	95040**	47970.0	13.1	23.4
Year	1	85872.3	620937.7	2911.6	440.7	166.3	0.7	1401000000	768000000	4.2	1761.8
Drought. Year	1	17.3	3931.4	28.1	57.6	0.2	1.0	8332000	9366000	116.4	8975.6
Genotype.Year	386	156.3**	1096.9**	44.6**	15.8**	19.9**	0.9**	1256000**	1021000**	32.0**	120.3**
Genotype. Drought. Year	386	12.5**	206.1**	16.0**	6.4**	8.5**	0.7**	441400**	283400**	16.1**	73.8**
Residual	1548	7.4	128.9	5.1	3.8	1.4	0.2	87390	46440	9.7	19.0
Total	4643										
CV%		3.7	5.1	12.0	8.6	15.4	16.4	13.3	13.9	6.4	13.1

\*, \*\* - Significant at 5% and 1% respectively, MS- Mean sum of squares, CV%- Co-efficient of variation.

Source	DE					Mean su	ım of squa	res			
Source	D.F	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	27.2	352.9	3.2	0.5	0.6	1.5	177035	41819	24.7	7.4
Drought	1	16.6	15574.2	684.9	26.3	58.0	0.0	51392822	52560210	68.1	5941.2
Residual	2	7.2	28.1	0.2	0.9	5.9	1.4	19284	6112	0.1	7.8
Genotype	38	463.2**	7328.1**	435.9**	297.3**	36.5**	12.6**	5951734**	3156927**	92.4**	149.2**
Drought. Genotype	38	6.1 <sup>NS</sup>	184.7*	10.8**	2.8 <sup>NS</sup>	4.0**	0.4 <sup>NS</sup>	551331**	505148**	3.2 <sup>NS</sup>	43.9**
Residual	152	6.5	107.3	5.1	2.4	0.8	0.3	43031	162658	6.2	13.9
Total	233										
CV%		4.0	5.5	11.4	7.6	13.9	17.5	7.8	10.7	4.8	11.0

 Table 9 a. Analysis of variance for flowering group 1 of sorghum reference set evaluated during 2008-09 post rainy (E1) at ICRISAT, Patancheru, India.

Table 9b Analysis of variance for flowering group 2 of sorghum reference set evaluated during 2008-09 post rainy (E1) at ICRISAT, Patancheru, India.

Source	DE										
Source	D.I	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	29.1	1315.9	28.8	2.9	22.7	1.4	731364	235567	134.9	82.8
Drought	1	74.1	1657.6	421.8	28.7	25.3	0.2	31364785	26576064	720.9	1767.2
Residual	2	24.1	872.8	11.3	4.0	56.6	1.3	695420	290907	22.8	16.5
Genotype	116	117.6**	10072**	356.8**	262.4**	63.0**	7.6**	4542911**	2996022**	113.3**	213.1**
Drought. Genotype	116	10.6 <sup>NS</sup>	179.0*	15.7**	4.0 <sup>NS</sup>	14.3**	0.9**	515191**	3239973**	10.3**	75.2**
Residual	464	9.6	137.4	5.6	3.5	1.4	0.2	154461	70113	7.1	22.4
Total	701										
CV%		4.4	5.7	12.8	8.7	15.0	18.1	14.2	13.3	5.2	14.7

Table 9c. Analysis of variance for flowering group 3 of sorghum reference set evaluated during 2008-09 post rainy (E1) at ICRISAT, Patancheru, India.

Source	DE					Mean su	m of squa	ares			
Source	D.F	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	26.3	262.9	41.6	41.4	126.5	0.2	1332762	547503.0	50.8	87.2
Drought	1	27.6	1011.6	262.2	44.7	19.9	1.0	8899936	15526076.0	259.0	10350.5
Residual	2	5.9	1197.2	34.3	48.5	96.6	0.8	170116	37708.0	91.6	54.2
Genotype	126	100.9**	10692.9**	391.8**	322.2**	76.0**	4.8**	4677362**	3243798**	106.8**	183.5**
Drought. Genotype	126	6.0**	121.2 <sup>NS</sup>	11.2**	3.5**	8.9**	0.8**	703463**	401857**	10.4 <sup>NS</sup>	42.6**
Residual	504	3.9	103.0	5.1	2.8	1.6	0.2	175942	87159.0	9.4	25.2
Total	761										
CV%		2.6	4.4	13.5	7.6	16.1	18.4	13.5	13.8	6.3	15.2
*, ** - Sigr	nificant	at 5% and	1% respective	ly, NS- Non	-significant	i, MS-Me	an sum o	f squares, CV	%- Co-efficient	of variation	l.

Source	DE					Mean sur	n of squa	ures			
Source	D.F	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	2.4	496.1	12.4	3.9	1.0	0.0	65876	160797	13.2	82.2
Drought	1	1.5	4515.1	394.9	0.2	18.6	7.4	334204	1049718	146.6	1872.2
Residual	2	7.2	440.5	2.5	13.8	3.2	0.4	176982	167237	62.4	198.6
Genotype	53	124.1**	15025.7**	265.0**	364.9**	46.3**	6.2**	4390819**	2609783**	125.2**	114.0**
Drought. Genotype	53	16.2**	313.9**	25.9**	6.5 <sup>NS</sup>	4.5**	1.9**	568810**	346041**	13.2 <sup>NS</sup>	31.7**
Residual	212	7.7	167.1	4.9	4.4	1.1	0.2	102720	61459	12.7	17.6
Total	323										
CV%		3.2	4.9	12.5	8.1	14.0	17.6	10.8	11.3	7.6	13.3

Table 9d. Analysis of variance for flowering group 4 of sorghum reference set evaluated during 2008-09 post rainy (E1) at ICRISAT, Patancheru, India.

Table 9e. Analysis of variance for flowering group 5 of sorghum reference set evaluated during 2008-09 post rainy (E1) at ICRISAT, Patancheru, India.

Source	DE					Mean sur	n of squa	res			
Source	D.F	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	19.3	611.1	22.9	12.9	22.9	0.2	646401	237978	103.0	69.3
Drought	1	17.2	593.2	298.0	9.9	30.4	0.0	2608783	55078	6258.5	373.8
Residual	2	5.0	1712.5	8.8	2.3	2.0	0.3	417777	154001	14.1	96.1
Genotype	40	318.9**	13059.7**	298.1**	259.9**	82.1**	5.8**	5191040**	3332564**	87.7**	107.9**
Drought. Genotype	40	43.6**	210.3 <sup>NS</sup>	29.6**	4.8 <sup>NS</sup>	6.1**	0.5**	357390**	236737**	20.9 <sup>NS</sup>	30.8**
Residual	160	15.7	247.0	4.6	4.2	1.3	0.2	105829	55115	14.9	14.4
Total	245										
CV%		4.2	5.7	11.8	8.2	13.8	17.7	14	15	8.7	10.8

Table 9f. Analysis of variance for flowering group 6 of sorghum reference set evaluated during 2008-09 post rainy (E1) at ICRISAT, Patancheru, India

Source	DE					Mean sum	of squares	8			
Source	DF	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	45.4	5.8	0.5	46.1	9.2	0.5	153596	65370	41.6	16.9
Drought	1	2.8	3617.4	72.8	56.5	3.6	4.2	998826	4755863	38.3	77.4
Residual	2	33.0	193.9	8.0	15.5	3.3	0.7	106040	69528	1.7	15.4
Genotype	15	843.2**	13539.8**	159.1**	506.6**	63.1**	3.8**	5928259**	3284119**	42.1**	32.8*
Drought. Genotype	15	42.3 <sup>NS</sup>	697.2**	41.1**	10.4 <sup>NS</sup>	4.5**	1.1**	547922**	354373**	20.3 <sup>NS</sup>	13.3 <sup>NS</sup>
Residual	60	50.7	240.8	3.5	6.3	1.6	0.2	59164	37077	15.1	14.3
Total	95	7.1	5.3	13.6	10.3	15.1	14.9	11	13	10.1	14.2
CV%	2	45.4	5.8	0.5	46.1	9.2	0.5	153596	65370	41.6	16.9

\*, \*\* - Significant at 5% and 1% respectively, NS- Non-significant, MS- Mean sum of squares, CV%- Co-efficient of variation.

Source	DE					Mean sum	of square	es			
Source	Dr	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	59.3	50.9	0.4	18.3	2.1	0.2	174971	49743	46.8	28.0
Drought	1	89.8	3248.0	292.5	186.4	2.7	0.6	5878998	4397319	7.7	27.4
Residual	2	67.0	981.8	2.1	8.0	2.8	0.4	8164	36060	4.5	2.4
Genotype	10	1729.6**	14185.8**	371.9**	373.1**	123.2**	5.3**	8024590**	5450232**	242**	222.1**
Drought. Genotype	10	222.4**	2225.4**	13.3**	85.5**	13.4**	0.5**	426360**	625437**	7.6 <sup>NS</sup>	49.0**
Residual	40	48.0	469.5	1.9	8.9	2.3	0.1	67573	31461	12.9	11.7
Total	65										
CV%		7.0	7.7	10.4	11.8	14.3	11.7	10.4	10.0	8.9	12.9

Table 9g. Analysis of variance for flowering group 7 of sorghum reference set evaluated during 2008-09 post rainy (E1) at ICRISAT, Patancheru, India.

 Table 10a. Analysis of variance for flowering group 1 evaluated during 2009-10 post rainy (E2) at ICRISAT, Patancheru, India.

Source	DE					Mean sum	of square	s				
Source	Dr -	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Rep	2	26.5	362.1	7.0	2.9	1.0	0.1	0.003	25209	10092	145.6	
Drought	1	136.2	3496.2	65.2	0.4	83.7	2.6	2.1	95774	1216969	167.5	
Residual	2	2.3	22.2	10.3	12.8	1.7	0.6	0.07	5636	338	58.6	
Genotype	38	499.7**	6330.7**	323.9**	185.2**	18.0**	3.8**	3.1**	2034403**	1000522**	61.7**	
Drought. Genotype	38	6.5 <sup>NS</sup>	599.5**	30.1**	4.4 <sup>NS</sup>	4.3**	0.2 **	0.1**	192252**	182495**	13.9**	
Residual	152	6.2	162.6	2.72	4.3	0.5	0.1	0.05	8258	8433	7.3	
Total	233											
CV%		4.1	6.8	7.9	10.0	9.6	13.8	8.1	6.5	10.1	5.5	

Table 10b. Analysis of variance for flowering group 2 evaluated during 2009-10 post rainy (E2) at ICRISAT, Patancheru, India.

Source	DE				]	Mean sum	of squar	es				
Source	D.F.	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Rep	2	93.7	5282.6	61.4	20.9	12.9	0.6	0.1	47550	46998	446.7	
Drought	1	176.0	2605.8	1888.5	80.1	52.2	1.4	4.7	2562793	7751307	37.9	
Residual	2	8.7	507.7	23.5	19.6	10.5	0.6	0.1	156697	41011	24.2	
Genotype	116	221.1**	9584.6**	306.5**	207.8**	25.9**	4.2**	3.5**	1701184**	704520**	109.2**	
Drought. Genotype	116	6.5**	183.8*	25.4**	7.2**	6.0**	0.3 <sup>NS</sup>	0.2**	251560**	209019**	13.7*	
Residual	464	4.2	125.9	3.8	2.2	0.7	0.2	0.1	43488	21804	10.0	
Total	701											
CV%		3.1	5.8	10.3	7.1	10.1	15.0	8.7	11.5	12.8	6.2	

\*, \*\* - Significant at 5% and 1% respectively, NS - Non- significant, MS- Mean sum of squares, CV%- Co-efficient of variation.

Source D.	DE					Mean sum	n of squar	es				
Source	D.F	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Rep	2	6.8	1966.5	21.0	101.4	14.0	0.6	0.007	122385	3752	617.8	
Drought	1	14.3	1690.9	4.1	285.2	183.5	0.4	0.003	9282269	2372669	140.8	
Residual	2	7.5	117.4	2.5	40.0	4.1	0.1	0.003	6829	19099	621.3	
Genotype	126	193.9**	8257.3**	376.3**	243.7**	20.4**	3.6**	4.4**	2206058**	1398790**	99.5**	
Drought. Genotype	126	3.3 <sup>NS</sup>	124.5 <sup>NS</sup>	14.5**	3.6 <sup>NS</sup>	5.3**	0.4**	0.1**	298136**	180933**	20.1**	
Residual	504	2.9	137.3	6.1	5.0	1.3	0.2	0.0	72432	34458	13.	
Total	761											
CV%		2.4	5.6	13.1	10.7	14.9	15.6	7.6	14.8	14.4	7.6	

 Table 10c. Analysis of variance for flowering group 3 evaluated during 2009-10 post rainy (E2) at ICRISAT, Patancheru, India.

 Table 10d. Analysis of variance for flowering group 4 evaluated during 2009-10 post rainy (E2) at ICRISAT, Patancheru, India.

Source	DE		Mean sum of squares										
Source	D.r	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2	
Rep	2	10.6	141.3	0.8	32.1	1.8	0.02	0.1	40642	44352	61.6		
Drought	1	32.7	487.7	169.4	25.3	66.2	0.1	0.1	2641928	1160617	4474.1		
Residual	2	1.6	342.4	6.8	27.8	0.6	0.2	0.1	22135	12645	35.4		
Genotype	53	129.2**	11658.8**	225.4**	259.4**	27.8**	3.2**	3.5**	2068425**	1231486**	165.7**		
Drought. Genotype	53	3.7 <sup>NS</sup>	202.4 <sup>NS</sup>	15.4**	5.2**	5.5**	0.1 <sup>NS</sup>	0.06 NS	327094**	158960**	12.0 <sup>NS</sup>		
Residual	212	2.9	157.2	5.4	3.1	0.5	0.1	0.0	52922	27355	10.8		
Total	323												
CV%		2.3	5.4	12.4	7.0	10.9	13.5	8.0	13.3	13.8	6.9		

Table 10e. Analysis of variance for flowering group 5 evaluated during 2009-10 post rainy (E2) at ICRISAT, Patancheru, India.

	Mean sum of squares											
Source	D.F	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Rep	2	2.1	193.8	14.7	7.5	1.5	0.6	0.02	58048	6940	39.1	
Drought	1	157.8	5276.4	104.9	12.1	72.4	0.1	0.7	1704	439	6030.6	
Residual	2	9.3	146.9	11.0	6.7	0.0	0.2	0.02	51487	1457	3.7	
Genotype	40	178.4**	7069.6**	284.2**	233.8**	11.5**	8.0**	4.5**	1792699**	1232374**	93.3**	
Drought.	40											
Genotype	40	6.1**	173 <sup>NS</sup>	5.0 <sup>NS</sup>	4.3 <sup>NS</sup>	3.6**	0.3**	0.2**	208636**	173450**	12.4*	
Residual	160	3.3	163.4	5.5	3.7	0.8	0.2	0.04	48151	20508	8.9	
Total	245											
CV%	2	2.1	193.8	14.7	7.5	1.5	0.6	0.02	58048	6940	39.1	

\*, \*\* - Significant at 5% and 1% respectively, NS - Non- significant, MS- Mean sum of squares, CV%- Co-efficient of variation.

Source D.F					Mean sun	n of squar	es				
		DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1
Rep	2	14.2	759.4	0.3	9.8	0.9	0.2	0.1	93597	5168	99.2
Drought	1	0.8	978.6	1.9	18.4	24.6	0.2	0.1	668453	1798378	506.5
Residual	2	0.7	154.2	2.6	3.1	0.5	0.2	0.2	46228	2838	13.1
Genotype	15	209.0**	7348.7**	282.6**	450.8**	15.5**	2.3**	7.7**	2062298**	1357443**	77.1**
Drought.	15										
Genotype	10	6.4 <sup>NS</sup>	143.6 <sup>NS</sup>	20.3**	7.5 <sup>NS</sup>	4.5**	0.2 <sup>NS</sup>	0.1 <sup>NS</sup>	476753**	128372**	14.7 <sup>NS</sup>
Residual	60	6.5	357.9	4.5	8.5	0.8	0.2	0.1	47459	19298	12.7
Total	95										
CV%		3.3	7.6	11.9	11.4	12.8	15.3	9.8	14.4	13.9	8.1

 Table 10f. Analysis of variance for flowering group 6 evaluated during 2009-10 post rainy (E2) at ICRISAT, Patancheru, India.

Table 10g. Analysis of variance for flowering group 7 evaluated during 2009-10 post rainy (E2) at ICRISAT, Patancheru, India.

			Mean sum of squares									
Source	D.F	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Rep	2	5.1	337.6	6.5	0.2	2.1	0.1	0.05	88105	11257	31.6	
Drought	1	30.7	373.5	51.9	0.02	25.5	0.02	0.51	197418	1716652	114.7	
Residual	2	9.1	653.0	6.6	4.7	2.5	0.1	0.01	86822	50387	25.6	
Genotype	10	1522.2**	7234.4**	259.7**	324.2**	12.1**	19.6**	7.3**	2970170**	1856956**	135.4**	
Drought.	10											
Genotype		8.6 <sup>NS</sup>	350.3 <sup>NS</sup>	10.24**	14.7 <sup>NS</sup>	2.2**	0.5 <sup>NS</sup>	0.1**	142073**	511998**	24.5 <sup>NS</sup>	
Residual	40	7.4	486.6	3.6	11.8	0.6	0.3	0.03	29669	14736	20.8	
Total	65											
CV%		3.3	9.2	14.2	13.6	11.2	13.7	9.2	12.7	11.4	10.8	

### Table 11a. Analysis of variance of flowering group 1 pooled over E1 and E2.

Source	DF					Mean s	um of Squa	ares			
Source	D.1	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	3.8	808.0	14.3	1.0	1.1	0.3	128100	20698	147.9	114.2
Genotype	38	954.8**	13896.9**	756.7**	448.0**	45.7**	12.9**	6349102**	3214050**	134.7**	415.8**
Drought. Genotype	38	5.4 <sup>NS</sup>	847.1**	28.7**	5.9 <sup>NS</sup>	5.6**	0.3**	412459**	386940**	11.3 <sup>NS</sup>	78.1**
Residual	152	8.1	246.0	4.5	7.1	0.8	0.2	23608	23537	9.2	17.9
Year	1	1945.2	1494.3	206.5	7.6	33.8	13.2	181745614	108799144	722.2	1438.8
Drought. Year	1	21.2 <sup>NS</sup>	3257.9**	117.5**	6.2 <sup>NS</sup>	0.09 <sup>NS</sup>	1.6*	21704262**	19983315**	9.3 <sup>NS</sup>	83.4**
Genotype. Year	38	68.3**	496.1**	42.4**	17.5**	6.9**	1.6**	1139586**	653541**	20.9**	115.6**
Genotype. Drought. Year	38	8.5 <sup>NS</sup>	207.0**	16.2**	2.8*	4.0**	0.3 <sup>NS</sup>	356120**	286229**	9.3 <sup>NS</sup>	69.9**
Residual	159	6.0	80.8	3.3	1.7	0.7	0.3	24611	23606	6.7	12.2
Total	467										
CV%	2	3.8	808.0	14.3	1.0	1.1	0.3	128100	20698	147.9	114.2

\*, \*\* - Significant at 5% and 1% respectively, NS-Non- significant, CV%- Co-efficient of variation.

Source	DE					Mean s	um of squa	ires			
Source	D.1	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	29.2	1471.2	3.5	19.1	1.1	1.9	551800	79385	492.8	427.1
Genotype	116	301.0**	19126.4**	619.1**	457.8**	75.7**	10.8**	4997000**	1968290**	198.8**	318.7**
Drought. Genotype	116	9.9**	225.4**	25.3**	5.0**	10.8**	0.5**	408100**	248406**	13.6**	92.0**
Residual	464	6.8	143.5	4.5	2.9	1.2	0.2	101900	46161	9.1	20.2
Year	1	8772.5	64854.4	66.6	133.5	168.9	1.0	324900000	248311321	16.2	4935.5
Drought. Year	1	10.8 <sup>NS</sup>	49.8 <sup>NS</sup>	262.6**	6.6 <sup>NS</sup>	75.0**	1.3**	7998000**	2811012**	214.2**	5313.5**
Genotype. Year	116	37.7**	538.4**	44.1**	12.5**	13.2**	1.0**	1248000**	1732253**	23.7**	79.1**
Genotype. Drought. Year	116	7.1 <sup>NS</sup>	136.9 <sup>NS</sup>	15.9**	6.2**	9.5**	0.7**	358700**	284610**	10.4 <sup>NS</sup>	80.6**
Residual	468	7.4	145.1	5.3	2.9	1.3	0.2	96650	46619	8.5	20.7
Total	1403										
CV%		4.0	6.0	12.3	8.0	13.8	16.1	13.6	13.7	5.7	13.3

Table 11b. Analysis of variance of flowering group 2 pooled over E1 and E2

Table 11c. Analysis of variance of flowering group 3 pooled over E1 and E2

Source	DF	Mean sum of squares										
Source	<b>D</b> .1 :	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2	
Rep	2	9.6	547.0	1.6	133.1	73.8	0.5	1048000	307000	300.8	378.0	
Genotype	126	262.7**	18470.5**	731.3**	558.2**	78.2**	8.0**	5826000**	3985000**	183.4**	279.6**	
Drought. Genotype	126	4.2 <sup>NS</sup>	148.4 <sup>NS</sup>	13.5**	4.5 <sup>NS</sup>	5.4	0.7**	500800**	300700**	17.2 <sup>NS</sup>	57.2**	
Residual	504	3.6	149.2	5.9	4.2	1.4	0.2	133100	65150	13.4	26.7	
Year	1	15508.0	175206.0	1673.4	403.8	10.2	0.7	630200000	277700000	286.0	134.4	
Drought. Year	1	1.0 <sup>NS</sup>	42.6 <sup>NS</sup>	100.3**	49.8**	162.1**	1.3 <sup>NS</sup>	2010 <sup>NS</sup>	2880000**	9.6 <sup>NS</sup>	4921.5**	
Genotype. Year	126	32.0**	480.0**	36.7**	8.3**	18.2**	0.3**	1058000**	657200**	23.6**	76.4**	
Genotype. Drought.Year	126	5.1**	97.7 <sup>NS</sup>	12.1**	2.5 <sup>NS</sup>	8.8**	0.4**	500800**	282100**	13.0 <sup>NS</sup>	55.1**	
Residual	508	3.3	100.5	5.6	3.6	1.9	0.2	116200	57050	11.7	22.0	
Total	1523											
CV%		2.5	4.6	13.2	8.9	18.2	16.7	13.9	13.9	7.1	14.1	

\*, \*\* - Significant at 5% and 1% respectively, NS - Non- significant, CV%- Co-efficient of variation.

		Mean sum of squares           DF         PH         EXE         PL         PW         BT         PWT         YLD         SPAD1         SPAD2           7.9         219.8         4.0         10.6         2.5         0.02         66381         122373         62.8         21.6           223.2**         25738.0         452.8**         607.5**         65.9**         8.6**         5478889**         3294665**         265.0**         230.1**           10.0**         311.2         29.3**         5.6**         4.6**         0.9**         576625**         297086**         15.6 NS         48.4**           4.9         225.9         5.5         3.2         0.8         0.2         73534         40329         13.8         20.4           17536.5         167138.3         207.4         112.8         288.1         2.5         251353861         162393734         31.1         7.0           10.1 <sup>NS</sup> 1017.5         23.5**         10.3 <sup>NS</sup> 7.2**         2.9**         548416**         1392**         1500.4**         722.9**           30.0**         946.5         37.6**         16.7**         8.1**         0.7**         980355**         546604**         25									
Source	D.F	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	7.9	219.8	4.0	10.6	2.5	0.02	66381	122373	62.8	21.6
Genotype	53	223.2**	25738.0	452.8**	607.5**	65.9**	8.6**	5478889**	3294665**	265.0**	230.1**
Drought. Genotype	53	10.0**	311.2	29.3**	5.6**	4.6**	0.9**	576625**	297086**	15.6 <sup>NS</sup>	48.4**
Residual	212	4.9	225.9	5.5	3.2	0.8	0.2	73534	40329	13.8	20.4
Year	1	17536.5	167138.3	207.4	112.8	288.1	2.5	251353861	162393734	31.1	7.0
Drought. Year	1	10.1 <sup>NS</sup>	1017.5	23.5**	10.3 <sup>NS</sup>	7.2**	2.9**	548416**	1392**	1500.4**	722.9**
Genotype. Year	53	30.0**	946.5	37.6**	16.7**	8.1**	0.7**	980355**	546604**	25.9**	58.6**
Genotype. Drought.Year	53	9.86**	205.1	12.00**	6.0 <sup>NS</sup>	5.4**	1.0**	319279**	207915**	9.6 <sup>NS</sup>	34.8**
Residual	216	5.7	103.0	4.9	4.7	0.8	0.2	81938	49287	9.6	18.1
Total	647										
CV%		3.0	4.1	9.1	8.4	13.1	15.7	12.2	13.1	6.6	13.4

Table 11d. Analysis of variance of flowering group 4 pooled over E1 and E2.

Table 11e. Analysis of variance of flowering group 5 pooled over E1 and E2.

		Mean sum of squares           DF         PH         EXE         PL         PW         BT         PWT         YLD         SPAD1         SPAD2           6.1         664.6         36.9         4.5         8.1         0.7         533084         110053         25.5         63.8           412.1**         18875.2**         533.2**         482.2**         68.4**         13.0**         5858285**         3765123**         152.7**         307.3**           25.9**         238.0         15.1**         4.8 <sup>NS</sup> 4.2**         0.5**         320888**         239232**         23.4         138.7**           10.7         276.7         5.6         4.0         1.1         0.2         81891         37498         15.2         18.2           37110.8         202792.9         1379.2         1.5         587.4         2.1         83234153         33035876         383.6         5494.6           35.4 <sup>NS</sup> 4704.0**         24.6*         0.05 <sup>NS</sup> 4.4 <sup>NS</sup> 0.07 <sup>NS</sup> 1238573**         22841 <sup>NS</sup> 1.5 <sup>NS</sup> 82.4**           85.2**         1254.1**         49.2**         11.5**         25.3**         0.8**         1125454**         79981									
Source	D.F	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	6.1	664.6	36.9	4.5	8.1	0.7	533084	110053	25.5	63.8
Genotype	40	412.1**	18875.2**	533.2**	482.2**	68.4**	13.0**	5858285**	3765123**	152.7**	307.3**
Drought. Genotype	40	25.9**	238.0	15.1**	4.8 <sup>NS</sup>	4.2**	0.5**	320888**	239232**	23.4	138.7**
Residual	160	10.7	276.7	5.6	4.0	1.1	0.2	81891	37498	15.2	18.2
Year	1	37110.8	202792.9	1379.2	1.5	587.4	2.1	83234153	33035876	383.6	5494.6
Drought. Year	1	35.4 <sup>NS</sup>	4704.0**	24.6*	0.05 <sup>NS</sup>	4.4 <sup>NS</sup>	0.07 <sup>NS</sup>	1238573**	22841 <sup>NS</sup>	1.5 <sup>NS</sup>	82.4**
Genotype. Year	40	85.2**	1254.1**	49.2**	11.5**	25.3**	0.8**	1125454**	799815**	29.1**	211.2**
Genotype. Drought. Year	40	23.7**	145.2 <sup>NS</sup>	19.5**	4.2 <sup>NS</sup>	5.5**	0.3**	245137**	170955**	10.3 <sup>NS</sup>	135.3**
Residual	164	8.5	138.2	4.6	4.1	1.2	0.2	74322	39667	10.0	12.5
Total	491										
CV%		3.4	4.6	10.8	8.1	15.2	15.7	14.2	14.8	7.0	11.1

\*, \*\* - Significant at 5% and 1% respectively, NS - Non- significant, CV%- Co-efficient of variation.

Source	D.F	Mean sum of squares           DF         PH         EXE         PL         PW         BT         PWT         YLD         SPAD1         SPAI           33.9         382.6         0.2         24.0         3.7         0.7         202485         23074         127.2         80.1           763.8**         19160.9**         396.9**         926.3**         64.9**         5.5**         6394166**         3746846**         89.2**         100.0           22.4 Ns         498.1 Ns         26.0**         10.1         3.7**         0.5**         526972**         224692**         26.3 Ns         21.9           25.6         351.1         2.7         6.3         1.2         0.2         49787         26762         15.7         20.2           27684.0         82510.4         723.8         63.7         92.4         0.2         28808872         14032794         1618.5         1915.           0.2 Ns         4179.5**         25.6*         5.2 Ns         23.5**         1.3*         16530 Ns         352597**         411.6**         2.9 Ns           288.3**         1727.6**         44.7**         31.4**         13.6**         0.5**         1596391**         894717**         3									
		DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Rep	2	33.9	382.6	0.2	24.0	3.7	0.7	202485	23074	127.2	80.1
Genotype	15	763.8**	19160.9**	396.9**	926.3**	64.9**	5.5**	6394166**	3746846**	89.2**	100.0**
Drought. Genotype	15	22.4 <sup>NS</sup>	498.1 <sup>NS</sup>	26.0**	10.1	3.7**	0.5**	526972**	224692**	26.3 <sup>NS</sup>	21.9
Residual	60	25.6	351.1	2.7	6.3	1.2	0.2	49787	26762	15.7	20.2
Year	1	27684.0	82510.4	723.8	63.7	92.4	0.2	28808872	14032794	1618.5	1915.2
Drought. Year	1	0.2 <sup>NS</sup>	4179.5**	25.6*	5.2 <sup>NS</sup>	23.5**	1.3*	16530 <sup>NS</sup>	352597**	411.6**	2.9 <sup>NS</sup>
Genotype. Year	15	288.3**	1727.6**	44.7**	31.4**	13.6**	0.5**	1596391**	894717**	30.0**	39.3**
Genotype. Drought.Year	15	26.4 <sup>NS</sup>	342.6 <sup>NS</sup>	35.4**	7.8 <sup>NS</sup>	5.3**	0.8**	497702**	258054**	8.6 <sup>NS</sup>	9.3 <sup>NS</sup>
Residual	64	30.8	247.0	5.0	9.1	1.4	0.2	58755	30070	11.9	15.5
Total	191										
CV%		6.2	5.8	14.2	12.2	15.2	15.6	12.8	13.6	8.3	13.2

Table 11f. Analysis of variance of flowering group 6 pooled over E1 and E2.

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$1 a \nu n 1 1 2$	• Analysis	UI VALIANCE		21000/	DUDICU U	VULLI ANUL	

		Mean sum of squares										
Source	D.F.	DF	РН	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2	
Rep	2	34.6	86.4	3.3	7.4	0.0	0.3	205917	53031	18.5	38.9	
Genotype	10	2518.41**	19202.40**	543.64**	608.86**	98.91**	22.45**	8847484**	6135087**	324.16**	275.35**	
Drought. Genotype	10	106.8**	1122.1	12.0**	33.3*	8.1**	0.9**	164672**	873767**	11.0 <sup>NS</sup>	41.9 <sup>NS</sup>	
Residual	40	29.8	512.2	2.8	12.3	1.5	0.2	57999	26871	17.9	17.3	
Year	1	11201.9	52920.1	0.0	0.1	510.6	9.3	42348624	16661150	117.9	941.3	
Drought. Year	1	7.7 <sup>NS</sup>	709.4 <sup>NS</sup>	49.0**	91.5**	5.7 <sup>NS</sup>	0.3 <sup>NS</sup>	1960887**	309502**	31.4 <sup>NS</sup>	159.2**	
Genotype. Year	10	733.3**	2217.8**	88.1**	88.5**	36.5**	2.5**	2147275**	1172100**	53.3**	104.0**	
Genotype. Drought.Year	10	124.1**	1453.6**	11.6**	66.9**	7.4**	0.5**	403762**	263668**	21.1 <sup>NS</sup>	42.7**	
Residual Total	44 131	25.3	418.1	2.9	8.5	1.6	0.2	41444	20841	17.6	12.6	
CV%		5.6	7.8	12.8	11.6	14.8	11.9	10.6	10.2	10.2	13.2	

Table 12. Variance components due to genotypes ( $\sigma^2 g$ ) and genotype x environment ( $\sigma^2 g \ x \ e$ ) in different environments for all traits

Environments	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
E3	46.5*	1617.3**	89.1**	42.4**	19.2**	2.1**	0.5**	610303**	401234**	24.6**	36.6**
E4	53.8**	1144.0**	77.1**	37.0**	9.1**	1.5**	0.6**	137311**	102995**	11.9**	17.2*
E5	79.1**	1326.0**	66.1**	32.0**	6.0**	0.9	0.3**	243108**	214123**	21.2**	41.0**
Pooled	23.3**	651.1**	17.4**	12.4**	2.1**	0.2	0.1**	115789**	62311**	4.5**	3.4**
$\sigma^2 g x e$	35.8**	671.9**	60.0**	24.5**	9.3**	1.2	$0.4^{**}$	214495**	130066**	14.9**	$27.4^{*}$

\*, \*\* - Significant at 5% and 1% respectively, NS - Non- significant, CV%- Co-efficient of variation.

			I	PCV (%	)			GCV (%)						
			POOLED				POOLED			POOLED				POOLED
Characters	<b>E1</b>	E2	(E1 and E2)	E3	<b>E4</b>	E5	(E3, E4, E5)	E1	E2	(E1 and E2)	E3	<b>E4</b>	E5	(E3, E4, E5)
DF	15.83	12.21	13.29	13.00	14.38	13.81	9.56	15.22	11.91	13.03	10.64	11.36	13.19	7.39
PH	22.96	21.96	21.21	20.02	20.80	25.09	14.69	22.29	19.84	20.91	17.48	14.64	18.53	11.63
EXER	44.40	38.94	38.99	57.27	57.09	58.28	39.77	40.76	35.23	37.35	56.49	56.56	57.66	27.02
PL	32.69	29.87	30.41	34.31	31.05	32.13	22.45	31.42	28.69	29.79	31.85	28.10	27.10	16.79
PW	49.32	34.06	36.17	64.86	53.15	49.57	38.34	40.09	23.93	30.55	62.73	50.31	46.67	24.12
BT	44.61	36.43	37.10	69.21	48.87	35.65	32.54	35.84	32.35	33.57	68.24	46.45	32.50	19.76
HSW	*	33.75	*	31.19	36.44	34.73	22.04	*	31.74	*	28.92	34.18	31.37	13.71
PWT	37.60	39.62	34.12	36.36	61.56	25.17	26.29	31.23	32.57	30.45	34.64	56.42	22.09	15.07
YLD	42.65	44.46	37.23	40.89	63.82	31.41	20.35	35.18	34.76	32.80	37.38	61.19	28.99	16.89
SPAD1	12.71	12.38	10.39	12.84	11.56	11.97	7.17	9.96	8.10	9.36	10.51	6.90	9.48	4.41
SPAD2	22.92	26.44	18.95	18.69	15.10	19.59	9.86	13.23	13.98	13.41	14.90	9.90	15.34	4.48

Table 13 Phenotypic (PCV) and genotypic (GCV) co-efficient of variation for the quantitative characters of the sorghum reference set in all the environments.

Table 14 Heritability in broad sense  $(h_b^2)$  and genetic advance as per cent of mean (GA) for the quantitative characters of sorghum reference set in all the environments.

				$h_{b}^{2}(\%)$				GA (per cent of mean)						
			POOLED				POOLED			POOLED				POOLED
Characters	E1	E2	(E1 and E2)	E3	<b>E4</b>	E5	(E3, E4, E5)	E1	E2	(E1 and E2)	E3	<b>E4</b>	E5	(E1 and E2)
DF	92.37	95.27	96.10	67.02	62.40	91.19	59.79	30.12	23.96	26.32	17.95	18.49	25.95	11.72
PH	94.27	81.64	97.18	76.20	49.57	54.57	62.65	44.59	36.93	42.46	31.43	21.24	28.20	18.87
EXER	84.30	81.86	91.75	97.31	98.14	97.88	46.15	77.10	65.66	73.69	83.59	84.05	85.56	37.62
PL	92.40	92.26	95.98	86.16	81.90	71.16	55.91	62.22	56.77	60.12	60.91	52.38	47.09	25.73
PW	66.06	49.36	71.34	93.52	89.60	88.66	39.58	67.12	34.63	53.15	90.99	98.10	90.53	31.11
BT	64.54	78.85	81.89	97.21	90.33	83.09	36.88	59.31	59.17	62.59	80.73	90.95	61.02	24.60
HSW	*	88.48	*	85.96	87.98	81.58	38.71	*	61.51	*	55.24	66.04	58.36	17.47
PWT	68.98	67.56	79.69	90.79	83.99	77.04	50.53	53.43	55.14	56.00	67.99	77.56	39.95	21.96
YLD	68.06	61.14	77.64	83.55	91.93	85.21	57.19	59.80	55.99	59.54	70.38	88.00	55.13	25.92
SPAD 1	61.44	42.86	81.14	67.07	35.60	62.70	37.73	16.08	10.93	17.37	17.73	8.48	15.46	5.55
SPAD2	33.32	27.98	50.02	63.50	43.04	61.28	20.63	15.74	15.24	19.53	24.45	13.38	24.74	4.17

\*data not recorded

ENVIRONMENT <sup>1</sup>	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
E1	38.0-125.5	82.2-383.5	1.0-47.0	6.2-48.6	3.2-27.4	1.0-9.0	*	286-5517	187-3817	34.2-62.6	21.1-53.2
E2	46.5-126.8	84.2-340.1	0.6-38.3	7.4-44.8	3.6-18.3	1.7-9.0	0.3-5.1	387-3313	224-2504	35.4-61.2	6.8-51.5
Pooled (E1 & E2)	42.5-123.4	84.2-361.8	1.9-42.6	6.8-45.2	3.4-19.7	1.5-8.7	*	422-4243	301-3140	35.0-61.3	17.2-50.3
E3	51.4-80.7	89.1-342.3	0.4-61.6	7.5-60.6	1.4-49.2	0.0-9.6	0.6-5.2	484-3980	458-3148	33.4-59.3	27.5-52.2
E4	50.9-77.7	93.5-270.3	0.2-42.3	8.7-51.3	0.7-36.1	0.3-9.1	0.5-4.3	581-3060	293-2638	41.3-56.1	33.5-47.7
E5	48.8-92.6	103.6-269.7	0.3-40.9	7.6-44.2	1.4-22.7	0.5-7.5	0.6-4.9	809-3498	396-3312	32.9-59.2	15.9-56.1
Pooled (E3, E4, E5)	52.6-81.1	114.9-284.8	1.4-39.2	10.8-48.3	3.1-24.2	1.0-6.7	1.1-3.7	816-3001	761-2361	37.6-55.8	31.1-47.8

Table 15 a Range of quantitative characters in sorghum reference set evaluated at different environments.

\*- Data not recorded

<sup>1</sup> E1- ICRISAT, Patancheru during 2008-09, E2- ICRISAT, Patancheru during 2009-10, E3- UAS, Dharwad irrigated condition,

E4- UAS, Dharwad un-irrigated condition, E5 - RARS, Bijapur un-irrigated condition,

Table 15bRange of quantitative characters in flowering groups of sorghum reference set evaluated during the 2008-2009post rainy (E1) season at ICRISAT, Patancheru, India.

Flowering Group	$\mathrm{DF}^2$	РН	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Group 1	38.0-82.8	119.5-263.2	1.0-47.0	13.5-45.5	4.2-16.6	1.6-9.0	665-4525	546-3300	42.5-59.4	24.2-45.0
Group 2	59.8-82.7	82.2-291.2	3.4-36.2	8.8-48.6	4.7-24.4	1.0-8.5	286-4990	187-3817	39.3-62.6	21.3-51.9
Group 3	68.6-96.5	108.2-333.2	1.6-36.8	6.2-45.6	4.2-27.4	1.3-7.5	983-5517	331-3777	36.8-58.3	21.1-49.1
Group 4	77.3-94.7	153.8-383.5	5.6-32.0	8.6-41.1	4.9-15.5	1.5-7.2	505-4486	366-3477	35.3-58.3	23.6-45.6
Group 5	78.3-114.0	94.0-374.2	2.4-36.1	11.2-41.6	4.0-21.1	1.5-5.7	640-4887	409-3516	35.7-54.2	26.9-48.8
Group 6	77.5-120.3	153.4-342.7	6.0-23.4	7.18-35.5	3.2-15.8	1.7-4.5	763-3810	377-3033	34.2-44.2	22.2-30.4
Group 7	72.0-125.5	153.7-330.3	2.9-26.2	14.1-41.3	5.9-20.6	2.2-5.0	1166-4325	732-3291	34.2-53.2	34.2-53.2

Flowering Group	DF	РН	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Group 1	46.5-79.8	120.9-258.6	4.4-38.3	13.1-39.8	4.0-11.7	2.0-5.7	0.8-4.3	408-2847	250-1847	42.2-57.2	24.5-49.7
Group 2	50. 0-84.5	84.2-270.7	3.1-33.8	10.0-41.7	5.4-15.1	1.8-9.0	0.3-5.1	444-3313	302.6-1979	39.6-61.2	24.5-51.5
Group 3	54.8-85.5	106.2-304.2	0.6-35.7	7.4-44.8	4.4-14.5	1.7-6.5	0.7-4.8	475-3169	303-2504	35.4-58.2	13.3-49.4
Group 4	67.5-83.3	133.4-340.1	6.0-31.4	9.9-39.2	4.5-18.3	1.7-5.3	1.1-4.5	340-2747	236-2013	37.0-59.6	20.7-48.1
Group 5	67.7-92.3	117.5-322.2	6.8-33.2	10.8-38.6	3.9-10.8	1.8-7.7	0.9-4.4	387-2581	205-2332	39.5-53.1	6.8-38.6
Group 6	67.7-85.0	153.5-290.7	7.7-28.5	8.0-34.6	3.6-9.8	2.0-4.2	0.8-4.4	659-2761	224-1844	37.2-50.1	24.8-42.5
Group 7	69.2-126.8	157.5-284.6	3.6-27.2	13.0-35.5	5.0-10.2	2.0-7.5	0.5-4.3	525-2681	386-2111	35.6-49.4	24.0-41.9

Table 15c. Range of quantitative characters in flowering groups of sorghum reference set evaluated during the 2009-2010 post rainy season (E2) at ICRISAT, Patancheru, India.

Table 15d. Range of quantitative characters in different flowering groups of sorghum reference set pooled E1 and E2.

Flowering Group	DF	РН	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Group 1	42.5-81.3	122.7-260.4	3.8-42.6	13.4-42.7	4.2-14.2	1.8-7.3	610-3343	446-2513	43.8-58.4	24.0-48.0
Group 2	55.2-81.3	84.2-277.8	3.4-35.0	9.4-44.3	5.4-18.4	1.5-8.7	568-3667	518-2720	40.2-61.3	24.7-50.3
Group 3	61.8-88.3	108.5-318.7	1.9-36.2	6.8-45.2	4.3-19.7	1.7-7.0	761-4243	317-3140	36.1-58.2	17.2-49.3
Group 4	72.7-87.8	143.6-361.8	6.2-30.5	9.3-40.1	4.9-16.9	1.8-6.2	422-3511	301-2706	36.2-58.9	23.2-46.9
Group 5	73.0-103.2	105.7-348.2	4.6-34.7	11.0-37.7	4.0-15.5	1.7-6.7	610-3679	381-2556	39.0-53.2	20.9-43.7
Group 6	73.2-102.7	153.4-316.7	7.7-25.5	7.6-34.3	3.4-12.1	1.9-4.3	820-3047	425-2387	36.8-45.7	23.5-36.5
Group 7	72.0-123.4	155.6-307.5	5.0-26.7	13.6-36.0	5.4-15.4	2.1-6.2	959-3357	602-2559	35.0-51.3	24.0-40.4

Table 16a Means of quantitative characters in entire sorghum reference set evaluated at different environments.

Environment <sup>1</sup>	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD 1	SPAD 2
E1 E2	70.8b 74.9a	220.4b 232.2a	16.9b 18.0a	21.8a 22.3a	7.0b 7.6a	2.6a 2.7a	2.6a	2820a 2542c	2090a 1790b	48.5b 46.6d	35.3d 33.4f
Pooled (E1 & E2)	72.2b	225.0b	17.8a	22.2a	7.3b	2.6a		2687b	1844b	47.7c	32.5e
E3	64.1c	230.1a	16.7b	20.4a	7.0c	2.2a	2.5a	2225d	1694b	47.2a	40.7c
E4	64.6c	231.1a	15.5c	21.7a	6.0c	2.6a	2.3b	2150d	1550c	50.1a	41.9c
E5	67.4c	196.6d	14.1d	20.9a	5.2d	2.9a	2.3b	2229d	1596c	48.6a	41.7a
Pooled (E3, E4, E5)	67.1c	213.1c	16.3b	21.6a	6.5c	2.6a	2.0c	2211d	1613b	49.8a	42.7b

<sup>1</sup> E1- ICRISAT, Patancheru during 2008-09, E2- ICRISAT, Patancheru during 2009-10, E3- UAS, Dharwad irrigated condition, E4- UAS, Dharwad un-irrigated condition, E5 – RARS, Bijapur un-irrigated condition.

Table 16b Means of quantitative characters in different flowering groups of sorghum reference set evaluated during 2008-2009 post rainy season (E1) at ICRSAT, Patancheru, India

Flowering Group	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Group 1	63.3e	187.8e	19.8a	20.3a	6.6c	3.0a	2672a	1881a	51.6a	33.8b
Group 2	70.1c	206.2d	18.5a	21.5a	7.9b	2.6a	2772a	1992a	51.3a	32.3b
Group 3	76.9d	230.9c	16.8a	21.9a	7.7b	2.6a	3100a	2145a	48.8b	33.0b
Group 4	85.5b	262.4b	17.6a	26.0a	7.6b	2.6a	2970a	2195a	46.9b	31.7b
Group 5	93.4a	276.4b	18.1a	25.1a	8.3b	2.7a	2327a	1605a	44.3c	35.1b
Group 6	100.9a	291.2a	13.8b	24.3a	8.4b	2.8a	2285a	1543a	38.4d	26.6c
Group 7	99.6a	280.7ba	13.3b	25.2a	10.6a	3.1a	2489a	1777a	40.3d	40.3a

 Table 16c Means of quantitative characters in different flowering groups of sorghum reference set evaluated during

 2009-2010 post rainy season (E2) at ICRSAT, Patancheru, India.

Flowering Group	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Group 1	60.7f	186.9e	20.9a	20.7a	7.4b	2.6b	2.7a	1399a	913a	49.5b	37.5a
Group 2	65.1e	192.6d	18.9b	20.8a	8.6a	2.6b	2.6a	1810a	1151a	51.1a	36.0a
Group 3	70.6d	209.8c	18.9b	20.9a	7.6b	2.7b	2.6a	1815a	1291a	47.9c	33.6b
Group 4	75.0c	229.9b	18.7b	25.4a	6.3b	2.4b	2.6a	1720a	1193a	47.4c	32.0b
Group 5	76.0c	235.8a	21.5a	25.2a	6.1c	2.8b	2.5a	1505a	1087a	46.1c	28.4c
Group 6	76.8b	249.8a	17.7b	25.2a	7.0b	2.9b	2.6a	1510a	1002a	44.2d	32.9b
Group 7	81.1a	240.7a	13.3c	25.2a	6.7b	3.7a	1.9b	1356a	1066a	42.2d	31.9b

 Table 16d Means of quantitative characters in different flowering groups of sorghum reference set pooled over

 E1 and E2.

Flowering Group	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Group 1	62.7e	188.6d	20.3a	20.8a	7.1a	2.7a	2022a	1395a	50.7a	35.7a
Group 2	67.6d	199.4c	18.7a	21.1a	8.2a	2.6a	2291a	1572a	51.2a	34.1b
Group 3	73.7d	220.2b	17.8a	21.4a	7.6a	2.6a	2457a	1719a	48.4b	33.3b
Group 4	80.3c	246.3a	18.2a	25.6a	6.9a	2.5a	2347a	1695a	47.1b	31.8b
Group 5	84.7b	256.1a	19.8a	25.1a	7.2a	2.7a	1916a	1346a	45.3b	31.7b
Group 6	88.8a	260.7a	15.8b	24.8a	7.7a	2.9a	1898a	1272a	41.3c	29.8c
Group 7	90.3a	221.3b	13.3b	25.2a	8.6a	3.4a	1922a	1421a	41.2c	29.2c

Means were tested following Newman-Keuls test. Means followed by same letter are non-significant at P = 0.05.

				CHARAC	CTERS <sup>1</sup>					
	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Races										
Bicolor	65.0-103.6	147.6-335.0	1.6-33.6	13.6-48.6	4.4-27.4	1.3-7.0	505-3876	366-2949	35.3-56.4	21.3-42.1
Caudatum	56.7-106.8	82.2-312.9	1.7-36.2	7.2-31.3	3.2-14.1	1.0-4.7	1326-5517	693-3505	34.9-58.4	23.6-50.1
Durra	59.8-104.7	104.2-336.3	1.0-32.3	6.2-36.6	4.0-8.3	1.0-4.5	1704-4990	1213-3817	36.8-62.0	21.1-51.1
Guinea	63.0-121.5	94.0-342.7	6.0-36.8	11.6-40.4	5.4-13.0	1.8-5.0	851-4325	377-3291	35.7-59.0	21.8-51.4
Kafir	67.0-102.0	148.7-275.7	10.1-26.2	21.2-41.6	4.9-20.2	1.2-5.7	834-4268	625-3063	41.4-59.9	30.7-49.1
Intermediate races										
Caudatum-bicolor	62.5-97.7	84.2-374.2	6.0-36.1	14.6-38.3	4.8-16.6	1.2-3.5	1161-3445	736-2639	41.5-62.6	27.0-51.9
Durra-bicolor	67.3-94.3	182.7-383.5	6.1-31.5	11.2-31.0	5.5-14.8	1.5-3.2	1701-4887	974-3516	40.2-53.8	26.1-40.4
Durra-caudatum	52.7-90.7	131.3-303.9	2.3-36.7	10.4-28.1	4.2-9.8	1.7-4.3	826-4302	603-2964	45.4-56.1	23.2-42.4
Guinea-caudatum	61.3-117.6	108.2-298.0	2.4-31.4	12.5-38.5	4.0-10.3	1.0-3.5	1665-4805	935-3777	34.2-57.8	21.4-41.9
Guinea-durra	78.8-81.8	227.1-253.1	9.8-11.7	15.6-23.1	5.9-7.9	1.8-2.3	2718-3391	1803-2705	43.1-50.0	28.2-32.4
Kafir-caudatum	55.7-68.4	136.2-152.1	14.8-15.0	19.2-22.6	5.2-6.7	2.5-2.8	2900-3227	1915-2150	48.5-55.1	29.8-40.8
Wild type										
Aethiopicum	38.0-77.8	119.5-315.1	17.9-21.4	16.9-40.6	5.7-15.9	4.0-9.0	665-983	546-596	42.8-47.1	30.8-45.0
Arundinaceum	53.8-109.3	225.6-321.6	15.9-47.0	26.3-41.3	8.2-21.1	4.5-5.0	640-2958	409-2455	34.9-49.8	25.6-34.9
Drummondii	55.0-114.0	180.2-326.2	2.4-30.3	18.3-37.2	5.0-15.2	2.7-7.2	830-2267	419-1549	35.3-53.2	26.6-53.2
Verticilliflorum	72.0-125.5	214.1-317.0	6.2-31.3	30.4-35.7	14.5-20.6	4.8-8.5	286-1667	187-824	34.2-48.2	32.5-35.0

Table 17a Range of quantitative characters in races, intermediate races and wild types of sorghum reference set evaluated during 2008-2009 post rainy season (E1) at ICRISAT, Patancheru, India.

	CHARACTERS <sup>1</sup>										
	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Races											
Bicolor	54.5-82.7	143.6-310.8	5.4-35.6	13.1-44.8	5.1-18.3	2.0-5.2	1.08-4.35	340-2761	236-1844	35.4-57.2	22.8-47.1
Caudatum	53.5-83.3	86.5-289.2	2.4-38.1	8.0-28.4	3.6-11.9	1.8-3.7	1.12-5.08	633-3169	352-2323	40.2-59.7	24.1-47.1
Durra	50.5-82.7	108.7-311.8	5.1-30.5	7.4-35.1	4.2-10.3	1.8-3.5	1.58-4.77	677-3076	642-2111	40.4-58.3	6.8-44.4
Guinea	54-1.83.0	117.5-294.2	3.6-34.0	12.0-38.6	4.8-11.0	2.0-4.7	0.80-4.25	387-2747	205-1823	35.6-58.2	15.6-45.4
Kafir	64.0-79.5	133.4-236.8	15.2-31.4	19.3-33.3	4.5-10.8	1.8-7.7	1.93-3.73	512-2725	383-2085	44.2-61.2	11.6-51.5
Intermediate races											
Caudatum-bicolor	57.7-83.8	84.2-322.2	7.3-33.2	14.5-32.3	5.9-11.7	2.0-3.2	2.0-3.9	607-2592	454-2036	42.1-60.0	22.5-49.2
Durra-bicolor	60.8-83.0	176.9-340.1	8.4-31.5	10.8-32.8	4.4-11.6	2.0-3.5	1.9-3.9	650-2847	374-1847	41.6-57.2	28.3-36.7
Durra-caudatum	46.5-76.8	106.2-233.5	0.8-35.7	10.2-29.3	4.0-9.7	2.0-4.0	1.5-4.5	408-2257	285-1493	43.4-55.2	11.6-42.3
Guinea-caudatum	53.7-84.5	108.8-26.0	0.6-30.1	12.1-33.0	3.9-12.3	1.7-3.0	1.4-4.0	1215-3313	321-2504	38.4-57.7	20.7-49.7
Guinea-durra	70.2-77.5	200.6-238.3	10.5-13.9	15.9-22.2	4.9-6.8	2.0-2.3	3.5-4.5	1607-2457	822-1582	45.5-51.1	29.6-39.2
Kafir-caudatum	52.8-61.8	130.7-140.9	14.8-21.2	19.2-22.7	6.2-6.93	2.2-2.2	2.4-2.4	1967-2128	1321-1428	50.0-53.6	33.0-40.3
Wilds											
Aethiopicum	47.0-64.5	165.3-256.4	22.2-24.8	23.8-34.4	8.5-9.8	3.7-5.7	1.0-2.4	555-711	414-503	45.9-46.4	31.2-40.2
Arundinaceum	51.2-81.7	202.4-255.8	17.5-38.3	23.2-30.7	5.7-10.2	4.2-7.5	0.6-1.7	580-956	224-1356	36.7-46.7	25.6-28.9
Drummondii	52.7-92.3	167.9-272.9	6.8-27.8	18.9-31.8	4.9-11.8	3.3-5.3	0.7-2.6	563-1356	355-1322	37.0-52.2	10.7-41.9
Verticilliflorum	69.4-85.5	181.2-276.4	10.5-25.3	28.3-31.3	6.7-15.0	5.2-9.0	0.3-1.0	506-2213	303-1479	35.7-49.5	24.0-39.6

Table17b Range of quantitative characters in races, intermediate races and wild types of sorghum reference set during 2009-2010 post rainy season (E2) at ICRSAT, Patancheru, India.

CHARACTERS											
	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2	
Races											
Bicolor	59.8-92.6	145.6-318.7	4.4-34.6	13.4-45.2	5.1-19.7	1.7-6.1	422-2865	301-2060	36.1-56.7	22.8-42.5	
Caudatum	55.1-103.2	84.5-301.7	2.1-37.4	7.6-29.7	3.4-12.8	1.5-4.1	1127-4243	787-2787	37.8-59.0	20.9-46.2	
Durra	55.2-92.9	105.7-324.1	5.3-30.9	6.8-35.8	4.0-8.8	1.5-4.0	800-3639	381-2720	38.8-60.2	17.2-46.4	
Guinea	58.5-123.4	180.5-316.7	5.3-34.5	11.8-38.47	5.3-15.5	1.8-6.7	610-3458	402-2461	37.7-58.6	21.9-42.5	
Kafir	65.5-90.0	143.6-348.2	13.1-34.7	20.2-29.13	4.9-9.4	1.6-3.0	1613-3361	1169-2369	41.8-60.5	23.7-49.3	
Intermediate races											
Caudatum-bicolor	60.1-88.5	84.2-307.9	6.7-31.1	14.8-35.3	5.4-14.2	1.7-3.3	884-2944	595-2337	40.7-61.3	27.2-50.3	
Durra-bicolor	64.1-86.2	179.8-361.8	7.4-31.5	13.5-31.9	5.4-12.9	1.7-3.3	1175-3295	674-2225	41.6-55.3	27.7-34.5	
Durra-caudatum	50.1-92.8	118.8-302.6	2.0-36.2	10.3-37.5	4.2-9.8	2.0-4.1	674-3279	446-2228	41.7-55.2	25.2-42.3	
Guinea-caudatum	58.6-99.5	108.5-276.9	3.8-28.7	12.3-36.6	4.7-9.6	1.7-3.2	620-3945	479-3140	37.4-58.4	23.2-48.0	
Guinea-durra	75.3-79.7	213.3-245.7	10.4-12.7	15.8-22.7	5.4-7.1	2.0-2.3	2162-2924	1422-2143	44.3-50.5	29.1-35.3	
Kafir-caudatum	54.2-65.1	133.4-146.5	14.9-18.0	19.2-22.7	5.7-6.8	2.3-2.5	2514-2597	1618-1789	49.2-54.3	31.4-40.5	
Wild types											
Aethiopicum	42.5-71.2	142.3-285.7	21.6-21.8	20.4-37.5	7.1-12.9	7.3-3.8	610-847	524-505	44.4-46.8	42.6-31.0	
Arundinaceum	52.5-95.5	214.0-288.7	16.9-42.6	24.8-36.0	7.0-15.4	3.6-6.2	820-1885	451-1906	35.8-48.3	25.1-38.3	
Drummondii	53.8-93.0	174.1-289.7	15.0-28.3	11.0-33.6	4.1-12.2	2.2-6.2	793-3679	452-2556	36.2-52.1	26.4-40.4	
Verticilliflorum	70.7-104.9	197.7-296.7	10.3-28.3	29.9-32.4	10.6-17.8	5.1-8.7	568-1249	317-846	35.0-48.3	25.6-36.8	

Table 17c Range of quantitative characters in races, intermediate races and wilds of sorghum reference set pooled over E1 and E2.

	CHARACTERS <sup>1</sup>										
	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Races											
Bicolor	58.1-80.0	119.3-299.3	0.4-61.6	10.1-34.2	2.7-19.6	0.0-5.8	0.7-5.2	647-2670	529-2052	41.4-53.6	28.9-47.7
Caudatum	51.5-78.7	128.1-304.5	0.4-58.9	9.8-30.6	2.7-14.7	0.0-9.6	1.3-4.0	489-3980	324-3148	37.8-56.2	30.6-52.0
Durra	55.4-78.7	165.1-287.0	0.4-35.0	10.8-38.8	2.9-15.3	0.0-6.3	1.0-4.2	1095-3808	717-2915	39.0-56.9	32.3-49.7
Guinea	51.5-80.0	159.1-290.3	0.4-32.2	9.3-47.5	1.4-40.4	0.2-8.4	1.0-4.5	981-2928	762-2449	35.8-59.3	30.7-49.2
Kafir	56.9-80.7	189.8-307.1	0.4-39.3	12.3-37.5	4.0-27.7	0.0-6.4	1.5-4.6	1177-2780	932-2231	39.9-53.0	33.8-52.2
Intermediate races											
Caudatum-bicolor	51.5-78.7	128.1-304.5	0.4-58.9	9.8-60.6	2.7-49.2	0.0-9.6	0.6-4.0	712-2584	348-2070	37.8-56.2	28.7-52.0
Durra-bicolor	60.9-73.4	183.8-307.6	2.0-40.9	12.3-27.9	4.7-14.3	0.3-6.3	2.1-3.5	1050-3649	785-2539	42.8-54.5	34.6-46.0
Durra-caudatum	51.4-76.0	138.5-342.3	0.5-32.1	7.5-30.3	1.4-15.3	0.0-6.3	1.2-4.0	889-3894	656-2842	40.7-54.9	32.4-49.9
Guinea-caudatum	55.9-77.4	89.1-271.3	0.4-45.8	10.2-32.5	2.8-16.2	0.0-5.4	0.7-4.0	1062-2636	630-2139	39.9-55.5	27.5-47.9
Guinea-durra	58.1-65.1	218.2-240.5	16.6-25.5	12.8-26.6	4.9-6.6	1.3-2.8	1.4-2.8	1446-2227	1163-1369	42.0-52.0	33.9-47.1
Wild types											
Aethiopicum	59.9-62.4	145.2-238.2	18.7-18.9	9.0-19.9	1.9-9.4	1.9-2.2	2.3-2.5	696-1053	477-934	35.4-39.9	28.0-32.4
Arundinaceum	60.8-68.0	175.8-245.9	8.8-26.5	16.7-18.9	4.5-7.2	1.0-5.3	2.3-2.8	732-1320	800-1201	33.4-56.1	34.5-48.1
Drummondii	58.9-72.7	129.6-272.9	3.7-27.4	12.3-39.1	3.4-25.5	0.0-3.3	0.6-4.1	484-1973	458-1746	38.0-50.5	29.9-48.9
Verticilliflorum	57.8-76.6	153.0-271.8	7.1-33.9	13.5-25.8	3.7-17.9	0.5-4.3	1.4-3.2	584-1533	543-1287	44.8-48.2	34.3-47.2

Table 17d Range of quantitative characters in races, intermediate races and wild types of sorghum reference set during 2009-2010 post rainy season at UAS, Dharwad under irrigated condition (E3).

	CHARACTERS <sup>1</sup>											
	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2	
Races												
Bicolor	51.9-75.2	151.9-262.5	0.2-41.8	11.3-46.0	3.5-36.1	0.6-5.8	1.0-4.0	1357-2849	429-2498	41.3-52.1	37.7-45.4	
Caudatum	55.4-77.11	160.7-270.3	0.2-33.7	13.1-32.4	2.2-10.1	0.2-7.7	1.2-4.3	1120-3060	752-2259	46.7-56.1	35.1-47.3	
Durra	55.1-73.2	191.8-260.7	0.3-32.7	13.7-31.1	3.3-8.3	0.4-7.5	1.1-4.2	1433-2862	993-2638	44.2-55.1	33.5-47.0	
Guinea	55.9-75.9	184.5-266.7	0.2-42.2	10.6-44.4	0.7-31.6	0.8-9.1	1.0-4.3	581-2829	293-2298	42.7-53.7	33.5-47.7	
Kafir	51.2-73.1	204.0-263.4	3.4-35.9	13.4-29.6	3.3-16.4	1.2-6.4	0.5-4.3	1533-2840	802-2148	46.3-53.2	36.5-45.0	
Intermediate races												
Caudatum-Bicolor	55.6-70.9	186.4-255.8	0.2-42.3	10.0-51.3	3.1-18.7	0.2-6.7	0.6-3.5	1628-2874	1018-2297	45.8-53.1	35.8-46.4	
Durra-Bicolor	60.9-73.0	183.3-266.5	0.6-27.4	12.4-37.7	4.9-12.1	1.3-3.0	1.5-3.2	1709-2825	1062-2063	47.9-53.3	39.1-45.7	
Durra-caudatum	51.9-75.5	161.1-261.2	0.3-29.0	8.7-35.4	2.8-8.9	0.6-4.6	0.8-3.9	1629-2829	1030-2606	46.9-53.5	37.1-46.1	
Guinea-caudatum	54.9-77.7	93.5-255.2	0.2-27.2	9.7-30.1	1.2-15.0	0.4-4.8	0.6-4.3	1640-3053	1117-2629	46.2-54.1	34.9-46.3	
Guinea-durra	62.5-68.1	209.3-233.6	5.5-15.2	16.5-27.7	4.4-5.6	1.9-2.5	1.3-2.4	2053-2202	1212-1699	48.2-51.9	37.6-44.6	
Kafir-caudatum	60.6-57.0	238.5-183.9	10.3-19.9	20.3-23.6	6.2-6.3	2.8-2.4	2.8-2.6	2109-2783	1699-1318	52.6-53.2	41.3-43.3	
Wilds												
Aethiopicum	60.1-72.0	176.4-240.0	12.0-21.8	15.0-27.2	5.8-8.1	2.4-2.6	2.3-2.3	938-1145	574-913	49.8-51.0	40.1-43.1	
Arundinaceum	57.7-71.5	222.1-254.3	0.3-22.2	17.2-23.1	4.6-7.2	1.9-5.3	2.4-4.3	864-1041	528-758	46.4-51.2	35.9-43.4	
Drummondii	56.0-77.3	173.8-250.7	1.0-24.9	13.6-39.0	2.9-15.0	0.8-3.1	1.3-2.6	712-1045	325-901	47.3-52.3	39.3-45.4	
Verticilliflorum	50.9-63.2	248.3-226.6	27.9-22.0	20.3-17.8	5.5-4.4	5.3-3.0	2.8-2.1	670-1052	352-838	52.0-49.5	47.2-42.7	

Table 17e Range of quantitative characters in races, intermediate races and wilds of sorghum reference set during 2009-2010 post rainy season at UAS, Dharwad under un-irrigated condition (E4).

CHARACTERS <sup>1</sup>											
	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Races											
Bicolor	52.4-81.6	157.6-239.7	0.3-40.9	14.1-34.7	2.2-22.7	1.3-4.6	0.9-2.6	1355-3498	682-2746	42.3-54.6	32.4-52.1
Caudatum	48.8-81.6	135.5-265.0	0.3-32.5	10.1-36.3	2.2-8.7	1.3-5.6	1.1-3.9	1406-3260	999-2754	41.0-56.3	32.1-52.6
Durra	55.2-88.9	144.5-247.7	0.3-29.1	10.2-30.0	1.4-11.4	1.8-4.0	1.0-4.9	1345-3234	1029-3333	41.0-55.3	33.9-49.7
Guinea	51.5-90.7	145.4-269.7	0.3-29.6	7.6-44.1	2.4-12.9	1.3-5.0	0.9-2.9	1157-3328	919-2366	32.9-56.9	28.4-56.1
Kafir	55.2-92.6	147.1-247.9	2.4-38.2	16.0-32.2	2.3-8.7	2.2-5.5	1.1-3.4	1426-3397	1099-2556	45.7-56.3	32.1-49.6
Intermediate races											
Caudatum-Bicolor	54.3-79.8	146.0-258.2	0.3-27.3	15.1-30.6	2.3-12.0	2.2-5.5	1.1-3.4	1932-3310	890-2111	41.5-55.2	30.4-50.8
Durra-Bicolor	60.6-74.3	159.8-230.8	4.0-24.0	15.4-26.4	2.3-8.9	1.7-4.0	0.6-2.3	1334-2653	1116-2156	40.4-50.8	31.5-43.6
Durra-caudatum	51.5-81.6	153.2-233.8	0.3-37.4	12.9-27.2	2.0-7.0	1.3-4.3	0.8-4.0	1791-3334	1190-2584	43.3-55.0	31.8-54.3
Guinea-caudatum	51.5-85.3	103.0-238.3	0.3-28.7	8.9-34.3	1.5-13.6	0.5-4.3	0.9-3.8	1468-3182	396-2636	41.4-55.6	15.9-54.5
Guinea-durra	68.9-77.1	196.8-224.0	0.3-11.1	22.7-29.1	4.2-5.2	3.3-4.5	1.9-2.3	1783-2333	1316-1761	47.6-51.6	38.8-51.4
Kafir-caudatum	59.7-55.2	198.0-163.1	12.0-13.0	17.0-24.7	4.7-4.1	0.5-1.3	2.7-2.7	2392-2764	1830-1886	48.7-54.5	52.0-49.0
Wilds											
Aethiopicum	53.4-67.9	146.6-242.1	16.9-33.1	21.5-23.3	7.0-11.9	3.0-4.6	1.5-2.1	953-1098	793-839	43.7-47.0	32.6-37.6
Arundinaceum	60.6-72.5	164.7-226.4	18.9-27.1	13.8-23.3	3.8-7.6	2.6-7.5	1.1-2.5	809-1140	633-826	43.2-51.2	37.6-44.1
Drummondii	54.3-80.7	185.3-257.7	0.3-29.1	12.7-25.7	2.4-8.6	2.4-6.0	1.0-3.2	839-1139	513-986	41.4-51.8	36.3-48.8
Verticilliflorum	63.4-81.6	200.6-247.1	9.5-26.5	22.8-29.7	3.2-15.7	3.0-6.3	1.1-2.1	819-1042	619-899	41.7-59.2	36.2-51.1

Table 17f. Range of quantitative characters in races, intermediate races and wild types of sorghum reference set evaluated during the 2009-2010 post rainy season at ARRS, Bijapur under un-irrigated condition (E5).

CHARACTERS <sup>1</sup>											
	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Races											
Bicolor	55.1-78.3	148.8-266.0	3.9-39.2	12.1-38.9	3.5-22.0	1.2-4.2	1.4-3.7	1479-2651	1116-1844	41.6-51.4	35.0-46.2
Caudatum	52.6-75.9	136.8-260.4	2.7-29.5	13.0-30.0	3.5-9.5	1.2-6.7	1.6-3.4	1518-2999	1142-2210	44.3-53.9	36.2-46.7
Durra	55.4-76.3	167.1-254.6	3.5-27.0	12.5-29.5	4.0-10.6	1.0-5.6	1.5-3.3	1881-3001	1249-2361	42.5-54.7	36.0-46.4
Guinea	55.4-81.1	175.1-284.8	4.1-27.7	11.8-37.1	3.3-20.6	1.3-6.1	1.3-3.2	1568-2690	1121-2171	37.6-54.4	35.4-47.2
Kafir	60.3-80.8	208.8-247.8	8.9-26.0	15.8-34.0	3.3-11.4	1.9-5.1	1.5-3.7	1638-2576	1222-1924	45.2-53.8	38.0-46.5
Intermediate races											
Caudatum-bicolor	58.2-74.2	168.2-264.0	2.9-33.3	11.9-48.3	4.1-24.2	1.4-5.3	1.2-3.6	1886-2444	1195-1799	40.8-52.2	31.1-46.6
Durra-bicolor	60.9-70.6	188.6-255.9	8.1-29.0	12.9-28.8	4.7-9.6	1.4-3.6	1.4-3.0	1746-2812	1313-1812	44.6-51.3	37.2-42.4
Durra-caudatum	54.8-75.5	146.7-272.5	2.9-28.5	10.8-27.3	3.1-8.9	1.2-4.6	1.4-3.3	1816-2902	1379-2115	44.3-52.9	36.6-47.7
Guinea-caudatum	54.4-76.6	114.9-247.2	1.4-28.2	13.0-26.9	3.6-11.4	1.0-3.8	1.6-3.7	1730-2780	1069-2081	44.6-53.7	32.3-47.4
Guinea-durra	64.2-70.5	205.7-236.2	10.9-13.7	17.5-26.4	4.7-5.4	2.3-3.2	1.6-2.4	1967-2210	1387-1495	47.3-49.4	36.2-47.8
Kafir-caudatum	55.9-63.7	156.3-222.4	13.2-17.6	20.1-23.1	5.6-5.6	1.5-2.1	2.5-2.7	2431-2459	1778-1634	51.9-55.8	44.8-46.0
Wild type											
Aethiopicum	61.7-63.7	142.4-245.5	19.2-21.3	15.7-23.0	4.88-10.1	2.5-3.1	2.1-2.3	993-1213	828-1065	44.3-45.1	35.1-36.1
Arundinaceum	55.4-76.4	154.2-265.4	11.2-18.0	18.2-34.9	4.63-15.1	2.3-2.9	1.1-2.6	1082-1256	940-1030	43.9-51.0	37.7-43.7
Drummondii	55.4-76.4	154.2-265.4	11.2-18.0	18.2-34.9	4.63-15.1	2.3-2.9	1.1-2.6	866-1390	761-1164	43.9-51.0	37.7-43.7
Verticilliflorum	58.9-73.4	169.8-256.2	12.5-27.0	19.2-24.1	5.00-10.3	2.4-4.7	1.4-2.4	896-1164	810-996	44.2-53.9	39.6-44.5

Table 17g. Range of quantitative characters in individual races, intermediate races and wilds of sorghum reference set pooled over E3, E4 and E5.

Table 18a Means of quantitative characters in races, intermediate races and wild types of sorghum reference set evaluated during the 2008-2009 post rainy season (E1) at ICRSAT, Patancheru, India

					CHAR	ACTEF	$RS^1$			
Races	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Bicolor	78.9c	251.6b	17.7b	28.8a	11.4a	3.0a	2483b	1691b	46.8c	30.3b
Caudatum	75.3b	216.6d	17.0b	19.4c	6.5c	2.4b	3184a	2313a	49.4b	32.8b
Durra	78.8c	234.3c	14.2b	16.0d	6.3c	2.2b	3238a	2377a	48.2b	31.4b
Guinea	84.7a	268.8a	21.1a	28.4a	8.6b	3.1a	2433b	1592b	46.0b	32.8b
Kafir	80.5c	207.1d	17.3b	25.6b	7.1c	2.1b	3216a	2389a	53.7a	39.3a
Intermediate races										
Caudatum-bicolor	73.1a	231.6a	20.2a	23.8a	8.0ab	2.4a	2698a	1902a	51.8a	33.7a
Durra-bicolor	81.5a	256.4a	15.2a	17.4a	7.1ab	2.2a	2999a	2232a	45.0a	31.6a
Durra-caudatum	69.8a	211.1a	22.1a	18.6a	5.9ab	2.7a	2285a	1505a	51.0a	35.0a
Guinea-bicolor	75.8a	235.5a	6.5a	23.3a	7.3ab	1.5a	3670a	1621a	50.0a	31.7a
Guinea-caudatum	75.7a	199.2a	14.3a	19.9a	6.5ab	2.3a	3312a	2406a	48.7a	31.4a
Guinea-durra	80.4a	243.3a	11.0a	19.3a	6.8ab	2.1a	2977a	2177a	47.1a	30.6a
Guinea-kafir	79.5a	158.2a	10.3a	22.3a	6.6ab	2.0a	3215a	1860a	51.9a	44.1a
Kafir-bicolor	69.2a	218.8a	23.0a	26.4a	10.2a	2.2a	2868a	1599a	56.4a	33.5a
Kafir-caudatum	62.0a	144.1a	14.9a	20.9a	5.9ab	2.7a	3063a	2032a	51.8a	35.3a
Kafir-durra	78.0a	227.2a	11.0a	16.4a	4.5b	2.5a	4172a	2778a	50.6a	30.6a
Wild types										
Aethiopicum	57.9a	217.3a	19.7a	28.7a	10.8a	6.5a	824a	571a	45.0a	37.9a
Arundinaceum	91.4a	287.1a	25.1a	34.5a	16.5a	4.8a	1559a	1179a	40.9a	30.9a
Drummondii	80.6a	257.4a	18.8a	27.2a	9.9a	4.3a	1572a	1130a	44.6a	33.1a
Verticilliflorum	85.2a	273.4a	17.6a	33.3a	17.2a	6.4a	959a	481a	43.1a	33.9a
Virgatum	75.2a	252.8a	18.0a	40.7a	17.2a	5.0a	715a	375a	39.3a	36.4a

Table 18b Means of quantitative characters in races, intermediate races and wild types of sorghum reference set evaluated during the 2009-2010 post rainy season (E2) at ICRSAT, Patancheru, India.

						CH	ARACT	ERS			
Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Bicolor	71.9b	229.1a	19.3a	27.5a	9.5a	2.9a	2.0c	1454b	949b	47.0b	32.6b
Caudatum	68.0b	199.2a	18.7a	19.2c	6.9b	2.4b	2.8b	1917a	1334a	49.3b	34.6b
Durra	72.5b	217.2a	16.1a	15.8d	6.9b	2.2b	3.2a	1989a	1343a	47.3b	31.4b
Guinea	71.4b	232.1a	22.1a	28.1a	7.5b	3.0a	2.2c	1472b	1001b	47.4b	33.5b
Kafir	71.3a	186.2a	21.6a	24.5b	6.8b	2.3b	2.6b	1902a	1296a	54.4a	38.3a
Intermediate races											
Caudatum-bicolor	68.5a	220.3a	20.2a	23.2b	8.7a	2.4a	2.8b	1604a	1113a	49.8a	36.3a
Durra-bicolor	74.8a	234.7a	17.2a	17.7b	7.2ab	2.3a	2.4b	1902a	1243a	46.0a	32.8a
Durra-caudatum	62.3a	193.1a	22.9a	18.6b	6.5ab	2.6a	3.2b	1285a	940a.	49.7a	34.8a
Guinea-bicolor	72.3a	220.7a	11.3a	20.0b	7.8ab	2.3a	3.5b	2700a	1371a	47.1a	36.2a
Guinea-caudatum	68.1a	181.4a	15.2a	19.9b	6.9ab	2.2a	2.9b	2025a	1358a	48.5a	33.5a
Guinea-durra	74.1a	218.2a	11.8a	19.4b	6.0ab	2.2a	3.8a	2054a	1316a	48.8a	32.9a
Guinea-kafir	74.7a	160.9a	18.0a	22.0b	8.5ab	2.0a	2.4c	1515a	1216a	55.7a	40.5a
Kafir-bicolor	62.5a	208.4a	25.5a	25.5b	10.8a	2.2a	1.7b	1517a	1095a	59.0a	48.2a
Kafir-caudatum	57.3a	135.8a	18.0a	21.0b	6.5ab	2.2a	2.4b	2048a	1374a	51.8a	36.7a
Kafir-durra	71.8a	204.7a	16.9a	15.8b	4.4b	2.5a	2.0b	1780a	1380a	48.9a	31.0a
Wild types											
Aethiopicum	55.7a	210.9a	23.5a	29.1b	9.2b	4.7a	1.7b	633a	458a	46.2a	35.7a
Arundinaceum	69.2a	234.5a	25.8a	27.6b	7.8c	5.6a	1.0b	806a	659a	40.0a	27.9a
Drummondii	69.2a	221.1a	20.8a	25.4b	7.3c	4.0a	1.5b	973a	629a	44.0a	29.8a
Verticilliflorum	76.2a	240.4a	16.6a	29.4b	12.6b	6.3a	0.7b	910a	635a	44.4a	31.9a
Virgatum	69.2a	270.7a	23.5a	38.1a	13.8a	4.3a	3.3a	991a	1338a	49.2a	33.4a

Means were tested following Newman-Keuls test. Means followed by same letter are non-significant at P = 0.05.

Table 18c Means of quantitative characters in races, intermediate races and wilds of sorghum reference set pooled over E1 and E2.

				CHARA	CTERS					
Races	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Bicolor	75.3b	241.7a	18.9b	28.32a	10.4a	2.9a	1968b	1352a	46.9c	31.5b
Caudatum	72.2c	208.9b	17.6c	19.10c	6.6c	2.4b	2512a	1791a	49.3b	33.4b
Durra	75.7b	221.3b	15.2c	16.33d	6.6c	2.3bc	2600a	1838a	47.9bc	31.5b
Guinea	77.9a	250.7a	21.8a	28.03a	8.2b	3.1a	1998b	1329b	46.5c	32.2b
Kafir	75.8b	202.8b	19.6b	24.25b	6.7c	2.1c	2540a	1841a	53.9a	38.1a
Intermediate races										
Caudatum-bicolor	70.4a	220.6a	19.3a	24.07a	8.5b	2.4a	2159a	1491a	50.9a	35.3a
Durra-bicolor	78.2a	249.4a	15.9a	18.61a	7.5b	2.2a	2352a	1718a	45.3a	31.1a
Durra-caudatum	66.8a	203.9a	21.9a	19.00a	6.5b	2.8a	1774a	1202a	49.8a	35.0a
Guinea-bicolor	74.1a	228.1a	8.9a	21.63a	7.5b	1.9a	3184a	1496a	48.5a	34.0a
Guinea-caudatum	72.1a	192.9a	15.1a	20.35a	6.8b	2.3a	2644a	1861a	48.9a	32.6a
Guinea-durra	77.2a	230.7a	11.4a	19.31a	6.4b	2.1a	2515a	1746a	47.9a	31.8a
Guinea-kafir	77.1a	159.5a	14.1a	22.17a	7.5b	2.0a	2365a	1538a	53.8a	42.3a
Kafir-bicolor	65.8a	213.6a	24.2a	25.97a	10.5a	2.2a	2192a	1347a	57.7a	40.8a
Kafir-caudatum	59.7a	140.0a	16.5a	20.96a	6.2b	2.4a	2556	1703a	51.8a	36.0a
Kafir-durra	74.9a	216.0a	13.9a	16.13a	4.4c	2.5a	2976a	2079a	49.8a	30.8a
Wilds										
Aethiopicum	56.8a	214.0a	21.7a	28.94b	10.0ca	5.6a	729a	514b	45.6a	36.8a
Arundinaceum	79.0a	250.8a	24.2a	30.34b	10.6a	4.7a	1271a	931a	41.5a	30.0a
Drummondii	74.0a	231.3a	20.3a	24.13c	8.0a	3.8a	1579a	1127a	45.0a	33.0a
Verticilliflorum	80.7a	256.9a	17.1a	31.39b	14.9a	6.4a	935a	558a	43.8a	32.3a
Virgatum	72.2a	261.8a	20.8a	39.43a	15.5a	4.7a	853a	857a	44.2a	34.9a

 Table 18d Means of quantitative characters in races, intermediate races and wilds of sorghum reference set evaluated during

 2009-2010 post rainy season at UAS, Dharwad under irrigated condition (E3).

	CHARACTERS <sup>1</sup> DE DH EXE DI DW BT HSW DWT VID SPAD1 SPAD2										
Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Bicolor	64.4a	236.7a	15.3a	19.8a	6.6a	2.4a	2.4a	1624a	1307a	47.4a	39.7a
Caudatum	63.6a	227.3a	18.3a	19.7a	6.3a	2.2a	2.6a	3059a	2279a	47.4a	41.3a
Durra	63.7a	229.3a	16.6a	20.3a	6.6a	2.0a	2.5a	2728a	2060	47.3a	40.1a
Guinea	63.4a	235.1a	16.7a	22.3a	8.0a	2.3a	2.5a	2112a	1536a	46.8a	40.3a
Kafir	65.8a	244.4a	16.8a	21.0a	7.3a	2.2a	2.4a	1870a	1387a	46.6a	41.3a
Intermediate races											
Caudatum-bicolor	6.7b	228.6b	17.6a	20.0a	6.9a	2.1a	2.6b	1939a	1386a	47.3a	41.3a
Durra-bicolor	65.1b	239.7b	18.4a	19.4a	6.7a	2.1a	2.7b	2039a	1603a	46.7a	40.8a
Durra-caudatum	64.3b	224.6b	16.6a	19.3a	6.0a	2.1a	2.4b	2484a	1907a	47.7a	40.9a
Guinea-bicolor	77.4a	258.2a	10.2a	27.7a	5.3a	0.3a	1.1c	2422a	1979a	42.9a	38.8a
Guinea-caudatum	64.1b	217.3b	15.6a	20.0a	6.8a	2.1a	2.5b	2115a	1559a	47.6a	38.7a
Guinea-durra	61.4b	226.5b	20.0a	20.3a	5.9a	1.8a	2.3b	1879a	1267a	47.1a	38.7a
Guinea-kafir	59.2b	231.0b	23.3a	17.8a	4.5a	0.6a	3.7a	2149a	1916a	38.9b	43.9a
Kafir-bicolor	58.2c	129.6c	9.8aa	19.9a	6.2a	0.8a	1.9b	2151a	1257a	55.5a	43.9a
Kafir-caudatum	64.4b	191.3b	17.6a	22.0a	6.1a	2.1a	2.4b	2407a	1857a	55.1a	43.4a
Kafir-durra	65.4b	257.2a	17.9a	23.4a	5.9a	1.6a	3.0b	2459a	1801a	54.9a	47.5a
Wilds											
Aethiopicum	58.2a	191.7a	18.8a	14.5a	5.7a	2.1a	2.4a	874a	705a	38.1a	30.3a
Arundinaceum	65.2a	227.6a	16.2a	17.9a	5.2a	2.8a	2.5a	1121a	994a	46.6a	39.0a
Drummondii	65.9a	227.2a	13.2a	22.4a	8.2a	1.7a	2.2a	1081a	927a	46.4a	39.6a
Verticilliflorum	63.0a	220.7a	18.1a	18.7a	8.3a	2.2a	2.2a	956a	828a	46.3a	41.0a
Virgatum	68.7a	199.3a	11.0a	13.0a	5.5a	0.9a	2.0a	1125a	1011a	46.9a	31.0a

Means were tested following Newman-Keuls test. Means followed by same letter are non-significant at P = 0.05.

Table 18e Means of quantitative characters in races, intermediate races and wild types of sorghum reference set evaluated during the 2009-2010 post rainy season at UAS, Dharwad under un-irrigated condition (E4).

						CH	HARAC	FERS			
Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Bicolor	64.7a	233.6a	14.9a	21.4a	6.5a	2.5a	2.2a	2208a	1593a	49.3a	41.7a
Caudatum	63.6a	231.9a	16.3a	21.3a	5.9a	2.6a	2.4a	2215a	1619a	50.7a	41.7a
Durra	64.5a	232.4a	16.7a	21.2a	5.8a	2.8a	2.4a	2291a	1621a	50.4a	41.6a
Guinea	64.6a	235.5a	15.7a	23.1a	6.4a	2.8a	2.3a	2147a	1536a	49.9a	42.2a
Kafir	66.8a	242.5a	17.7a	22.0a	5.8a	2.9a	2.2a	2144a	1510a	50.2a	42.1a
Intermediate races											
Caudatum-bicolor	63.3a	233.1a	13.5a	21.8a	6.7b	2.7a	2.4a	2150a	1578a	49.7a	42.4b
Durra-bicolor	67.2a	237.6a	17.0a	23.8a	7.1a	2.3a	2.4a	2211a	1494a	50.8a	41.4b
Durra-caudatum	64.9a	226.8a	15.0a	20.9a	5.1b	2.5a	2.2a	2152a	1541a	50.0a	42.3b
Guinea-bicolor	72.2a	246.6a	17.8a	24.6a	9.0a	2.6a	2.4a	2131a	1487a	47.0a	40.6b
Guinea-caudatum	64.9a	218.7a	14.1a	20.7a	5.6b	2.4a	2.2a	2426a	1808a	50.2a	41.7b
Guinea-durra	66.0a	217.8a	9.2a	21.0a	4.9b	2.1a	2.0a	2150a	1423a	49.8a	42.1b
Guinea-kafir	57.4a	235.6a	20.3a	16.0a	2.3c	3.3a	2.3a	2431a	1849a	48.9a	44.5a
Kafir-bicolor	57.2a	165.3a	12.7a	17.0a	4.6b	3.7a	2.1a	2474a	1798a	54.6a	43.3a
Kafir-caudatum	58.8a	211.2a	15.1a	21.9a	6.3b	2.6a	2.7a	2446a	1509a	52.9a	42.3b
Kafir-durra	70.8a	245.0a	20.3a	30.0a	5.8b	2.6a	2.6a	2499a	1831a	47.8a	39.2c
Wilds											
Aethiopicum	66.0a	208.20a	16.9a	21.1b	7.0a	2.5a	2.3a	1042a	744a	50.4a	41.6a
Arundinaceum	64.0a	239.23a	11.0a	20.6b	6.0a	3.8a	2.9a	921a	662a	48.8a	40.5a
Drummondii	68.3a	216.22a	11.8a	23.4a	6.2a	2.2a	1.8a	857a	563a	49.4a	42.4a
Verticilliflorum	58.7a	226.58a	22.0a	17.8b	4.4a	3.0a	2.1a	910a	613a	49.5a	42.7a
Virgatum	72.4a	252.50a	13.4a	18.7b	5.3a	3.3a	1.7a	990a	564a	47.6a	41.9a

Table 18f Means of quantitative characters in races, intermediate races and wild types of sorghum reference set evaluated during 2009-2010 post rainy season at ARRS Bijapur under un-irrigated condition (E5).

	CHARACTERS										
Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Bicolor	66.8c	202.1b	14.8a	22.4b	5.8a	2.8a	1.7c	2180a	1545a	48.0b	40.1c
Caudatum	65.0c	189.9c	12.7a	19.7b	4.4c	2.8a	2.1a	2440a	1771a	49.0b	42.0b
Durra	68.4c	191.5c	11.4a	18.1c	5.1b	2.7a	2.1a	2193a	1585a	49.4b	41.9b
Guinea	70.2a	208.2a	15.9a	22.8a	5.8a	3.1a	1.8b	2323a	1747a	47.4b	41.8b
Kafir	71.9a	192.3c	14.5a	21.6b	4.7c	3.1a	2.0a	2326a	1557a	51.1a	43.3a
Intermediate races											
Caudatum-bicolor	66.1a	197.4a	15.7a	22.0a	5.9a	2.8a	1.9a	2360a	1482a	48.1a	41.7a
Durra-bicolor	66.7a	204.1a	14.8a	20.0a	5.4a	2.7a	1.8a	2164a	1535a	46.4a	38.0a
Durra-caudatum	63.9a	198.3a	16.4a	20.1a	4.5a	2.8a	2.1a	2537a	1853a	49.2a	42.8a
Guinea-bicolor	81.6a	223.8a	3.4b	15.7a	6.1a	3.0a	2.4a	2348a	1911a	49.0a	40.1a
Guinea-caudatum	66.7a	183.4a	11.9a	19.3a	5.2a	2.8a	2.2a	2152a	1481a	49.5a	41.7a
Guinea-durra	73.7a	212.2a	7.3b	25.3a	4.7a	3.7a	2.0a	2117a	1544a	49.0a	43.2a
Guinea-kafir	77.1a	150.4a	11.6a	19.5a	3.3a	2.2a	1.6a	2061a	1451a	47.2a	46.1a
Kafir-bicolor	60.6a	205.2a	12.2a	23.1a	8.8a	3.2a	1.6a	2248a	1766a	50.5a	35.6a
Kafir-caudatum	57.5a	180.5a	13.5a	20.8a	4.4a	0.9b	2.7a	2578a	1858a	51.6a	50.5a
Kafir-durra	76.2a	176.5a	13.0c	20.0a	5.6a	4.0a	2.0a	2208a	1246a	50.6a	45.0a
Wilds											
Aethiopicum	60.7a	194.3a	25.0a	22.4a	9.5c	3.8a	1.8a	1025a	816a	45.3a	35.1a
Arundinaceum	66.8a	205.9a	22.9a	19.9a	5.1c	4.4a	1.7a	976a	742a	46.1a	41.7a
Drummondii	68.6a	206.9a	15.1a	22.3a	5.2b	3.8a	1.8a	992a	724a	47.2a	40.7a
Verticilliflorum	70.7a	218.2a	19.4a	26.8a	9.1a	4.8a	1.5a	953a	729a	48.3a	43.6a
Virgatum	54.3a	247.3a	14.6a	30.1a	6.3b	3.9a	1.0a	1035a	846a	44.8a	33.1a

Means were tested following Newman-Keuls test. Means followed ay same letter are non-significant at P = 0.05

Table 18g Means of quantitative characters in races, intermediate races and wild types of sorghum reference set pooled over E1 and E2.

	CHARACTERS										
Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Bicolor	65.2a	226.1a	14.8a	21.4b	6.3a	2.6a	2.1a	1994a	1481a	48.0b	40.4c
Caudatum	64.0a	216.2a	15.7a	20.2b	5.6a	2.6a	2.4a	2544a	1838a	49.2a	41.7b
Durra	65.5a	217.3a	15.2a	19.6c	5.7a	2.5a	2.3a	2401a	1751a	49.1a	41.0b
Guinea	65.9a	228.4a	16.0a	23.0a	6.8a	2.7a	2.2a	2191a	1600a	47.9b	41.5b
Kafir	68.7a	228.6a	16.6a	21.6b	5.6a	2.8a	2.2a	2130a	1517a	49.5a	42.3a
Intermediate races											
Caudatum-bicolor	64.4b	221.7b	14.7a	21.7a	7.0a	2.4a	2.3a	2158a	1522a	48.2b	41.8a
Durra-bicolor	66.5b	228.3b	16.7a	21.0a	6.4a	2.3a	2.3a	2150a	1569a	48.1b	40.0a
Durra-caudatum	64.6b	217.4b	16.2a	19.9a	5.2a	2.5a	2.3a	2376a	1742a	49.0b	42.2a
Guinea-bicolor	78.6a	247.0a	10.4a	22.3a	6.9a	2.0a	2.0a	2291a	1739a	45.4c	39.8a
Guinea-caudatum	65.3b	203.1b	13.6a	19.8a	5.9a	2.4a	2.3a	2239a	1625a	49.0b	41.5a
Guinea-durra	66.7b	218.5b	12.1a	22.5a	5.1a	2.6a	2.1a	2061a	1444a	48.5b	41.3a
Guinea-kafir	63.2b	200.9b	18.4a	17.4a	3.3a	2.1a	2.4a	2289a	1796a	44.8c	45.2a
Kafir-bicolor	57.6c	157.8c	11.6a	20.0a	6.6a	2.6a	1.9a	2365a	1661a	54.7b	41.3a
Kafir-caudatum	59.8c	189.4b	15.4a	21.6a	5.6a	1.8a	2.6a	2445a	1706a	53.9a	45.4a
Kafir-durra	71.6b	227.5	22.9a	24.7a	5.8a	2.7a	2.6a	2463a	1695a	50.6a	43.4a
Wilds											
Aethiopicum	62.7a	193.9a	20.3a	19.3a	7.5a	2.8a	2.2a	1103a	946a	44.7a	35.6c
Arundinaceum	64.7a	227.0a	16.7a	19.4a	5.5a	3.7a	2.4a	1130a	983a	46.8a	40.2b
Drummondii	68.1a	215.6a	13.4a	22.8a	6.5a	2.6a	1.9a	1109a	938a	47.5a	41.0a
Verticilliflorum	63.3a	223.4a	19.9a	21.5a	7.2a	3.6a	1.9a	1073a	925a	47.9a	42.6a
Virgatum	66.3a	248.7a	12.7a	21.3a	5.6a	2.8a	1.5a	1177a	1001a	45.6a	35.5c

Means were tested following Newman-Keuls test. Means followed ay same letter are non-significant at P = 0.05

		Mean <sup>†</sup>			Range	Variance <sup>‡</sup>				
Characters <sup>1</sup>	Races	Intermediate races	Wild	Race	Intermediate race	Wild	Race	Intermediate race	Wild	p>f
DF	79.4a	73.9b	81.5a	56.7-121.5	52.7-117.6	38.0-125.5	135.4	99.3	406.7	< 0.0001**
РН	237.3a	217.0c	263.0a	82.2-342.7	84.2-383.5	119.5-326.2	2707.5	2406.8	2663.33	0.781
EXE	17.9a	18.0a	19.6a	1.6-36.9	2.3-36.7	2.4-47.0	53.5	57.7	82.1	0.309
PL	23.4b	20.8b	30.8a	6.2-48.6	10.4-38.5	16.9-41.3	59.7	24.8	44.4	0.001**
PW	7.8b	6.9b	13.4a	3.2-27.4	4.0-16.6	5.0-21.1	10.8	3.8	24.8	0.018
BT	2.6b	2.4b	5.2a	1.0-7.0	1.0-4.3	2.7-9.0	0.7	0.3	2.9	< 0.001**
PWT	2883a	2870b	1307b	505-5517	826-4887	286-2958	727405	743872	441985	0.344
YLD	2034a	2025a	888b	366-3817	603-3777	187-2455	481501	471944	305944	0.358
SPAD1	48.5a	50.2a	43.3b	34.9-62.0	35.2-62.6	34.2-53.2	28.5	20.0	28.4	0.110
SPAD2	33.0a	33.1a	33.5a	21.1-51.4	21.4-51.9	25.6-53.2	32.6	27.2	33.4	0.620

Table 19a Mean, range and variance of quantitative characters in the races, intermediate races and wild types as group of sorghum reference set evaluated during 2008-09 post rainy season (E1) at ICRISAT, Patancheru, India.

 Table 19b Mean, range and variance of quantitative characters in races, intermediate races and wild types as a group of sorghum reference set during 2009-10 post rainy season (E2) at ICRISAT, Patancheru, India.

		Mean <sup>†</sup>			Range					
		Intermediate			Intermediate					
Characters <sup>1</sup>	Races	races	Wild	Races	races	Wild	Races	races	Wild	p>f
DF	70.4a	67.2a	69.8a	50.5-126.8	46.5-84.5	47.0-92.3	65.0	62.3	122.0	0.38
PH	213.4b	199.4b	229.7a	86.7-311.8	84.2-340.1	165.3-276.4	1740.7	1767.4	1197.6	0.56
EXE	19.8a	19.0a	20.9a	2.4-38.1	0.6-35.7	6.8-38.3	49.1	55.8	47.4	0.63
PL	22.9b	20.6b	27.7a	7.4-44.8	10.2-33.0	18.9-38.1	50.5	22.0	19.3	< 0.0001**
PW	7.4b	7.4b	9.2a	3.6-18.3	3.9-12.3	4.9-15.0	3.9	3.5	10.5	$0.00^{**}$
BT	2.6b	2.4b	4.9a	1.8-7.7	1.7-4.0	3.3-9.0	0.5	0.2	2.2	< 0.0001**
HSW	2.5b	2.9a	1.3c	0.8-5.1	1.7-4.0	0.3-3.3	0.6	0.5	0.5	0.43
PWT	1737a	1719a	899.2b	34-3169	400-3313	506.3-2213	290946	379404	147398	0.03*
YLD	1183a	1171a	652.5b	205-2323	220-2504	224-1479	166243	212117	142940	0.17
SPAD1	48.7a	49.4a	43.9b	35.4-61.2	38.4-60.0	35.7-52.2	21.8	16.6	23.6	0.23
SPAD2	33.9a	34.9a	30.7b	6.8-51.5	11.6-49.7	10.7-41.9	40.5	35.9	60.5	0.42

<sup>†</sup>Means were tested following Newman-Keuls test. Means followed by same letter are non-significant at P = 0.05. <sup>‡</sup>Variances were tested using Levene's test.

\*, \*\* - Significant at 5% and 1% respectively.
		Mean <sup>†</sup>			Range		Variance <sup>‡</sup>				
		Intermediate			Intermediate			Intermediate			
Characters	Races	races	Wild	Race	races	Wild	Race	races	Wild	p>f	
DF	75.0a	70.7b	75.0a	55.1-123.4	50.1-99.5	42.5-104.9	88.9	72.2	202.6	$0.009^{**}$	
PH	225.7b	208.8b	241.2a	84.5-348.2	84.2-361.8	142.3-296.7	2163.2	2064.6	1546.5	0.605	
EXE	18.9a	18.3a	20.3a	2.1-37.4	2.0-36.2	10.3-42.6	50.4	51.3	47.9	0.944	
PL	23.0b	21.3b	28.2a	6.8-45.2	10.3-37.7	11.0-39.4	53.0	27.0	42.7	0.003**	
PW	7.6b	7.3b	10.8a	3.4-19.7	4.2-14.2	4.1-17.8	6.0	3.1	16.2	$0.0009^{**}$	
BT	2.6b	2.4b	4.8a	1.5-6.7	1.7-4.1	2.2-8.7	0.6	0.2	2.6	$0.0001^{**}$	
PWT	2301a	2262a	1252b	422-4243	620-3945	568-3679	413201	484386	422971	0.63	
YLD	1605a	1568a	879b	301-2787	450-3140	317-2556	242902	269970	276674	0.8	
SPAD1	48.6a	49.8a	44.1b	36.1-60.5	37.4-61.3	35-52.1	23.3	16.0	22.4	0.08	
SPAD2	33.1a	37.1a	32.7a	17.2-49.3	23.5-50.3	25.1-42.6	27.4	23.8	22.7	0.6175	

Table 19c Mean, range and variance of quantitative traits in the races, intermediate races and wild types as group of sorghum reference set pooled over E1 and E2.

Table 19d Mean, range and variance of quantitative characters in races, intermediate races and wild type as group of sorghum reference set in UAS, Dharwad under irrigated condition (E3).

Dhai waa aha	ier mingute							*		
		Mean <sup>†</sup>			Range			<b>Variance</b> <sup>‡</sup>		
		Intermediate			Intermediate	!		Intermediate		
Characters <sup>1</sup>	Races	races	Wild	Races	races	Wild	Races	races	Wild	p>f
DF	64.0a	64.3a	64.4a	51.5-80.7	51.4-77.4	57.9-76.6	32.0	30.1	27.8	0.820
PH	233.2a	225.1a	222.1a	119.3-307.1	89.1-342.3	129.6-272.9	1055.0	1511.2	1793.6	0.087
EXE	17.1a	16.3a	15.4a	0.4-61.6	0.4-47.9	3.7-33.9	89.0	87.5	61.5	0.713
PL	20.7a	20.1a	19.6a	9.3-47.5	7.5-60.6	9.0-39.1	33.9	40.9	38.6	0.860
PW	7.0a	6.9a	7.3a	1.4-40.4	1.4-49.2	1.9-25.5	15.2	22.8	27.1	0.760
BT	2.3a	1.9a	2.2a	0.0-9.6	0.0-7.2	0.0-5.3	2.2	2.0	1.6	0.760
HSW	2.5a	2.5a	2.3b	0.7-5.2	0.6-4.0	0.6-4.1	0.4	0.5	0.5	0.980
PWT	2413a	2163a	1040b	489-3980	854-3894	484-1973	572824	259884	95052	0.270
YLD	1807a	1615a	898b	524-3148	571-2842	458-1746	353947	192611	78725	0.132
SPAD1	47.1a	47.5a	45.7a	35.8-59.3	37.8-57.5	33.4-56.1	15.1	16.7	24.7	0.230
SPAD2	40.6a	41.1a	38.7b	28.9-52.2	27.5-50.9	28.0-48.9	20.2	25.4	40.1	0.010

<sup>†</sup>Means were tested following Newman-Keuls test. Means followed by same letter are non-significant at P = 0.05. <sup>‡</sup>Variances were tested using Levene's test.

\*, \*\* - Significant at 5% and 1% respectively.

		Mean <sup>†</sup>			Range		Variance <sup>‡</sup>				
		Intermediate			Intermediate			Intermediate			
Characters <sup>1</sup>	Races	races	Wild	Race	races	Wild	Races	races	Wild	p>f	
DF	64.5a	64.6a	65.0a	51.2-77.1	51.9-77.7	50.9-77.3	32.7	31.4	53.0	0.82	
PH	234.3a	225.4a	222.5a	151.9-270.3	93.5-266.5	168.7-254.3	409.7	877.3	858.0	0.09	
EXE	16.1a	14.3a	14.9a	0.2-42.2	0.2-42.3	0.3-27.9	80.5	66.1	70.1	0.82	
PL	21.9a	21.3a	21.1a	10.6-46.0	8.7-51.3	13.6-39.0	27.7	35.4	32.4	0.86	
PW	6.1a	5.9a	5.7a	0.7-36.1	1.2-18.7	2.9-15.0	9.9	5.1	6.0	0.76	
BT	2.7a	2.5a	2.7a	0.2-9.1	0.2-6.7	0.2-5.3	1.5	0.9	1.7	0.76	
HSW	2.3a	2.3a	2.2b	0.5-4.3	0.6-4.3	1.2-4.3	0.5	0.5	0.4	0.65	
PWT	218a	2219a	1497b	1330-2626	1876-2623	1376-1625	51612	41799	3806	0.27	
YLD	1565a	1609a	1105b	966-2052	1297-2068	972-1261	39755	34790	6059	0.13	
SPAD1	50.2a	50.1a	49.4a	41.3-56.1	45.8-54.6	46.4-52.3	4.4	4.0	3.1	0.23	
SPAD2	41.8a	42.0a	42.1a	33.5-47.7	34.9-46.4	35.9-47.1	7.4	7.4	6.4	0.01	

Table 19e Mean, range and variance of various traits in the races, intermediate races and wilds as a group of sorghum reference set in UAS, Dharwad under un-irrigated condition (E4).

Table 19f. Mean, range and variance of quantitative characters in the races, intermediate races and wild type as a group of sorghum reference set in ARRS, Bijapur under un-irrigated condition (E5).

		Mean <sup>†</sup>			Range		Variance <sup>‡</sup>				
		Intermediate			Intermediate			Intermediate			
Characters <sup>1</sup>	Races	races	Wild	Races	races	Wild	Races	races	Wild	p>f	
DF	68.0a	66.2a	67.5a	48.8-92.6	51.5-85.3	53.4-81.6	77.1	62.6	64.8	0.24	
PH	197.1a	192.5a	208.6a	135.5-269.7	103-258.2	146.6-257.7	719.1	704.5	661.0	0.30	
EXE	13.9b	13.7b	18.6a	0.3-4.9	0.3-37.4	0.3-33.1	64.9	60.0	75.4	0.80	
PL	20.9a	20.4a	23.1a	7.6-44.2	8.9-34.3	12.7-29.7	25.4	18.1	16.8	0.35	
PW	5.1b	5.2b	6.6a	1.4-22.7	1.5-13.6	2.4-15.7	5.0	4.4	11.9	0.32	
BT	2.9b	2.8b	4.2a	1.3-5.6	0.5-5.5	2.4-7.5	0.6	0.6	1.8	0.12	
HSW	2.0a	2.1a	1.7b	0.9-4.9	0.6-4.0	1.04-3.2	0.3	0.4	0.3	0.47	
PWT	2290a	2296a	1277b	1411-3506	1546-3199	1145-1398	149975	109015	6254	0.08	
YLD	1664a	1597a	865b	817-3312	574-2584	673-1076	140202	132977	12382	0.94	
SPAD1	48.7a	48.9a	47.1aa	32.9-56.9	40.4-55.6	41.4-59.2	13.3	12.0	16.6	0.94	
SPAD2	41.8a	41.9a	41.2a	28.4-56.1	15.9-54.5	32.6-51.1	20.9	33.3	23.8	0.31	

<sup>†</sup>Means were tested following Newman-Keuls test. Means followed by same letter are non-significant at P = 0.05. <sup>‡</sup>Variances were tested using Levene's test.

\*, \*\* - Significant at 5% and 1% respectively.

		Mean <sup>†</sup>			Range		Variances <sup>‡</sup>				
Characters <sup>1</sup>	Race	Intermediate race	Wild	Race	Intermediate race	Wild	Race	Intermediate race	Wild	p>f	
DF	65.4a	65.1a	65.7a	52.6-81.1	54.4-78.6	55.4-76.4	28.9	28.9	36.6	0.73	
PH	222.2a	213.4a	219.2a	136.8-284.8	114.9-272.5	142.4-265.4	507.4	778.9	1091.3	0.01*	
EXE	15.7a	14.7a	16.2a	2.7-39.2	1.4-33.3	9.3-27.0	38.4	35.9	22.5	0.35	
PL	21.2a	20.5a	21.5a	11.8-38.9	10.8-48.3	15.7-34.9	17.4	19.7	13.7	0.83	
PW	6.1a	6.0a	6.6a	3.3-22.0	3.1-24.2	4.4-15.1	4.9	4.9	6.1	0.98	
ВТ	2.6a	2.4a	3.1a	1.0-6.7	1.0-5.3	2.2-6.2	0.6	0.5	0.9	0.40	
HSW	2.3a	2.3a	2.0a	1.3-3.7	1.2-3.7	1.1-3.2	0.2	0.23	0.2	0.68	
PWT	2299a	2244a	1106b	1479-3001	1730-2902	866-1390	103747	58462	11772	0.48	
YLD	1672a	1620a	946b	1116-2361	1069-2115	761-1164	56869	38608	8332	$0.02^*$	
SPAD1	48.7a	48.9a	47.1a	37.6-54.7	40.8-55.8	40.1-53.9	5.6	6.3	9.0	0.39	
SPAD2	41.4a	41.8a	40.6a	35.0-47.2	31.1-47.8	35.1-44.1	6.3	10.0	8.2	0.07	

Table. 19g Mean range and variance of various traits in the races, intermediate races and wilds as a group of sorghum reference set collection pooled overE3, E4andE5.

<sup>†</sup>Means were tested following Newman-Keuls test. Means followed by same letter are non-significant at P = 0.05. <sup>‡</sup>Variances were tested using Levene's test.

\*, \*\* - Significant at 5% and 1% respectively.

Basic Races							Charact	ers			
Environments	DF	РН	PE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
E1	79.48a	237.76a	17.67b	23.15a	7.81a	2.61b		2898d	2053d	48.36b	32.83b
E2	70.67c	214.24d	19.50a	22.68a	7.41a	2.60b	2.59a	1744f	1188f	48.61b	33.79b
Pooled (E1&E2)	75.18b	226.35c	18.68a	22.80a	7.59a	2.61b		2317e	1619e	48.46b	32.97b
E3	63.92e	234.23b	17.08b	20.69b	6.94b	2.27c	2.53a	4198c	3217a	47.06c	40.43a
E4	64.54e	237.28a	16.05c	22.01a	6.13c	2.67b	2.33b	4041c	2662c	50.39a	41.62a
E5	67.99d	198.43e	14.06e	20.81b	5.11d	2.88a	1.96c	4675a	2935b	48.78b	41.63a
Pooled (E3,E4,E5)	65.45e	222.46c	15.70d	21.18b	6.07c	2.62b	2.27b	4295b	2935b	48.72b	41.39a
Variance	114.66	2207.75	65.34	47.11	9.68	1.10	0.58	2149424	1268746	29.48	56.61
F value	10.49	16.80	8.16	7.48	2.27	15.67	12.90	40.45	52.82	16.58	25.08
P>F	$0.001^{**}$	0.001**	0.001**	0.001**	$0.034^{*}$	0.001**	0.001**	0.001**	0.001**	0.001**	0.001**
Intermediate races											
E1	74.56a	215.81a	17.10b	20.32a	6.84a	2.38b		2935b	2075b	49.54b	32.80b
E2	67.87c	199.18c	18.10a	20.16a	7.28a	2.35b	2.85a	1771d	1206b	48.90b	34.53b
Pooled (E1&E2)	71.35b	208.11b	17.39a	20.73a	7.22a	2.38b		2331c	1623c	49.23b	33.65b
E3	64.31d	224.28a	16.24b	20.17a	6.97a	1.92c	2.49b	4309a	3038a	47.97c	41.63a
E4	64.55d	220.58a	14.56c	21.15a	5.79b	2.52b	2.24c	4101a	2785a	50.12a	42.46a
E5	66.24c	189.23d	13.28c	20.23a	5.26b	2.79a	2.11c	4499a	2845a	48.93b	42.22a
Pooled (E3,E4,E5)	65.08d	212.97b	14.74c	20.51a	6.00b	2.40b	2.27c	4313a	2887a	48.80b	41.71a
Variance	86.86	2365.35	65.57	35.18	8.05	0.81	0.59	2701613	1158528	26.97	61.88
F value	4.68	6.42	4.59	3.18	1.65	15.97	7.01	2.22	24.24	15.65	12.66
P>F	$0.001^{**}$	$0.001^{**}$	$0.001^{**}$	$0.004^{**}$	0.130	0.001**	$0.001^{**}$	$0.039^{*}$	0.001**	0.001**	0.001**
Wilds											
E1	81.46a	263.03a	19.63a	30.81a	13.37a	5.17a		1307c	888d	43.35a	33.50b
E2	69.84c	229.72b	20.94a	27.70b	9.23b	4.94a	1.30c	899c	652d	43.86a	30.70b
Pooled (E1&E2)	75.04b	241.21b	20.28a	28.19b	10.78b	4.82a		1252c	879d	44.12a	32.72b
E3	64.52d	216.66c	15.14a	19.36d	7.49c	2.19b	2.20a	1358a	1042a	44.62a	37.93a
E4	64.64d	218.38c	14.79a	20.61d	5.65d	2.82b	2.11a	1171b	988b	47.55a	42.25a
E5	67.30c	221.47c	18.72a	25.13c	6.80c	4.40a	1.61b	1067a	937b	45.99a	40.95a
Pooled (E3,E4,E5)	65.73c	219.19c	16.23a	21.49d	6.58c	3.10b	2.01b	1088a	926c	47.14a	40.59a
Variance	180.62	2528.35	61.87	52.21	22.18	3.25	0.59	3213166	1669695	34.21	68.35
F value	4.84	2.06	0.99	1.00	1.41	0.92	0.71	7.87	5.57	2.11	5.01
P>F	0.001**	0.612	0.436	0.430	0.212	0.478	0.585	0.001**	0.001**	0.055	0.001**

Table Means of quantitative traits in basic races, intermediate races and wilds as a group of sorghum reference set evaluated at different environments.

Means were tested following Newman-Keuls test. Means followed by same letter are non-significant at P = 0.05

Table 20 Variance components of quantitative characters of entire sorghum reference set in diff	erent
environments.	

Environment <sup>1</sup>	DF	PH	EXE	PL	PW	BT	HSW	PET	YLD	SPAD1	SPAD2
E1	119.2	2113.3	62.8	46.1	9.5	1.2	-	2076948	1269733	23.0	25.2
E2 Pooled	107.9	2197.2	54.2	55.0	10.0	1.1	0.7	1290336	741476	21.0	14.3
(E1 & E2)	102.8	2103.8	61.0	51.2	7.4	0.9	-	1699191	838019	25.0	16.0
E3	31.2	1234.7	86.6	36.3	18.2	2.1	0.4	558503	337394	16.1	23.1
E4	33.3	560.7	75.4	30.2	8.2	1.4	0.5	163467	76669	4.1	7.0
E5 pooled	72.3	711.2	64.7	23.1	5.3	0.8	0.3	187368	157915	13.1	24.8
(E3,E4,E5)	29.2	635.5	36.4	17.8	5.0	0.6	0.2	163467	76669	6.2	7.5
F Value	23.8	39.7	10.2	15.0	2.5	9.3	38.0	67.7	55.1	32.1	23.2
P>F	0.001**	0.001*	0.0.01**	0.001**	0.018*	0.001**	0.001**	0.001**	0.001**	0.002**	0.001**

<sup>1</sup> E1- ICRISAT, Patancheru during 2008-09, E2- ICRISAT, Patancheru during 2009-10, E3- UAS, Dharwad irrigated condition, E4- UAS, Dharwad un-irrigated condition, E5 – RARS, Bijapur un-irrigated condition.

Table 21a Variance components of quantitative characters in different flowering groups of sorghum reference set evaluated during the 2008-2009 post rainy season (E1) at ICRSAT, Patancheru, India.

CHARACTERS <sup>2</sup>											
Flowering Group	DF	РН	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2	
Group 1	63.0	996.3	59.3	40.4	5.0	1.7	809258	429175	12.6	20.3	
Group 2	19.6	1678.7	59.5	43.7	10.5	1.3	757129	499335	18.9	35.5	
Group 3	16.8	1782.1	65.3	53.7	12.7	0.8	779550	540633	17.8	30.6	
Group 4	20.7	2504.3	44.2	60.8	7.7	1.0	731687	434917	20.9	19.0	
Group 5	53.1	2177.3	49.7	43.3	13.7	1.0	865253	555346	14.6	18.0	
Group 6	140.5	2255.8	26.5	84.5	10.5	0.6	987904	547257	7.0	5.4	
Group 7	288.2	2362.6	62.0	62.2	20.5	0.9	1337175	908241	40.3	40.3	
F Value	9.4	2.3	1.0	0.6	0.3	0.3	0.4	0.6	3.6	1.7	
P>F	< 0.001**	0.016*	0.4	0.7	0.9	0.9	0.9	0.745	0.004**	0.09	

 Table 21b Variance components of quantitative characters in different flowering groups of sorghum reference set evaluated during 2009-2010 post rainy season (E2) at ICRSAT, Patancheru, India.

CHARACTERS <sup>2</sup>											
Flowering Group	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Group 1	83.3	1055.1	54.0	30.9	3.0	0.6	0.5	339062	166751	10.3	50.5
Group 2	36.8	1597.4	51.1	34.6	4.3	0.7	0.6	283529	117415	18.2	30.8
Group 3	32.6	1378.0	62.3	40.3	3.4	0.6	0.7	364939	231311	16.9	29.2
Group 4	21.6	1973.1	38.0	43.9	4.7	0.5	0.6	350244	209130	27.3	28.6
Group 5	29.7	1178.3	47.4	39.0	1.9	1.3	0.8	298852	205396	15.5	68.9
Group 6	34.8	1224.6	47.1	75.1	2.6	0.4	1.3	343723	226152	12.9	17.8
Group 7	253.7	1205.9	43.3	54.0	2.0	3.3	1.2	494878	309662	22.6	26.2
F Value	3.7	1.3	1.1	1.00	0.6	1.1	1.6	0.5	2.2	2.0	2.2
P>F	0.003**	0.2	0.4	0.5	0.7	0.3	0.1	0.8	$0.02^*$	0.05	$0.02^{*}$

Variances were tested using Levene's test. \*, \*\* - Significant at 5% and 1% respectively

	CHARACTERS <sup>2</sup>											
Flowering Group	DF	РН	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2		
Group 1	79.6	1158.1	63.1	37.3	3.8	1.1	529098	267837	11.2	34.6		
Group 2	25.1	1593.8	51.6	38.1	6.3	0.9	416388	164026	16.6	26.6		
Group 3	21.9	1539.2	60.9	46.5	6.5	0.7	485477	332122	15.3	23.3		
Group 4	18.6	2144.8	37.7	50.6	5.5	0.7	456658	274555	22.1	19.2		
Group 5	34.3	1572.9	44.4	40.2	5.7	1.1	488179	313761	12.7	25.6		
Group 6	63.7	1597.2	33.1	77.2	5.4	0.5	532669	312210	7.4	8.3		
Group 7	209.9	1600.4	45.3	50.7	8.2	1.9	737409	511198	27.0	23.0		
F Value	7.1	1.5	1.2	0.7	0.2	0.3	0.3	2.25	2.7	1.11		
P>F	< 0.001**	0.1	0.3	0.7	0.9	0.9	0.9	$0.02^{*}$	0.001**	0.3		

Table 21c Variance components of quantitative characters in different flowering groups of entire sorghum reference set pooled over E1 and E2.

Variances were tested using Levene's test. \*, \*\* - Significant at 5% and 1% respectively

Table 22a Variance components of	quantitative characters	s in races, intermediate	races and wild type of s	orghum reference
set evaluated during the 2008-2009	post rainy season (E1) a	at ICRSAT, Patancheru	, India.	

					CHARA	ACTERS <sup>1</sup>				
Races	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Bicolor	94.4	1970.2	49.2	86.8	32.9	1.3	616161	354328	33.4	24.6
Caudatum	106.6	2852.3	55.1	17.3	3.3	0.4	617257	401100	22.8	28.2
Durra	74.3	1625.4	61.9	40.4	0.8	0.4	536650	369058	19.8	37.0
Guinea	210.1	2125.5	47.4	28.6	3.4	0.4	595995	345619	24.2	22.0
Kafir	73.4	1549.3	22.1	16.6	8.1	0.6	609561	351412	19.8	25.5
F-Value	0.2	0.8	1.2	0.1	1.8	1.1	2.2	0.7	1.0	0.5
P>F	0.9	0.5	0.3	1.0	0.1	0.4	0.1	0.6	0.4	0.7
Intermediate races										
Caudatum-bicolor	81.6	2582.6	38.6	21.6	5.7	0.3	410007	283220	25.3	27.9
Durra-bicolor	68.1	1702.0	60.4	25.7	6.8	0.3	637211	365901	18.4	19.0
Durra-caudatum	97.5	1359.9	73.1	18.4	1.3	0.5	1009671	481295	9.8	32.0
Guinea-caudatum	94.0	2339.7	48.4	22.8	1.4	0.3	626348	388484	23.9	25.4
Guinea-durra	2.3	199.7	1.0	14.2	1.0	0.1	131251	221188	12.7	4.9
F-Value	4.8	1.4	1.7	8.6	10.1	2.7	0.1	0.2	0.9	0.7
P>F	$0.001^{**}$	0.2	0.1	$0.0001^{**}$	$0.0001^{**}$	$0.031^{*}$	1.0	1.0	0.5	0.6
Wilds										
Arundinaceum	642.8	1791.0	219.2	37.9	34.7	0.7	1178411	795207	45.5	15.3
Drummondii	281.6	2158.8	65.2	26.3	10.3	1.7	237764	171768	33.1	56.3
Verticilliflorum	411.9	1417.4	80.7	4.0	4.6	2.8	299853	82601	23.7	0.6
F-Value	0.30	0.4	1.2	1.2	3.1	1.7	4.8	3.4	0.3	0.7
P>F	0.7	0.7	0.3	0.3	0.1	0.2	$0.02^{*}$	0.1	0.7	0.5

Table 22 b Variance components of quantitative characters in races, intermediate races and wild type of sorghum reference set evaluated during the 2009-2010 post rainy season (E2) at ICRSAT, Patancheru, India.

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						CHA	ARACTE	ERS <sup>1</sup>			
Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Bicolor	49.0	1313.9	46.3	58.8	8.1	0.6	0.4	215859	108508	28.7	45.9
Caudatum	62.5	2096.0	56.2	17.7	2.0	0.2	0.6	277675	168057	16.4	28.6
Durra	60.1	1296.3	54.3	34.0	1.9	0.1	0.6	214308	137729	14.6	41.9
Guinea	92.5	1240.8	39.5	24.0	2.2	0.3	0.5	218489	106422	15.8	29.4
Kafir	16.4	886.5	29.0	10.1	3.8	1.2	0.2	256465	188277	15.2	65.2
F-Value	0.8	2.5	1.5	5.9	7.6	1.9	2.0	0.4	1.8	2.1	1.4
P>F	0.6	0.0	0.2	$0.0002^{**}$	$0.0001^{**}$	0.1	0.1	0.8	0.1	0.1	0.2
Intermediate races											
Caudatum-bicolor	41.7	1565.6	43.1	16.8	2.9	0.1	0.3	262019	162857	18.0	43.2
Durra-bicolor	64.8	1467.2	56.6	35.7	5.7	0.2	0.3	358740	159377	18.5	7.0
Durra-caudatum	68.0	797.8	69.4	18.5	2.2	0.3	0.6	345946	164760	9.8	41.9
Guinea-caudatum	50.2	1704.0	49.8	18.9	2.3	0.1	0.4	348274	279441	20.5	36.4
Guinea-durra	13.6	361.3	3.4	10.1	1.0	0.0	0.3	182488	183141	8.5	29.4
F-Value	0.9	0.8	0.8	0.8	2.1	2.4	1.4	0.3	1.4	1.0	0.9
P>F	0.4	0.6	0.5	0.5	0.1	0.1	0.3	0.9	0.2	0.4	0.5
Wilds											
Arundinaceum	166.4	631.3	90.1	10.5	3.6	2.8	0.3	26305	248091	21.5	2.4
Drummondii	122.3	1192.0	41.5	16.4	4.4	0.4	0.3	89600	81432	24.6	110.1
Verticilliflorum	56.8	1132.6	33.9	1.2	9.4	2.1	0.1	421133	222066	26.9	37.5
F-Value	0.5	0.5	0.7	2.3	0.6	2.4	1.2	1.4	0.8	0.1	2.0
P>F	0.6	0.6	0.5	0.1	0.6	0.1	0.3	0.3	0.5	0.9	0.2

\*, \*\* - Significant at 5% and 1% respectively Variances were tested using Levene's test.

Table 22 c Variance components of quantitative characters in races, intermediate races and wild types of sorghum reference set pooled over E1 and E2.

					CHA	RACTER	$S^1$			
Races	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
Bicolor	61.8	1627.8	47.1	69.8	15.4	0.9	311732	166849	28.5	26.7
Caudatum	94.2	2519.2	58.2	16.5	1.8	0.2	367475	213837	18.2	23.2
Durra	64.1	1669.3	51.6	40.2	1.1	0.3	337037	215682	14.8	26.8
Guinea	119.5	1111.0	37.7	26.7	3.6	0.7	388933	199079	18.3	16.3
Kafir	36.4	2078.8	33.1	5.2	1.9	0.1	236098	128624	17.8	40.9
F-Value	1.7	2.4	1.4	8.3	1558.0	3.5	0.6	0.7	1.4	2.0
P>F	0.1	0.05	0.2	$0.001^{**}$	$0.0001^{**}$	$0.008^{**}$	0.7	0.6	0.2	0.09
Intermediate races										
Caudatum-Aicolor	35.8	1628.4	35.3	20.3	3.7	0.2	269246.0	158860.0	18.5	27.9
Durra-Aicolor	62.1	1596.7	59.1	31.5	5.2	0.2	299756.0	166001.0	16.3	3.3
Durra-Caudatum	107.0	1266.1	72.0	30.0	1.9	0.3	601469.0	268742.0	11.7	18.4
Guinea-Caudatum	60.0	2233.5	47.3	24.4	1.4	0.1	474292.0	283839.0	18.0	27.3
Guinea-Durra	4.9	256.8	1.3	11.9	0.8	0.0	147484.0	133932.0	10.5	10.1
F-Value	1.6	0.9	1.6	0.2	2.8	2.5	1.7	1.1	0.4	1.7
P>F	0.2	0.5	0.2	0.9	$0.03^{*}$	0.04	0.2	0.4	0.8	0.2
Wilds										
S. arundinaceum	352.2	1014.2	153.9	21.9	15.0	1.3	231240	455114	37.9	33.6
S. drummondii	133.5	1077.7	24.8	39.0	7.3	1.3	654230	338417	24.2	19.4
S. verticilliflorum	170.2	1253.0	49.0	1.0	5.6	1.9	62964	33139	23.8	17.8
F-Value	0.7	0.1	2.6	1.3	1.0	0.2	0.6	0.7	0.1	0.3
P>F	0.5	0.9	0.1	0.3	0.4	0.8	0.5	0.5	0.9	0.7

Table 22d Variance components of quantitative characters in races, intermediate races and wild type of sorghum reference set evaluated during the 2009-2010 post rainy season at UAS, Dharwad under irrigated condition (E3).

						(	CHARA	CTERS <sup>1</sup>			
Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Bicolor	33.5	1150.1	143.9	36.4	8.5	2.3	0.5	224073	136034	10.1	20.3
Caudatum	30.5	1336.2	98.7	26.0	5.3	2.3	0.4	441987	281083	13.6	19.4
Durra	30.3	959.7	72.2	28.1	6.1	2.3	0.4	412583	341067	18.9	23.4
Guinea	30.3	906.6	62.5	41.4	31.9	2.2	0.4	125239	104728	18.2	18.6
Kafir	38.5	425.0	80.8	38.4	23.6	1.9	0.6	127354	114209	13.8	20.4
F-Value	0.3	1.6	1.3	0.6	1.4	0.0	0.9	1.5	2.5	2.7	0.5
P>F	0.9	0.2	0.3	0.6	0.2	1.0	0.5	0.2	$0.04^*$	$0.03^{*}$	0.7
Intermediate races											
Caudatum-bicolor	28.5	910.9	75.7	81.6	69.2	1.8	0.6	157010	114898	12.8	35.7
Durra-bicolor	17.8	1287.8	150.1	34.9	9.2	3.1	0.2	548293	311677	14.2	20.6
Durra-caudatum	39.7	1926.6	62.2	30.4	8.7	3.0	0.4	442177	279093	17.3	22.5
Guinea-caudatum	28.0	1593.8	91.0	28.1	8.1	1.8	0.5	126357	125011	14.7	23.6
Guinea-durra	12.5	149.3	23.7	48.6	0.8	0.6	0.7	157909	10610	25.0	53.5
F-Value	0.8	1.0	1.0	0.6	0.7	0.8	0.6	0.8	0.4	1.2	0.8
P>F	0.5	0.4	0.4	0.7	0.6	0.5	0.7	0.5	0.8	0.3	0.5
Wilds											
Arundinaceum	10.2	1177.1	57.7	1.1	1.7	3.4	0.1	51132	35357	90.6	39.7
Drummondii	30.5	2061.7	51.4	50.7	41.0	0.9	0.8	135394	112606	14.9	43.1
Verticilliflorum	47.4	2163.2	113.8	30.6	30.5	1.6	0.5	101584	69065	1.4	23.9
F-Value	0.8	0.4	1.6	0.7	0.4	1.2	0.9	0.6	0.9	5.2	1.3
P>F	0.5	0.7	0.2	0.5	0.7	0.3	0.4	0.5	0.4	0.0	0.3

Variances were tested using Levene's test. \*, \*\* - Significant at 5% and 1% respectively

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Table 22e Variance components of quantitative characters in races, intermediate races and wild type of sorghum reference set evaluated during 2009-2010 post rainy season at UAS, Dharwad under un-irrigated condition (E4).

						(	CHARAG	CTERS <sup>1</sup>			
Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Bicolor	32.0	478.7	127.9	42.6	26.9	1.2	0.5	48552	38982	3.8	5.6
Caudatum	33.1	440.0	63.8	19.6	2.1	1.6	0.5	47534	38635	3.3	7.4
Durra	30.6	351.3	77.1	17.8	1.4	1.9	0.6	49721	54007	5.8	11.0
Guinea	33.7	442.4	92.1	37.1	15.8	1.5	0.6	64430	35814	4.9	6.7
Kafir	30.5	196.4	44.3	19.6	7.8	1.7	0.7	36979	34879	3.7	6.5
F-Value	0.5	1.2	3.7	2.4	1.0	0.1	0.5	0.7	2.4	1.1	1.1
P>F	0.7	0.3	$0.006^{**}$	$0.053^{*}$	0.4	1.0	0.8	0.6	0.0	0.4	0.3
Intermediate races											
Caudatum-bicolor	19.9	377.5	85.6	58.8	6.9	1.4	0.5	39122	29455	4.0	9.0
Durra-bicolor	17.9	676.7	77.3	68.3	4.8	0.4	0.2	41645	34527	3.2	4.6
Durra-caudatum	47.1	926.8	62.7	29.6	2.0	1.0	0.7	31194	35205	2.8	6.0
Guinea-caudatum	31.8	1162.2	63.5	21.2	5.3	0.7	0.6	43590	32327	4.3	8.2
Guinea-durra	9.3	186.9	28.0	34.6	0.4	0.1	0.4	1906	14442	3.7	15.4
F-Value	2.5	1.3	0.3	1.3	0.3	0.9	1.0	1.0	0.7	0.5	1.5
P>F	$0.050^{*}$	0.3	0.9	0.3	0.9	0.4	0.4	0.4	0.6	0.7	0.2
Wilds											
Arundinaceum	48.3	2284.5	98.3	20.8	3.2	3.2	1.2	9189824	4393671	77.1	83.9
Drummondii	172.5	3608.0	60.0	83.9	14.7	0.7	0.2	1976795	1321539	49.8	24.3
Verticilliflorum	59.1	5473.2	29.2	5.3	1.1	3.3	0.4	2561319	796831	39.9	59.4
F-Value	2.1	0.7	1.1	1.2	0.7	2.0	2.1	4.3	3.7	0.3	1.8
P>F	0.2	0.5	0.4	0.3	0.5	0.2	0.2	0.031*	0.0	0.7	0.2

Table 22f Variances components of quantitative characters in races, intermediate races and wild type of sorghum reference set during 2009-2010 post rainy season at ARRS, Bijapur under un-irrigated condition (E5).

							CHARA	CTERS <sup>1</sup>			
Races	DF	PH	EXE	PL	PW	AT	HSW	PWT	YLD	SPAD1	SPAD2
Bicolor	61.9	468.9	85.6	28.0	13.7	0.5	0.2	184498	154235	9.8	23.6
Caudatum	65.9	862.2	63.8	20.0	1.8	0.7	0.3	102821	100917	10.5	19.4
Durra	79.2	586.0	62.3	20.8	3.5	0.4	0.4	178735	190427	11.5	18.7
Guinea	81.8	594.3	50.1	26.0	4.7	0.6	0.2	142435	141595	16.3	22.1
Kafir	70.4	705.4	64.5	16.9	2.8	0.7	0.2	177078	108345	11.9	18.7
F-Value	0.6	1.5	1.4	0.9	2.2	1.0	1.6	0.8	1.0	1.0	0.5
P>F	0.6	0.2	0.3	0.4	0.1	0.4	0.2	0.5	0.4	0.4	0.7
Intermediate races											
Caudatum-bicolor	49.0	779.0	39.3	17.6	6.2	0.7	0.3	64112	73141	13.3	25.7
Durra-bicolor	25.5	536.8	47.6	16.3	4.2	0.5	0.3	94775	108406	10.5	13.6
Durra-caudatum	65.8	412.4	83.6	13.4	1.6	0.6	0.6	75159	135544	9.8	30.4
Guinea-caudatum	70.6	761.6	57.2	19.8	4.8	0.5	0.4	158184	167498	12.7	41.2
Guinea-durra	18.6	195.0	37.0	11.5	0.3	0.2	0.1	50356	36133	5.0	49.5
F-Value	1.2	0.5	1.6	0.8	1.1	0.3	0.8	0.8	1.2	0.8	0.4
P>F	0.3	0.7	0.2	0.5	0.3	0.9	0.5	0.5	0.3	0.5	0.8
Wilds											
Arundinaceum	25.7	793.7	14.4	17.5	2.9	4.5	0.4	11737	4712	13.9	9.3
Drummondii	80.0	493.0	92.0	15.8	3.8	1.3	0.5	6871	20523	9.0	18.1
Verticilliflorum	35.6	297.4	60.3	5.0	22.7	1.4	0.1	4474	9987	40.0	36.8
F-Value	1.2	0.2	1.9	0.3	5.7	1.7	1.1	0.0	0.8	1.6	0.8
P>F	0.3	0.8	0.2	0.7	0.0	0.2	0.4	1.0	0.5	0.2	0.5

Variances were tested using Levene's test. \*, \*\* - Significant at 5% and 1% respectively

						C	HARAC	TERS <sup>1</sup>			
Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
Bicolor	24.6	473.2	77.5	24.3	8.9	0.4	0.2	564771	415074	4.0	7.9
Caudatum	23.4	610.0	33.1	10.5	1.5	0.6	0.2	486429	403398	4.3	6.2
Durra	26.6	348.7	37.3	11.4	1.4	0.8	0.2	676680	451928	5.1	6.3
Guinea	32.8	551.3	30.5	20.0	8.5	0.6	0.2	583703	413450	7.2	5.8
Kafir	31.8	146.5	26.6	17.6	3.5	0.7	0.3	549660	385834	5.7	5.6
F-Value	0.9	2.1	4.5	1.6	1.3	0.3	1.8	0.4	0.1	1.0	0.5
P>F	0.5	0.1	$0.001^{**}$	0.2	0.3	0.9	0.1	0.8	1.0	0.4	0.8
Intermediate races											
Caudatum-bicolor	22.6	449.1	46.0	39.3	13.0	0.6	0.2	21017	25909	5.7	12.4
Durra-bicolor	10.9	418.6	31.3	28.5	2.0	0.4	0.2	103265	34790	3.7	3.4
Durra-caudatum	32.6	965.9	30.5	13.0	1.6	0.7	0.3	76552	34227	7.2	6.8
Guinea-caudatum	31.9	779.3	36.8	11.1	2.1	0.4	0.2	57271	40786	5.1	10.8
Guinea-durra	11.3	252.0	2.1	20.4	0.1	0.3	0.2	17031	2943	1.2	34.8
F-Value	1.4	1.1	0.6	0.8	0.8	0.4	0.6	0.7	0.9	0.7	1.3
P>F	0.2	0.3	0.7	0.5	0.5	0.8	0.7	0.6	0.5	0.6	0.3
Wilds											
Arundinaceum	28.3	225.7	32.2	1.3	1.1	3.3	0.3	2278960	1018459	23.8	8.0
Drummondii	51.6	1198.5	6.0	22.9	9.6	0.1	0.2	488642	415040	5.4	4.4
Verticilliflorum	27.6	919.7	26.8	4.1	4.4	0.8	0.2	817541	709178	11.6	3.0
F-Value	0.8	1.1	2.5	0.8	0.4	6.7	0.3	2.5	1.1	1.8	0.9
P>F	0.5	0.4	0.1	0.5	0.7	$0.007^*$	0.8	0.1	0.4	0.2	0.4

Table 22g Variance components of quantitative characters in individual basic races, intermediate races and wilds of sorghum reference set pooled over E3, E4 and E5.

Variances were tested using Levene's test.

\*, \*\* - Significant at 5% and 1% respectively

Environments <sup>1</sup>	Characters <sup>2</sup>	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1
E1		0.593**									
E2		0.513**									
Pooled (E1&E2)	PH	0.562**									
E3		0.287**									
E4		0.190**									
E5		0.174**									
Pooled(E3,E4,E5)		0.339**									
E1		-0.282**	0.231**								
E2		-0.335**	0.235**								
Pooled (E1&E2)		-0.305**	0.249**								
E3	EXE	-0.142**	0.288**								
E4		-0.214**	0.281**								
E5		-0.131*	0.294**								
Pooled(E3,E4,E5)		-0.206**	0.248**								
E1		0.209**	0.428**	0.260**							
E2		0.141**	0.401**	0.305**							
Pooled (E1&E2)		0.193**	0.422**	0.296**							
E3	PL	0.189**	0.307**	0.265**							
E4		0.102*	0.271**	0.172**							
E5		0.061	0.215**	0.158**							
Pooled(E3,E4,E5)		0.174**	0.300**	0.232**							
E1		0.198**	0.415**	0.045	0.710**						
E2		-0.064	0.168**	0.073	0.398**						
Pooled (E1&E2)		0.074	0.329**	0.067	0.630**						
E3	PW	0.062	0.227**	0.028	0.633**						
E4		-0.036	0.168**	-0.110*	0.513**						
E5		0.022	0.188**	0.190**	0.168**						
Pooled(E3,E4,E5)		0.059	0.209**	0.02	0.602**						
E1		-0.026	0.094	0.286**	0.273**	0.331**					
E2		-0.018	0.136**	0.238**	0.332**	0.324**					
Pooled (E1&E2)		-0.012	0.130**	0.278**	0.324**	0.415**					
E3	BT	-0.115*	0.022	0.139**	0.025	0.015					
E4		-0.1	0.138**	0.319**	0.03	-0.065					
E5		0.095	0.136**	0.135**	0.120*	0.119*					
Pooled(E3,E4,E5)		-0.105*	0.087	0.261*	0.018	-0.002					

Table 23 Correlation coefficient of quantitative characters of sorghum reference set in all the environments.

Environments <sup>1</sup>	Characters <sup>2</sup>	DF	РН	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1
E2		-0.179**	-0.035	-0.015	-0.266**	-0.262**	-0.494**				
E3		-0.153**	-0.148**	-0.033	-0.207**	-0.084	-0.072				
E4	HSW	-0.113*	-0.031	0.011	-0.272**	-0.146**	-0.003				
E5		-0.107*	-0.120*	-0.083	-0.159**	-0.168**	-0.153**				
Pooled(E3,E4,E5)		-0.172**	-0.133**	-0.015	-0.254**	-0.192**	-0.122*				
E1		-0.100*	-0.133**	-0.279**	-0.293**	-0.283**	-0.607**				
E2		0.077	-0.180**	-0.293**	-0.303**	-0.143**	-0.533**	0.330**			
Pooled (E1&E2)		-0.023	-0.160**	-0.308**	-0.322**	-0.280**	-0.630**				
E3	PWT	-0.040	-0.003	0.051	-0.025	-0.036	-0.017	0.097			
E4		-0.099	-0.015	0.014	-0.086	-0.024	0.092	0.237**			
E5		0.025	0.06	-0.013	-0.022	0.01	0.057	0.048			
Pooled(E3,E4,E5)		-0.017	-0.001	0.021	-0.038	-0.074	-0.033	0.136			
E1		-0.107*	-0.120**	-0.254**	-0.327**	-0.308**	-0.590**		0.940**		
E2		0.093	-0.136**	-0.234**	-0.276**	-0.189**	-0.414**	0.302**	0.781**		
Pooled (E1&E2)		-0.011	-0.130**	-0.283**	-0.347**	-0.309**	-0.587**		0.928**		
E3	YLD	-0.053	-0.024	0.041	-0.071	-0.051	0.007	0.100	0.924**		
E4		-0.085	-0.025	0.011	-0.157**	-0.061	0.091	0.316**	0.919**		
E5		0.007	0.06	-0.002	0.035	0.026	0.076	0.064	0.793**		
Pooled(E3,E4,E5)		-0.056	-0.025	0.025	-0.073	-0.086	-0.018	0.182**	0.734**	-0.056	
E1		-0.596**	-0.560**	0.119*	-0.164**	-0.281**	-0.240**		0.144**	0.135**	
E2		-0.403**	-0.486**	0.130**	-0.138**	0.064	-0.260**	0.196**	0.175**	0.124*	
Pooled (E1&E2)	(D + D 4	-0.537**	-0.554**	0.120*	-0.167**	-0.166**	-0.266**		0.154**	0.123*	
E3	SPADI	-0.033	-0.079	-0.042	-0.024	-0.071	0.091	0.158**	0.078	0.084	
E4		-0.244**	-0.183*	0.026	-0.109*	-0.006	0.014	0.176**	0.179**	0.126*	
E5		-0.216**	-0.082	0.045	-0.111*	0.076	-0.029	0.178**	-0.056	-0.033	
Pooled(E3,E4,E5)		-0.196**	-0.194**	0.022	-0.087	-0.087	-0.011	0.191**	0.023	0.002	
E1		-0.054	-0.266**	-0.002	0.061	-0.063	-0.031		-0.163**	-0.191**	0.464**
E2		-0.369**	-0.333**	0.065	-0.058	0.101*	-0.140**	0.108*	0.093	0.084	0.649**
Pooled (E1&E2)		-0.353**	-0.397**	0.086	-0.007	-0.089	-0.095		-0.017	-0.033	0.710**
E3	SPAD2	0.02	0.027	-0.039	0.011	-0.03	-0.015	-0.024	-0.002	0.005	0.240**
E4		-0.025	0.111*	0.088	0.052	0.014	0.052	0.048	-0.021	-0.01	0.271**
E5		-0.042	-0.049	-0.073	-0.034	-0.084	0.012	0.175**	0.01	0.043	0.147**
Pooled(E3.E4 E5)		-0.002	0.084	0.041	0.011	-0.007	0.001	0.026	-0.013	-0.012	0.302**

<sup>1</sup> E1- ICRISAT, Patancheru during 2008-09, E2- ICRISAT, Patancheru during 2009-10, E3- UAS, Dharwad irrigated condition, E4- UAS, Dharwad un-irrigated condition, E5 – RARS, Bijapur un-irrigated condition.

<sup>2</sup> DF- Days to 50% flowering, PH- Plant height, EXE- Panicle exerstion, PL- Panicle length, PW- Panicle width, BT- Basal tiller, HSW-Hundred seed weight, PWT- Panicle weight, YLD- Grain yield, SPAD1- SCMR at flowering, SPAD2- SCMR 30 days after flowering.

\*, \*\* significane at 5% and 1 % respectively.

		_		Er	nvironm	ents		
Pair o reco useful co	of traits orded orrelation	E1	E2	Pooled over E1 and E2	E3	E4	E5	Pooled over E3, E4 and E5
DE	PH	0.593	0.513	0.562	-	-	-	-
DF	SPAD1	-0.596	-	0.560	-	-	-	-
PW	PL	0.710	-	0.630	0.633	-	-	0.602
PWT	BT	0.607	-0.533	-0.630	-	-	-	-
YLD	BT	0.590	-	0.940	-	-	-	-
	PWT	0.587	0.781	0.940	0.624	0.667	0.793	0.734
SPAD2	SPAD1	-	0.649	0.710	-	-	-	-

 Table 23b Useful correlation recorded by the qualitative traits in different environments

Characters <sup>1</sup>	Flowering									
Characters	group	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1
	G1	0.357*								
	G2	0.126								
	G3	0.193*								
PH	G4	0.278*								
	G5	0.113								
	G6	0.685**								
	G7	0.592								
	G1	-0.562**	0.266							
	G2	-0.469**	0.388**							
	G3	-0.462**	0.378**							
EXE	G4	-0.288*	0.368**							
	G5	-0.314*	0.434**							
	G6	0.013	0.418							
	G7	-0.063	0.480							
	G1	0.039	0.273	0.262						
	G2	0.158	0.203*	-0.054						
	G3	-0.050	0.475**	0.413**						
PL	G4	-0.181	0.420**	0.614**						
	G5	-0.053	0.302	0.399*						
	G6	0.143	0.621*	0.451						
	G7	0.367	0.549	0.469						
	G1	0.237	0.450**	0.063	0.772**					
	G2	0.246**	0.343**	-0.099	0.791**					
	G3	0.120	0.506**	0.083	0.723**					
PW	G4	0.111	0.600**	0.399**	0.618**					
	G5	0.030	0.244	0.059	0.630**					
	G6	0.315	0.589*	0.439	0.806**					
	G7	0.426	0.487	0.244	0.935**					
	G1	-0.677**	-0.400*	0.277	-0.178	-0.144				
	G2	-0.135	0.089	0.332**	<b>0.198</b> <sup>*</sup>	0.292**				
	G3	-0.105	0.264**	0.384**	0.443**	0.325**				
BT	G4	0.186	0.219	0.257	0.285*	0.502**				
	G5	0.250	0.026	0.055	0.603**	0.650**				
	G6	0.537*	0.394	-0.010	0.312	0.440				
	G7	0.345	0.423	0.283	0.807**	0.793**				
	G1	0.597**	0.139	-0.434**	-0.166	-0.085	-0.692**			
DW/T	G2	<b>0.193</b> <sup>*</sup>	0.096	-0.299**	-0.178	-0.208*	-0.639**			
r w I	G3	0.048	-0.141	-0.277**	-0.323**	-0.248**	-0.606			
	G4	-0.050	-0.286*	-0.412**	-0.367**	-0.521**	-0.644**			
	G5	-0.283	-0.034	-0.063	-0.438**	-0.310*	-0.653**			

 Table. 24a
 Correlation coefficient of quantitative characters in flowering group of sorghum reference

 set evaluated during 2008-09 post rainy season (E1) at ICRISAT centre, Patancheru, India.

Table 24a Contd...

Characters <sup>1</sup>	Flowering									
Characters	group	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1
	G6	-0.648**	-0.578*	-0.178	-0.476	-0.675**	-0.552*			
	G7	-0.395	-0.704*	-0.402	-0.343	-0.293	-0.355			
	G1	0.636**	0.171	-0.495**	-0.143	-0.059	-0.698**	0.949**		
	G2	0.163	0.100	-0.274**	-0.255**	-0.260**	-0.586**	0.957**		
	G3	0.018	-0.099	-0.227**	-0.366**	-0.305**	-0.612**	0.924**		
YLD	G4	-0.049	-0.319*	-0.408**	-0.442**	-0.582**	-0.642**	0.955**		
	G5	-0.328*	-0.033	-0.019	-0.495**	-0.289	-0.648**	0.941**		
	G6	-0.641**	-0.584*	-0.333	-0.442	-0.494	-0.568*	0.841**		
	G7	-0.465	-0.643*	-0.355	-0.262	-0.203	-0.223	0.972		
	G1	-0.015	-0.032	0.174	0.247	0.071	-0.378**	0.026	-0.017	
	G2	-0.324**	-0.364**	-0.024	0.035	-0.193*	-0.309**	0.014	-0.010	
	G3	-0.404**	-0.449**	0.059	-0.217*	-0.405**	-0.237**	0.123	0.126	
SPAD1	G4	-0.145	-0.599**	-0.049	-0.108	-0.298*	-0.273*	0.295*	0.304**	
	G5	0.079	-0.305	0.010	-0.041	-0.335*	-0.325*	0.145	0.077	
	G6	0.244	0.510*	0.368	0.095	-0.087	-0.180	-0.108	-0.154	
	G7	-0.425	0.243	0.384	0.045	-0.090	-0.272	-0.300	-0.251	
	G1	-0.479**	-0.420**	-0.034	0.055	-0.231	0.262	-0.249	-0.251	0.140
	G2	-0.261**	-0.409**	-0.009	0.143	0.001	-0.069	-0.302**	-0.324**	0.673**
	G3	0.024	-0.408**	-0.094	-0.058	-0.157	-0.154	-0.125	-0.169	0.622**
SPAD2	G4	-0.141	-0.463**	0.127	0.063	-0.168	-0.040	0.070	0.069	0.696**
	G5	-0.048	-0.289	0.065	0.267	-0.108	-0.010	0.041	-0.036	0.734**
	G6	0.467	0.663**	0.269	0.370	0.190	0.136	-0.506*	-0.509*	0.643**
	G7	-0.034	0.494	0.387	0.359	0.215	0.046	-0.601	-0.564*	0.844**

<sup>1</sup> DF- Days to 50% flowering, PH- Plant height, EXE- Panicle exerstion, PL- Panicle length, PW- Panicle width, BT- Basal tiller, HSW- Hundred seed weight, PWT- Panicle weight, YLD- Grain yield, SPAD1-SCMR at flowering, SPAD2- SCMR 30 days after flowering.

Characters <sup>1</sup>	Flowering groups	DF	РН	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1
	G 1	0.336**									
	G 2	0.401**									
	G 3	0.404**									
PH	G 4	0.457**									
	G 5	0.185									
	G 6	0.399									
	G 7	0.224									
	G 1	-0.528**	0.170								
	G 2	-0.399**	0.311**								
	G 3	-0.385**	0.318**								
EXE	G 4	-0.345*	0.201								
	G 5	-0.439**	0.232								
	G 6	-0.248	0.471								
	G 7	-0.417	0.455								
	G 1	-0.090	0.259	0.321*							
	G 2	0.201*	0.258**	0.025							
	G 3	-0.076	0.399**	0.429**							
PL	G 4	-0.235	0.349*	0.532**							
	G 5	-0.357*	0.182	0.471**							
	G 6	-0.267	0.597*	0.592*							
	G 7	0.316	0.386	0.380							
	G 1	0.113	0.193	-0.217	0.503**						
	G 2	0.312**	0.442**	0.018	0.738**						
	G 3	0.238**	0.418**	0.118	0.578**						
PW	G 4	0.214	0.399**	0.269*	0.364**						
	G 5	-0.002	0.274	0.116	0.537**						
	G 6	0.111	0.669**	<b>0.613</b> <sup>*</sup>	0.792**						
	G 7	-0.067	0.067	0.450	<b>0.618</b> <sup>*</sup>						
	G 1	-0.413**	-0.133	0.333*	-0.071	-0.136					
	G 2	-0.114	0.031	0.224*	0.281**	0.366**					
	G 3	-0.120	0.226*	0.293**	0.461**	0.475**					
BT	G 4	-0.150	0.191	0.380**	0.314*	0.564**					
	G 5	-0.113	-0.010	0.272	0.359 <sup>*</sup>	0.523**					
	G 6	0.134	0.256	0.139	0.456	0.398					
	G 7	0.078	0.223	0.329	0.573	0.732					
	G 1	0.140	0.175	-0.268	-0.301	-0.025	-0.470**				
	G 2	-0.109	0.063	0.143	-0.345	-0.385**	-0.437**				
	G 3	-0.232**	-0.118	-0.102	-0.329**	-0.395 <sup>**</sup>	-0.568 <sup>**</sup>				
HSW	G 4	-0.229	-0.094	-0.262	-0.114	-0.335*	-0.307				
	G 5	-0.267	0.185	0.092	-0.054	-0.089	-0.383*				
	G 6	-0.401	0.061	0.207	0.064	0.007	-0.665				
	G 7	-0.328	-0.132	-0.183	-0.743**	-0.596	-0.794**				
	G 1	0.350	0.106	-0.297	-0.049	0.130	-0.453	0.136			
PWT	G 2	0.356**	-0.043	-0.344 **	-0.177	-0.162	-0.402	0.158			
	G 3	0.077	-0.270	-0.223	-0.326	-0.272	-0.609**	0.344**			
	G 4	0.178	-0.301*	-0.414 <sup>**</sup>	-0.341	-0.414**	-0.644	0.358			
	G 5	0.004	-0.133	<b>-0.371</b> *	-0.416**	-0.249	-0.621**	0.401**			
	G 6	-0.207	-0.106	-0.138	-0.195	-0.344	-0.685	0.743			
	G 7	-0.441	-0.437	-0.359	-0.916	-0.615	-0.665	0.881			
YLD	G 1	0.335*	0.111	-0.255	-0.035	0.119	-0.432**	0.247	0.927**		

 Table 24b. Correlation coefficient of quantitative characters in flowering group of sorghum reference set during the 2009-2010 post rainy season (E2) at ICRISAT centre, Patancheru, India.

Table 24b Contd...

Characters <sup>1</sup>	Flowering groups	DF	РН	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1
	G 2	0.143	-0.082	-0.202*	-0.128	-0.175	-0.016	-0.062	0.232*		
	G 3	0.036	-0.275***	-0.200*	-0.331**	-0.284**	-0.593**	0.341**	0.954**		
	G 4	0.151	-0.273*	-0.315*	-0.332*	-0.414**	-0.618**	0.368**	0.937**		
	G 5	-0.109	-0.036	-0.340*	-0.375*	-0.188	-0.623**	0.551**	$0.847^{**}$		
	G 6	-0.053	0.054	-0.086	-0.239	-0.319	-0.715**	0.728**	0.928**		
	G 7	-0.292	-0.512	-0.367	-0.854**	-0.277	-0.397	0.705*	0.865**		
	G 1	0.049	-0.296	0.050	0.021	-0.088	-0.353*	0.337*	0.069	0.114	
	G 2	-0.261**	-0.357**	0.116	0.066	0.007	-0.101	-0.023	-0.061	-0.034	
SDAD1	G 3	-0.293**	-0.426**	0.156	-0.123	-0.185*	-0.112	0.171	0.139	0.129	
SFADI	G 4	-0.147	-0.590**	0.031	-0.170	-0.258	-0.403**	0.169	0.348*	0.336*	
	G 5	-0.332*	-0.200	0.155	0.311*	0.062	-0.309*	0.505**	0.267	0.209	
	G 6	0.140	0.075	0.231	-0.127	-0.073	-0.145	0.146	0.043	0.254	
	G 7	-0.490	0.096	0.302	-0.485	-0.426	-0.621*	0.641*	0.477	0.266	
	G 1	-0.230	-0.028	0.105	0.209	0.157	-0.144	0.284	0.132	0.156	0.449**
	G 2	-0.182*	-0.327**	0.051	0.150	0.054	0.083	-0.138	-0.183*	-0.053	0.737**
	G 3	-0.192*	-0.249**	0.117	-0.008	-0.060	-0.106	0.092	0.107	0.086	0.716**
SPAD2	G 4	-0.286*	-0.453**	0.063	-0.138	-0.332*	-0.179	0.262	0.158	0.149	0.710**
	G 5	-0.318*	0.001	-0.062	0.022	-0.046	-0.354*	0.213	0.431**	0.410**	0.330**
	G 6	-0.140	0.357	0.620*	0.261	0.097	0.205	0.032	-0.203	-0.033	0.665**
	G 7	-0.145	0.179	0.144	-0.383	-0.384	-0.424	0.439	0.290	0.255	0.829**

<sup>1</sup> DF- Days to 50% flowering, PH- Plant height, EXE- Panicle exerstion, PL- Panicle length, PW- Panicle width, BT-Basal tiller, HSW- Hundred seed weight, PWT- Panicle weight, YLD- Grain yield, SPAD1- SCMR at flowering, SPAD2- SCMR 30 days after flowering.

Characteral	Flowering									
Characters	groups	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1
	G 1	0.331 <sup>*</sup>								
	G 2	0.276 <sup>**</sup>								
	G 3	0.311**								
PH	G 4	-0.320***								
	G 5	0.107								
	G 6	0.571*								
	G 7	0.505								
	G 1	-0.541**	0.232							
	G 2	-0.445	0.368							
	G 3	-0.450	0.357**							
EXE	G 4	-0.320*	0.286*							
	G 5	-0.354*	0.371							
	G 6	-0.028	0.510 <sup>°</sup>							
	G 7	-0.180	0.519							
	G 1	-0.009	0.289	0.306						
	G 2	0.176	0.227*	-0.015						
	G 3	-0.067	0.446	0.431**						
PL	G 4	-0.226	0.385	0.594						
	G 5	-0.203	0.258	0.468						
	G 6	0.027	0.637**	0.531*						
	G 7	0.399	0.518	0.566						
	G 1	0.179	0.303	-0.126	0.634**					
	G 2	0.294 <sup>**</sup>	0.409 <sup>**</sup>	-0.050	0.798					
	G 3	0.203*	0.504	0.092	0.709					
$\mathbf{PW}$	G 4	0.175	0.521**	0.345*	0.526					
	G 5	-0.030	0.266	0.142	0.599					
	G 6	0.312	0.645	0.480	0.794					
	G 7	0.292	0.344	0.392	0.831**					
	G 1	-0.552**	-0.265	0.303	-0.127	-0.150				
	G 2	-0.165	0.056	0.306**	0.249**	0.358**				
	G 3	-0.137	0.254**	0.355**	0.465	0.422**				
BT	G 4	0.018	0.219	0.346*	0.309	0.595				
	G 5	0.067	0.013	0.176	0.519**	0.715				
	G 6	0.528*	0.386	0.070	0.386	0.479				
	G 7	0.260	0.378	0.303	0.770**	0.867**				
	G 1	0.398	0.111	-0.316 <sup>*</sup>	-0.102	0.026	-0.600**			
	G 2	0.316**	0.047	-0.354**	-0.196	-0.212	-0.610			
	G 3	0.101	-0.213 <sup>*</sup>	-0.262**	-0.345	-0.310**	-0.655			
PWT	G 4	0.092	-0.314*	-0.478**	-0.380**	-0.545 <sup>**</sup>	-0.715			
	G 5	-0.164	-0.070	-0.225	-0.458***	-0.351	-0.671**			
	G 6	-0.541*	-0.400	-0.217	-0.399	-0.624*	-0.742**			
	G 7	-0.541	-0.775*	-0.474	-0.708*	-0.446	-0.508			
	G 1	0.432**	0.147	-0.345*	-0.087	0.053	-0.605**	0.955		
YLD	G 2	0.265**	0.064	-0.333**	-0.276 <sup>**</sup>	-0.275 <sup>**</sup>	- <b>0.518</b> <sup>**</sup>	0.861**		
	G 3	0.069	-0.185*	-0.226**	-0.371**	-0.354**	-0.645**	0.949**		

Table 24c. Correlation coefficient of quantitative characters in different flowering groups of sorghum reference set pooled over E1 and E2.

Table Late contain	Tab	le 24c	contd.	•••
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Characters	Flowering									
Characters	groups	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1
	G 4	0.095	-0.326*	-0.429**	-0.423**	-0.586**	-0.691**	0.966**		
	G 5	-0.236	-0.028	-0.169	-0.490**	-0.304	-0.668**	0.927**		
	G 6	-0.422	-0.331	-0.350	-0.432	-0.559*	-0.735**	0.919**		
	G 7	-0.529	-0.697*	-0.419	-0.591	-0.237	-0.315	0.954**		
	G 1	0.017	-0.217	0.123	0.146	-0.046	-0.370*	0.049	0.035	
	G 2	-0.300**	-0.385**	0.029	0.055	-0.111	-0.207*	-0.057	-0.099	
	G 3	-0.360**	-0.463**	0.095	-0.187*	-0.372**	-0.189*	0.148	0.128	
SPAD1	G 4	-0.188	-0.629**	-0.012	-0.151	-0.329*	-0.361**	0.352**	0.375**	
	G 5	-0.163	-0.270	0.118	0.140	-0.268	-0.324*	0.228	0.133	
	G 6	0.346	0.356	0.304	-0.069	-0.206	-0.130	-0.058	-0.022	
	G 7	-0.481	0.140	0.389	-0.208	-0.289	-0.443	-0.028	-0.059	
	G 1	-0.365*	-0.164	0.172	0.195	0.027	0.016	0.065	0.061	0.419**
	G 2	-0.253**	-0.415**	0.021	0.155	-0.003	0.034	-0.305**	-0.310**	0.763**
SDAD2	G 3	-0.103	-0.349**	-0.006	-0.037	-0.176*	-0.147	0.005	-0.044	0.775**
SFAD2	G 4	-0.258	-0.507**	0.107	-0.055	-0.307*	-0.136	0.141	0.168	0.774**
	G 5	-0.362*	-0.117	0.003	0.106	-0.135	-0.289	0.355*	0.299	0.497**
	G 6	0.279	0.567*	<b>0.565</b> <sup>*</sup>	0.317	0.048	0.257	-0.302	-0.329	0.764**
	G 7	-0.238	0.341	0.390	0.071	-0.062	-0.185	-0.368	-0.352	0.906**

Characters <sup>1</sup>	Races	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1
	Races	0.571**								
PH	Intermediate Races	0.527**								
	Wilds	0.824**								
	Races	-0.253**	0.199**							
EXE	Intermediate Races	-0.283**	0.400**							
	Wilds	-0.628**	-0.414*							
	Races	0.183**	0.400**	0.271**						
PL	Intermediate Races	0.062	0.308**	0.287**						
	Wilds	0.317	0.620**	-0.015						
	Races	0.168**	0.399**	-0.023	0.672**					
PW	Intermediate Races	0.030	0.312**	<b>0.188</b> <sup>*</sup>	0.644**					
	Wilds	0.290	0.467*	-0.076	0.849**					
	Races	0.043	0.049	0.301**	0.158*	0.106				
BT	Intermediate Races	-0.363**	-0.027	0.435**	0.010	-0.168				
	Wilds	-0.353	-0.338	0.177	0.120	0.316				
	Races	-0.211**	-0.067	-0.226**	-0.253**	-0.165**	-0.541**			
PWT	Intermediate Races	0.177*	-0.119	-0.422**	-0.097	-0.037	-0.499**			
	Wilds	0.082	0.002	0.070	-0.190	-0.309	-0.579**			
	Races	-0.229**	-0.088	-0.209**	-0.300**	-0.225**	-0.532**	0.931**		
YLD	Intermediate Races	$0.187^{*}$	-0.039	-0.372**	-0.144	-0.044	-0.493**	0.933**		
	Wilds	0.092	-0.043	0.056	-0.197	-0.300	-0.585**	0.917**		
	Races	-0.590**	-0.634**	0.104	-0.179**	-0.288**	-0.221**	0.137*	0.166**	
SPAD1	Intermediate Races	-0.623**	-0.362**	0.165	0.247**	0.114	0.132	-0.126	-0.189*	
	Wilds	-0.607**	-0.388	0.404	-0.289	-0.206	-0.064	0.144	0.037	
	Races	0.006	-0.310**	0.014	0.050	-0.100	-0.161*	-0.117	-0.127*	0.521**
SPAD2	Intermediate Races	-0.135	-0.226**	0.003	0.110	-0.092	0.080	-0.288**	-0.368**	0.451**
	Wilds	-0.280	-0.198	-0.199	-0.080	0.028	0.215	-0.034	0.009	0.270

 Table 25a Correlation coefficient for quantitative characters in the races, intermediate races and wild type as a group of sorghum reference set evaluated during 2008-09 post rainy season (E1) at ICRISAT, Patancheru, India.

Characters 1	Races	DF	РН	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1
	Races	0.499**									
PH	Intermediate Races	0.475**									
	Wilds	0.760**									
	Races	-0.325**	0.192*								
EXE	Intermediate Races	-0.324**	0.346**								
	Wilds	-0.790***	-0.402								
	Races	0.120	0.392**	0.296**							
PL	Intermediate Races	0.125	0.323**	0.330**							
	Wilds	0.135	0.458*	0.073							
	Races	-0.092	0.154*	0.037	0.356**						
PW	Intermediate Races	-0.060	0.168	0.150	0.429**						
	Wilds	-0.002	0.030	-0.108	0.561**						
	Races	-0.009	0.075	0.280**	0.315**	0.276**					
BT	Intermediate Races	-0.332**	0.071	0.415**	-0.023	-0.065					
	Wilds	0.104	-0.030	-0.077	0.304	0.505*					
	Races	-0.141*	0.038	-0.038	-0.281**	-0.269**	-0.419**				
HSW	Intermediate Races	-0.270**	0.002	0.136	0.071	-0.088	-0.052				
	Wilds	-0.071	0.248	0.116	0.243	-0.063	-0.455*				
	Races	-0.009	-0.124*	-0.240**	-0.352**	-0.163**	-0.530**	0.375**			
PWT	Intermediate Races	0.283**	-0.194*	-0.405**	-0.038	0.036	-0.473**	-0.015			
	Wilds	-0.104	-0.172	0.105	-0.205	0.075	-0.277	0.049			
	Races	0.034	-0.115	-0.224**	-0.313**	-0.212**	-0.449**	0.343**	0.786**		
YLD	Intermediate Races	0.274**	-0.090	-0.278**	-0.101	-0.120	-0.289**	0.003	0.731**		
	Wilds	-0.184	-0.153	0.173	0.139	0.297	0.099	0.066	0.655**		
	Races	-0.456**	-0.567**	0.149*	-0.179*	0.037	-0.196*	0.151*	0.190*	0.151*	
SPAD1	Intermediate Races	-0.315**	-0.317**	0.152	<b>0.193</b> *	0.253**	0.039	0.018	-0.081	-0.167	
	Wilds	-0.476**	-0.344	0.206	-0.093	0.300	-0.191	0.131	0.386	0.465*	
	Races	-0.363**	-0.339**	0.082	-0.043	0.055	-0.180*	0.116	0.122	0.123	0.682**
SPAD2	Intermediate Races	-0.355**	-0.254**	0.057	0.016	0.228**	0.140	-0.040	-0.092	-0.128	0.583**
	Wilds	-0.451**	-0.509**	0.157	0.039	0.333	0.073	-0.079	0.292	0.366	0.535**

Table 25b Correlation coefficient for quantitative characters in the races, intermediate races and wild type as a group of sorghum reference set evaluated during 2009-10 post rainy season (E2) at ICRISAT, Patancheru, India.

Characters <sup>1</sup>	Races	DF	PH	EXE	PL	PW	BT	PWT	YLD	SPAD1
	Races	0.554**								
PH	Intermediate Races	0.494**								
	Wilds	0.803**								
	Races	-0.280**	0.223**							
EXE	Intermediate Races	-0.351**	0.349**							
	Wilds	-0.685**	-0.463*							
	Races	0.155**	0.378**	0.304**						
PL	Intermediate Races	0.222*	0.441**	0.308**						
	Wilds	0.171	0.513***	-0.073						
	Races	0.057	0.314**	0.018	0.598**					
PW	Intermediate Races	0.029	0.317**	$0.177^{*}$	0.598**					
	Wilds	0.094	0.324	-0.116	0.796**					
	Races	0.032	0.084	0.296**	0.260**	0.277**				
BT	Intermediate Races	-0.276**	0.117	0.483**	0.100	-0.105				
	Wilds	-0.174	-0.138	0.036	0.436*	0.678**				
	Races	-0.133*	-0.114	-0.288**	-0.329**	-0.227***	-0.619**			
PWT	Intermediate Races	0.191*	-0.17*	-0.389**	-0.090	-0.049	-0.591**			
	Wilds	0.109	-0.074	0.061	-0.627**	-0.430*	-0.550**			
	Races	-0.115	-0.105	-0.266**	-0.352**	-0.276***	-0.585**	0.925**		
YLD	Intermediate Races	0.198 <sup>*</sup>	-0.102	-0.350**	-0.163	-0.106	-0.539**	0.910**		
	Wilds	0.098	-0.104	0.049	-0.517*	-0.345	-0.446*	0.930**		
	Races	-0.560**	-0.639**	0.121	-0.184**	-0.195***	-0.248**	0.180**	0.183**	
SPAD1	Intermediate Races	-0.492**	-0.360**	0.160	0.119	0.171	0.063	-0.123	-0.214*	
	Wilds	-0.609**	-0.416*	0.355	-0.274	-0.072	-0.140	0.181	0.111	
	Races	-0.338**	-0.469**	0.079	-0.020	-0.134*	-0.206**	0.078	0.073	0.754**
SPAD2	Intermediate Races	-0.348**	-0.229**	0.140	0.135	0.073	0.146	-0.231**	-0.275***	0.666**
	Wilds	-0.475*	-0.440*	-0.034	-0.248	-0.118	0.093	0.024	0.010	0.625**

Table 25c Correlation coefficient for quantitative characters in the races, intermediate races and wild type as a group of sorghum reference set pooled over E1 and E2.

<sup>1</sup> DF- Days to 50% flowering, PH- Plant height, EXE- Panicle exerstion, PL- Panicle length, PW- Panicle width, BT- Basal tiller, HSW-Hundred seed weight, PWT- Panicle weight, YLD- Grain yield, SPAD1- SCMR at flowering, SPAD2- SCMR 30 days after flowering.

Characters <sup>1</sup>	Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1
	Races	0.373**									
PH	Intermediate Races	0.278**									
	Wilds	0.570**									
EVE	Races	-0.200**	0.282**								
EXE	Intermediate Races	-0.047	0.303**								
	Wilds	0.101	0.358								
DI	Races	0.248**	0.368**	0.317**							
PL	Intermediate Races	0.141	0.205*	0.245**							
	Wilds	0.146	0.514*	-0.002							
	Races	0.138*	0.226*	0.061	0.591**						
PW	Intermediate Races	0.005	0.231**	0.004	0.709**						
	Wilds	0.020	0.423*	-0.029	0.819**						
DT	Races	-0.084	-0.037	0.121	0.056	0.033					
BI	Intermediate Races	-0.173	-0.016	0.127	-0.003	-0.027					
	Wilds	-0.242	-0.131	0.336	-0.018	0.108					
HSW	Races	-0.124	-0.161*	-0.006	-0.182**	-0.052	-0.088				
	Intermediate Races	-0.278**	-0.152	-0.063	-0.364**	-0.211*	-0.093				
	Wilds	-0.200	-0.152	0.005	-0.050	0.002	0.220				
PWT	Races	-0.033	-0.033	0.054	-0.087	-0.051	-0.034	0.099			
	Intermediate Races	-0.090	-0.134	-0.040	0.031	0.008	-0.080	-0.068			
	Wilds	0.412	0.231	0.096	0.003	-0.014	0.421*	0.399			
YLD	Races	-0.034	-0.081	0.018	-0.124	-0.073	-0.028	0.094	0.912**		
	Intermediate Races	-0.142	-0.092	0.019	-0.001	-0.012	0.013	-0.019	0.904**		
	Wilds	0.393	0.279	0.112	0.094	0.058	0.434*	0.373	0.978**		
SPAD1	Races	0.040	-0.124	-0.016	0.002	-0.067	-0.066	0.196**	0.004	0.036	
	Intermediate Races	-0.097	-0.212*	-0.141	-0.066	-0.078	0.108	0.082	$0.187^{*}$	0.131	
	Wilds	-0.163	-0.087	-0.183	0.118	0.077	0.463*	0.059	0.171	0.197	
SPAD2	Races	0.078	0.005	-0.046	-0.057	-0.039	0.040	0.023	0.045	0.055	0.247**
	Intermediate Races	0.059	0.061	-0.009	0.076	0.135	-0.104	-0.088	0.012	-0.004	0.282**
	Wilds	0.082	-0.267	-0.226	-0.073	-0.110	0.258	-0.204	0.063	0.031	0.374

Table 25d Correlation coefficient for quantitative characters in the races, intermediate races and wild type as a group of sorghum reference set evaluated during 2009-10 at UAS dharwad, under irrigated condition (E3).

 Table 25e Correlation coefficient for quantitative characters in the races, intermediate races and wild type as a group of sorghum reference set evaluated during 2009-10 at UAS dharwad, under un-irrigated condition (E4).

Characters <sup>1</sup>	Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1
DII	Races	0.254**									
PH	Intermediate Races	0.209*									
	Wilds	0.059									
	Races	-0.257**	0.288**								
EXE	Intermediate Races	-0.113	0.299**								
	Wilds	-0.415*	0.041								
	Races	0.095	0.272**	0.174**							
PL	Intermediate Races	0.144	0.425**	0.250**							
	Wilds	0.061	-0.005	-0.0037							
	Races	0.018	0.140*	-0.163**	0.475**						
PW	Intermediate Races	-0.049	0.237*	-0.001	0.532**						
	Wilds	-0.104	0.192	-0.256	0.740**						
	Races	-0.158*	0.123	0.315**	0.043	-0.112					
BT	Intermediate Races	-0.003	0.080	0.253**	0.027	0.011					
	Wilds	-0.248	0.205	0.449**	0.047	0.002					
	Races	-0.089	-0.041	0.055	-0.240**	-0.150**	-0.002				
HSW	Intermediate Races	-0.086	-0.098	-0.132	-0.337**	-0.132	-0.060				
	Wilds	-0.339	-0.096	0.207	-0.254	-0.129	0.317				
	Races	0.004	0.049	-0.001	-0.052	-0.094	0.042	0.047			
PWT	Intermediate Races	-0.018	0.035	0.118	-0.049	-0.210*	0.028	0.080			
	Wilds	-0.062	0.310	-0.028	-0.280	-0.097	-0.283	0.164			
	Races	-0.016	0.084	-0.015	-0.072	-0.073	-0.034	0.078	0.805**		
YLD	Intermediate Races	-0.031	0.069	0.212**	0.013	-0.195*	0.082	0.019	0.853**		
	Wilds	-0.038	0.172	-0.010	-0.362	-0.301	-0.342	0.333	0.786**		
	Races	-0.269**	-0.118	0.086	-0.119	-0.016	0.066	0.157*	0.054	0.085	
SPAD1	Intermediate Races	-0.195*	-0.214*	-0.095	-0.030	0.077	-0.066	0.186*	-0.035	-0.162	
	Wilds	-0.222	-0.434*	0.114	-0.008	0.032	-0.139	0.041	-0.215	-0.104	
	Races	0.012	0.033	0.091	0.023	-0.050	0.004	0.113	0.038	0.071	0.227**
SPAD2	Intermediate Races	-0.043	0.055	0.033	-0.035	-0.059	0.156	0.007	-0.132	-0.181*	0.290**
	Wilds	0.259	0.044	0.333	0.226	-0.139	0.255	-0.469*	-0.367	-0.330	0.089

Characters <sup>1</sup>	Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1
	Races	0.204**									
PH	Intermediate Races	0.165									
	Wilds	0.201									
	Races	-0.048	0.308**								
EXE	Intermediate Races	-0.250**	0.249**								
	Wilds	-0.322	-0.118								
	Races	0.103	0.249**	$0.177^{*}$							
PL	Intermediate Races	-0.035	0.144	0.073							
	Wilds	-0.228	0.486*	0.049							
	Races	0.013	0.153**	0.177**	0.240**						
PW	Intermediate Races	0.049	0.181*	0.183*	0.047						
	Wilds	-0.003	0.209	0.304	0.256						
	Races	0.120	0.109	0.098	0.068	0.088					
BT	Intermediate Races	0.117	0.010	-0.048	-0.040	-0.076					
	Wilds	-0.025	-0.041	0.426*	0.072	0.269					
	Races	-0.079	-0.109	-0.053	-0.142*	-0.143*	-0.145*				
HSW	Intermediate Races	-0.108	-0.181*	-0.167	-0.103	-0.199*	0.054				
	Wilds	-0.123	-0.388	-0.050	-0.452*	-0.390	-0.274				
	Races	0.116	-0.005	0.023	0.046	0.026	0.017	-0.050			
PWT	Intermediate Races	0.063	0.110	0.151	0.122	-0.134	0.091	0.088			
	Wilds	0.049	-0.147	0.171	-0.190	0.063	0.143	-0.186			
	Races	0.135*	-0.026	-0.014	-0.014	-0.022	-0.014	0.035	0.780**		
YLD	Intermediate Races	0.067	0.213*	0.089	0.112	-0.061	0.054	0.029	0.649**		
	Wilds	0.028	-0.086	0.188	-0.062	0.059	0.047	-0.220	0.836**		
	Races	-0.195**	-0.051	0.024	-0.150*	0.048	-0.115	0.147*	0.069	0.036	
SPAD1	Intermediate Races	-0.241**	-0.184*	-0.004	-0.025	0.018	0.119	0.229*	0.138	0.021	
	Wilds	0.013	-0.133	0.073	0.029	0.452*	0.312	-0.144	-0.067	-0.124	
	Races	-0.022	-0.023	-0.061	-0.076	-0.112	0.054	0.127*	0.007	-0.020	0.114
SPAD2	Intermediate Races	-0.033	-0.015	-0.120	0.022	-0.055	0.067	0.085	0.102	0.095	0.298**
	Wilds	0.202	0.040	-0.028	-0.055	0.056	-0.100	0.190	-0.008	-0.096	-0.133

 Table 25f. Correlation coefficient for quantitative characters in the races, intermediate races and wild type as a group of sorghum reference set evaluated during 2009-10 at ARRS, Bijapur, under un-irrigated condition (E5).

Characters <sup>1</sup>	Races	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1
	Races	0.345**									
PH	Intermediate races	0.302**									
	Wild type	0.468*									
	Races	-0.222**	0.301**								
EXE	Intermediate races	-0.185*	0.170								
	Wild type	-0.213	0.090								
	Races	0.184**	0.281**	0.261**							
PL	Intermediate races	0.178	0.327**	0.204**							
	Wild type	0.020	0.262	-0.138							
	Races	0.089	0.184**	0.020	0.581**						
PW	Intermediate races	0.038	0.232*	0.009	0.628**						
	Wild type	-0.132	0.319	0.032	0.711**						
	Races	-0.125	0.092	0.250**	0.056	-0.003					
BT	Intermediate races	-0.025	0.079	0.208*	-0.057	-0.004					
	Wild type	-0.326	-0.057	0.548**	-0.227	-0.126					
	Races	-0.169**	-0.083	0.030	-0.215**	-0.161*	-0.094				
HSW	Intermediate races	-0.137	-0.169	-0.117	-0.344**	-0.257**	-0.165				
	Wild type	-0.368	-0.392	0.167	-0.105	-0.088	0.061				
	Races	-0.061	-0.123	-0.003	-0.126*	-0.046	-0.037	0.157*			
PWT	Intermediate races	0.056	-0.072	-0.032	-0.011	-0.050	-0.051	0.080			
	Wild type	0.286	0.315	0.026	-0.066	-0.122	0.158	0.105			
	Races	-0.073	-0.178**	-0.062	-0.192**	-0.077	-0.070	0.149*	0.866**		
YLD	Intermediate races	0.035	-0.005	0.051	-0.073	-0.130	0.070	-0.006	0.832**		
	Wild type	0.349	0.370	0.068	-0.174	-0.135	0.109	0.161	0.929**		
	Races	-0.152*	-0.115	0.085	-0.131*	-0.131*	-0.036	0.223**	0.140*	0.092	
SPAD1	Intermediate races	-0.249**	-0.272**	-0.058	0.014	-0.002	0.074	0.103	0.236*	0.122	
	Wild type	-0.310	-0.380	-0.097	-0.099	0.026	0.239	0.091	-0.150	-0.145	
	Races	0.056	0.056	0.018	-0.046	-0.025	-0.023	0.119	0.083	0.035	0.234**
SPAD2	Intermediate races	-0.105	0.186	0.122	0.123	0.089	0.089	-0.134	0.120	0.140	0.365**
	Wild type	0.086	-0.083	-0.099	-0.010	-0.270	0.103	-0.036	-0.253	-0.203	0.409

 Table 25g Correlation coefficient for quantitative characters in the races, intermediate races and wild type as a group of sorghum reference set pooled over E3, E4 and E5.

Environments <sup>1</sup>	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2	Mean±SE
E1	0.61	0.61	0.61	0.60	0.52	0.54	*	0.62	0.62	0.62	0.62	0.60±0.011
E2	0.62	0.63	0.63	0.61	0.59	0.46	0.63	0.63	0.64	0.62	0.61	0.60±0.017
Pooled (E1 & E2	0.62	0.62	0.62	0.61	0.55	0.49	0.62	0.62	0.63	0.62	0.62	0.60±0.014
E3	0.60	0.62	0.59	0.60	0.47	0.62	0.57	0.54	0.63	0.64	0.64	0.59±0.015
E4	0.61	0.60	0.59	0.62	0.46	0.63	0.59	0.61	0.62	0.63	0.62	0.59±0.014
E5	0.62	0.62	0.59	0.63	0.55	0.60	0.61	0.63	0.62	0.59	0.63	$0.60 \pm 0.007$
Pooled (E3, E4, E5)	0.61	0.62	0.62	0.60	0.48	0.59	0.62	0.63	0.59	0.63	0.62	0.60±0.013
Mean± se	$0.61 \pm 0.004$	$0.62{\pm}0.003$	$0.60{\pm}0.008$	$0.61 \pm 0.005$	0.50±0.021	$0.57 \pm 0.004$	$0.62 \pm 0.020$	$0.61 \pm 0.005$	$0.61 \pm 0.016$	$0.62 \pm 0.008$	$0.62 \pm 0.003$	0.60±0.013

Table 26 Shannon Weaver diversity index (H') for quantitative characters of sorghum reference set in all the environments.

\*data not recorded, <sup>1</sup> E1- ICRISAT, Patancheru during 2008-09, E2- ICRISAT, Patancheru during 2009-10, E3- UAS, Dharwad irrigated condition, E4- UAS, Dharwad un-irrigated condition, E5 – RARS, Bijapur un-irrigated condition,

Table. 27a Shannon Weaver diversity index (H') for quantitative characters in different flowering groups of sorghum
reference set evaluated during the 2008-2009 post rainy season (E1) at ICRSAT, Patancheru, India.

	Group 1	Group2	Group 3	Group 4	Group 5	Group 6	Group 7	Maan   SE
	(36) <sup>a</sup>	(114)	(124)	(51)	(38)	(13)	(8)	Mean±SE
DF	0.55	0.62	0.58	0.58	0.53	0.56	0.54	0.57±0.012
PH	0.58	0.58	0.62	0.55	0.55	0.38	0.40	$0.53 \pm 0.033$
EXE	0.52	0.60	0.61	0.58	0.59	0.55	0.46	$0.56 \pm 0.018$
PL	0.48	0.58	0.61	0.62	0.60	0.50	0.49	$0.56 \pm 0.022$
PW	0.41	0.38	0.39	0.42	0.47	0.53	0.40	$0.44 \pm 0.021$
BT	0.44	0.51	0.55	0.36	0.51	0.54	0.39	$0.48 \pm 0.026$
PWT	0.58	0.60	0.63	0.57	0.58	0.58	0.37	$0.57 \pm 0.029$
YLD	0.60	0.61	0.63	0.61	0.57	0.54	0.43	$0.58 \pm 0.023$
SPAD1	0.54	0.61	0.62	0.64	0.60	0.54	0.33	$0.56 \pm 0.036$
SPAD2	0.58	0.59	0.61	0.58	0.56	0.58	0.33	$0.55 \pm 0.033$
Mean±SE	$0.53 \pm 0.020$	$0.57 \pm 0.023$	$0.58 \pm 0.023$	$0.55 \pm 0.028$	0.56±0.013	0.53±0.019	$0.41 \pm 0.021$	$0.54 \pm 0.022$

<sup>a</sup> Numbers within parenthesis indicate number of accessions in each flowering group

DF- Days to 50% flowering, PH- Plant height, EXE- Panicle exerstion, PL- Panicle length, PW- Panicle width, BT- Basal tiller,

HSW- Hundred seed weight, PWT- Panicle weight, YLD- Grain yield per plot, SPAD1- SCMR at flowering, SPAD2- SCMR 30 days after flowering.

	Group 1	Group2	Group 3	Group 4	Group 5	Group 6	Group 7	Moon+SE
	(36) <sup>a</sup>	(114)	(124)	(51)	(38)	(13)	(8)	Ivicali=3E
DF	0.55	0.60	0.59	0.56	0.51	0.42	0.13	0.50±0.056
PH	0.62	0.60	0.62	0.58	0.58	0.46	0.51	$0.57 \pm 0.021$
EXE	0.61	0.61	0.61	0.60	0.54	0.54	0.55	$0.59 \pm 0.012$
PL	0.53	0.60	0.60	0.63	0.60	0.53	0.56	$0.58 \pm 0.013$
PW	0.57	0.57	0.56	0.32	0.54	0.54	0.40	$0.51 \pm 0.035$
BT	0.33	0.32	0.52	0.40	0.38	0.53	0.45	$0.42 \pm 0.028$
HSW	0.57	0.61	0.60	0.60	0.60	0.53	0.51	$0.58 \pm 0.015$
PWT	0.59	0.60	0.61	0.60	0.60	0.53	0.49	$0.58 \pm 0.017$
YLD	0.61	0.63	0.61	0.57	0.61	0.58	0.51	$0.59 \pm 0.015$
SPAD1	0.62	0.62	0.62	0.58	0.58	0.57	0.47	$0.58 \pm 0.018$
SPAD2	0.57	0.61	0.63	0.60	0.51	0.60	0.54	$0.58 \pm 0.014$
Mean±SE	$0.56 \pm 0.027$	$0.57 \pm 0.029$	$0.60{\pm}0.011$	$0.54{\pm}0.032$	$0.55 \pm 0.021$	$0.53 \pm 0.017$	$0.46 \pm 0.040$	$0.55 \pm 0.023$

Table. 27b Shannon Weaver diversity index (H') for quantitative characters in different flowering groups of sorghum reference set evaluated during the 2009-2010 post rainy season (E<sub>2</sub>)at ICRSAT, Patancheru, India.

Table 27c Shannon Weaver diversity index (H') for quantitative characters in different flowering groups of sorghum reference set pooled over E1 and E2.

	Group 1	Group2	Group 3	Group 4	Group 5	Group 6	Group 7	Moon±SE
	(36) <sup>a</sup>	(114)	(124)	(51)	(38)	(13)	(8)	Wieali±5E
DF	0.59	0.62	0.59	0.57	0.61	0.57	0.51	0.58±0.013
PH	0.59	0.59	0.62	0.58	0.50	0.53	0.40	$0.55 \pm 0.026$
EXE	0.56	0.58	0.62	0.58	0.61	0.53	0.50	$0.58 \pm 0.015$
PL	0.50	0.59	0.61	0.62	0.62	0.48	0.56	$0.58 \pm 0.020$
PW	0.54	0.47	0.51	0.40	0.50	0.58	0.41	$0.50 \pm 0.024$
BT	0.33	0.44	0.50	0.36	0.38	0.53	0.45	$0.44 \pm 0.025$
PWT	0.55	0.61	0.59	0.57	0.58	0.54	0.43	$0.56 \pm 0.021$
YLD	0.56	0.61	0.61	0.57	0.59	0.53	0.43	$0.56 \pm 0.021$
SPAD1	0.58	0.61	0.62	0.61	0.56	0.56	0.50	$0.59{\pm}0.015$
SPAD2	0.62	0.59	0.64	0.58	0.61	0.48	0.45	$0.57 \pm 0.025$
Mean±SE	0.54±0.026	$0.57 \pm 0.020$	0.59±0.015	$0.55 \pm 0.028$	$0.56 \pm 0.024$	0.53±0.010	$0.46 \pm 0.017$	0.55±0.021

<sup>a</sup> Numbers within parenthesis indicate number of accessions in each

			Races				Intermed	iate Races		Wild	
	B (37) <sup>a</sup>	C (76)	D (47)	G (66)	K (26)	CB (29)	DB (15)	DC (25)	GC (52)	Sd (10)	Mean±SE
DF	0.56	0.60	0.60	0.56	0.53	0.47	0.54	0.57	0.53	0.56	0.55±0.012
PH	0.60	0.62	0.58	0.60	0.54	0.52	0.31	0.59	0.59	0.57	$0.55 \pm 0.028$
EXE	0.57	0.59	0.57	0.60	0.54	0.60	0.41	0.60	0.60	0.56	$0.56 \pm 0.018$
PL	0.57	0.61	0.53	0.62	0.44	0.55	0.41	0.54	0.53	0.53	$0.53 \pm 0.020$
PW	0.48	0.40	0.59	0.58	0.25	0.52	0.21	0.51	0.59	0.56	$0.47 \pm 0.043$
BT	0.51	0.57	0.57	0.57	0.36	0.58	0.46	0.48	0.62	0.52	$0.52 \pm 0.024$
PWT	0.58	0.62	0.60	0.61	0.57	0.54	0.55	0.55	0.59	0.47	$0.57 \pm 0.014$
YLD	0.63	0.61	0.60	0.60	0.54	0.50	0.49	0.52	0.59	0.27	$0.53 \pm 0.034$
SPAD1	0.57	0.60	0.58	0.61	0.61	0.59	0.49	0.58	0.56	0.56	$0.57 \pm 0.011$
SPAD2	0.62	0.59	0.54	0.57	0.54	0.52	0.53	0.55	0.61	0.28	$0.53 \pm 0.030$
Mean±se	$0.57 \pm 0.014$	$0.58 \pm 0.020$	$0.58 \pm 0.008$	$0.59{\pm}0.006$	$0.49 \pm 0.034$	$0.54{\pm}0.013$	$0.44 \pm 0.034$	$0.55 \pm 0.012$	$0.58 \pm 0.010$	$0.49 \pm 0.037$	$0.54 \pm 0.009$

Table 28a Shannon-Weaver diversity index (H') for quantitative characters in races, intermediate races and wild types of sorghum reference set evaluated during 2008-2009 (E1) post rainy season at ICRSAT, Patancheru, India.

Table 28b Shannon-Weaver diversity index (H') for quantitative characters in races, intermediate races and wild types of sorghum reference set evaluated during the 2009-2010 (E2) post rainy season at ICRSAT, Patancheru, India.

			Races				Intermed	iate Races		Wild	
	B (37) <sup>a</sup>	C (76)	D (47)	G (66)	K (26)	CB (29)	DB (15)	DC (25)	GC (52)	Sd (10)	Mean±SE
DF	0.58	0.59	0.59	0.48	0.56	0.55	0.40	0.56	0.59	0.39	0.53±0.024
PH	0.60	0.58	0.62	0.62	0.58	0.52	0.35	0.55	0.57	0.56	$0.55 \pm 0.025$
EXE	0.59	0.61	0.55	0.59	0.48	0.55	0.49	0.55	0.62	0.57	0.56±0.014
PL	0.59	0.62	0.53	0.60	0.53	0.59	0.43	0.57	0.56	0.53	$0.55 \pm 0.017$
PW	0.59	0.58	0.59	0.61	0.47	0.57	0.50	0.55	0.58	0.53	$0.56 \pm 0.014$
BT	0.49	0.57	0.42	0.58	0.07	0.45	0.37	0.44	0.51	0.47	$0.44{\pm}0.045$
HSW	0.52	0.63	0.62	0.60	0.58	0.51	0.32	0.60	0.61	0.53	$0.55 \pm 0.029$
PWT	0.56	0.61	0.64	0.62	0.58	0.58	0.57	0.53	0.57	0.46	0.57±0.016
YLD	0.60	0.60	0.56	0.59	0.57	0.57	0.54	0.47	0.60	0.35	$0.54{\pm}0.025$
SPAD1	0.60	0.60	0.59	0.62	0.57	0.60	0.44	0.54	0.57	0.57	0.57±0.017
SPAD2	0.56	0.62	0.52	0.57	0.54	0.60	0.51	0.51	0.60	0.45	$0.55 \pm 0.017$
Mean±se	$0.57 \pm 0.011$	$0.60 \pm 0.006$	$0.57 \pm 0.019$	$0.59 \pm 0.012$	$0.50\pm0.045$	$0.55 \pm 0.014$	$0.45 \pm 0.025$	$0.53 \pm 0.013$	$0.58 \pm 0.009$	$0.49 \pm 0.022$	$0.54 \pm 0.022$

<sup>a</sup>-Numbers within parenthesis indicate number of accessions in each race, intermediate and wild. B-Bicolor, C-Caudatum, D-Durra, G-Guinea, K-Kafir, sd-S. drummondii

			Races				Intermed	iate Races		Wild	
	B (37) <sup>a</sup>	C (76)	D (47)	G (66)	K (26)	CB (29)	DB (15)	DC (25)	GC (52)	Sd (10)	Mean±SE
DF	0.62	0.60	0.59	0.55	0.60	0.53	0.28	0.58	0.55	0.56	0.55±0.031
PH	0.60	0.58	0.57	0.60	0.51	0.56	0.41	0.61	0.59	0.56	$0.56 \pm 0.018$
EXE	0.60	0.60	0.55	0.59	0.48	0.60	0.50	0.60	0.55	0.41	$0.55 \pm 0.020$
PL	0.53	0.60	0.54	0.59	0.57	0.59	0.41	0.51	0.56	0.47	$0.54{\pm}0.018$
PW	0.52	0.55	0.61	0.51	0.48	0.56	0.43	0.58	0.59	0.56	$0.54{\pm}0.017$
BT	0.50	0.59	0.53	0.51	0.51	0.55	0.44	0.55	0.57	0.51	0.53±0.013
PWT	0.61	0.61	0.60	0.60	0.48	0.55	0.55	0.55	0.61	0.39	$0.55 \pm 0.022$
YLD	0.64	0.62	0.60	0.61	0.58	0.60	0.42	0.53	0.60	0.39	$0.56 \pm 0.027$
SPAD1	0.59	0.62	0.57	0.60	0.56	0.60	0.41	0.57	0.58	0.58	$0.57{\pm}0.018$
SPAD2	0.57	0.64	0.61	0.63	0.60	0.55	0.55	0.56	0.54	0.56	$0.58{\pm}0.011$
Mean±se	0.58±0.013	$0.60{\pm}0.007$	$0.58 \pm 0.009$	0.58±0.012	0.54±0.015	$0.57 \pm 0.008$	$0.44 \pm 0.024$	$0.56 \pm 0.009$	$0.58 \pm 0.009$	$0.50 \pm 0.023$	$0.55 \pm 0.015$

Table 28c Shannon-Weaver diversity index (H') for quantitative characters in different races, intermediate races and wild types of sorghum reference set pooled over E1 and E2.

Table 28d Shannon-Weaver diversity index (H') for quantitative characters in different races, intermediate races and wild type of sorghum reference set evaluated during 2009-2010 post rainy season at UAS, Dharwad under irrigated condition (E3).

			Races				Intermed	iate Races		Wild	
	B (37) <sup>a</sup>	C (76)	D (47)	G (66)	K (26)	CB (29)	DB (15)	DC (25)	GC (52)	Sd (10)	Mean±SE
DF	0.56	0.57	0.59	0.62	0.54	0.49	0.50	0.58	0.54	0.45	0.54±0.017
PH	0.55	0.62	0.60	0.59	0.58	0.55	0.57	0.47	0.56	0.53	0.56±0.013
EXE	0.50	0.58	0.60	0.59	0.59	0.57	0.53	0.56	0.56	0.51	$0.56 \pm 0.011$
PL	0.60	0.58	0.51	0.58	0.52	0.40	0.46	0.56	0.60	0.39	$0.52 \pm 0.025$
PW	0.47	0.57	0.54	0.48	0.35	0.17	0.15	0.48	0.49	0.14	$0.38 \pm 0.053$
BT	0.56	0.54	0.55	0.55	0.57	0.46	0.37	0.50	0.60	0.56	0.53±0.021
HSW	0.55	0.61	0.57	0.62	0.53	0.54	0.55	0.53	0.61	0.47	$0.56 \pm 0.014$
PWT	0.59	0.61	0.58	0.60	0.55	0.33	0.55	0.59	0.55	0.57	$0.55 \pm 0.026$
YLD	0.60	0.61	0.58	0.58	0.57	0.57	0.46	0.56	0.59	0.41	$0.55 \pm 0.020$
SPAD1	0.59	0.61	0.62	0.60	0.58	0.59	0.48	0.58	0.60	0.39	$0.56 \pm 0.023$
SPAD2	0.60	0.59	0.59	0.58	0.56	0.61	0.41	0.56	0.62	0.56	0.57±0.019
Mean±se	0.56±0.013	$0.59{\pm}0.007$	0.58±0.089	0.58±0.012	$0.48 \pm 0.040$	0.46±0.036	0.54±0.012	0.57±0.011	0.57±0.011	0.45±0.037	0.53±0.022

<sup>a</sup> Numbers within parenthesis indicate number of accessions in each race, intermediate and wild . B-Bicolor, C-Caudatum, D-Durra, G-Guinea, K-Kafir, sd-S. drummondii

			Races				Intermed	iate Races		Wild	
	B (37) <sup>a</sup>	C (76)	D (47)	G (66)	K (26)	CB (29)	DB (15)	DC (25)	GC (52)	Sd (10)	Mean±SE
DF	0.58	0.59	0.59	0.59	0.54	0.56	0.50	0.58	0.59	0.45	0.56±0.015
PH	0.57	0.60	0.58	0.57	0.55	0.62	0.55	0.53	0.56	0.47	$0.56 \pm 0.013$
EXE	0.53	0.57	0.52	0.59	0.53	0.52	0.55	0.55	0.55	0.52	$0.54{\pm}0.007$
PL	0.55	0.63	0.60	0.61	0.58	0.47	0.46	0.56	0.63	0.39	$0.55 \pm 0.026$
PW	0.05	0.61	0.57	0.44	0.44	0.44	0.37	0.57	0.52	0.35	$0.44{\pm}0.051$
BT	0.55	0.59	0.58	0.55	0.53	0.52	0.46	0.49	0.58	0.56	$0.54{\pm}0.014$
HSW	0.55	0.61	0.58	0.59	0.58	0.60	0.50	0.55	0.60	0.56	$0.57 \pm 0.014$
PWT	0.54	0.58	0.60	0.58	0.59	0.59	0.37	0.55	0.56	0.46	$0.54{\pm}0.023$
YLD	0.63	0.61	0.60	0.55	0.58	0.54	0.53	0.53	0.59	0.57	$0.57 \pm 0.011$
SPAD1	0.53	0.59	0.63	0.61	0.57	0.59	0.50	0.56	0.59	0.46	$0.56 \pm 0.017$
SPAD2	0.59	0.58	0.59	0.59	0.55	0.54	0.41	0.56	0.61	0.41	$0.54{\pm}0.023$
Mean±se	0.51±0.047	$0.60 \pm 0.005$	$0.59 \pm 0.008$	$0.57 \pm 0.014$	$0.55 \pm 0.013$	$0.54 \pm 0.017$	$0.47 \pm 0.020$	$0.55 \pm 0.008$	$0.58 \pm 0.009$	$0.47 \pm 0.022$	$0.54 \pm 0.019$

Table 28e Shannon-Weaver diversity index (H') for quantitative characters in different races, intermediate races and wilds of sorghum reference set evaluated during 2009-2010 post rainy season at UAS, Dharwad under un-irrigated condition (E4).

Table 28f. Shannon-Weaver diversity index (H) for quantitative characters in different races, intermediate races and wilds of sorghum reference set evaluated during 2009-2010 post rainy season at ARRS, Bijapur under un-irrigated condition (E<sub>5</sub>).

			Races				Intermed	iate Races		Wild	
	B (37) <sup>a</sup>	C (76)	D (47)	G (66)	K (26)	CB (29)	DB (15)	DC (25)	GC (52)	Sd (10)	Mean±SE
DF	0.58	0.58	0.62	0.60	0.54	0.51	0.46	0.57	0.59	0.46	0.55±0.018
PH	0.60	0.61	0.61	0.62	0.57	0.55	0.53	0.62	0.60	0.56	$0.59{\pm}0.010$
EXE	0.51	0.62	0.58	0.60	0.53	0.60	0.30	0.60	0.60	0.41	$0.54{\pm}0.033$
PL	0.57	0.62	0.62	0.58	0.55	0.42	0.48	0.57	0.59	0.35	$0.53 \pm 0.028$
PW	0.33	0.54	0.51	0.43	0.53	0.24	0.42	0.46	0.51	0.14	$0.41 \pm 0.043$
BT	0.56	0.53	0.55	0.55	0.46	0.49	0.53	0.60	0.61	0.46	$0.53 \pm 0.017$
HSW	0.57	0.59	0.59	0.62	0.53	0.60	0.53	0.53	0.52	0.56	$0.56{\pm}0.011$
PWT	0.60	0.60	0.60	0.62	0.61	0.40	0.41	0.50	0.62	0.29	$0.53 \pm 0.038$
YLD	0.59	0.61	0.60	0.61	0.52	0.60	0.43	0.58	0.60	0.47	$0.56 \pm 0.020$
SPAD1	0.56	0.62	0.60	0.58	0.57	0.56	0.57	0.56	0.57	0.57	$0.58 \pm 0.007$
SPAD2	0.60	0.60	0.59	0.61	0.56	0.56	0.46	0.60	0.59	0.45	$0.56 \pm 0.019$
Mean±se	0.55±0.023	$0.60 \pm 0.009$	$0.59 \pm 0.010$	0.58±0.017	$0.54 \pm 0.011$	$0.50\pm0.034$	$0.46 \pm 0.023$	$0.56 \pm 0.014$	$0.58 \pm 0.011$	$0.43 \pm 0.039$	$0.54 \pm 0.022$

<sup>a</sup> Numbers within parenthesis indicate number of accessions in each race, intermediate and wild . B-Bicolor, C-Caudatum, D-Durra, G-Guinea, K-Kafir, sd-S. drummondii

			Races				Intermed	iate Races		Wild	
	B (37) <sup>a</sup>	C (76)	D (47)	G (66)	K (26)	CB (29)	DB (15)	DC (25)	GC (52)	Sd (10)	Mean±SE
DF	0.59	0.59	0.56	0.60	0.61	0.52	0.46	0.53	0.57	0.47	0.55±0.016
PH	0.61	0.59	0.58	0.64	0.54	0.60	0.53	0.56	0.59	0.39	$0.56 \pm 0.022$
EXE	0.56	0.57	0.54	0.60	0.57	0.63	0.42	0.58	0.53	0.47	$0.55 \pm 0.019$
PL	0.57	0.60	0.61	0.59	0.52	0.55	0.43	0.59	0.59	0.51	$0.56 \pm 0.017$
PW	0.33	0.60	0.61	0.51	0.48	0.51	0.50	0.56	0.53	0.47	$0.51 \pm 0.025$
BT	0.61	0.59	0.56	0.61	0.50	0.42	0.41	0.56	0.55	0.46	$0.53 \pm 0.024$
HSW	0.57	0.58	0.51	0.60	0.51	0.58	0.53	0.53	0.61	0.51	$0.55 \pm 0.012$
PWT	0.56	0.58	0.60	0.60	0.49	0.54	0.48	0.56	0.59	0.58	0.56±0.013
YLD	0.54	0.58	0.55	0.58	0.51	0.50	0.46	0.53	0.57	0.45	0.53±0.015
SPAD1	0.60	0.60	0.61	0.58	0.58	0.56	0.50	0.57	0.56	0.52	0.57±0.011
SPAD2	0.60	0.63	0.56	0.59	0.61	0.50	0.50	0.53	0.58	0.51	0.56±0.015
Mean±se	$0.56 \pm 0.024$	$0.60 \pm 0.005$	$0.57 \pm 0.010$	$0.59 \pm 0.009$	$0.54 \pm 0.013$	$0.54{\pm}0.017$	$0.47 \pm 0.013$	$0.55 \pm 0.007$	$0.57 \pm 0.008$	$0.48 \pm 0.014$	0.55±0.017

Table 28g Shannon-Weaver diversity index (H') for quantitative characters in different races, intermediate races and wild types of sorghum reference set pooled over E<sub>3</sub>, E<sub>4</sub> and E5.

<sup>a</sup> Numbers within parenthesis indicate number of accessions in each race, intermediate and wild . B-Bicolor, C-Caudatum, D-Durra, G-Guinea, K-Kafir, sd-S. drummondii.

				Phenotypic Diversity index					
Flowering group	Mean	Maximum Similarity	Between genotypes	Minimum Similarity	Between genotypes				
Group1	0.28	0.03	IS 28849 and IS 28740	0.63	IS 33844 and IS 18821				
Group2	0.27	0.00	IS 29472 and IS 29407	0.54	IS 13848 and IS 13				
Group3	0.25	0.01	IS 13827 and IS 8685	0.57	IS 41724 and IS 35				
Group4	0.24	0.01	IS 26554 and IS 26457	0.57	IS 14206 and IS 9527				
Group5	0.24	0.03	IS 14414 and IS 4963	0.48	IS 24786 and IS 14216				
Group6	0.28	0.10	IS 27390 and IS 6828	0.47	IS 27855 and IS 18758				
Group7	0.30	0.10	IS 33844 and IS 18758	0.56	IS 18829 and IS 18758				
Entire set	0.24	0.00	IS 29472 and IS 29407	0.54	IS 36563 and IS 31533				

 Table 29a
 Phenotypic diversity index in flowering groups and entire sorghum reference set.

## Table.29b Phenotypic diversity index of sorghum reference set at different Environments.

				Phenotypic Diversity index					
Locations	Mean	Maximum Similarity	Between genotypes	Minimum Similarity	Between genotypes				
E <sub>3</sub>	0.22	0.00	IS 23100 and IS 13827	0.50	IS 41724 and IS 2678				
E <sub>4</sub>	0.23	0.01	IS 26457 and IS 25077	0.52	IS 41(52)500 and IS 13				
E <sub>5</sub>	0.23	0.00	IS 22506 and IS 22291	0.50	IS 18821 and IS 9303				
Pooled( $E_3$ , $E_4$ , $E_5$ )	0.22	0.00	SSM 215 and IS 24139	0.50	IS 41(52)500 and IS 13				

E3- UAS, Dharwad irrigated condition, E4- UAS, Dharwad un-irrigated condition, E5 – RARS, Bijapur un-irrigated condition

Table. 30a Least similar (First five accessions) and most similar (First five accessions) accessions based on phenotypic diversity index in each flowering group and in entire set of sorghum reference set at ICRISAT centre, Patancheru, India.

Flowering		Diversity		Diversity
group	Least similar accessions	index	Most similar accessions	index
	IS 33844 and IS 18821	0.63	IS 28849 and IS 28740	0.03
	IS 30436 and IS 18821	0.57	IS 31852 and IS 28740	0.07
Group 1	IS 36563 and IS 18879	0.56	IS 19453 and IS 14963	0.07
	IS 18821 and IS 2205	0.55	IS 3511 and IS 3507	0.08
	IS 30417 and IS 18821	0.54	IS 18919 and IS 18879	0.09
	IS 13848 and IS 13	0.54	IS 29472 and IS 29407	0.00
	IS 32050 and IS 13	0.53	IS 4821 and IS 4285	0.01
Group 2	IS 393(411)659 and IS 18868	0.53	IS 29496 and IS 29375	0.01
	IS 28645 and IS 13	0.53	IS 29569 and IS 29375	0.01
	IS 24009 and IS 14259	0.53	Image: Sity         Image: Most similar accessions           3         IS 28849 and IS 28740           7         IS 31852 and IS 28740           6         IS 19453 and IS 14963           5         IS 3511 and IS 3507           4         IS 18919 and IS 18879           4         IS 29472 and IS 29407           3         IS 4821 and IS 4285           3         IS 29496 and IS 29375           3         IS 29569 and IS 29496           7         IS 13827 and IS 8685           5         IS 19053 and IS 20700           4         IS 27490 and IS 22291           4         SSM12 and IS 7277           7         IS 26554 and IS 7889           0         IS 24139 and IS 23100           0         IS 23100 and IS 11026           8         IS 24939 and IS 3885           6         IS 14414 and IS 4963           8         IS 24939 and IS 11374           7         IS 27390 and IS 6828           4         IS 31195 and IS 16186           3	0.01
	IS 41724 and IS 35	0.57	IS 13827 and IS 8685	0.01
	IS 102(111)525 and IS 18800	0.55	IS 19053 and IS 2416	0.01
Group 3	IS 13989 and IS 35	0.55	IS 32569 and IS 20700	0.01
	Diversity         index         Most similar accessions           Least similar accessions         index         Most similar accessions           S 33844 and IS 18821         0.63         IS 28849 and IS 28740           S 36563 and IS 18879         0.56         IS 19453 and IS 14963           S 18821 and IS 2205         0.55         IS 3511 and IS 3507           S 30417 and IS 18821         0.54         IS 18919 and IS 18879           IS 13848 and IS 13         0.54         IS 29472 and IS 29407           IS 32050 and IS 13         0.53         IS 29496 and IS 29375           IS 28645 and IS 13         0.53         IS 29459 and IS 29375           IS 24009 and IS 14259         0.53         IS 29569 and IS 29496           IS 12724 and IS 35         0.57         IS 13827 and IS 8685           IS 102(111)525 and IS 18800         0.55         IS 19053 and IS 22291           SM1049 and IS 447(471)496         0.54         SSM12 and IS 22291           SM1049 and IS 447(471)496         0.54         IS 26554 and IS 7889           IS 12266 and IS 14206         0.57         IS 26554 and IS 7889           IS 14206 and IS 9227         0.57         IS 26554 and IS 23100           IS 14206 and IS 14206         0.50         IS 24139 and IS 23100           IS 14266 and IS	0.02		
	SSM1049 and IS 447(471)496	0.54	SSM12 and IS 7277	0.02
	IS 14206 and IS 9527	0.57	IS 26554 and IS 26457	0.01
	IS 18758 and IS 14206	0.57	IS 26554 and IS 7889	0.01
Group 4	IS 21126 and IS 13926	0.51	IS 26457 and IS 7889	0.02
DIS33844 and IS18821 $0.6$ IS30436 and IS18821 $0.5$ Group 1IS36563 and IS18879 $0.5$ IS18821 and IS2205 $0.5$ IS30417 and IS18821 $0.5$ IS32050 and IS13 $0.5$ IS32050 and IS13 $0.5$ IS23050 and IS13 $0.5$ IS24009 and IS14868 $0.5$ IS24009 and IS14259 $0.5$ IS120(111)525 and IS18800 $0.5$ IS102(111)525 and IS18800 $0.5$ IS102(111)525 and IS18800 $0.5$ IS102(111)525 and IS $0.5$ IS102(111)525 and IS $0.5$ IS1120(111)525 and IS $0.5$ IS1202(111)525 and IS $0.5$ IS14206 and IS $9527$ 0.57IS18758 and IS1S14206 and IS $1926$ 0.59IS14206 and IS1S24786 and IS142060.59IS24786 and IS1S24786 and IS142060.59IS24786 and IS1S24786 and IS142160.44IS24786 and IS1S27855 and IS144IS27855 and IS187580.44IS187580.451S278551S18876 and IS187580.44IS187580	0.50	IS 24139 and IS 23100	0.02	
	IS 14206 and IS 10882	0.50	IS 23100 and IS 11026	0.03
	IS 24786 and IS 14216	0.48	IS 14414 and IS 4963	0.04
	IS 24786 and IS 24503	0.48	IS 24939 and IS 3885	0.04
Group 5	IS 24786 and IS 19466	0.46	IS 14414 and IS 14216	0.06
	IS 24786 and IS 21401	Diversityindex\$\$ 188210.63IS 28849 and IS 28740\$\$ 188210.57IS 31852 and IS 28740\$\$ 188790.56IS 19453 and IS 14963\$\$ 22050.55IS 3511 and IS 3507\$\$ 188210.54IS 18919 and IS 18879\$\$ 130.54IS 29472 and IS 29407\$\$ 130.53IS 29476 and IS 29375\$\$ 130.53IS 29496 and IS 29375\$\$ 130.53IS 29569 and IS 29375\$\$ 142590.53IS 29569 and IS 29375\$\$ 142590.53IS 29569 and IS 29496\$\$ 350.57IS 13827 and IS 8685\$\$ and IS 188000.55IS 19053 and IS 2416\$\$ 350.55IS 32569 and IS 20700\$\$ and IS 350.54IS 27490 and IS 22291IS 447(471)4960.54SSM12 and IS 7277\$\$ 95270.57IS 26554 and IS 26457\$\$ 142060.50IS 24139 and IS 23100\$\$ 108820.50IS 23100 and IS 11026\$\$ 142160.48IS 14414 and IS 4963\$\$ 245030.48IS 24939 and IS 3885\$\$ 194660.46IS 14216 and IS 4963\$\$ 245030.48IS 214139 and IS 22099\$\$ 187580.44IS 31195 and IS 22059\$\$ 187580.44IS 31195 and IS 22059\$\$ 187580.44IS 31195 and IS 23254\$\$ 187580.55IS 2369 and IS 23554\$\$ 187580.56IS 33844 and IS 18758\$\$ 220	0.06	
	IS 18758 and IS 14216	0.43	SSM249 and IS 11374	0.07
	IS 27855 and IS 18758	0.47	IS 27390 and IS 6828	0.10
	IS 33844 and IS 27855	0.44	IS 31195 and IS 22609	0.10
Group 6	IS 18876 and IS 18758	0.44	IS 31195 and IS 16186	0.11
	Diversity           Least similar accessions         index         Most similar accessions           IS 33844 and IS 18821         0.63         IS 28849 and IS 28740           IS 30436 and IS 18821         0.57         IS 31852 and IS 28740           IS 36563 and IS 18879         0.56         IS 19453 and IS 14963           IS 18821 and IS 2205         0.55         IS 3111 and IS 3507           IS 30417 and IS 18821         0.54         IS 29472 and IS 29407           IS 32050 and IS 13         0.53         IS 4821 and IS 4285           IS 393(411)659 and IS 18868         0.53         IS 29472 and IS 29375           IS 24009 and IS 14259         0.53         IS 29569 and IS 29375           IS 24009 and IS 14259         0.55         IS 19053 and IS 29496           IS 41724 and IS 35         0.57         IS 13827 and IS 8685           IS 102(111)525 and IS 18800         0.55         IS 2769 and IS 22291           SSM1049 and IS 447(47)1496         0.54         IS 27490 and IS 22291           SSM1049 and IS 14206         0.57         IS 2654 and IS 7889           IS 21126 and IS 13926         0.51         IS 2654 and IS 24657           IS 18758 and IS 14206         0.50         IS 24139 and IS 14206           IS 24786 and IS 14206         0.50         IS 241	0.11		
	IS 18876 and IS 2205	Index         Most similar accessions           11         0.63         IS 28849 and IS 28740           121         0.57         IS 31852 and IS 28740           129         0.56         IS 19453 and IS 14963           130         0.55         IS 3511 and IS 3507           141         0.54         IS 29472 and IS 29407           0.54         IS 29472 and IS 29407           0.53         IS 4821 and IS 4285           S 18868         0.53         IS 29569 and IS 29375           09         0.53         IS 29569 and IS 29375           09         0.53         IS 29569 and IS 29375           0.53         IS 29569 and IS 29375           0.54         IS 29569 and IS 29375           0.55         IS 13827 and IS 8685           S 18800         0.55           0.55         IS 2569 and IS 20700           S 35         0.54           0.57         IS 26554 and IS 26457           04         0.57           15 26554 and IS 7889           06         0.50           0.50         IS 23100 and IS 11026           06         0.50           0.50         IS 24139 and IS 3485           06         0.51	0.11	
	IS 31533 and IS 18758	0.56	IS 33844 and IS 18758	0.10
	IS 18829 and IS 18758	0.55	IS 25077 and IS 3957	0.11
Group 7	IS 18835 and IS 18758	0.51	IS 32454 and IS 23669	0.13
-	IS 33844 and IS 18829	0.47	IS 23669 and IS 3957	0.13
IS 30505 and IS 1000         IS 18821 and IS 220         IS 30417 and IS 188         IS 13848 and IS 13         IS 32050 and IS 13         Group 2       IS 393(411)659 and         IS 28645 and IS 13         IS 24009 and IS 142         IS 41724 and IS 35         IS 102(111)525 and         Group 3       IS 13989 and IS 35         IS 102(111)525 and         SSM1049 and IS 44         IS 14206 and IS 952         IS 18758 and IS 142         Group 4       IS 21126 and IS 139         IS 14206 and IS 142         IS 24786 and IS 142         IS 27855 and IS 187         IS 33844 and IS 278         Group 6       IS 18876 and IS 187         IS 18829 and IS 187         IS 18829 and IS 187         IS 33844 and IS 188         IS 33844 and IS 315         IS 36563 and IS 315         IS 41724 and IS 142         Entire set       IS 18758 and IS	IS 33844 and IS 31533	0.46	IS 33844 and IS 32454	0.15
	IS 36563 and IS 31533	0.54	IS 29472 and IS 29407	0.00
	IS 41724 and IS 14206	0.54	IS 26554 and IS 26457	0.00
Entire set	IS 18758 and IS 14571	0.54	IS 6154 and IS 5972	0.00
	SSM19 and IS 18821	0.54	IS 23053 and IS 20351	0.00
	IS 31179 and IS 18821	Diversity           index         Most similar accessions           0.63         IS 28849 and IS 28740           0.57         IS 31852 and IS 28740           0.56         IS 19453 and IS 14963           0.55         IS 3511 and IS 3507           0.54         IS 29472 and IS 29407           0.53         IS 4821 and IS 4285           0.53         IS 29496 and IS 29375           0.53         IS 29569 and IS 29375           0.53         IS 29569 and IS 29375           0.53         IS 29569 and IS 29496           0.57         IS 13827 and IS 8685           18800         0.55         IS 19053 and IS 2416           0.55         IS 32569 and IS 20700           35         0.54         IS 27490 and IS 22291           71)496         0.54         SSM12 and IS 7277           0.57         IS 26554 and IS 7489           0.51         IS 26554 and IS 7489           0.50         IS 24139 and IS 23100           0.50         IS 24139 and IS 3885           0.46         IS 14414 and IS 4963           0.48         IS 24939 and IS 3885           0.46         IS 14216 and IS 4963           0.48         IS 24939 and IS 31374           0.4	0.00	

		Diversity		Diversity
Environment	Least similar accessions	index	Most similar accessions	index
	IS 41724 and IS 2678	0.50	IS 7889 and IS 2848	0.00
	IS 18821 and IS 2678	0.48	IS 22506 and IS 7889	0.00
$E_3$	IS 18821 and IS 9303	0.46	IS 29569 and IS 22239	0.01
	IS 22332 and IS 18821	0.46	IS 32986 and IS 23669	0.01
	SSM1123 and IS 18821	0.45	IS 24887 and IS 19026	0.01
	IS 41 (52) 500 and IS 13	0.52	IS 26457 and IS 25077	0.01
	IS 19455 and IS 13	0.50	IS 26457 and IS 7889	0.01
$E_4$	SSM275 and IS 30409	0.50	IS 29496 and IS 22239	0.01
	IS 36563 and IS 30335	0.49	IS 29876 and IS 2848	0.01
	IS 36563 and IS 30409	0.49	IS 22291 and IS 7889	0.01
	IS 18821 and IS 9303	0.49	IS 22506 and IS 22291	0.00
	IS 19455 and IS 13	0.48	IS 29496 and IS 27164	0.01
$E_5$	IS 30175 and IS 18821	0.47	IS 29407 and IS 22334	0.01
	IS 24939 and IS 19455	0.47	IS 28409 and IS 8685	0.01
	IS 36563 and IS 12804	0.47	IS 32986 and IS 14331	0.01
	IS 41(52)500 and IS 13	0.50	SSM215 and IS 24139	0.01
	IS 41724 and IS 2678	0.48	SSM215 and IS 5910	0.01
Pooled ( $E_3$ , $E_4$ , $E_5$ )	IS 18821 and IS 9303	Diversity         Diversity           index         Most similar accessions         ind           0.50         IS 7889 and IS 2848         ind           0.48         IS 22506 and IS 7889         ind           0.46         IS 29569 and IS 22239         ind           0.46         IS 32986 and IS 23669         ind           0.46         IS 32986 and IS 23669         ind           0.46         IS 24887 and IS 19026         is 24887 and IS 19026           1         0.45         IS 26457 and IS 25077           0.50         IS 26457 and IS 7889         is 22239           0.50         IS 29496 and IS 22239           0.49         IS 22506 and IS 22239           0.49         IS 22506 and IS 22291           0.49         IS 22506 and IS 22291           0.48         IS 29496 and IS 27164           0.47         IS 29407 and IS 22334           0.47         IS 29407 and IS 22334           0.47         IS 32986 and IS 14331           0.47         IS 32986 and IS 14331           0.48         SSM215 and IS 24139           0.48         SSM215 and IS 16173           0.47         IS 30441 and IS 30436           0.47         IS 26457 and IS 7889 <td>0.01</td>	0.01	
	IS 36633 and IS 13	0.47	IS 30441 and IS 30436	0.01
	IS 18821 and IS 2678	0.47	IS 26457 and IS 7889	0.01

Table.30b Least similar (First five accessions) and most similar (First five accessions) accessions based on phenotypic diversity index of sorghum reference set at different environments.

 $E_3$ - UAS dharwad, irrigated condition;  $E_4$ - UAS dharwad, Un-irrigated condition;  $E_5$ -ARRS, Bijapur, Un-irrigated condition.

	Principal	Eigen	Variability	Cumulative											
Environments	Components	value	percentage	percentage	DF	PH	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
	PC1	3.4	34.4	34.42	-0.259	-0.351	-0.135	-0.362	-0.371	-0.337	*	0.374	0.376	0.347	0.085
	PC2	2.2	21.7	56.15	0.393	0.369	-0.241	0.030	0.067	-0.288		0.395	0.390	-0.369	-0.344
E1	PC3	1.2	12.1	68.22	-0.453	0.154	0.668	0.096	0.029	0.109		0.175	0.208	0.018	-0.479
	PC4	1.2	11.9	80.15	-0.057	0.084	0.070	0.573	0.446	-0.275		0.217	0.180	0.344	0.428
	PC5	0.8	8.4	88.50	0.339	0.394	0.526	-0.115	-0.456	-0.296		-0.086	-0.073	0.045	0.360
	PC1	3.3	30.2	30.15	0.182	0.327	0.138	0.333	0.197	0.382	-0.309	-0.381	-0.349	-0.340	-0.258
	PC2	2.1	19.1	49.24	0.503	0.295	-0.288	-0.049	-0.197	-0.211	0.084	0.298	0.302	-0.379	-0.400
E2	PC3	1.3	11.7	60.92	0.053	0.421	0.365	0.488	0.393	-0.148	0.222	0.267	0.269	0.173	0.224
	PC4	1.2	11.2	72.09	-0.223	0.215	0.540	-0.098	-0.487	-0.150	0.468	-0.188	-0.156	-0.133	-0.214
	PC5	0.8	7.1	79.15	-0.366	-0.174	0.350	-0.127	0.095	0.403	-0.225	0.333	0.455	-0.230	-0.322
	PC1	3.5	35.2	35.20	-0.226	-0.353	-0.144	-0.348	-0.325	-0.359	*	0.369	0.361	0.356	0.234
Pooled (E1,E2)	PC2	2.3	22.5	57.70	0.437	0.312	-0.274	-0.044	-0.062	-0.262		0.363	0.365	-0.371	-0.399
	PC3	1.2	12.1	69.82	-0.070	0.249	0.264	0.553	0.443	-0.200		0.319	0.294	0.246	0.270
	PC4	1.0	10.3	80.16	-0.257	0.261	0.779	-0.152	-0.370	-0.035		0.058	0.107	-0.102	-0.270
	PC5	0.8	7.8	87.91	0.523	0.289	0.095	0.070	-0.425	-0.346		-0.227	-0.233	0.170	0.440
	PC1	2.0	18.2	18.19	-0.202	-0.193	0.027	-0.376	-0.343	0.013	0.298	0.507	0.505	0.242	0.047
	PC2	1.8	16.7	34.93	0.129	0.471	0.260	0.444	0.249	0.123	-0.171	0.430	0.437	-0.116	0.028
E3	PC3	1.5	14.0	48.97	-0.398	0.117	0.584	0.062	-0.089	0.505	0.138	-0.200	-0.202	0.267	0.223
	PC4	1.3	11.4	60.35	-0.296	-0.224	-0.198	0.269	0.546	-0.268	0.019	0.040	0.041	0.566	0.239
	PC5	1.1	10.0	70.39	0.506	0.261	-0.050	-0.060	-0.135	-0.139	0.281	-0.076	-0.050	0.137	0.725
	PC1	2.2	20.1	20.05	0.276	0.403	0.182	0.498	0.427	0.016	-0.299	-0.294	-0.316	-0.146	-0.034
	PC2	1.9	17.4	37.41	0.086	0.235	0.212	0.275	0.212	0.028	0.620	-0.016	0.610	0.056	0.100
E4	PC3	1.3	12.0	49.45	0.553	0.052	-0.508	-0.068	-0.003	-0.393	0.019	-0.074	0.010	0.258	0.448
	PC4	1.2	11.2	60.67	-0.192	-0.135	0.163	0.167	0.129	0.418	-0.132	0.113	-0.119	0.647	0.485
	PC5	1.0	9.3	69.95	-0.277	-0.364	-0.340	0.288	0.586	-0.307	0.012	0.356	0.002	0.001	-0.166
	PC1	2.1	19.3	19.27	-0.057	-0.304	-0.269	-0.280	-0.304	-0.295	0.307	0.464	0.451	0.195	0.151
	PC2	1.7	15.4	34.69	0.278	0.383	0.252	0.309	0.223	0.046	-0.222	0.497	0.509	-0.060	-0.079
E5	PC3	1.3	12.0	46.66	-0.535	0.057	0.438	0.033	0.329	-0.012	0.181	0.046	-0.007	0.597	0.133
	PC4	1.1	9.8	56.43	0.302	0.230	-0.072	-0.017	-0.111	0.463	0.183	-0.038	-0.035	0.153	0.751
	PC5	0.9	8.4	64.85	0.194	-0.340	-0.266	-0.345	0.399	0.439	-0.359	0.076	0.057	0.358	-0.198
	PC1	2.5	22.2	22.23	-0.197	-0.301	-0.128	-0.384	-0.328	-0.134	0.320	0.437	2.45	22.23	22.23
	PC2	1.7	15.8	38.06	0.220	0.352	0.145	0.411	0.353	-0.073	-0.088	0.491	1.74	15.83	38.06
Pooled(E3,E4,E5)	PC3	1.5	13.3	51.33	-0.485	0.015	0.584	0.098	0.021	0.458	0.079	-0.060	1.46	13.26	51.33
	PC4	1.2	10.5	61.83	-0.053	-0.246	-0.334	0.208	0.330	-0.377	0.040	-0.187	1.16	10.50	61.83
	PC5	1.1	9.9	71.73	0.466	0.414	-0.004	-0.263	-0.419	0.114	-0.013	-0.113	1.09	9.90	71.73

Table. 31 Vector loading and percentage of variation explained by the first five principal components in different environments of sorghum reference set.

\*-Data not recorded.

E1- ICRISAT, Patancheru during 2008-09, E2- ICRISAT, Patancheru during 2009-10, E3- UAS, Dharwad irrigated condition, E4- UAS, Dharwad un-irrigated condition, E5 – RARS, Bijapur un-irrigated condition.

## PC- Principal Component.
Flowering group	РС	Eigen value	Variability percentage	Cumulative Percentage	DF	РН	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
	PC1	3.7	36.9	36.9	0.454	0.204	-0.270	0.001	0.089	-0.440	0.451	0.463	0.031	-0.243
Group 1	PC2	2.3	23.3	60.3	0.040	0.412	0.322	0.546	0.546	-0.111	-0.176	-0.170	0.175	-0.163
	PC3	1.4	13.5	73.8	-0.110	-0.297	-0.044	0.242	-0.051	-0.288	0.101	0.074	0.687	0.515
	PC1	3.0	29.8	29.8	0.141	-0.053	-0.247	-0.267	-0.277	-0.441	0.521	0.523	0.025	-0.167
Group 2	PC2	2.4	23.9	53.8	-0.360	-0.432	0.040	-0.234	-0.362	-0.126	-0.115	-0.108	0.491	0.463
	PC3	1.8	17.7	71.5	-0.317	0.209	0.496	-0.475	-0.407	0.193	-0.054	0.007	-0.266	-0.329
	PC1	3.5	35.4	35.4	0.000	0.332	0.260	0.405	0.371	0.401	-0.371	-0.373	-0.254	-0.138
Group 3	PC2	2.1	21.4	56.8	-0.357	-0.326	0.209	-0.017	-0.199	0.166	-0.337	-0.337	0.477	0.447
	PC3	1.5	14.8	71.6	0.577	-0.199	-0.549	-0.136	0.056	0.021	-0.291	-0.336	-0.160	0.282
	PC1	4.1	41.0	41.0	-0.051	-0.335	-0.286	-0.323	-0.401	-0.340	0.402	0.417	0.261	0.137
Group 4	PC2	2.0	20.0	60.9	-0.356	-0.305	0.340	0.270	0.021	0.061	-0.133	-0.137	0.481	0.565
	PC3	1.3	13.2	74.1	0.433	-0.321	-0.366	-0.367	-0.086	0.422	-0.335	-0.300	0.129	0.192
	PC1	3.5	34.9	34.9	0.139	0.156	0.106	0.404	0.377	0.468	-0.439	-0.438	-0.186	-0.049
Group 5	PC2	2.0	19.5	54.4	0.155	-0.399	-0.136	0.093	-0.144	0.060	-0.177	-0.233	0.575	0.590
	PC3	1.7	17.0	71.4	-0.431	0.267	0.599	0.396	0.108	-0.081	0.179	0.171	0.204	0.326
	PC1	4.9	48.5	48.5	0.323	0.398	0.206	0.316	0.335	0.264	-0.387	-0.381	0.158	0.306
Group 6	PC2	1.8	17.6	66.1	-0.064	0.182	0.287	-0.051	-0.249	-0.433	0.193	0.120	0.648	0.396
	PC3	1.4	14.4	80.5	-0.469	-0.012	0.493	0.482	0.415	-0.191	0.127	0.144	-0.135	-0.200
	PC1	4.3	42.9	42.9	0.270	0.413	0.271	0.394	0.361	0.340	-0.382	-0.350	0.080	0.080
Group 7	PC2	2.8	27.7	70.5	-0.306	0.077	0.238	-0.137	-0.228	-0.284	-0.180	-0.172	0.561	0.561
	PC3	1.5	15.1	85.6	-0.411	-0.159	0.244	0.400	0.349	0.280	0.355	0.455	0.164	0.164

Table. 32a Vector loading and percentage of variation explained by the first three principal components in flowering groups of sorghum reference set at E1.

Flowering	РС	Eigen value	Variability Percentage	Cumulative Percentage	DF	рн	EXE	PL.	PW	BT	HSW	рут	VLD	SPAD1	SPAD2
group	10	value	Tertentage	I creentage	0.000		EAE	112		0.101	11517	1.01	1110	STADT	STAD2
	PCI	3.1	28.0	28.0	0.356	0.112	-0.322	-0.053	0.131	-0.434	0.306	0.452	0.456	0.167	0.118
Group 1	PC2	1.8	16.5	44.5	-0.037	0.381	0.255	0.659	0.508	-0.034	-0.190	0.064	0.061	-0.100	0.205
	PC3	1.8	16.4	60.8	-0.354	-0.256	0.244	0.085	-0.080	-0.119	0.262	-0.074	-0.026	0.571	0.567
	PC1	2.6	23.9	23.9	0.112	0.273	0.139	0.488	0.532	0.387	-0.345	-0.276	-0.149	-0.017	0.076
Group 2	PC2	2.3	21.2	45.1	-0.471	-0.358	0.231	-0.033	-0.120	0.132	-0.042	-0.309	-0.128	0.475	0.474
	PC3	1.7	15.6	60.7	-0.303	0.308	0.534	-0.178	-0.128	0.086	0.312	-0.308	-0.273	-0.305	-0.338
	PC1	3.8	34.3	34.3	0.058	0.298	0.194	0.350	0.341	0.408	-0.313	-0.397	-0.395	-0.188	-0.133
Group 3	PC2	2.1	19.4	53.6	-0.485	-0.254	0.349	0.124	-0.073	0.162	0.027	-0.154	-0.146	0.517	0.467
	PC3	1.3	11.9	65.6	0.165	0.354	0.317	0.402	0.377	-0.124	0.024	0.424	0.412	0.127	0.249
	PC1	4.1	37.4	37.4	-0.011	-0.287	-0.246	-0.274	-0.342	-0.375	0.244	0.405	0.394	0.300	0.236
Group 4	PC2	2.2	19.6	57.0	0.535	0.350	-0.363	-0.190	0.079	-0.153	-0.045	0.203	0.185	-0.352	-0.439
	PC3	1.1	10.4	67.4	-0.187	0.373	0.315	0.565	-0.035	-0.176	0.465	0.233	0.283	-0.120	-0.103
	PC1	3.6	32.8	32.8	-0.015	-0.088	-0.223	-0.278	-0.251	-0.432	0.291	0.464	0.461	0.182	0.264
Group 5	PC2	2.4	21.4	54.2	0.473	-0.081	-0.388	-0.439	-0.216	-0.025	-0.324	-0.003	-0.058	-0.448	-0.265
	PC3	1.3	11.9	66.1	0.371	0.765	-0.042	0.067	0.395	-0.072	0.235	0.077	0.166	-0.147	-0.011
	PC1	3.9	35.2	35.2	0.083	0.273	0.257	0.342	0.372	0.418	-0.277	-0.405	-0.384	-0.026	0.183
Group 6	PC2	2.8	25.6	60.8	-0.172	0.314	0.422	0.300	0.242	-0.176	0.433	0.267	0.318	0.237	0.313
	PC3	1.6	14.9	75.7	0.259	-0.022	0.034	-0.325	-0.270	0.007	-0.183	-0.156	0.019	0.655	0.516
	PC1	5.4	49.3	49.3	-0.155	-0.154	-0.142	-0.391	-0.304	-0.346	0.390	0.407	0.338	0.288	0.227
Group 7	PC2	2.2	19.8	69.2	-0.268	0.409	0.548	0.106	0.049	-0.024	0.077	-0.109	-0.199	0.472	0.408
	PC3	1.5	14.0	83.2	0.604	0.358	-0.284	0.089	-0.438	-0.285	0.024	-0.153	-0.276	0.034	0.212

Table. 32b Vector loading and percentage of variation explained by the first three principal components in flowering groups of sorghum reference set at E2.

PC- Principal Component.

DF- Days to 50% flowering, PH- Plant height, EXE- Panicle exerstion, PL- Panicle length, PW- Panicle width, BT- Basal tiller, HSW- Hundred seed weight, PWT- Panicle weight, YLD- Grain yield per plot, SPAD1- SCMR at flowering, SPAD2- SCMR 30 days after flowering.

Flowering group	РС	Eigen value	Variability Percentage	Cumulative Percentage	DF	РН	EXE	PL	PW	BT	PWT	YLD	SPAD1	SPAD2
	PC1	3.2	31.6	31.6	0.427	0.162	-0.312	-0.007	0.122	-0.457	0.475	0.486	0.049	-0.075
Group 1	PC2	2.0	19.6	51.2	-0.013	0.371	0.301	0.644	0.514	-0.130	-0.081	-0.067	0.158	0.198
	PC3	1.7	17.2	68.4	-0.256	-0.351	0.118	-0.009	-0.201	-0.159	0.189	0.166	0.571	0.585
	PC1	3.1	30.5	30.5	0.223	-0.009	-0.275	-0.264	-0.249	-0.403	0.504	0.500	-0.119	-0.250
Group 2	PC2	2.5	24.8	55.3	0.357	0.464	-0.002	0.306	0.429	0.165	0.032	0.021	-0.442	-0.394
	PC3	1.7	17.1	72.4	0.311	-0.172	-0.454	0.454	0.375	-0.166	0.126	0.050	0.361	0.380
	PC1	3.7	36.8	36.8	0.011	0.326	0.232	0.384	0.376	0.402	-0.391	-0.389	-0.244	-0.160
Group 3	PC2	2.2	22.2	58.9	-0.448	-0.282	0.279	0.051	-0.161	0.175	-0.251	-0.255	0.504	0.448
	PC3	1.3	12.9	71.8	-0.372	0.276	0.579	0.295	0.047	-0.111	0.390	0.419	0.054	-0.136
	PC1	4.3	42.8	42.8	-0.022	-0.314	-0.265	-0.296	-0.383	-0.363	0.407	0.413	0.294	0.206
Group 4	PC2	2.2	21.6	64.3	-0.462	-0.325	0.368	0.230	-0.027	0.111	-0.181	-0.164	0.416	0.496
	PC3	1.1	11.0	75.3	-0.134	0.385	0.391	0.535	0.054	-0.404	0.342	0.321	0.000	-0.086
	PC1	3.6	36.4	36.4	0.070	0.148	0.182	0.355	0.368	0.455	-0.448	-0.435	-0.187	-0.215
Group 5	PC2	2.0	20.0	56.3	0.494	-0.079	-0.432	-0.417	-0.118	0.018	-0.078	-0.074	-0.397	-0.453
	PC3	1.4	13.5	69.8	-0.047	0.694	0.278	-0.029	0.169	-0.132	0.255	0.339	-0.419	-0.193
	PC1	4.6	46.2	46.2	-0.271	-0.367	-0.262	-0.329	-0.361	-0.336	0.384	0.376	-0.110	-0.266
Group 6	PC2	2.0	20.3	66.5	0.043	0.205	0.278	-0.075	-0.252	-0.274	0.212	0.199	0.623	0.511
	PC3	1.6	15.5	82.0	0.504	-0.118	-0.438	-0.475	-0.311	0.273	-0.246	-0.168	0.225	0.060
	PC1	4.7	46.6	46.6	-0.250	-0.366	-0.271	-0.415	-0.335	-0.337	0.425	0.374	0.047	-0.099
Group 7	PC2	2.6	26.4	73.0	-0.258	0.157	0.289	-0.097	-0.210	-0.269	-0.111	-0.147	0.595	0.558
	PC3	1.4	14.4	87.4	0.542	0.221	-0.372	-0.224	-0.412	-0.341	-0.227	-0.350	-0.096	-0.013

 Table. 32c Vector loading and percentage of variation explained by the three five principal components in flowering groups of sorghum reference set pooled over E1 and E2.

PC- Principal Component.

DF- Days to 50% flowering, PH- Plant height, EXE- Panicle exerstion, PL- Panicle length, PW- Panicle width, BT- Basal tiller, HSW- Hundred seed weight, PWT- Panicle weight, YLD- Grain yield per plot, SPAD1- SCMR at flowering, SPAD2- SCMR 30 days after flowering.

Environments	Races	РС	Eigen value	Variability (%)	Cumulative %	DF	РН	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
		PC1	3.2	32.2	32.2	-0.310	-0.367	-0.134	-0.350	-0.327	-0.300	*	0.370	0.387	0.362	0.122
	Races	PC2	2.2	21.5	53.7	0.286	0.366	-0.279	-0.014	0.125	-0.300	*	0.421	0.404	-0.387	-0.332
		PC3	1.4	13.6	67.3	-0.217	0.107	0.245	0.579	0.486	-0.279	*	0.210	0.172	0.290	0.275
E1	Intermediate	PC1	3.1	30.7	30.7	0.306	0.025	-0.352	-0.164	-0.068	-0.380	*	0.468	0.479	-0.301	-0.260
	Races	PC2	2.2	22.1	52.8	0.363	0.583	0.272	0.398	0.415	-0.047	*	-0.106	-0.071	-0.259	-0.196
		PC3	1.7	16.5	69.3	-0.236	-0.155	-0.043	0.463	0.468	-0.287	*	0.290	0.234	0.488	0.158
		PC1	3.3	33.0	33.0	0.450	0.473	-0.285	0.404	0.378	-0.014	*	-0.151	-0.144	-0.358	-0.122
	Wilds	PC2	2.7	27.2	60.2	-0.273	-0.173	0.147	0.136	0.236	0.515	*	-0.506	-0.507	0.067	0.127
		PC3	1.3	13.5	73.6	-0.186	0.099	0.581	0.488	0.398	-0.054	*	0.264	0.225	0.263	-0.169
		PC1	3.3	29.8	29.8	-0.164	-0.284	-0.154	-0.346	-0.206	-0.375	0.304	0.412	0.390	0.304	0.244
	Races	PC2	2.3	20.9	50.6	0.475	0.342	-0.299	-0.089	-0.190	-0.198	0.127	0.222	0.232	-0.451	-0.402
		PC3	1.2	11.2	61.9	-0.046	0.511	0.489	0.426	0.200	-0.157	0.354	0.217	0.208	0.066	0.181
E2	Intermediate	PC1	2.8	25.5	25.5	0.375	-0.010	-0.392	-0.149	-0.159	-0.358	-0.073	0.436	0.416	-0.291	-0.277
	Races	PC2	2.0	18.6	44.1	0.352	0.609	0.270	0.290	0.071	0.093	-0.034	-0.205	-0.134	-0.356	-0.384
		PC3	1.7	15.5	59.6	0.155	0.117	0.037	0.512	0.566	-0.289	-0.061	0.288	0.149	0.351	0.250
		PC1	3.3	30.1	30.1	0.450	0.408	-0.319	0.096	-0.103	0.060	-0.010	-0.292	-0.318	-0.407	-0.391
	Wilds	PC2	2.2	19.8	49.9	0.160	0.184	-0.146	0.491	0.594	0.443	-0.072	0.023	0.279	0.092	0.190
		PC3	1.7	15.5	65.4	0.196	0.369	-0.101	0.133	-0.040	-0.471	0.545	0.388	0.288	0.196	-0.077
		PC1	3.5	34.7	34.7	-0.250	-0.346	-0.144	-0.325	-0.288	-0.342	*	0.378	0.378	0.360	0.275
	Races	PC2	2.3	23.0	57.7	-0.391	-0.319	0.330	0.135	0.061	0.265	*	-0.342	-0.342	0.404	0.382
		PC3	1.3	12.8	70.4	-0.109	0.276	0.222	0.552	0.499	-0.259	*	0.315	0.280	0.148	0.207
Pooled over (F1 and F2)	Intermediate	PC1	3.2	31.6	31.6	0.270	-0.056	-0.373	-0.179	-0.131	-0.391	*	0.455	0.462	-0.274	-0.296
(ET and E2)	Races	PC2	2.3	23.0	54.6	0.422	0.577	0.164	0.400	0.299	0.048	*	-0.087	-0.064	-0.345	-0.281
		PC3	1.7	16.7	71.3	-0.043	-0.020	-0.010	0.432	0.518	-0.337	*	0.300	0.215	0.427	0.333
		PC1	3.7	36.6	36.6	0.258	0.335	-0.200	0.442	0.377	0.268	*	-0.359	-0.325	-0.298	-0.222
	Wilds	PC2	2.8	28.2	64.8	0.485	0.348	-0.293	-0.136	-0.195	-0.355	*	0.333	0.313	-0.291	-0.287
		PC3	1.1	11.4	76.1	0.167	0.104	-0.652	-0.071	0.075	0.025	*	-0.019	-0.043	0.291	0.662

Table. 33 Vector loading and percentage of variation explained by the first three principal components in races intermediate races and wilds as group of sorghum reference set in different environments.

Environments	Races	РС	Eigen value	Variability (%)	Cumulative %	DF	РН	EXE	PL	PW	BT	HSW	PWT	YLD	SPAD1	SPAD2
		PC1	2.3	20.7	20.7	0.256	0.399	0.179	0.492	0.391	0.058	-0.241	-0.352	-0.378	-0.120	-0.077
	Races	PC2	1.8	16.5	37.2	0.152	0.275	0.239	0.287	0.240	-0.002	-0.023	0.603	0.581	-0.024	0.036
		PC3	1.4	12.4	49.5	0.534	0.100	-0.401	0.008	0.036	-0.325	0.120	-0.032	-0.012	0.468	0.450
		PC4	1.2	11.2	60.7	-0.339	-0.091	0.466	0.193	0.115	0.236	0.379	-0.090	-0.092	0.531	0.334
F2		PC1	2.3	20.6	20.6	0.279	0.398	0.223	0.479	0.421	-0.019	-0.329	-0.259	-0.265	-0.236	0.074
E3	Intermediate races	PC2	2.0	18.0	38.6	-0.040	0.006	0.057	0.313	0.280	-0.012	-0.221	0.611	0.593	0.166	0.134
		PC3	1.3	12.1	50.7	0.226	-0.176	-0.477	0.030	0.136	-0.302	-0.062	-0.102	-0.196	0.447	0.572
		PC4	1.3	11.3	62.0	-0.541	-0.188	0.162	0.208	0.250	0.560	0.085	-0.204	-0.160	0.357	0.155
		PC1	2.9	26.0	26.0	0.291	0.342	0.173	0.244	0.221	0.273	0.187	0.506	0.525	0.140	-0.009
		PC2	2.3	21.3	47.3	0.237	0.444	0.084	0.402	0.355	-0.372	-0.258	-0.235	-0.199	-0.286	-0.266
	Wilds	PC3	1.7	15.8	63.1	-0.317	-0.083	-0.236	0.436	0.476	0.251	-0.065	-0.189	-0.142	0.470	0.276
		PC4	1.4	12.9	76.0	0.490	0.064	-0.317	-0.061	-0.173	-0.189	-0.482	0.077	0.053	0.166	0.563
		PC1	2.0	18.2	18.2	-0.225	-0.154	0.084	-0.377	-0.363	0.090	0.297	0.464	0.472	0.290	0.160
	Races	PC2	1.7	15.7	33.9	0.224	0.464	0.139	0.405	0.248	0.068	-0.174	0.467	0.463	-0.146	0.035
		PC3	1.6	14.9	48.8	-0.348	0.234	0.618	0.204	-0.032	0.483	0.065	-0.192	-0.206	0.233	0.168
		PC4	1.2	11.1	59.9	-0.314	-0.247	-0.191	0.280	0.551	-0.257	-0.007	0.020	0.070	0.507	0.307
F4	<b>x</b> . <b>x</b> .	PC1	2.2	19.5	19.5	0.170	0.480	0.346	0.538	0.335	0.157	-0.331	0.059	0.133	-0.241	-0.076
L7	Intermediate races	PC2	2.1	19.1	38.6	-0.024	-0.016	0.161	-0.167	-0.325	0.070	0.095	0.610	0.624	-0.174	-0.184
		PC3	1.4	12.6	51.2	-0.412	0.032	0.391	0.026	0.027	0.413	0.096	0.073	0.056	0.448	0.535
		PC4	1.2	10.8	62.0	-0.371	-0.093	-0.148	0.284	0.469	-0.452	0.128	0.232	0.178	0.395	-0.264
		PC1	2.7	24.8	24.8	-0.094	0.087	-0.021	-0.397	-0.264	-0.164	0.299	0.479	0.521	-0.103	-0.358
		PC2	2.1	18.9	43.8	-0.421	-0.120	0.539	-0.177	-0.240	0.467	0.361	-0.163	-0.090	0.189	0.106
	Wilds	PC3	1.7	15.1	58.9	-0.131	0.602	0.134	0.266	0.366	0.370	0.092	0.198	0.033	-0.459	-0.040
		PC4	1.6	14.6	73.5	-0.397	-0.248	-0.167	0.286	0.494	-0.115	0.293	-0.014	-0.036	0.299	-0.488
E5		PC1	1.9	17.4	17.4	0.299	0.419	0.324	0.420	0.332	0.252	-0.312	0.258	0.211	-0.205	-0.171
	Races	PC2	1.8	16.4	33.8	0.086	-0.174	-0.150	-0.153	-0.140	-0.092	0.118	0.642	0.663	0.135	0.069
		PC3	1.3	11.6	45.4	-0.451	0.156	0.457	0.075	0.338	-0.190	0.208	0.074	0.028	0.595	0.069
		PC4	1.1	10.1	55.5	0.261	0.315	0.132	-0.072	-0.221	0.391	0.277	-0.037	-0.040	0.100	0.720

Table 33. Contd...

Environments	Races	РС	Eigen value	Variability (%)	Cumulative %	DF	РН	EXE	PL	PW	вт	HSW	PWT	YLD	SPAD1	SPAD2
		PC1	1.9	17.1	17.1	0.071	0.337	0.244	0.235	-0.005	0.104	-0.037	0.604	0.609	0.058	0.125
	Intermediate races	PC2	1.8	16.4	33.5	-0.174	-0.383	-0.269	-0.137	-0.346	0.178	0.466	0.186	0.091	0.453	0.339
		PC3	1.4	12.6	46.1	0.659	0.033	-0.515	-0.135	-0.261	0.236	0.013	0.059	0.111	-0.369	-0.067
		PC4	1.1	10.1	56.2	0.258	0.208	-0.113	0.037	0.484	0.385	-0.197	-0.177	-0.154	0.350	0.527
		PC1	2.4	21.9	21.9	0.066	-0.188	-0.315	-0.307	-0.453	-0.382	0.468	-0.226	-0.241	-0.262	0.137
		PC2	2.1	18.6	40.5	-0.042	-0.409	0.204	-0.395	-0.134	0.075	0.146	0.557	0.518	-0.093	-0.037
	Wilds	PC3	1.7	15.0	55.5	0.386	0.423	-0.346	0.142	-0.106	-0.285	-0.293	0.287	0.339	-0.377	0.122
		PC4	1.3	11.9	67.4	0.640	-0.076	-0.185	-0.378	0.267	0.166	0.002	0.022	-0.101	0.431	0.336
		PC1	2.4	22.1	22.1	-0.224	-0.338	-0.134	-0.422	-0.325	-0.101	0.289	0.419	0.441	0.245	0.097
	Races	PC2	1.6	14.5	36.5	0.125	0.267	0.251	0.389	0.387	0.063	-0.026	0.542	0.490	0.012	0.101
		PC3	1.5	13.4	50.0	-0.448	0.111	0.614	0.035	-0.111	0.422	0.220	-0.108	-0.164	0.328	0.151
		PC4	1.3	11.4	61.3	0.396	0.308	-0.072	-0.018	-0.051	-0.317	0.274	-0.100	-0.148	0.386	0.620
Pooled (F3 F4 and F5)	<b>x</b> , <b>x</b> ,	PC1	2.3	20.6	20.6	0.213	0.408	0.165	0.502	0.446	0.062	-0.368	-0.255	-0.239	-0.209	0.071
(E3, E4 and E3)	Intermediate races	PC2	2.0	17.9	38.5	0.005	0.117	0.153	0.218	0.143	0.124	-0.154	0.558	0.556	0.303	0.380
		PC3	1.5	13.6	52.1	0.567	0.205	-0.284	-0.027	-0.083	-0.238	0.030	0.300	0.298	-0.435	-0.349
		PC4	1.3	11.5	63.5	0.020	0.237	0.502	-0.277	-0.393	0.557	-0.123	-0.066	0.136	-0.332	-0.039
		PC1	2.7	24.2	24.2	0.410	0.458	-0.032	0.096	0.075	-0.123	-0.159	0.442	0.451	-0.344	-0.223
		PC2	2.3	20.5	44.7	0.092	0.159	-0.271	0.474	0.422	-0.384	-0.283	-0.345	-0.368	-0.089	-0.001
	Wilds	PC3	1.7	15.4	60.1	-0.399	0.104	0.464	0.306	0.494	0.320	0.209	0.062	0.025	-0.057	-0.352
		PC4	1.3	11.8	71.9	-0.170	-0.366	-0.334	-0.010	-0.008	-0.470	0.495	0.100	0.086	-0.189	-0.454

\*Data not recorded

PC- Principal Component.

E1- ICRISAT, Patancheru during 2008-09, E2- ICRISAT, Patancheru during 2009-10, E3- UAS, Dharwad irrigated condition, E4- UAS, Dharwad un-irrigated condition, E5 - RARS, Bijapur un-irrigated condition.

DF- Days to 50% flowering, PH- Plant height, EXE- Panicle exerstion, PL- Panicle length, PW- Panicle width, BT- Basal tiller, HSW- Hundred seed weight, PWT- Panicle weight, YLD- Grain yield per plot, SPAD1- SCMR at flowering, SPAD2- SCMR 30 days after flowering.

Flowering		Eigen	Variability	Cumulative							
Group	PC	value	Percentage	Percentage	YP	YS	STI	MP	GMP	SSI	TOL
Crown 1	PC1	5.1	63.6	63.6	0.991	0.869	0.947	0.974	0.965	0.436	0.436
Group 1	PC2	2.8	35.5	99.1	0.052	0.471	0.268	0.220	0.257	-0.900	-0.900
C	PC1	4.8	59.6	59.6	0.965	0.918	0.985	0.998	0.997	0.112	0.112
Group 2	PC2	3.2	39.8	99.4	0.247	-0.384	-0.103	-0.046	-0.072	0.994	0.994
C	PC1	5.8	72.9	72.9	0.984	0.846	0.912	0.950	0.947	0.712	0.712
Group 3	PC2	2.1	26.2	99.1	-0.134	-0.513	-0.372	-0.308	-0.318	0.702	0.702
Creare A	PC1	5.2	63.3	63.3	0.990	0.833	0.944	0.955	0.953	0.529	0.529
Gloup 4	PC2	3.1	33.9	97.2	-0.063	-0.542	-0.284	-0.292	-0.299	0.849	0.849
Crear 5	PC1	4.8	60.5	60.5	0.977	0.963	0.982	0.999	0.999	-0.003	-0.003
Group 5	PC2	3.1	38.9	99.4	0.195	-0.251	0.097	-0.016	-0.020	1.000	1.000
Caracara (	PC1	5.8	72.8	72.8	0.831	0.988	0.931	0.935	0.950	-0.710	-0.710
Group 6	PC2	2.0	26.5	99.4	0.546	0.130	0.317	0.352	0.308	0.704	0.704
C	PC1	4.8	60.3	60.3	0.974	0.885	0.968	0.992	0.982	0.263	0.263
Group /	PC2	3.1	38.8	99.1	0.148	-0.446	-0.217	-0.119	-0.185	0.964	0.964
Entire reference	PC1	4.8	61.2	61.2	0.991	0.869	0.947	0.974	0.965	0.436	0.436

DTE

-0.436

0.900

-0.112

-0.994

-0.712

-0.702

-0.529

-0.849

0.003

-1.000

0.710

-0.704

-0.263

-0.964

-0.436

0.900

-0.900

-0.900

Table 34 Principal Component analysis for drought tolerance indices

PC- Principal Component

set

PC2

3.1

38.0

## Table 35 Mean of Clusters of drought tolerance indices in each flowering group and in entire sorghum reference set

99.2

0.052

0.471

0.268

0.220

0.257

GROUP	Class	YP	YS	STI	МР	GMP	SSI	TOL	DTE
C1	1	2199.31	1575.22	1.26	1887.27	1854.34	0.78	25.82	74.18
01	2	1724.06	1004.98	0.64	1364.52	1314.07	1.27	42.15	57.85
	3	822.88	666.74	0.21	744.81	738.16	0.51	16.82	83.18
	1	1152.77	1308.90	0.55	1230.84	1227.52	-0.79	-13.69	113.69
	2	2337.33	2337.02	1.85	2337.18	2331.70	-0.12	-2.02	102.02
G2	3	2083.69	1738.16	1.23	1910.93	1901.10	0.91	15.92	84.08
	4	1325.60	1110.99	0.51	1218.29	1212.17	0.93	16.23	83.77
	5	1847.86	1251.18	0.79	1549.52	1518.69	1.86	32.34	67.66
	1	589.00	797.56	0.15	693.28	684.42	-3.56	-38.79	138.79
	2	1798.34	1705.40	0.94	1751.87	1749.22	0.46	5.05	94.95
G3	3	1049.88	1036.73	0.35	1043.31	1040.79	0.12	1.32	98.68
	4	2603.91	2180.80	1.73	2392.35	2377.42	1.43	15.64	84.36
	5	2092.36	1450.00	0.92	1771.18	1739.32	2.82	30.74	69.26
	1	2067.42	1485.59	1.02	1776.51	1750.81	4.25	28.26	71.74
	2	1762.24	1690.16	0.98	1726.20	1725.24	0.57	3.81	96.19
G4	3	1055.24	1325.09	0.48	1190.17	1180.02	-4.16	-27.65	127.65
	4	2364.64	2242.44	1.73	2303.54	2299.12	0.66	4.40	95.60
	5	688.75	595.83	0.16	642.29	640.23	2.32	15.46	84.54
	1	1915.34	1798.92	1.93	1857.13	1851.48	3.25	3.90	96.10
G5	2	987.62	1215.94	0.70	1101.78	1095.07	-18.29	-21.98	121.98
	3	908.72	673.86	0.39	791.29	781.78	22.06	26.52	73.48
	1	2159.00	1858.75	1.92	2008.88	2000.29	0.52	12.76	87.24
G6	2	1191.00	997.86	0.63	1094.43	1089.84	0.65	15.99	84.01
	3	1253.20	613.60	0.40	933.40	874.86	2.08	51.34	48.66
	1	2342.25	1986.75	1.78	2164.50	2153.21	0.53	13.52	86.48
G7	2	1447.40	742.40	0.45	1094.90	1022.71	1.69	43.48	56.52
	3	669.00	836.50	0.21	752.75	747.91	-0.99	-25.51	125.51
	1	1876.56	1426.92	0.96	1651.74	1631.87	1.59	22.97	77.03
	2	1381.51	1399.45	0.7	1390.48	1389.65	-0.11	-1.52	101.52
Entire reference	3	1168.48	810.1	0.37	989.29	967.13	1.87	27.12	72.88
501	4	2290.13	2002.6	1.65	2146.36	2136.49	0.79	11.46	88.54
	5	939.32	1204.04	0.45	1071.68	1062.76	-2.07	-30.01	130.01

Yp = Potential yield in non-stress environment, Ys = Yield in stress environment, STI- Stress tolerance index, MP- Mean productivity, GMP- Geometric mean productivity, SSI- Stress susceptibility index, TOL- Tolerance, DTE- Drought tolerant efficiency.



Figure 1. Number of accessions in basic races, intermediate races and wild types in sorghum reference set.

Figure 2. Country wise distribution of accessions in sorghum reference set





Figure 3. Frequency distribution of mid rib color in entire reference set, races, intermediate races, wild types and flowering groups of sorghum reference set.

Figure 4. Frequency distribution of plant pigmentation in entire reference set, races, intermediate races, wild types and flowering groups of sorghum reference set.





Figure 5. Frequency distribution of nodal tillers in entire reference set, races, intermediate races, wild types and flowering groups of sorghum reference set.

Figure 6. Frequency distribution of glume color in entire reference set, races, intermediate races, wild types and flowering groups of sorghum reference set.









Figure 8a. Shannon Weaver diversity index (H') for qualitative traits in entire sorghum reference set and in different flowering groups.

Figure 8b. Shannon Weaver diversity index (H') for qualitative traits in basic races, intermediate races, wild types of sorghum reference set.





Figure 9a. Phenotypic coefficient of variation for quantitative characters in sorghum reference set.



Figure 9b. Genotypic coefficient of variation for quantitative characters in sorghum reference set.

DF- Days to 50% flowering, Plant height, EXE- Panicle exerstion, PL- Panicle length, PW – Panicle width, BT- Basal tillers, PWT-Panicle weight, YLD - Grain yield per plot, SPAD1- SCMR at the time of flowering, SPAD2 – SCMR 30 days after flowering.



Figure 9c. Broad sense heritability (h<sup>2</sup><sub>b</sub>) for quantitative characters in sorghum reference set.



Figure 9d. Genetic advance as percent of mean (GA) for quantitative characters in sorghum reference set.

DF- Days to 50% flowering, Plant height, EXE- Panicle exerstion, PL- Panicle length, PW – Panicle width, BT- Basal tillers, PWT-Panicle weight, YLD - Grain yield per plot, SPAD1- SCMR at the time of flowering, SPAD2 – SCMR 30 days after flowering.



Figure 10. Mean performance of sorghum reference set for quantitative characters

Environments



Environments



Environments





Environments



Environmetns





Environmetns





Environments

Figure 10. Mean performance of sorghum reference set for quantitative characters contd...

## Figure 11a Scatter plot of sorghum reference set in pooled over E1 and E2



Figure 11b Scatter plot of sorghum reference set in pooled over E3, E4 and E5







Figure 12b. Dendrogram constructed based on the first three principal components of basic races, intermediate races and wild sub species in E2







Figure 12d. Dendrogram constructed based on the first three principal components of basic races, intermediate races and wild sub species in E3







Figure 12f. Dendrogram constructed based on the first three principal components of basic races, intermediate races and wild sub species in E5







Plate 1. Varibility for grain color in sorghum reference set







Straw (IS 2814)



Purple (IS 25733)



Grey (IS 15428)



Yellow (IS 23053)



Red (IS 25077)



Light Red (IS 16396)



Light Brown (IS 13827)



Reddish Brown (IS 14963)



Brown (IS 24939)



Plate 2b. Variability for panicle width in sorghum reference set.

