

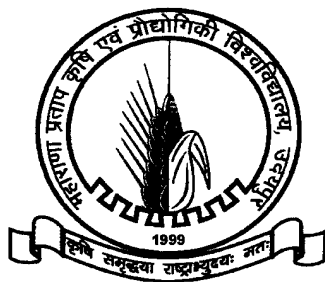
# Genetic Divergence in Sorghum [*Sorghum bicolor* (L.) Moench]

Tokj [I kj?ke ckbdyj (, y-) eks llp] ea vkuokk' kd  
vi I j.k dk v/; ; u

**VIRENDRA KUMAR BHAGASARA**

Thesis

**Master of Science in Agriculture**  
(Plant Breeding & Genetics)



**2017**

**DEPARTMENT OF PLANT BREEDING AND GENETICS**  
RAJASTHAN COLLEGE OF AGRICULTURE  
MAHARANA PRATAP UNIVERSITY OF AGRICULTURE AND TECHNOLOGY  
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**CERTIFICATE-I**

Dated: 18-01-2017

This is to certify that **Mr. Virendra Kumar Bhagasara** has successfully completed the Comprehensive Examination held on 02-06-2016 as required under the regulation for the degree of **Master of Science in Agriculture**.

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Dated: 18-01-2017

This is to certify that the thesis entitled “**Genetic divergence in Sorghum [Sorghum bicolor (L.) Moench]**” submitted for the degree of **Master of Science in Agriculture** in the subject of **Plant Breeding and Genetics**, embodies bonafide research work carried out by **Mr. Virendra Kumar Bhagasara** under my guidance and supervision and that no part of this thesis has been submitted for any other degree. The assistance and help received during the course of investigation have been fully acknowledged. The draft of the thesis was also approved by the advisory committee on 14-09-2016.

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Dated: 15-04-2017

This is to certify that the thesis entitled “**Genetic divergence in Sorghum [Sorghum bicolor (L.) Moench]**” submitted by **Mr. Virendra Kumar Bhagasara** to the Maharana Pratap University of Agriculture and Technology, Udaipur in partial fulfilment of the requirements for the degree of **Master of Science in Agriculture** in the subject of **Plant Breeding and Genetics** after recommendation by the external examiner was defended by the candidate before the following members of the examination committee. The performance of the candidate in the oral examination on his thesis has been found satisfactory; we therefore, recommend that the thesis be approved.

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Dated: 17-04-2017

This is to certify that **Mr. Virendra Kumar Bhagasara**, student of **Master of Science in Agriculture**, Department of Plant Breeding and Genetics, Rajasthan College of Agriculture, Udaipur has made all the corrections / modifications in the thesis entitled “**Genetic divergence in Sorghum [*Sorghum bicolor* (L.) Moench]**” which were suggested by the external examiner and the advisory committee in the oral examination held on 15-04-2017. The final copies of the thesis duly bound and corrected were submitted on 17-04-2017, are enclosed herewith for approval.

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Enclose: One original and three copies of bound thesis forwarded to the Director, Resident Instructions, Maharana Pratap University of Agriculture and Technology, Udaipur through the Dean, Rajasthan College of Agriculture, Udaipur.

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## ABSTRACT

### Genetic Divergence in Sorghum [*Sorghum bicolor* (L.) Moench]

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P. G. Research Scholar

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The present investigation entitled “Genetic Divergence in Sorghum [*Sorghum bicolor* (L.) Moench]” was carried out with 1700 germplasm lines along with 4 checks *i.e.* CSV17, CSV20, CSV27 and CSV21F provided by National Bureau of Plant Genetic Resources (NBPGR) through ICAR- Indian Institute of Millet Research (IIMR) Hyderabad. The experiment was laid out in augmented RBD with 60 replications during *Kharif* 2015 at Instructional Farm, Rajasthan College of Agriculture, Udaipur. Observations were recorded for 26 characters *i.e.* 17 qualitative and 9 quantitative characters on five competitive plants selected at random for each germplasm lines except early vigour and days to 50 percent flowering which were recorded on whole plot basis. Availability of genotypes in different replication at the time of observations was not conform on account of germinations and shoot fly dead hearts therefore, data were analysed in augmented CRD. Analysis of variance revealed significant difference between genotypes for 9 quantitative characters. Variability parameters, correlations coefficients, path coefficients, MANOVA and genetic divergence were studied using these 9 characters.

Majority of the accessions showed good early plant vigour (52.7 %), dark green leaf (96.1 %), non-tan leaf sheath pigmentation (94.4 %), drooping leaves (100 %), green midrib colour (52.5 %), non senescence (91.8 %), compact panicle density (53.6 %), elliptical panicle shape (34.9 %), straw glume colour (35.3 %), ½ glume coverage (42.8 %), presence of awns (89.2 %), creamy straw seed (40.6 %), sub lenticular round but flat from other side grain shape (35.0 %), medium seed size (35.2 %), non-lustrous seed (93.8 %), intermediate endosperm texture (44.8 %) and durra race (30.0 %).

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Tan type leaf sheath pigmentation, drooping leaf orientation, straw glume colour, ½ glume covering, oval grain shape, intermediate endosperm texture present in all the 4 check. Three checks were belongs to kafir race *viz.*, CSV17, CSV20 and CSV27, and CSV21F were belongs to bicolor.

Mean square due to germplasm was significant for all the characters. CSV17 was the best check for days to 50 percent flowering. CSV27 was the best check for leaf length, leaf width, panicle length and grain yield per panicle. CSV21F was the best check for panicle width, plant height and number of leaves.

GCV, PCV and genetic gain were high for grain yield per panicle and heritability for 100-seed weight.

Association study indicated grain yield per panicle exhibited positively significant correlation with 100-seed weight at both genotypic and phenotypic level. Whereas, it was significantly negative correlated with panicle length, leaf length and plant height at both genotypic and phenotypic level and number of leaves and panicle width at genotypic level.

The residual effect 0.5336 at genotypic level and 0.8000 at phenotypic level indicated that 53.36 and 20 per cent variability of seed yield per panicle was explained by these 8 independent characters at genotypic and phenotypic level.

Multivariate analysis of variance using wilks lambda indicates that there was significant difference between genotypes over the 9 quantitative characters. The seed yield was most affected by leaf length as it was having highest direct effect.

The 599 germplasm grouped in 10 clusters based on equilibrium distance over 9 characters. Among them Cluster-VII was the largest with 137 germplasm. Maximum inter cluster distance was between cluster-I and VI (240.654).

The analysis of variance revealed significant difference between cluster means for all nine characters. Germplasm belong to cluster VIII having lower mean values for days to 50 % flowering. Higher mean values of plant height, total number of leaves, leaf length and leaf width belonging to cluster VI. Higher mean values of 100-seed weight, panicle length, grain weight and panicle width belonging to cluster V, II, IX and II, respectively. Three lines IC-286998, IC-286992 and IC-286993 and five lines IC-287950, IC-286922, IC-288160, IC-287253 and IC-287866 were identified for earliness and panicle length characters. Ten lines IC-287651, IC-287444, IC-287529, IC-288281, IC-287454, IC-287482, IC-288006, IC-288270, IC-287769 and

IC-287743) and five lines IC-287836, IC-287072, IC-288215, IC-288008 and IC-287078 were identified for making hybridization for obtaining transgressive segregants for high seed yield per panicle.

vuqki .k

Tokj (I kj?ke ckbdyj , y eks Up) ea vkuqk'kd vi I j.k dk v/; ; u

fojnz d'ekj Hkxkl jk\*  
'kk'kd'rkz

Mkw ch- vkj- j.kok\*\*  
e[; I ykgdkj

or'eku 'kk'k Tokj (I kj?ke ckbdyj , y eks Up) ea vkuqk'kd vi I j.k dk v/; ; u 'kh''kd ds v'rx' 1700 tuun0; rFkk pkj r'ud de'k% I h-, I -oh- 17] I h-, I -oh- 20] I h-, I -oh- 27 , oa I h-, I -oh- 21 , Q tks fd jk''Vh; ikni vkuqk'kd C; j'ks (, u-ch-i h-t h-vkj-) I s Hkkjrh; df''k vuq' akku ifj''kn~(vkbZl h-, -vkj-) Hkkjrh; dnlu vuq' akku I h.Fkku (vkbZvkbZ, e-vkj- ds ek/; e I s i k r fd; } dk v/; ; u fd; k x; k A ifj'f.k [kj h Q 2015 ea I o'k'k' ; knfPNd [k.M vfhkdYiuk ea jktLFkku df''k egkfo/kky;] mn; ij fun'kkRed i'ks= ij mxk; k x; kA tuu n0; ka dh foHkku ifrdfr; ka ea voykdu ds I e; v'qj.k ugha gkus , oa ruk eD[kh ds nekjk erl Ro ds vk'k' dks I o'f/kr I h-vkj-Mh- ea fo'y's''kr fd; k x; k A

dy 26 y{k.kka dk voykdu fd; k ftuea 17 xq'kkRed rFkk 9 ek=kRed y{k.k I f'efyr FkA tuun0; i'Dr ea iR; d y{k.k dk voykdu ; knfPNd #i I s p'us x; s ikp ifr; ksch ik'kks ij fd; k x; k gS fl ok; ikj'k'kd vkst , 0 50 ifr''kr iq'ikoLFkk ea yxsfnu ftudk voykdu I Ei w'kZ tul [; k ds vk/kkj ij fd; k x; kA

vf/kdk'k tuu n0; dk vPNk ikj'fEHkd vkst (52-7%) xgjs gjs jax dh i'Ukh; ka (96-1%) x'ru i'Ykh E; kujatdrk (94-4 %) yVdrh g'pZ i'fYk; k; (100%) e/; f'kjk dk gjk jax (52-5%) x'j th.k'k (91-8%) I ?ku iq'lkx'N ?kuRo (53-6%) nh?'k'rh; ckyh 'kh''kZ vkdkj (34-9%) Xy' dk jax Hk' s t' s k (35-3%) vk/kk <dk nkuk (42-8%) 'k'wd dh mifLFkr (89-2%) eyk'bh'kj fruds ds jax dk nkuk (40-6%) mi el'jkdj x'ky y'sdu nh'jh rjQ I s lery vkdkj dk nkuk (35%) cht dk e/; e vkdkj (35-2%) vpedhys nkus (93-8%) e/; or'hZ Hk'ki k's'k I j'puk (44-8%) vk'j ng'kZ tkfr (30%) ik; s x; kA

\*'kk'kd'rkZ Luk'k'kd'rk-j] ikni iztuu , oa vkuqk'f' kch foHk'x] jktLFkku df''k egkfo|ky;] mn; ij v'kpk; ; ikni iztuu , oa vkuqk'f' kch foHk'x] jktLFkku df''k egkfo|ky;] mn; ij

vPNk ikj'fEHkd vkst] ru i'Ykh E; ku jatdrk] yVdrh i'fYk; k; vfhk'fou; kl ] Xy' dk jax Hk' s t' s k] vk/kk <dk nkuk] v'k'kdj nkuk , 0 e/; or'hZ Hk'ki k's'k I j'puk I Hkh pkjks r'ud ea ik; h x; hA rhu r'ud d'f'Qj tkfr ds v'rx' ik; s x; s tks fd I h-, I -oh- 17] I h-, I -oh- 20] I h-, I -oh- 27 , oa I h-, I -oh- 21 , Q ckbdyj tkfr ds v'rx' ik; k x; kA

tuun0; ds dkj.k ox'ek/; I Hkh y{k.kka ds fy, egRo i w'kZ FkA I h-, I -oh- 17 50 ifr''kr iq'ikoLFkk ea yxsfnu ds fy, I cl s vPNk r'ud FkA I h-, I -

oh- 27 iYkh dh yEckbz iYkh dh pk&lkbz ckyh 'kh'kz yEckbz vks ifr iqlkx&Nk nkuk mit dsfy, lcl svPNk rnyud ik; k x; kA l h-, l -oh- 21 , Q iqlkx&Nk dh yEckbz iksks dh mpkbz , o ifYk; ka dh l d; k dsfy, lcl svPNk rnyud Fkk A

mPp l efi=d id j.k xqkkad (th-l h-oh-) vks ik#fid id j.k xqkkad (ih-l h-oh-) ,oa tufur ykHk ifr iqlkx&Nk nkuk mit dsfy, mPp rFkk fi=xE; rk 100 nkuka ds Hkkj dsfy, mPp ik; k x; kA

l kgp; l v/; ; u ea ifr iqlkx&N nkuk mit nksuks Lrj thu i#ih vks i#ih Lrj ea 100 nksuks ds Hkkj ds l kFk egRoiwkZ l dkjkRed l e/k inf'kz fd; k] tcf d ; g egRoiwkZ vks udkjkRed l gl Ecak iqlkx&N yEckbz ifYk; ka dh yEckbz vks iksks dh mpkbz nksuka Lrj thui#ih vks i#ih Lrj ij ik; k x; k , o ifYk; ka dh l d; k o iqlkx&N dh pk&lkbz thu i#ih Lrj ij ik; k x; kA

vof'k"V iHkko 0-5336 l sthui#ih Lrj 0-8000 i#ih Lrj ij ik; k x; k ftlea l dr fn; k fd 53-36 vks 20 ifr'kr cht ifr iqlkx&N dh ifjorU'khyrk thui#ih o i#ih Lrj ij 8 Loræ y{k.kka nekjk l e>k; k x; k A

cgfHkUu#ih fo'y's'k.k dk id j.k foYdl ySCMk dk mi; kx dj baxr fd; k fd 9 ek=kRed y{k.kka l s vf/kd tuunD; ka ds chp egRoiwkZ varj Fkk A cht mit dks iYkh dh yEckbz us lcl svf/kd iHkfor fd; k ftl dk mPpre iR; {k iHkko jgk A

599 l Ei s dka dks 10 l engka ea cka/k x; k tksfd 9 y{k.kka ij vk/kkfjr Fks A muea l s vi lcl s cMk Fkk bl ea l okZ/kd 137 thunD; ik; s x; s A l okZ/kd varjkl eng njih l , oa VI (240.654) l eng ds e/; ik; h x; h A

fopj.k ds fo'y's'k.k l sirk pyk] l Hkh 9 o.kkz dsfy, l Ei s d l k/ku ds chp egRoiwkZ varj ik; k x; k A 50 ifr'kr Qny cuus dsfy, lcl s de e/; eku l Ei s d VIII dk FkkA iksks dh mpkbz ifYk; ka dh l d; k] iYkh dh yEckbz , o iYkh dh pk&lkbz dsfy, lcl svf/kd e/; eku l Ei s d VI dk Fkk A 100 chtka dk otu] iqlkx&N yEckbz vukt otu , oa iqlkx&N pk&lkbz dsfy, mPp e/; eku de'k%V, II, IX , oa II l Ei s dka dk Fkk A

rhu IC-286998, IC-286992 IC-286993 , oa IC-287950, IC-286922, IC-288160, IC-287253 vks IC-287866 i k p ykbuka dks de'k% 'kh'kz i q i u , oa iqlkx&N yEckbz ds y{k.k grq igpkuk x; kA nl IC-287651, IC-287444, IC-287529, IC-288281, IC-287454, IC-287482, IC-288006, IC-288270, IC-287769 vks IC-287743 o IC-287836, IC-287072, IC-288215, IC-288008 vks IC-287078 i k p ykbuka dks ifrx&N vf/kd mit i l r djus dsfy, l dj.k cukus grq igpkuk x; kA

# 1. INTRODUCTION

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*Sorghum bicolor* (L.) Moench ( $2n = 20$ ) is one of the most important crop in the world because of its adaptation to a wide range of ecological conditions, suitability for low input cultivation and diverse uses (Doggett, 1988 a). Sorghum belongs to family Poaceae and tribe Andropogoneae (Harlan & de, 1972). The height of cultivated varieties varies from 0.5 m to 6.0 m. According to the inflorescence (panicle), which varies from very open or loose to very compact, cultivated sorghum have been classified into 5 races *viz.*, Bicolor, Guinea, Caudatum, Durra and Kafir and ten intermediate races corresponding to the pair wise combination of major races. These are identified according to the morphological traits, especially panicle, grain and glume traits (Harlan & de Wet, 1972).

Worldwide, it is cultivated on 42.64 million ha with a production of 67.57 million tones in the year 2014-15. The crop is widely grown for food, feed, fodder, forage and fuel in the semi-arid tropics (SAT) of Asia, Africa, America and Australia. In India, sorghum is having 6.00 m ha area, 5.50 mt production and 917 kg/ha productivity in the year 2014-15 (Source: Directorate of Economics and Statistics, Department of Agriculture and Cooperation, 2014-15, New Delhi). The major sorghum growing states in the country are Maharashtra, Karnataka, Rajasthan, Madhya Pradesh, Andhra Pradesh, Tamil Nadu, Uttar Pradesh and Gujarat. In Rajasthan, 6.61 lac ha area is under cultivation and production is 5.05 lac tones with 763 kg per ha productivity in the year 2014-15. Major emphasis of farmers on fodder cause low grain productivity in this crop.

Nutritional value per 100 g of grain is 1,418 kJ (339 kcal) energy, 74.63 g carbohydrates , 6.3 g dietary fibre, 3.30 g fat and 11.30 g protein.

Worldwide, there are four crops *viz.*, rice, wheat, maize, and potato that supply approximately 85% of the world's food energy where sorghum stands at 5<sup>th</sup> position. For 500 million people in over 30 countries of the semi arid tropics, sorghum is a dietary staple. Sorghum is used not only for human food, but also used as fodder and feed for animals, building material, fencing, or for brooms (Doggett, 1988 b; House, 1985; Rooney and Waniska, 2000).

In the USA, sorghum grain has traditionally been used for livestock feed and stems and foliage for green chop, hay, silage, and pasture. Forage crops are important for the economy of India as these crops provide major nutritional base for livestock. With the increase in the world human population and economic growth, the demand of animal products such as milk, meat and eggs in the human diet is bound to increase. Improvement in the quality of cattle and buffalo depends upon the adequate supply of required feed and fodder (Patil and Singh, 2006).

Before planning any breeding programme, the assessment of genetic variability in germplasm and relationship between characters are necessary step. At present, ICRISAT is sharing a major repository for world sorghum germplasm with a total of 39,234 accessions from 93 countries. The USA sorghum germplasm collection contains over 41,000 accessions that represent landraces and cultivars from 115 countries. Traditionally, this collection has been evaluated for traits such as abiotic or biotic stress and other agronomic characters. Sorghum is a gluten-free cereal and recent research has begun to evaluate it for flour characteristics that would make it more amenable to baking and other processing technologies. New technologies are allowing sorghum germplasm to be screened for high levels of anti-oxidants that show promise in cancer research and glycemic control (Dahlberg *et al.* 2011).

Variability over the characters are known as genetic diversity which plays an important role in plant breeding and it arises due to geographical separation or genetic barriers to crossing ability. The evaluation of diversity is important to know the source of genes for particular trait within the available germplasm. So, it is essential to know about diversity among genotypes before undertaking any crop improvement programme. It can be studied by ward analysis (1963) using euclidian distances. This technique is intensively used in plant breeding and genetics for the study of genetic divergence in various breeding materials. This is one of the potent technique of measuring genetic divergence.

Genetic improvement for quantitative and qualitative traits depends on the nature and amount of variability present in the genetic stock. If desirable traits having high heritability more are the chances of improvement through selection. Indian sorghum possesses wide range of genetic variability. The present study is based on 17 qualitative characters and nine quantitative characters majored on 1700 germplasm

lines and four checks. Information on the variability was majored by genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic gain for individual quantitative characters and through equilibrium distance over the characters. Relationship between characters was studied by correlation coefficients and path coefficients analysis.

Elimination of heterogeneity in one direction is possible in augmented randomized block designs (augmented RBD). Federer (1956, 1961) gave the analysis, randomization procedure and construction of this design by adding the new treatments to the blocks of RBD for evaluation of large number of germplasm. The analysis of augmented designs can be easily carried out by making use of the control treatments which are appearing in every block to compare the test treatments against control treatments. Even if control treatments are missing in own or other block data can be analysed in augmented CRD.

In view of the above facts, an experiment entitled “**Genetic divergence in Sorghum [*Sorghum bicolor* (L.) Moench]**” was plan in augmented RBD and conducted during *Kharif* 2015 at Instructional Farm, Rajasthan College of Agriculture, Udaipur with the following objectives:

1. To study the variability parameters
2. To study the character association
3. To study the genetic divergence

## 2. REVIEW OF LITERATURE

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A thorough understanding of the nature of variation, character association and genetic diversity helps in development of sound plant improvement programmes. In this regard, past studies forms the basis for the formulation of new strategies. Hence, brief review of literature available in Sorghum pertaining to various aspects of present investigation has been presented in this chapter under following heads:

1. Variability parameters
2. Association studies
3. Genetic divergence

### 1. Variability parameters

Possibility of improvement in any crop mainly depends on the nature and magnitude of variability. In germplasm study phenotypic variability can be partitioned into genotypic and environmental components. In homozygous genotypes its genotypic components being the heritable part of the total variability, therefore magnitude influence the selection strategies.

Fisher (1918) was the first to realized the importance of genotypic variance and partitioned the genetic variance into three parts *viz.*, (a) additive (b) dominance and (c) epistatic components. According to him, additive genetic variance is mainly responsible for genetic advance and can be exploited through selection.

Fisher (1925) suggested a field design (randomized block design) to separate the environmental variance from genotypic variance. Lush (1940) defined heritability in broad sense as a ratio of genotypic variance to the phenotypic variance.

Johnson *et al.* (1955) advocated that genetic gain, which is genetic advance expressed as per cent of mean, provides a direct comparison of the expected efficiency of selection for different characters.

According to Panse (1957), if heritability is due to dominance and epistasis effects, the genetic gain would be low, while in other cases where heritability is due to additive gene effects, a high genetic advance would be expected.

Geleta *et al.* (2005) evaluated 64 sorghum germplasm for 12 quantitative traits. Genotypic and phenotypic coefficients of variation were greater than 12 per cent for plant height, panicle length, head weight, grain yield per plant, 100-kernel weight and kernel number per panicle. Higher estimates of heritability (greater than 80 %) coupled with higher predicted genetic advance as percentage of mean (greater than 20 %) were obtained for plant height, panicle length and 100-kernel weight, suggesting involvement of additive gene action.

Chaudhary *et al.* (2005) studied variability in 130 germplasm lines of sorghum for stover yield and its components. They reported high estimates of PCV, GCV, heritability and genetic gain for number of leaves per plant.

Kishore and Singh (2005) observed 30 genetically diverse strains of fodder sorghum and 11 hybrids of sorghum and sudan grass grown under both irrigated and rainfed conditions for two years. They reported sufficient genetic variability among the genotypes for all the characters studied. High estimates of GCV and PCV for green fodder and dry matter yield were reported. The heritability estimates were high for crude protein and moderate for almost all the traits. High genetic advance was for green fodder yield and dry fodder yield under irrigated conditions.

Yadav *et al.* (2005) studied variability in lines generated at Hisar and germplasm collected from different sources for forage traits like multicut traits, leaf characteristics, plant height and fodder yield over three to five years. Higher variability was observed for leaf length, number of leaves per plant, plant height, regeneration potential, TSS, green fodder yield and dry fodder yield per plant.

Bello *et al.* (2007) conducted an experiment to estimate the genetic variability in cultivated strains of sorghum and reported high broad sense heritability for plant height and number of leaves per plant.

Deepalakshmi and Ganesamurthy (2007) revealed that the magnitude of PCV and GCV were more or less equivalent for days to maturity, number of leaves per plant, ear head weight, number of primaries per panicle, 100 grain weight, grain mould score and single plant yield showing that these characters are less affected by environmental fluctuations and might offer scope for selection. High heritability accompanied with high GA as per cent of mean was observed for days to fifty per cent flowering, plant height, number of leaves per plant, leaf length, ear head weight,

number of primaries per panicle, 100 grain weight, grain mould score and single plant yield and suggested that these characters by were growned under additive gene action thus give better scope for selection.

Elangovan and Reddy (2007) studied 157 sorghum accessions for 28 agromorphological and one biochemical character. Wide range of variability was recorded in both qualitative and quantitative characters. Majority of the accessions showed tan type, dark green leaf colour, erect leaf orientation and stay green types (non-senescence). However, variation was observed in seedling vigour, midrib colour, ear head shape, ear head compactness, glume colour, glume covering, seed size, seed colour, and races. The quantitative characters also showed wide variation in the evaluated sorghum germplasm. The characters *viz.*, stem dry weight (70-665 g), stem fresh weight (110-1040 g), grain yield (3-75 g), brix (3-25 %), and 100-seed weight (0.6-4.5 g) were highly variable based on coefficient of variability percentage.

Warkad *et al.* (2008) studied variability in sixty-four sorghum germplasm accessions collected from various districts of Vidarbha region. Significant genetic variability was observed among the genotypes studied. Highest PCV and GCV values were observed for dry fodder yield per plant followed by ear head breadth and ear head length, grain yield per plant, stem girth and 1000-seed weight. High heritability accompanied with high genetic advance over mean was observed for grain yield, dry fodder yield, stem girth, ear head length and breadth, suggesting the influence of additive genes and scope for selection. Also, high of heritability along with low genetic advance over mean was observed for the characters *viz.*, days to maturity and number of leaves per plant indicating that variability is mainly governed by non-additive gene effects and hence heterosis breeding can be fruitfully exploited in improving such characters.

Kumar *et al.* (2009) showed that there is considerable genetic variability and high heritability for grain Fe and Zn contents and it is possible to genetically enhance the grain micronutrient content (Fe and Zn) in sorghum and other major staples. However, limited information is available on the extent of variability in the sorghum germplasm accessions and breeding lines and the character association between grain Fe and Zn contents and with other agronomic traits. Significant positive correlation was observed between grain Fe and Zn contents ( $r=0.75$ ). The five accessions *viz.*, IS 5427, IS 5514, IS 55, IS 3760 and IS 3283 with high grain Fe ( $>50$  mg kg<sup>-1</sup>) and Zn

(>37 mg kg<sup>-1</sup>) contents were identified and can be utilized to increase the diversity and micronutrient density of sorghum hybrid parents in future.

Sharma *et al.* (2009) studied analysis of variance indicated highly significant differences among genotypes for all the characters except ear head length. The highest phenotypic and genotypic coefficients of variation were recorded for ear head width (37.49 and 34.72), grain yield per plant (35.35 and 32.32), days to maturity (34.63 and 34.25), number of primaries per panicle (30.06 and 29.52), plant height (28.49 and 26.45), ear length (25.91 and 19.39) and peduncle exertion (25.59 and 22.80). Estimates of heritability varied from 56.04 per cent (ear head length) to 97.80 per cent (days to maturity). All the characters except ear head length and days to 50 per cent flowering showed more than 75 per cent heritability.

Umadevi and Kumaravadivel (2009) studied 60 sorghum germplasm grown in the *Rabi* season of 2003. Among the seven characters studied, plant height, ear head length, stem girth, leaf length, single plant yield and 100-seed weight showed high variability. Plant height, ear head length, stem girth, leaf breadth, single plant yield and 100-seed weight showed high heritability. The highest and moderate genetic advance was recorded for plant height and single plant yield respectively.

Vinodhana *et al.* (2009) studied genetic variability of 100 sorghum genotypes for fifteen characters. Phenotypic co-efficient of variation (PCV) was higher than the genotypic co-efficient of variation (GCV) for all the characters indicating the influence of environment on the expression of these traits. The characters *viz.*, stay green, root volume, leaf area index, plant height and harvest index showed high value for phenotypic and genotypic co-efficient of variation showed higher estimates of heritability and expected genetic gain indicating the presence of additive gene effect.

Chavan *et al.* (2010) observed genetic variability in 24 sorghum genotypes for ten quantitative traits. The analysis of variance revealed significant differences among genotypes for all characters. GCV and PCV were high for harvest index followed by grain yield per plant and panicle width. The highest value of GCV and PCV were observed for harvest index and least value for days to maturity. High heritability was observed for grain yield per panicle followed by harvest index, panicle width, number of primary branches per panicle, plant height and number of grains per panicle. High heritability coupled with high genetic advance was observed for number of grains per

panicle, plant height and grain yield per panicle. These traits were governed primarily by additive genetic effect and selection based on phenotypic performance could be worth in achieving desired results.

Godhbarle *et al.* (2010) revealed that the genotypic variance was lower than the phenotypic variance for all the characters. High genotypic and phenotypic variance, heritability and genetic advance were observed for the characters *viz.*, panicle length, fodder yield, number of primary branches per panicle, grains per primary branches, harvest index, grain yield and plant height indicating that additive gene effects were operating for these traits.

Singh *et al.* (2010) evaluated 32 diverse accessions of forage sorghum for green fodder yield and its component traits. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were found maximum for leaf : stem ratio followed by stem girth, total soluble solid, green fodder yield, leaf breadth, green fodder yield per day whereas, days to milking stage exhibited lowest value. High heritability coupled with high genetic advance was observed for plant height, number of nodes per plant, internode length, stem girth, leaf breadth, leaves per plant, leaf:stem ratio, total soluble solids and green fodder yield per day. It revealed substantial contribution of additive genetic variance in the expression of these traits.

Kumar *et al.* (2011) revealed that the estimates of PCV were generally higher than their corresponding GCV for all the characters studied. The GCV was maximum for leaf stem ratio, followed by leaf area, green fodder yield, total soluble solids, stem girth, protein content and internode length, whereas minimum being for leaf breadth, leaves per plant, plant height, leaf length, nodes per plant and days to 50 per cent flowering. The highest PVC was observed for leaf stem ratio followed by leaf area, green fodder yield, total soluble solid, protein content, stem girth, number of nodes per plant and internode length whereas leaf breadth, number of leaves per plant, plant height, leaf length, and days to 50 per cent flowering exhibited lowest value. Leaf area, leaf stem ratio, stem girth, total soluble solids, leaf breadth, nodes per plant, leaves per plant, internode length and plant height exhibited high heritability combined with high genetic advance as per cent of mean. Thus these traits may be useful for further improvement in quality and yielding capacity in forage sorghum varieties.

Jain and Patel (2012) evaluated 102 land races of forage sorghum for days to 50 per cent flowering, plant height, number of leaves per plant, leaf length, leaf breadth and fodder yield per plant in augmented block design during 2009-10 and 2010-11. High heritability accompanied with high GA as per cent of mean was observed for days to 50 per cent flowering, plant height, number of leaves per plant, leaf length and green fodder yield per plant suggested that these characters are under additive gene action and having better scope for selection.

Tomar *et al.* (2012) studied genotypic variability of 52 sweet sorghum genotypes for 17 quantitative traits. Analysis of variance showed significant differences among the accessions for all the characters studied. The GCV was near to PCV for days to fifty per cent flowering, days to physiological maturity, plant height, juice yield and sucrose yield, indicating significant effect of genotype on phenotypic expression of these traits with very little effect of environment. The genotypes under study showed high heritability for sixteen characters and moderate heritability for only one character *i.e.* number of leaves. High heritability combined with high genetic advance (as per cent of mean) was observed for sucrose yield, juice yield, cane yield, juice extraction per cent, sucrose per cent, juice volume, juice weight, millable cane weight, fresh cane weight, stay green trait, stem girth and plant height. High heritability estimates along with high GA indicates that variation for these characters is due to additive gene effects and consequently the scope for improving sucrose and cane yield through selection is more.

Seetharam and Ganesamurthy (2013) evaluated thirty nine genotypes for nine quantitative characters *viz.*, days to 50 per cent flowering, plant height, number of leaves per plant, leaf length, leaf width, stem width, panicle length, panicle weight and single plant yield. The genotypes exhibited considerable amount of variability for all characters. Higher estimates of genotypic and phenotypic coefficients of variation were observed for grain yield, panicle weight, panicle length and plant height. A moderate values of phenotypic and genotypic co-efficient of variation were observed for all other characters. High heritability coupled with high genetic advance was recorded for single plant yield, panicle weight, panicle length and plant height. Thus these traits would be more fruitful for direct selection in existing populations.

Elangovan *et al.* (2014) studied variability for 11 agro-morphological and seven biochemical traits during *Kharif* 2008 to 2010. Analysis of variance showed

significant differences among genotypes for all traits studied. The PCV and GCV were higher for ear head length, ear head width, stem fresh weight, stem dry weight, grain yield, 100 grain weight, juice volume and reduced sugars. The lower degree or equal GCV and PCV for presence of awns, grain size, grain color, and grain lustrue indicated that improvement for such traits might be achieved only up to some extent. High heritability coupled with high genetic advance as percentage of mean was found for the trait juice volume suggesting the presence of additive gene action better and response to selection.

Hariprasanna *et al.* (2014) characterised grains of adapted cultivars, parental lines, advance breeding lines and selected germplasm accessions of sorghum the levels of micronutrient viz., iron (Fe) and zinc (Zn). Considerable variability for grain Fe (12.1-83.4 mg/kg) and Zn (6.3-51.4 mg/kg) contents was observed. In general, germplasm lines had higher values for Fe and Zn compared to cultivars and breeding lines. The availability of high variability for grain Fe and Zn contents among the genotypes tested holds promise for grain micronutrient enrichment through breeding programmes.

Dossu-Aminon *et al.* (2015) collected 142 accessions of landraces from Northern Benin and evaluated in Central Benin for 10 qualitative and 14 quantitative agro morphological traits. High variability among both qualitative and quantitative traits was observed. Broader variability was observed for grain yield (0.72–10.57 tons/ha), panicle weight (15–215.95 g), days to 50 per cent flowering (57–200 days) and plant height (153.27–636.5 cm). The results obtained will help enhancing sorghum production and diversity and developing new varieties that will be better adapted to the current soil and climate conditions in Benin.

Malik *et al.* (2015) observed higher estimates of genotypic and phenotypic coefficient of variation for leaf breadth, leaves per plant, leaf area, leaf stem ratio and green fodder yield, moderate for leaf length, internode length, stem girth, total soluble solids and protein content and low for days to 50 per cent flowering. Heritability (broad sense) was high for days to 50 per cent flowering, plant height, leaf breadth, leaf length, internode length, stem girth, leaves per plant, leaf area, leaf stem ratio, total soluble solids, protein content and green fodder yield. The genetic advance as per cent of mean were high for plant height, leaf breadth, leaf length, internode length, stem girth, leaves per plant, leaf area, leaf stem ratio and green fodder yield. High

heritability coupled with high genetic advance was observed for plant height, leaf breadth, leaf length, internode length, stem girth, leaves per plant, leaf area, leaf stem ratio and green fodder yield. This leaves scope for selection.

## 2. Association studies

Association of economically important character with other quantitative characters determined by correlation coefficient is quite helpful for selection. Information on correlation between two yield contributing characters can be used in predicting the correlated response for directional selection as well as in the identification of some characters which may not have value in themselves but are useful indices of consideration in improvement of yield.

Galton (1889) developed the basic concept of correlation and was later elaborated and discussed by Fisher (1918, 1936) and Wright (1921) for the plant breeding programme. Genetic correlation provides a measure of genetic association between characters and is used in selection of one character for the improvement of other (Miller *et al.* 1958) and helpful to the breeders since they are based on transmissible genetic variance (Jermon *et al.* 1956). Genetic correlation is the net effect of all genes that affect the character, some are causing positive and some are negative association. The major cause underlying genetic correlations are pleiotropy, linkage and development induced relationship (Adams, 1967; Stebbins, 1950). Crop yield is end products of the interaction of a number of inter related attributes. Hence, the efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its components and among the components themselves. Knowledge of the strength and type of such association is an important prerequisite for the formulation of breeding procedures (Breese and Haywards, 1972).

Plant breeders are generally concerned with two types of correlation *i.e.* (i) phenotypic correlation and (ii) genotypic correlation. The association between two characters that can be observed directly is the phenotypic correlation which depends upon both genotypic and environmental effect. The correlation between breeding values of two characters is the genotypic correlation.

Path co-efficient is standardized partial regression coefficient where correlation coefficient is split into direct and indirect effects. Wright (1921) coined the term path coefficient and gave the theory of path analysis. Li (1955) gave a

detailed account of both basic and applied aspect of path coefficient analysis by means of formulating a path diagram of cause and effect relationship showing the inter-relationship of variables.

Dewey and Lu (1959) for the first time applied the techniques of path coefficient in plant breeding and reported that it provides important information about the specific forces acting to produce a particular correlation. They partitioned the total correlation coefficient into direct and indirect effect and assigned the values of path coefficient contributing to yield which help to ascertain with much more precision and clarity the complex association in the selection programme.

Chaudhary *et al.* (2005) studied character association in 130 germplasm lines of sorghum. Stover yield exhibited positive and significant correlation with plant height, stem girth and green fodder yield. Leaf length revealed positive and significant association with stem girth at genotypic level.

Elangovan and Reddy (2005) evaluated 699 sorghum accessions and control cultivars M 35-1 and CS14R (or CSV 15R) under restoration programme during 2 *Rabi* seasons at Hyderabad, Andhra Pradesh and Solapur, Maharashtra India for different characters. All the characters (days to 50 per cent flowering, leaf number, leaf length, leaf width, plant height, ear head length, ear head width, stem thickness, grain yield, 100-seed weight and days to maturity) showed high variation among accessions. High and positive correlation days to flowering was observed with leaf number, leaf length, stem thickness and days to maturity; leaf number with leaf length, plant height and stem thickness; leaf length with leaf width and plant height; and leaf width with stem thickness. Thirty-nine accessions were identified as potential donors for days to flowering, leaf length, leaf width, plant height, ear head length, ear head width, grain yield, 100-seed weight and days to maturity.

Iyanar and Khan (2005) reported significant negative correlation of green fodder yield with total soluble solids at genotypic and phenotypic level.

Negash and Chemedda (2005) reported significant positive correlation of green fodder yield with green fodder yield per day, leaf length and plant height at genotypic and phenotypic level.

Premalatha *et al.* (2006) showed that grain yield was significant and positively correlated with number of grains per panicle and 100-grain weight. The results of path

analysis revealed that the direct contribution of 100-grain weight was high on grain yield followed by number of grains per panicle, leaf area index, plant height and days to 50 per cent flowering. Hence, along with grain yield, the component traits also be considered for selection of superior and dual-purpose sorghum genotypes.

Kenga *et al.* (2006) reported significant positive genotypic correlation between grain yield and most of the traits. Days to anthesis was negatively correlated with vegetative and reproductive traits.

Singh *et al.* (2006) reported significant positive correlation of green fodder yield with green fodder yield per day, leaf length and plant height at genotypic and phenotypic level.

Alhassan *et al.* (2008) reported significant positive correlation of days to 50 per cent flowering and grain yield per plant were positively with grain yield per hectare. However, beta -amylase activity was negatively and significantly correlated with days to 50 per cent flowering and 1000-grain yield. The path coefficient analysis indicated positive and significant correlation as well as high direct effect of grain yield per plant and days to 50 per cent flowering on grain yield per hectare. Apart from this, beta-amylase activity also had positive and significant direct effect on alpha-amylase activities. Selection for days to 50 per cent flowering, grain yield per plant and alpha - and beta -amylase activities are the most reliable traits for sorghum improvement programme for grain yield and malting quality.

Aruna and Audilakshmi (2008) evaluated 135 germplasm lines belonging to different races. In an augmented design during 2002 and in Randomized complete block design (RCBD) for selected lines during 2003. The correlation studies indicated that besides panicle weight, the number of grains/unit length of primary branch and the number of secondary branches/primary branch had significant positive relation with grain yield. IS nos 1259, 5447, 5725 and 2036 were promising for more than one yield component. The study indicated that besides caudatum race, the lines belonging to guinea, kafir and inter-races are good sources for different yield components.

Singh (2008) reported high significant positive correlation coefficients of dry matter yield with green forage yield, leaves per plant, leaf length and leaf breadth however, these characters showed negative phenotypic correlation coefficient with leaf:stem ratio in path coefficients analysis for dry matter yield, only green forage

yield had high direct effect. Leaf length, leaves per plant, leaf breadth, plant height and stem thickness had positive indirect effects on dry matter yield through green forage yield.

Singh *et al.* (2008) reported higher value of genotypic correlations as compared to their corresponding phenotypic correlations for most of the character combinations. Green fodder yield had positively and significant correlation with green fodder yield per day, leaf length and plant height at genotypic and phenotypic level. This indicates that any selection based on these characters will enhance performance and improvement in forage sorghum. The negatively significant correlation of green fodder yield with total soluble solids observed at genotypic and phenotypic level. Leaf length had positive and significant association with stem girth at genotypic level. The correlation of leaves per plant was positive and significant with stem girth and leaf length.

Kachapur and Salimath (2009) revealed the presence of positive and significant genotypic correlation between brix and pol per cent but significantly and negative relation between brix and ear head weight and brix and grain yield. Partitioning of the correlation coefficient through path analysis indicated that the direct effects of brix and juice volume was maximum (38.11) followed by brix and CCS yield (17.01).

Sharma *et al.* (2009) studied 100 sorghum germplasm lines with 5 controls to identify qualify direct and indirect contributors of grain yield.

Singh *et al.* (2009) showed that path coefficient of green fodder yield per day was most important and directly controlling the green fodder yield. High indirect positive contribution of green fodder yield per day was mainly *via* number leaves per plant and leaf length. This indicates that, effectiveness of selection for high fodder yield could be enhanced by inclusion of green fodder yield per day as a selection criterion.

Bisen *et al.* (2010) suggested that number of grain per panicle had the highest positive direct effect on grain yield per plant followed by plant height, length of panicle, number of secondary branches per primary branches, 1000-grain weight, number of nodes per plant and length of last internode, indicating their importance in determining the grain yield.

Chavan *et al.* (2010) reported significant and positive correlation of seed yield with panicle length, number of grains per panicle, panicle width, test weight, number of primary branches per panicle and harvest index. The panicle length was positively correlated with panicle width, plant height, number of primary branches per panicle, test weight and harvest index. Results of path analysis showed that the days to 50 per cent flowering, panicle length, plant height and number of grains per panicle were important characters for seed yield of *Kharif* sorghum.

Cunha and Lima (2010) reported significantly positive correlation between dry matter and plant height both at genotypic and phenotypic level.

Iyanar *et al.* (2010) studied genotypic correlation coefficient and path analysis in 109 genotypes of multicut fodder sorghum for 14 fodder yield and yield related characters of each cut and over the cuts. Green fodder per plant was significant and positively correlated with plant height, number of tillers, leaf length, number of leaves, leaf: stem ratio, stem thickness, dry fodder yield and green fodder yield per plot and negatively correlated with HCN and crude protein. Dry fodder yield exhibited high correlation coefficient with green fodder yield per plant followed by leaf length, plant height and number of leaves. Number of tillers had positive association with leaf length and dry fodder yield. Leaf length had highest positive association with dry fodder yield and green fodder yield per plant. Dry fodder yield had positive association with green fodder yield in first cut.

Jain *et al.* (2010) reported positive and significant correlation as well as high direct effect of dry fodder yield per plant, plant height, number of leaves per plant and stem girth on green fodder yield per plant.

Prakash *et al.* (2010) carried out an investigation with 7 lines, 5 testers and their 35 hybrids to assess the direct and indirect effect for green fodder yield per plant in sorghum. Path analysis showed that plant height contributed high direct effect towards green fodder yield per plant followed by leaf length. Stem diameter also exerted positive direct effect on green fodder yield. Thus, the present study indicated that the plant height, leaf length and stem diameter are important characters in deciding the green fodder yield per plant. Hence these characters may be used in selection for improvement of green fodder yield.

Kumar *et al.* (2011) studied the correlation between yield components and seed yield in interspecific crosses of sorghum grown in Tandur, Andhra Pradesh, India, during the *Rabi* season. The experimental materials consisted of 29 segregating progenies of two interspecific crosses in the F<sub>4</sub> generation *i.e.*, *Sorghum bicolor* (cs3541) x *S. usamberense* [*S. arundinaceum*] (Sb x Su) and *Sorghum bicolor* (cs3541) x *Sorghum lewisonii* (Sb x Sl). The number of days to 50 per cent flowering, plant height, panicle length, test weight and fodder yield had positive direct effects on seed yield, whereas the number of days to maturity had a direct negative effect on seed yield. Plant height, panicle length, test weight and fodder yield should be considered in the selection for yield improvement.

Patted *et al.* (2011) revealed significant positive correlation between grain yield and 1000-grain mass, grain yield and fodder yield and plant height and fodder yield at both genotypic and phenotypic levels. Similarly, significant but negative correlation existed between grain yield and days to flowering and grain yield and days to maturity at both genotypic and phenotypic levels. Partitioning of correlation between yield and yield components into direct and indirect effects revealed that 1000-grain mass had the highest positive direct effect on grain yield while days to maturity had the highest negative direct effect on grain yield.

El-Din *et al.* (2012) reported that panicle length had low but positive direct effect on grain yield, whereas number of kernels per head had high positive direct effect on grain yield. Positive indirect effect was through days to flowering, plant height, panicle length, panicle width and panicle internodes whereas, its indirect effect was negative through leaf area and 1000-kernel weight.

Gayathri *et al.* (2012) reported that all the characters showed positive indirect effect through 100-grain weight and days to 50 per cent flowering, indicating that direct selection for grain size might be helpful in improving the grain iron content. Negative indirect effects of 100-grain weight through other characters were more prominent than its positive direct effect on the grain iron content, thus direct selection for grain weight should be practiced to reduce the undesirable indirect effect. The days to 50 per cent flowering exhibited a positive direct effect and a positive non-significant association with the grain iron content. Hence, selection for this character may be rewarding during the development of iron-rich cultivars. A very high residual

effect (0.836) revealed that some more characters closely related with grain iron content need to be included apart from the characters studied.

Jankovic *et al.* (2012) studied phenotypic and genotypic correlation coefficients in three species of Sorghum genus - forage sorghum (*S. bicolor* Moench genotype NS-Dzin), Sudan grass (*S. sudanense* L. genotype Zora) and interspecies hybrid (*S. bicolor* x *S. sudanense* genotype Siloking). Coefficients of simple correlations indicate the presence of very strong to almost complete positive correlations. Plant height and number of leaves were indirectly related to yield of green biomass and correlations varied from non significant to very weak.

Kumar *et al.* (2012) reported maximum direct effects of juice volume, number of nodes per plant, days to 50 per cent flowering, grain yield and plant height on green cane yield. Hence, these traits contributed maximum to higher green cane yield compared to other traits. The residual value (0.24) was high, indicating that more traits need to be included in future evaluation programme. Based on the overall performance, genotypes Urja, IS 11161, IS 18164, IS 14904, SSV 74, NSSV 256, SPV 422, IS 21036, IS 7546 and IS 5352 were found promising for possessing higher green cane yield and brix content.

Navneet and Singh (2012) reported higher magnitude of phenotypic correlation than their corresponding genotypic correlations for most of the character combinations. Green fodder yield had positive and significant association with leaf breadth, leaves per plant and leaf area both at genotypic and phenotypic level. This indicates that any selection based on these characters will enhance performance and improvement in forage sorghum. Path coefficient analysis showed that leaf length, leaf breadth, leaves per plant and leaf area were the most important characters controlling directly to green fodder yield. High indirect positive contribution of leaf length, leaf breadth, leaves per plant and stem girth *via* leaf area and leaf stem: ratio, total soluble solids and protein content was *via* leaves per plant. This indicates that, effectiveness of selection for high fodder yield can be enhanced by inclusion of leaf length, leaf breadth, leaves per plant, stem girth and leaf area in selection criterion along with the leaf: stem ratio.

Abubakar and Bubuche (2013) reported positive significant correlation of leaf number with plant height, leaf area index and straw weight and negative significant

correlation with flag leaf area. Leaf length had significant positive correlation with flag leaf length and straw weight. Plant height, recorded significant positive correlation with leaf number and straw weight and negative correlation with flag leaf length and grain yield. Leaf area index has significant positive correlation with leaf number, plant height and negatively correlated with hundred grain weight and grain yield. Flag leaf area had significant positive correlation with flag leaf length and negative correlation with leaf number and straw weight. Straw weight has the significant and positive correlation with leaf number, leaf length and plant height and significantly and positive correlation with flag leaf area. Selection for straw weight can be therefore carried out simultaneously with plant height, leaf length and leaf number.

Hmon *et al.* (2013) analysed the variation in panicle-related traits of 206 sorghum accessions collected from 27 Asian and African countries. Path coefficient analysis indicated that panicle length, the total number of branches, rachis length and panicle width had a positive direct effect on grain yield. Finally, they showed that the variation in the inflorescence architecture of sorghum accessions was dependent not only on the panicle length, but also on the total number of branches, the maximum length of primary branches, rachis length, panicle diameter and panicle width. Thus, there are major panicle determinants that are strongly associated with grain yield which should be considered in breeding programmes. These results will serve as a starting point for further evaluation of sorghum germplasm *via* quantitative trait loci analysis and may be useful for improving yield based on careful consideration of trait selection and inflorescence morphology.

Pahuja and Dharmveer (2013) reported positive significant correlation of dry fodder yield per plant with green fodder yield per plant, 1000-grain weight and plant height. The results of path coefficient analysis showed that green fodder yield, TSS, width of flag leaf, leaf length, plant height and panicle length of branches had positive direct effect on dry fodder yield per plant.

Seetharam and Ganesamurthy (2013) reported that out of 36 correlations, 24 were significant at  $P=0.05$  and 21 were significant at 0.01 and 14 were found to be of useful correlations ( $r>+or-0.500$ ). Among the useful correlations, yield had significant correlation with days to 50 per cent flowering, leaf length, leaf width and panicle weight. In path analysis, panicle weight had positive direct effect on yield. First three

principal components explained more than 70 per cent of variation which reduced nine characters into seven characters and confirmed the correlation analysis.

Iraddi *et al.* (2013) revealed significant and positive correlation of fresh stalk yield with total biomass, grain yield, plant height, nodes per plant, stem girth, days to 50 per cent flowering and days to maturity, while sugar yield with juice yield, fresh stalk yield, total biomass, grain yield and positive correlation of fresh stalk yield with total biomass, grain yield, plant height, nodes per plant, stem girth, days to 50 per cent flowering and days to maturity. Sugar yield has positive correlation with juice yield, fresh stalk yield, total biomass, grain yield, total soluble sugars, brix per cent, bio ethanol yield and juice extraction per cent. These correlated traits can be effectively utilized in formulating indirect selection schemes. While path analysis studies revealed maximum positive direct effect of total soluble sugars and juice yield on sugar yield.

Jain and Patel (2014) studied the genetic variability and nature of character association in 9 parental lines and their thirty-six F<sub>1</sub>s of dual purpose sorghum (*Sorghum bicolor* (L) Moench) in randomized block design during *kharif* 2012. High heritability coupled with high genetic advance and GCV were noticed for seed yield/plant and dry fodder yield/plant. Whereas, high heritability combined with low genetic advance was recorded for leaf length and days to 50 per cent flowering. The seed yield/plant showed positive and significant correlation with plant height, number of leaves/plant, 100-seed weight and dry fodder yield/plant. While the dry fodder yield/plant showed positive and significant correlation with days to maturity, plant height, number of leaves/plant, leaf length, leaf width, 100-seed weight and seed yield/plant. The characters, 100-seed weight, plant height, number of leaves/plant and leaf width had positive and high direct effects on seed yield/plant and dry fodder yield/plant. Hence, due consideration should be given to these characters while planning a breeding strategy for dual purpose sorghum.

Emendack *et al.* (2014) studied the relationships between early-season cold temperature germination and pre flowering drought stress in eight grain sorghum inbreds using morpho physiological traits. Final germination per cent (FGP) differed among lines (range 30-80 %) and was positively correlated with leaf area index, plant height (HGT), and harvest index (HI). These three traits and single plant biomass (SPB) were also positively correlated with grain yield (SPY) under pre-flowering

drought. Most significant correlations among measured traits were observed at the heading to flowering phase. HI explained 75 and 91 per cent variability in SPY for the limited and no irrigation treatments respectively. Other predictors for SPY were; FGP, HGT and SPB under limited irrigation, and FGP and HGT under no irrigation. Therefore the ability to cease growth, maintain LAI, retain high CLC and high HI, will be important selection traits to develop sorghum cultivars for temperate and highland regions, with possibility of pre-flowering drought occurrence.

Patil *et al.* (2014) reported that the grain yield per plant exhibited significant positive association with 1000-grain weight, stem girth, leaf length, panicle length, panicle diameter, panicle weight and protein per cent in grain at both genotypic and phenotypic levels. Path co-efficient analysis considering 15 characters as causal variables showed that the number of leaves per plant had highest positive direct effect on grain yield per plant followed by panicle diameter, leaf length, protein per cent in grain and 1000-grain weight.

Kalpande *et al.* (2015) reported positive and significant correlation of plant height, panicle length, panicle width, test weight, primary branches per panicle, grains per primary branches and harvest index with grain yield per plant indicating the importance of these characters for improving grain yield per plant. Path coefficient analysis revealed that the characters *viz.*, panicle length, test weight, plant height, harvest index, threshed grade score, relative water content and panicle width had high positive direct effect on grain yield per plant.

### **3. Genetic Divergence**

The assessment of genetic diversity using quantitative traits is very important for differentiating the well defined populations. Several methods of divergence analysis based on quantitative traits have been proposed to suit various objectives, of which Mahalanobis's generalized distance occupy a unique place and an efficient method to gauge the extent of diversity among genotypes, which quantify the differences among several quantitative traits.

Murthy *et al.* (1970) studied genetic divergence in 1086 exotic collections. The 86 per cent of the variation was accounted by the three factors *viz.* I -panicle length, length of primaries, distance between whorls, number of fertile spikelet's, II – angle of primaries, number of secondary's and distance with whorls and III – growth

rate, days to flower and number of primaries. They concluded that reproductive and growth factors played significant role in the divergence of the genus Sorghum.

Rana and Murthy (1971) subjected 20 varieties of Eu-sorghum of diverse origin to multivariate analysis for four years. They evaluated these varieties for six traits and grouped them into six clusters.

Mehindiratta and Sindhy (1972) grouped 36 indigenous and exotic varieties into nine clusters. They also reported high contribution of leaf length and plant height towards genetic divergence.

Goyal and Asawa (1980) studied genetic divergence between genotypes including parents, hybrids,  $F_2$ s and  $F_3$ s derived from common male sterile line Kafir-60. These genotypes were grouped into 12 clusters, of which six accounted for 26 forms.

Giriraj and Goud (1981) assessed the genetic divergence in eight grain sorghum lines and their 28  $F_{1s}$  and grouped into 12 clusters.

Kukadia *et al.* (1981) through an analysis of dispersion reported that the highest contribution towards divergence was from plant height, followed by panicle length, grain yield, primaries per panicle, panicle breadth and days to flowering. The 27 varieties grouped into six clusters.

Dabholkar *et al.* (1983) studied 11 parents, 21  $F_1$ s and 21  $F_2$ s for genetic divergence. Genotypes grouped into seven clusters in  $F_2$  and eight in  $F_1$ . The greatest contribution to divergence was by days to 50 per cent flowering followed by plant height.

Sisodia *et al.* (1983) divided 30 genotypes into eight clusters. Important contributors for genetic divergence were plant height, days to maturity, ear length, ear diameter and leaf number.

Salilkumar and Singhania (1984) assessed the genetic divergence between 50 lines and these lines grouped into nine clusters. Major contributors to genetic divergence were days to 50 per cent blooming, leaf size, number of leaves per plant, grain yield per panicle, grain weight and stover yield.

Asthana *et al.* (1998) assessed genetic diversity among 52 sorghum genotypes from USA, Mexico, Africa and India using 20 yield related characters and partitioned

them into 13 clusters. There was absence of any relationship between geographic distance and genetic diversity. The trait, panicle size contributed maximum towards genetic divergence followed by grains per panicle, gross panicle weight and leaf area.

Ayana and Bekele (1999) assessed genetic divergence among 415 sorghum accessions for 15 quantitative characters using cluster analysis. They grouped the accessions into ten clusters.

Singh *et al.* (2001) investigated the genetic diversity in 46 genotypes of *S. bicolor* during summer season using multivariate analysis. The genotypes were divided in 8 clusters indicating the wide range of genetic diversity among the strains. There was no definite relationship between geographic and genetic diversity.

Nirmala *et al.* (2004) studied genetic divergence in 26 genotypes of sorghum using Mahalanobis  $D^2$  statistics. The genotypes grouped in 8 clusters. Cluster I was largest and having 19 genotypes and the rest of the clusters were of single genotype. Cluster VII was having high mean values for 100-seed weight and primaries, cluster VI for panicle length, cluster V for number of seeds per primary branch, and cluster VIII for grain yield, fodder weight and leaf area at 50 percent flowering.

Ashish *et al.* (2007) evaluated 24 sorghum genotypes in three environments, *viz.*, early sowing ( $E_1$ ), timely sowing ( $E_2$ ) and late sowing ( $E_3$ ), to know the influence of Genotype x Environment interaction on genetic diversity. Considerable genetic diversity was recorded in the material. The environment influenced clustering pattern of the genotypes. The mean values for different traits varied from environment to environment, which indicated the impact of different environments on the gene expression and ultimate effect on phenotypic expression for producing diversity among the genotypes. The intra and inter cluster distances also varied with environments. Mean values were higher in  $E_1$  followed by  $E_2$  and  $E_3$ . Some genotypes were occupying position in same cluster in two different environments indicating their stability. It is revealed that for better understanding of genetic diversity among the genotypes, they should be tested in variable environments.

Khapre *et al.* (2007) assessed genetic divergence in 74 local land races (70 local germplasm lines and 4 checks *viz.*, Swati, CSV 14 R and M-35-1) of *Rabi* sorghum was assessed using  $D^2$  analysis. All genotypes were grouped in to 9 clusters.

The study revealed that the local land races of *Rabi* sorghum possess diverse gene combinations and genetic diversity was independent of geographic origin. The path coefficient analysis revealed maximum contribution of ear head weight followed by ear head girth, number of secondaries and number of leaves towards the grain yield.

Rohman *et al.* (2007) studied genetic diversity in 35 sorghum genotypes based on 9 characters during *Rabi* 2002-03 in Gazipur, Bangladesh, using  $D^2$  and principal component analysis. The genotypes were grouped into 4 clusters. Cluster I contained the highest number of genotypes and cluster III contained the lowest number. The intercluster distance was higher than the intracluster distance. The highest intercluster distance was recorded between cluster III and IV. The highest intracluster distance was observed in cluster IV and the lowest in cluster II. Days to maturity, number of tillers per plant and 1000-grain weight showed the high contribution to genetic diversity.

Shridhar *et al.* (2007) assessed the genetic diversity in 39 germplasm lines of sorghum based on eight traits (days to first flowering, plant height, number of leaves, leaf length, leaf width, green fodder yield, dry matter yield and brix values). The genotypes grouped into nine clusters. The cluster means estimated over the genotypes for the eight characters reveal considerable inter cluster variation. This variation may be utilized in selection of parents for obtaining heterotic hybrids and recovering desirable segregates.

Savion *et al.* (2008) studied genetic diversity among accessions of sorghum in different conditions of P availability in nutrient solution and determined the characteristics that contributed in discriminating this divergence. The experiment was conducted under greenhouse conditions using a 9x4 factorial arrangement, with nine sorghum hybrids and four doses of P (3, 32, 97 and 129 m M P per liter of nutrient solution), in a randomized blocks design with three replications. Genetic dissimilarity was determined using the Mahalanobis generalized distance matrix and relative contribution of traits towards genetic divergence was calculated. Significant differences among hybrids were observed for all characteristics at the P concentrations 32, 97 and 129 mM P.L<sup>-1</sup>. The concentration 97 m M of P.L<sup>-1</sup> generated the largest number of groups of genotypes, however, genetic variability was also observed for the other P concentrations. Total dry mass presented the highest contribution to the expression of genetic dissimilarity between the hybrids, at all the P

concentrations. The experimental hybrid 0735019 demonstrated both efficiency and responsiveness to P, showing the highest values for the characteristics evaluated at the different levels of P.

Singh *et al.* (2008) revealed considerable genetic diversity among 32 genotypes of forage sorghum (*S. bicolor*), grown in Meerut, Uttar Pradesh, India, during *Kharif* 2006. The genotypes were grouped into 7 clusters (cluster I had 14 genotypes, cluster II had 11 genotypes, cluster VI had 3 genotypes and cluster III, IV, V and cluster VII had one genotype each). This envisaged that the genotypes grouped within a particular cluster were more or less genetically similar to each other and apparent. The maximum intra cluster distance was recorded for cluster VI (53.36) and the lowest for cluster I (45.60). The maximum inter cluster distance was observed between cluster IV and VI (125.10), whereas the minimum between clusters I and III (56.97). The hybridization of CPVI-1724, Varsha and SPV-1725 with SSG-59-3, Pant Chari-3 and SSG 59-3 with JHV-14 and, HC-260 with SSG-59-3, would produce heterotic hybrids and wide spectrum variability in subsequent generations. The leaves per plant had the greatest contribution (45.16 %) towards genetic divergence, followed by green fodder yield per day (19.76 %), internode length (14.31 %) and leaf breadth (13.31 %).

Rani and Rao (2009) estimated genetic divergence in 41 sorghum genotypes comprising tropical land races, derivatives of temperate and tropical lines (B and R lines), varieties and hybrids, by multivariate analysis. Based on  $D^2$  values, seven clusters were formed. Eight diverse genotypes were selected for the study of heterosis and were crossed in all possible combinations. Relationship between heterosis for important yield components and genetic divergence between parents was analysed in five top heterotic crosses and also in five commercial hybrids. There was no perfect correspondence between heterosis and genetic divergence between parents. Hence, this study established importance of even within group divergence for obtaining high heterosis.

Umadevi *et al.* (2009) studied genetic divergence in 60 germplasm using Mahalanobis  $D^2$  statistic in the *Rabi*. Observations recorded on seven characters. By applying Tocher's method, 60 germplasm were grouped into 21 clusters. Maximum inter cluster distance was observed between cluster VI and VII ( $D=41.76$ ). Plant height and single plant yield had contributed high towards genetic divergence.

Jain and Patel *et al.* (2012) evaluated 102 land races of forage sorghum for days to 50 % flowering, plant height, number of leaves per plant, leaf length, leaf breadth and fodder yield per plant in augmented block design during 2009-10 and 2010-11 revealed highly significant differences among the accessions. High heritability accompanied with high GA as per cent of mean was observed for days to 50 % flowering, plant height, number of leaves per plant, leaf length and fodder yield per plant suggested that these characters are under additive gene action and gives better scope for selection. Fodder yield was positive and significantly correlated with number of leaves per plant, leaf length, leaf width and panicle length. The characters leaf width, number of leaves per plant, days to 50 % flowering and panicle length showed positive direct effect on fodder yield. Whereas, leaf length showed positive significant correlation with fodder yield but the direct effect was negative. This indicated that positive correlation of this trait was due to its indirect effect via other traits. Based on the results of the means of the two years considering together for the various traits, the accession E-143 and E-JN-11 was superior for earliness, EA-2 and GUB-50 for plant height, E-159 for leaf characters and E-203 and GGUB-39 for fodder yield. Therefore, these accessions recommended for utilization in further breeding program for developing superior varieties.

Mahajan and Wadikar (2012) studied genetic divergence among twenty four sorghum genotypes using mahalanobis  $D^2$  staistic. The genotypes grouped into eight clusters, which revealed wide diversity in the experimental material. Harvest index contributed maximum towards genetic divergence. The maximum inter cluster distance was observed between clusters VII and VIII followed by clusters II and VIII and clusters II and VI. The high diverse clusters could serve as potential sources of the accessions for their use in hybridization programme.

Chittapur *et al.* (2013) used one hundred *Rabi* sorghum germplasm lines of diverse origin to estimate genetic diversity. Among the 15 quantitative traits studied, the highest contribution towards the divergence was by plant height followed by days to flowering, panicle weight, panicle length, number of primaries per panicle, dead heart percentage and grain yield. The genotypes were grouped into 23 clusters. Clustering pattern obtained in the present study indicates that no relationship was observed between the geographical diversity and genetic diversity.

Kannababu *et al.* (2013) characterized 15 parental lines and 32 varieties belonging to different categories of sorghum for DUS traits during the *Kharif* 2006 and 2007. Plant height contributed >70 % towards diversity. The 47 genotypes clustered in three clusters when diversity based on quantitative and in four clusters when diversity based on qualitative data alone. Combination of qualitative and quantitative traits in establishing distinctiveness was more effective than any type of traits alone.

Seetharam and Ganesamurthy (2013) studied genetic diversity in 39 sorghum genotypes for nine characters and highest diversity index (0.879) was observed between TNS598 and IS5030. Hierarchical clustering divided the genotypes into six clusters. Promising genotypes were identified for early flowering, plant height, number of leaves, leaf length and yield based on cluster mean values.

Shegro *et al.* (2013) conducted field experiments in Potchefstroom, South Africa, during the summer seasons of 2009 and 2010, to estimate the level of phenotypic diversity among 22 sorghum accessions. The experiment was laid out in a randomized complete block design with three replications. Nine qualitative and 20 quantitative traits were recorded. Analysis of variance for the quantitative traits revealed that differences among accessions were highly significant for all traits. Diversity index varied from 31 % (panicle compactness and shape) to 84 % (glume color). The pair-wise genetic distances based on phenotypic traits showed varying genetic distances. Cluster analysis of the phenotypic traits resulted in four distinct groups of accessions with genetic distances ranging from 0.40 to 1.59. Therefore, the phenotypic markers provide a useful measure of genetic distances among sorghum accessions to identify potential donors or parental material for future breeding efforts.

Ahamad *et al.* (2015) estimated divergence based on morphological traits using Mahalanobis generalized distance ( $D^2$ ) analysis to group the sorghum genotypes. Significant variations among sorghum genotypes were observed with respect to days to flowering, days to maturity, plant height, number of seeds per panicle, 100 seed weight and grain yield per plant. The highest grain yield per genotype (124.90 g) was recorded in BD-755 genotype while the lowest (4.50 g) was in BD-736 genotype. The highest number of genotypes (26) was in cluster VII and the lowest (7) was included in cluster II. The highest class mean values for days to flowering (84.1 days), days to maturity (148.0 days), inflorescence width (7.7 cm),

number of seeds per panicle (3989.7) and seed yield per plant (106.7 g) were found in cluster II. The highest inter-cluster distance was obtained between the cluster VIII and II (25.880) followed by VI and II (22.842), while the lowest inter-cluster was between VII and V (2.859). The intra-cluster distance was the highest (0.994) in cluster VIII. The maximum value of inter-cluster distance indicated that genotypes belonging to cluster VIII were far diverged from those of cluster II.

Sujatha *et al.* 2015 assessed the divergence among the 45 *Rabi* sorghum landraces, 13 advanced breeding lines and 4 popular cultivars. The 62 genotypes were grouped into 15 clusters, where cluster I was the largest comprising of 41 genotypes followed by cluster III with 7 genotypes and cluster XI with 2 genotypes. The inter cluster distance was maximum between cluster XIII and XIV followed by cluster XIV and XV, cluster XII and XV, cluster XII and XIII and cluster V and XIV. Based on the inter cluster distance and *per se* performance, the elite variety Phule Anuradha, the land races RSV 1426, SSRG 147, Pusegaon local and the advanced breeding line RSV 1420 can be utilized in breeding programmes as potential parents for crop improvement. Seed yield contributed maximum to divergence (31.84%) followed by plant height (20.62%) and days to 50% flowering (14.38%).

### 3. MATERIALS AND METHODS

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The present investigation entitled “**Genetic divergence in Sorghum [Sorghum bicolor (L.) Moench]**” was conducted during *Kharif* 2015 at Instructional Farm, Rajasthan College of Agriculture, Udaipur (Rajasthan). The material used and methods followed were as follows:

#### **EXPERIMENTAL MATERIAL**

The experimental material consists of 1700 germplasm lines of sorghum (given in Appendix-II) along with four checks *i.e.* CSV17, CSV20, CSV27 and CSV21F provided by National Bureau of Plant Genetic Resources (NBPGR) through ICAR- Indian Institute of Millet Research (IIMR), Hyderabad.

#### **EXPERIMENTAL DESIGN AND CROP GEOMETRY**

The experimental material was planted in augmented RBD with 60 replications. Inter and intra row spacing was 45 and 15 cm, respectively. Each genotype was grown in 2 m long single row plot. The date of sowing was 12/07/2015. But, later on account of shoot fly, stem borer or any other reason in number of plots observation cannot be recorded for one or more characters. Therefore, the experiment was analysed in augmented CRD.

#### **OBSERVATIONS RECORDED**

Five or available competitive normal appearing plants from each line were randomly selected for recording the observations for all the qualitative and quantitative characters.

A brief description of the procedure adopted for recording the observations for each character is given below.

#### **A. Qualitative Characters**

##### **1. Early plant vigour**

Early vigour was scored on 1 to 3 scale for each line. Where, 1 indicate poor, 2 good and 3 very good on the visual basis at 25 DAS.

**2. Leaf Colour**

Leaf colour was scored on 1 to 3 scale in each line. Where, 1 indicate pale green, 2 light green and 3 dark green on the visual basis at full foliage stage.

**3. Leaf Sheath Pigmentation**

Leaf sheath pigmentation was scored on 1 to 2 scale in each line. Where, 1 indicate tan, and 2 non-tan on the visual basis at full foliage stage.

**4. Leaf Orientation**

Leaf orientation was scored on 1 to 2 scale in each line. Where, 1 indicate erect and 2 drooping on the visual basis at full foliage stage.

**5. Leaf Midrib Colour**

Leaf midrib colour was scored on 1 to 7 scale in each line. Where, 1 indicate white, 2 green, 3 yellow, 4 brown, 5 purple, 6 colourless and 7 dark green on the visual basis at full foliage stage.

**6. Stay Green**

Stay green was scored on 0 and 1 scale in each line. Where, 0 indicate non senescence and 1 senescence on the visual basis for each lines at full foliage stage.

**7. Panicle Compactness**

Panicle compactness was scored on 1 to 6 scale in each line. Where, 1 indicate compact, 2 semi-compact, 3 loose, 4 very loose, 5 broom corn and 6 others on the visual basis at near maturity stage.

**8. Panicle Shape**

Panicle shape was scored on 1 to 7 scale in each line. Where, 1 indicate round, 2 oblong, 3 ovate, 4 elliptical, 5 cylindrical, 6 broom corn and 7 others on the visual basis at maturity stage.

**9. Glume Colour**

Glume colour was scored on 1 to 12 scale in each line. Where, 1 indicate white, 2 straw, 3 light brown, 4 brown, 5 reddish brown, 6 light red, 7 red, 8 dark red, 9 purple, 10 black, 11 straw brown and 12 straw purple on the visual basis at near maturity stage.

**10. Glume Covering**

The glume covering was categorized as covering of  $\frac{1}{4}$ ,  $\frac{1}{2}$ ,  $\frac{3}{4}$  and fully grain covered on the visual basis at near maturity stage and it was scored as 0.25, 0.50, 0.75 and 1, respectively.

**11. Presence of Awn**

Presence of awn was scored on 0 and 1 scale in each line. Where, 0 indicate absent and 1 present on the visual basis at maturity stage.

**12. Grain Colour**

Grain colour was scored on 1 to 14 scale in each line. Where, 1 indicate white, 2 chalky white, 3 creamy straw, 4 light yellow, 5 yellow, 6 light brown, 7 brown, 8 reddish brown, 9 light red, 10 red, 11 grey, 12 purple, 13 white and red mixed and 14 black on the visual basis after threshing.

**13. Grain Shape**

Grain shape was scored on 1 to 5 scale in each line. Where, 1 indicate compactly flat, 2 round, 3 sub lenticular round but flat from other side, 4 oval and 5 elliptical on the visual basis after threshing.

**14. Grain Size**

Grain size was scored on 1 to 3 scale in each line. Where, 1 indicate small, 2 medium and 3 bold on the visual basis after threshing.

**15. Endosperm Texture**

Endosperm texture was scored on 1 to 7 scale in each line. Where, 1 indicate compactly corneous, 2 mostly corneous, 3 intermediate, 4 mostly starchy, 5 completely starchy floury, 6 waxy, 7 yellow endosperm on the visual basis after threshing.

**16. Grain Lusture**

Grain lusture was scored on 0 and 1 scale in each line. Where, 0 indicate non lustrous, and 1 lustrous on the visual basis after threshing.

## **17. Race**

Race was identified on the basis of panicle, glume and grain characters. Where, 1 indicates durra, 2 bicolor, 3 caudatum, 4 guinea and 5 kafir. Durra race having characters are compact panicle, glume coriaceous and strongly nerved on the lower half and obovate shaped seed. Characters for bicolor race are open and medium size panicle, three-fourths or more of the grain covered by glume and small size seed. Caudatum race having characters are dense to slightly open panicle, grain partially covered by glume and flat on one side and bulging on the other shaped seed. Characters for guinea race are long size and loose panicle, most of the grain covered by glume and ovate or flattened shape and small to medium size seed. Kafir race having characters are cylindrical and semi-compact panicle, glume variable in length and elliptical or flattened shaped seed.

### **B. Quantitative Characters**

#### **1. Days to 50 per cent Flowering**

The date on which panicle emergence was noticed in 50 per cent of the plants in a plot was recorded and the number of days were counted from the date of sowing.

#### **2. Plant Height (cm)**

It was recorded from ground level to the tip of the panicle at maturity stage. The mean plant height was worked out for each plot.

#### **3. Number of Leaves**

Number of leaves for randomly selected plants was counted at full foliage stage. Then average was taken over number of plants.

#### **4. Leaf Length (cm)**

Lengths of 7<sup>th</sup> leaf from the base of the plant on randomly selected plants were recorded in centimetre (cm) at full foliage stage and mean leaf length was worked out.

#### **5. Leaf Width (cm)**

Width of above selected leaves were recorded from middle of the leaf where leaf width was maximum at full foliage stage and mean leaf width was worked out.

**6. Panicle Length (cm)**

It was recorded from tip to the base of the panicle on randomly selected plants at maturity stage. The mean panicle length was worked out for each plot.

**7. Panicle Width (cm)**

Panicle width was recorded on randomly selected plants. It was recorded at broad middle portion of the panicle at maturity stage and mean panicle width was worked.

**8. 100- Seed Weight (g)**

From the bulk seed of selected plants three samples of 100-seed were drawn and weighed on electronic balance in grams. The mean 100-seed weight was worked out for each plot.

**9. Grain Yield per Panicle ( g )**

After threshing, weight of dried grains of selected plants were recorded in grams and averaged.

**STATISTICAL METHODOLOGY**

The mean values of each plot were subjected to various standard statistical procedures as mentioned below.

**1. Analysis of Variance**

The analysis of variance for different characters in augmented CRD was done following Federer (1956). The skeleton of ANOVA is given in Table 3.1:

**Table 3.1 skeleton of ANOVA of augmented CRD**

| S.N. | Source              | d.f.  | SS  | MS | F | EMS                      |
|------|---------------------|-------|---|----|---|--------------------------|
| 1.   | Check               | c-1   | $\sum_{i=1}^c (\sum_{j=1}^r X_{ij})^2 / r - (\sum_{i=1}^c \sum_{j=1}^r X_{ij})^2 / n$ |    |   | $\sigma^2 + r\sigma^2 c$ |
| 2.   | Error               | (n-c) | Total SS – Block SS – Check SS  |    |   | $\sigma^2$               |
| 3.   | Total               | n-1   | $\sum_{i=1}^c \sum_{j=1}^r X_{ij}^2 - (\sum_{i=1}^c \sum_{j=1}^r X_{ij})^2 / n$       |    |   |                          |
| 4.   | Germplasm           | g-1   | $\sum_{j=1}^g X_i^2 - (\sum_{i=1}^g X_i)^2 / g$                                       |    |   | $\sigma^2 + \sigma^2 g$  |
| 5.   | Check v/s Germplasm | 1     | $(\sum_{i=1}^c \sum_{j=1}^r X_{ij})^2 / n + (\sum_{i=1}^g X_i)^2 / g$                 |    |   |                          |

**Where**  $X_{ij}$  = Value of  $i^{\text{th}}$  check in  $j^{\text{th}}$  block

$X_i$  = Value of  $i^{\text{th}}$  germplasm

$r$  = Number of blocks

$c$  = Number of checks

$n$  = Number of observations including number of blocks and checks

$g$  = Number of germplasm

$MS = SS_i / df_i$

F was calculated by dividing the MS of checks, germplasm and check v/s germplasm by error MS and was tested on respective degrees of freedom.

**Least significant difference for adjusted means:**

1. Difference between two check means =  $t \alpha \sqrt{2MSE/r}$
2. Difference between two germplasm in same block =  $t \alpha \sqrt{2MSE}$
3. Difference between two germplasm in different block =  $t \alpha \sqrt{2MSE (c+1)/c}$
4. Difference between germplasm and check mean =  $t \alpha \sqrt{MSE (1 + \frac{1}{r} + \frac{1}{c} + \frac{1}{rc})}$

For all L.S.D. the t value is two tail value at  $\alpha$  level and at error degree of freedom.

## 2. Estimation of variability parameters

The following genetic parameters were estimated for the character having significant mean square due to the germplasm.

- (a) **Genotypic variance:** It was calculated using following formula.

$$V_g = \text{MSG} - \text{MSE}$$

Where,

$V_g$  = Genotypic variance,                       $\text{MSG}$  = Mean square due to germplasm

$\text{MSE}$  = Error mean square

- (b) **Phenotypic variance:** It was calculated as follows:

$$V_p = V_g + V_e$$

Where,

$V_p$  = Phenotypic variance,                       $V_g$  = Genotypic variance, and

$V_e$  = Error variance *i.e.*  $\text{MSE}$

- (c) **Genotypic coefficient of variation (GCV):** It was calculated using the following formula as suggested by the Burton (1952).

$$\text{GCV} = \frac{\sqrt{V_g}}{\bar{X}} \times 100$$

Where,

$V_g$  = Genotypic variance, and                       $\bar{X}$  = Germplasm mean

- (d) **Phenotypic coefficient of variation (PCV):** It was calculated using the following formula as suggested by Burton (1952).

$$\text{PCV} = \frac{\sqrt{V_p}}{\bar{X}} \times 100$$

Where,

$V_p$  = phenotypic variance, and                       $\bar{X}$  = Germplasm mean

- (e) **Heritability ( $h^2$ ):** It was estimated in broad sense by using following formula as suggested by Lush (1940).

$$h^2 = \frac{V_g}{V_p} \times 100$$

Where,

$h^2$  = Heritability in broad sense

$V_g$  = Genotypic variance

$V_p$  = Phenotypic variance

**(f) Genetic gain**

It is percent expected genetic advance over the population mean. It was computed as follows using the formula of Johnson *et al.* (1955)

$$GG = \frac{GA}{\bar{X}} \times 100$$

Where,

$\bar{X}$  = Germplasm mean

$$GA = \text{Genetic advance} = \frac{K \cdot V_g}{\sqrt{V_p}}$$

Where,

$V_g$  = Genotypic variance

$V_p$  = Phenotypic variance

$K$  = Selection differential at 5 per cent selection pressure *i.e.* 2.06

**3. Correlation coefficient**

Genotypic and phenotypic correlation coefficients between different characters were calculated by using the genotypic and phenotypic variances and covariances in basic formula of Pearson (1902).

**(a) Genotypic correlation coefficient**

$$r_{xy}(g) = \frac{Cov_{xy}(g)}{\sqrt{V_x(g) \cdot V_y(g)}}$$

**(b) Phenotypic correlation coefficient**

$$r_{xy}(p) = \frac{Cov_{xy}(p)}{\sqrt{V_x(p) \cdot V_y(p)}}$$

Where,

$r_{xy}(g)$  = Genotypic correlation coefficient between X and Y traits

$r_{xy}(p)$  = Phenotypic correlation coefficient between X and Y traits

$Cov_{xy}(g)$  = Genotypic covariance between X and Y traits

$Cov_{xy}(p)$  = Phenotypic covariance between X and Y traits

$V_x(g)$  = Genotypic variance for X trait

$V_y(g)$  = Genotypic variance for Y trait

$V_x(p)$  = Phenotypic variance for X trait

$V_y(p)$  = Phenotypic variance for Y trait

The significance of correlation was tested by using the procedure of 't' test given by William Sealy Gosset (1908).

#### 4. Path coefficient analysis

Path coefficient is the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect. Path coefficients were calculated using the methodology described by Wright (1921), Li (1955) and Dewey and Lu (1959).

The detail procedure was as follows:

Direct effects  $P_{iy} = r_{ij}^{-1} \cdot r_{iy}$

Matrix of direct and indirect effects  $P_{ij} = r_{ij} \cdot P_{iy}$

Residual effect =  $\sqrt{1 - R^2}$

$$\text{Where } R^2 = \sum_{i=1}^c r_{iy} \cdot P_{iy}$$

Where,

$R^2$  = determinant

$r_{iy}$  = vector of correlations between  $i^{\text{th}}$  independent character and 'y' dependent character

$P_{iy}$  = vector of direct effect of  $i^{\text{th}}$  character on dependent character 'y'

$P_{ij}$  = matrix of direct and indirect effects

$r_{ij}$  = correlation matrix between  $i^{\text{th}}$  and  $j^{\text{th}}$  independent characters

$r^{-1}_{ij}$  = inverse correlation matrix

## 5. MANOVA (Multivariate Analysis of Variance)

Multivariate Analysis of Variance was performed using Wilk's lambda.

$$\lambda = \frac{|E|}{|H+E|}$$

Where, the determinant of the error sums of squares and cross products matrix **E** is divided by the determinant of the total sum of squares and cross products matrix **T = H + E**. If **H** is large relative to **E**, then **|H + E|** will be large relative to **|E|**. Thus, we will reject the null hypothesis if Wilk's lambda is small (close to zero).

## 6. Genetic divergence

Since, experimental design was augmented therefore, diversity analysis was carried out using ward (1963) method using euclidian distances and calculated through SPSS version 16 by using means of checks and germplasm having observations for all the quantitative characters.

## 4. EXPERIMENTAL RESULTS

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The results obtained from the present investigation entitled “**Genetic Divergence in Sorghum [*Sorghum bicolor* (L.) Moench]**” have been presented separately for qualitative characters and quantitative characters.

### 4.1 Qualitative characters

The germplasm lines were evaluated along with four checks in augmented RBD with 60 blocks. Out of the 1700 germplasm lines, 44 entries did not germinate and 503 germinated but affected by shoot fly and could not complete critical growth stages. Observations recorded on various qualitative traits are given below in Table 4.1.

#### Early plant vigour

Frequency of good early plant vigour was (64.4), (61.0), (59.3) and (53.7) per cent for CSV17, CSV20, CSV21F and CSV27 checks, respectively. At this stage 1656 germplasm lines were available and scored. Out of them 131, 872 and 653 lines having very good, good and poor early plant growth *i. e.* 52.6, 39.5 and 7.9 per cent, respectively.

#### Leaf colour

Leaf colour was dark green in CSV17 and CSV20, light green in CSV27 and CSV21F checks. At this stage 1153 germplasm lines were evaluated. Out of these 1108 were dark green, 45 light green being 96.1 and 3.9 per cent, respectively.

#### Leaf sheath pigmentation

Leaf sheath pigmentation was found tan type in all the four checks. Out of 1153 germplasm lines 1089 were non-tan and 64 were tan being 94.4 and 5.6 per cent, respectively.

#### Leaf orientation

Leaf orientation was drooping type for all the four checks as well as for all the 1153 germplasm lines evaluated.

### **Leaf midrib colour**

The check CSV20 showed white mid-rib and CSV17, CSV27 and CSV 21F green midrib colour. Among the 1153 germplasm lines 605 had green, 251 white, 212 yellow, 77 dark green and 8 colourless midrib colour being 52.5, 21.8, 18.4, 6.6 and 0.7 per cent, respectively.

### **Stay green**

Stay green indicating delayed senescence of leaves was found in CSV20 and non-stay green indicating senescence in CSV17, CSV27 and CSV21F checks. Whereas, in the germplasm 1059 were not having senescence and 94 lines were having senescence. This indicated that 91.8 per cent were having stay green character and rest 8.5 per cent lacking stay green character.

### **Panicle compactness**

It was found semi-compact in CSV17 and CSV20 and loose in CSV27 and CSV21F. Whereas, out of 1153 germplasm accessions 618 were compact, 294 were semi-compact, 156 were very loose, 75 were loose and 10 were broom corn being 53.6, 25.5, 13.5, 6.5 and 0.9 per cent, respectively.

### **Panicle shape**

Panicle shape was cylindrical in CSV17, elliptical in CSV20 and CSV27 and ovate in CSV21F. Whereas, out of 1153 germplasm lines 402 were elliptical, 291 broom corn, 270 cylindrical, 171 oblong, 18 ovate and 1 round being 34.9, 25.2, 23.4, 14.8, 1.6 and 0.1 per cent, respectively.

### **Glume colour**

Glume colour was found straw in all the four checks. Whereas, out of 1153 germplasm accessions, 407 were having straw, 355 light brown, 128 reddish brown, 93 brown, 56 red, 39 straw brown, 29 dark red, 25 light red, 12 black and 9 purple colour being 35.3, 30.8, 11.1, 8.1, 4.8, 3.4, 2.5, 2.2, 1.0 and 0.8 per cent, respectively.

### **Glume covering**

Glume covering was  $\frac{1}{2}$  in all the four checks. Whereas, out of 1153 germplasm accessions 493 were covered  $\frac{1}{2}$  seed, 417 were covered  $\frac{3}{4}$  of the seed, 170

were covered ¼ seed and 73 were fully covered being 42.8, 36.2, 14.7 and 6.3 per cent, respectively.

**Table 4.1 Frequency of genotypes in different categories of characters**

| Character                | Type           | Genotype (%) |          |        |        |        |         |
|--------------------------|----------------|--------------|----------|--------|--------|--------|---------|
|                          |                | Germplasm    | Per cent | CSV 17 | CSV 20 | CSV 27 | CSV 21F |
| Early plant vigour       | Poor           | 653          | 39.4     | 8.5    | 22.0   | 34.5   | 27.1    |
|                          | Good           | 872          | 52.7     | 64.4   | 61.0   | 60.3   | 59.3    |
|                          | Very good      | 131          | 7.9      | 27.1   | 16.9   | 5.2    | 13.6    |
|                          | Total          | 1656         |          |        |        |        |         |
| Leaf colour              | Light green    | 45           | 3.9      |        |        | 100    | 100     |
|                          | Dark green     | 1108         | 96.1     | 100    | 100    |        |         |
|                          | Total          | 1153         |          |        |        |        |         |
| Leaf sheath pigmentation | Non-tan        | 1089         | 94.4     |        |        |        |         |
|                          | Tan            | 64           | 5.6      | 100    | 100    | 100    | 100     |
|                          | Total          | 1153         |          |        |        |        |         |
| Leaf orientation         | Drooping       | 1153         | 100      | 100    | 100    | 100    | 100     |
|                          | Total          | 1153         |          |        |        |        |         |
| Leaf midrib colour       | White          | 251          | 21.8     |        | 100    |        |         |
|                          | Green          | 605          | 52.5     | 100    |        | 100    | 100     |
|                          | Yellow         | 212          | 18.4     |        |        |        |         |
|                          | Dark green     | 77           | 6.6      |        |        |        |         |
|                          | Colour less    | 8            | 0.7      |        |        |        |         |
|                          | Total          | 1153         |          |        |        |        |         |
| Stay green               | Non-Senescence | 1059         | 91.8     |        | 100    |        |         |
|                          | Senescence     | 94           | 8.2      | 100    |        | 100    | 100     |
|                          | Total          | 1153         |          |        |        |        |         |
| Panicle compactness      | Compact        | 618          | 53.6     |        |        |        |         |
|                          | Semi-compact   | 294          | 25.5     | 100    | 100    |        |         |
|                          | Loose          | 75           | 6.5      |        |        | 100    | 100     |
|                          | Very loose     | 156          | 13.5     |        |        |        |         |
|                          | Broom corn     | 10           | 0.9      |        |        |        |         |
|                          | Total          | 1153         |          |        |        |        |         |
| Panicle                  | Round          | 1            | 0.1      |        |        |        |         |

| Character       | Type          | Genotype (%) |          |        |        |        |         |
|-----------------|---------------|--------------|----------|--------|--------|--------|---------|
|                 |               | Germplasm    | Per cent | CSV 17 | CSV 20 | CSV 27 | CSV 21F |
| shape           |               |              |          |        |        |        |         |
|                 | Oblong        | 171          | 14.8     |        |        |        |         |
|                 | Ovate         | 18           | 1.6      |        |        |        | 100     |
|                 | Elliptical    | 402          | 34.9     |        | 100    | 100    |         |
|                 | Cylindrical   | 270          | 23.4     | 100    |        |        |         |
|                 | Broom corn    | 291          | 25.2     |        |        |        |         |
|                 | Total         | 1153         |          |        |        |        |         |
| Glume colour    |               |              |          |        |        |        |         |
|                 | Straw         | 407          | 35.3     | 100    | 100    | 100    | 100     |
|                 | Light brown   | 355          | 30.8     |        |        |        |         |
|                 | Brown         | 93           | 8.1      |        |        |        |         |
|                 | Reddish brown | 128          | 11.1     |        |        |        |         |
|                 | Light red     | 25           | 2.2      |        |        |        |         |
|                 | Red           | 56           | 4.8      |        |        |        |         |
|                 | Dark red      | 29           | 2.5      |        |        |        |         |
|                 | Purple        | 9            | 0.8      |        |        |        |         |
|                 | Black         | 12           | 1.0      |        |        |        |         |
|                 | Straw & brown | 39           | 3.4      |        |        |        |         |
|                 | Total         | 1153         |          |        |        |        |         |
| Glume covering  |               |              |          |        |        |        |         |
|                 | ¼             | 170          | 14.7     |        |        |        |         |
|                 | ½             | 493          | 42.8     | 100    | 100    | 100    | 100     |
|                 | ¾             | 417          | 36.2     |        |        |        |         |
|                 | 1             | 73           | 6.3      |        |        |        |         |
|                 | Total         | 1153         |          |        |        |        |         |
| Presence of awn |               |              |          |        |        |        |         |
|                 | Absent        | 125          | 10.8     | 100    | 100    | 100    |         |
|                 | Present       | 1028         | 89.2     |        |        |        | 100     |
|                 | Total         | 1153         |          |        |        |        |         |
| Grain colour    |               |              |          |        |        |        |         |
|                 | White         | 98           | 8.5      |        |        | 100    | 100     |
|                 | Chalky white  | 240          | 20.8     |        |        |        |         |
|                 | Creamy straw  | 468          | 40.6     | 100    | 100    |        |         |
|                 | Light yellow  | 111          | 9.6      |        |        |        |         |
|                 | Yellow        | 33           | 2.9      |        |        |        |         |

| Character         | Type  | Genotype (%) |          |        |        |        |         |
|-------------------|---|--------------|----------|--------|--------|--------|---------|
|                   |   | Germplasm    | Per cent | CSV 17 | CSV 20 | CSV 27 | CSV 21F |
|                   | Light brown                                   | 81           | 7.0      |        |        |        |         |
|                   | Brown   | 8            | 0.7      |        |        |        |         |
|                   | Reddish brown                                 | 44           | 3.8      |        |        |        |         |
|                   | Light red                                     | 24           | 2.0      |        |        |        |         |
|                   | Red   | 17           | 1.5      |        |        |        |         |
|                   | White & red mixed                             | 29           | 2.5      |        |        |        |         |
|                   | Total   | 1153         |          |        |        |        |         |
| Grain shape       | Compactly flat                                | 31           | 2.7      |        |        |        |         |
|                   | Round   | 142          | 12.3     |        |        |        |         |
|                   | Sub lenticular round but flat from other side | 403          | 35.0     |        |        |        |         |
|                   | Oval  | 188          | 16.3     | 100    | 100    | 100    | 100     |
|                   | Elliptical                                    | 389          | 33.7     |        |        |        |         |
|                   | Total   | 1153         |          |        |        |        |         |
| Grain size        | Small   | 404          | 35.0     | 100    |        |        |         |
|                   | Medium  | 406          | 35.2     |        |        | 100    | 100     |
|                   | Bold  | 343          | 29.8     |        | 100    |        |         |
|                   | Total   | 1153         |          |        |        |        |         |
| Endosperm texture | Compactly corneous                            | 349          | 30.3     |        |        |        |         |
|                   | Mostly corneous                               | 153          | 13.3     |        |        |        |         |
|                   | Intermediate                                  | 516          | 44.8     | 100    | 100    | 100    | 100     |
|                   | Mostly starchy                                | 134          | 11.6     |        |        |        |         |
|                   | Completely starchy floury                     | 1            | 0.1      |        |        |        |         |
|                   | Total   | 1153         |          |        |        |        |         |
| Grain lusture     | Non Lustrous                                  | 1081         | 93.8     | 100    | 100    | 100    |         |
|                   | Lustrous                                      | 72           | 6.2      |        |        |        | 100     |
|                   | Total   | 1153         |          |        |        |        |         |

| Character | Type     | Genotype (%) |          |        |        |        |         |
|-----------|----------|--------------|----------|--------|--------|--------|---------|
|           |          | Germplasm    | Per cent | CSV 17 | CSV 20 | CSV 27 | CSV 21F |
| Race      | Durra    | 347          | 30.0     |        |        |        |         |
|           | Bicolor  | 138          | 12.0     |        |        |        | 100     |
|           | Caudatum | 206          | 17.9     |        |        |        |         |
|           | Guinea   | 131          | 11.4     |        |        |        |         |
|           | Kafir    | 331          | 28.7     | 100    | 100    | 100    |         |
|           | Total    | 1153         |          |        |        |        |         |

### **Presence of awn**

Awn was present in CSV21F and absent in CSV17, CSV20 and CSV27 checks. Whereas, out of 1153 germplasm accessions 1028 were awned and 125 were non-awned being 89.2 and 10.8 per cent, respectively.

### **Grain colour**

Grain colour was creamy straw in CSV17 and CSV20 and white in CSV27 and CSV21F checks. Whereas, out of 1153 germplasm lines 468 were with creamy straw, 240 chalky white, 111 light yellow, 98 white, 81 light brown, 44 reddish brown, 33 yellow, 29 white and red mixed, 24 light red, 17 red and 8 brown being 40.6, 20.8, 9.6, 8.5, 7.0, 3.8, 2.9, 2.5, 2.0, 1.5 and 0.7 per cent, respectively.

### **Grain shape**

In all the four checks grain shape was oval. Whereas, out of 1153 germplasm lines, grain shape in 403 lines were sub-lenticular round but flat from other side, in 389 lines elliptical, in 188 lines oval, in 142 round and in 31 compactly flat germplasm was found being 35.0, 33.3, 16.3, 12.3, and 2.7 per cent, respectively.

### **Grain size**

Grain size was small in CSV17, medium in CSV27 and CSV21F and bold in CSV20 checks. Whereas, out of 1153 germplasm accessions 406 were medium, 404 small and 343 bold being 35.2, 35.0 and 29.8 per cent, respectively.

### **Endosperm texture**

Endosperm texture was intermediate in all the four checks. Whereas, 516 germplasm accessions exhibited intermediate, 349 compactly corneous, 153 mostly corneous, 134 mostly starchy and 1 completely starchy floury endosperm texture being 44.8, 30.3, 13.3, 11.6 and 0.1 per cent, respectively.

### **Grain lusture**

It was non-lustrous in CSV17, CSV20 and CSV27 and lustrous in CSV21F checks. Out of 1153 germplasm lines, 1081 were having non-lustrous and 72 lustrous grains being 93.8 and 6.2 per cent, respectively.

## **Race**

Three checks were belongs to kafir race CSV17, CSV20 and CSV27 while CSV21F were belongs to bicolor. Out of 1153 germplasm, 347 were durra, 331 were kafir, 206 were caudatum, 138 lines were bicolor type and 131 were guinea being 30.0, 28.7, 17.9 12.0 and 11.4 per cent, respectively.

### **4.2 Quantitative Characters**

Apart from above qualitative characters nine quantitative characters were also studied. The data recorded on quantitative traits were subjected to various statistical and biometrical analysis and the results obtained are presented under the following sub-heads:

- 4.2.1 Analysis of variance
- 4.2.2 Mean performance
- 4.2.3 Variability analysis
- 4.2.4 Correlation coefficient analysis
- 4.2.5 Path-coefficient analysis
- 4.2.6 MANOVA
- 4.2.7 Genetic divergence

#### **4.2.1 Analysis of variance**

The mean squares of augmented CRD design in respect of nine quantitative characters are presented in Table 4.2. The mean squares due to treatment, check and germplasm were highly significant for all the characters. The mean square due to checks v/s germplasm was also highly significant for all the characters except leaf length.

**Table 4.2 Mean square for different characters**

| SN Character         | Treatment<br>[1156] | Check<br>[3] | Germplasm<br>[1152] | C v/s G<br>[1] | Error<br>[206] |
|----------------------|---------------------|--------------|---------------------|----------------|----------------|
| 1. Days to flowering | 264.50**            | 5397.25**    | 215.08**            | 41791.34**     | 23.90          |
| 2. Plant height      | 4831.60**           | 176848.45**  | 3986.03**           | 462880.67**    | 891.08         |
| 3. Number of leaves  | 15.06**             | 77.92**      | 13.20**             | 1972.87**      | 1.33           |
| 4. Leaf length       | 173.29**            | 2684.40**    | 166.75**            | 173.50         | 83.83          |
| 5. Leaf width        | 2.60**              | 12.98**      | 2.53**              | 50.83**        | 0.99           |
| 6. Ear head length   | 41.64**             | 271.54**     | 38.54**             | 2930.97**      | 15.00          |
| 7. Ear head width    | 6.66**              | 71.82**      | 6.48**              | 15.90*         | 3.24           |
|                      | [598]               | [3]          | [594]               | [1]            | [202]          |
| 8. 100 Seed weight   | 0.94**              | 15.50**      | 0.75**              | 69.91**        | 0.07           |
| 9. Grain weight      | 492.07**            | 12449.15**   | 401.55**            | 18391.05**     | 207.23         |

\*, \*\* significant at 5% and 1% level of significance respectively

[ ] Degree of freedom

#### 4.2.2 Mean Value for Different Characters:

The mean values are presented in appendix II and III and salient results are presented character-wise as follows.

##### Days to 50 per cent flowering

Days to 50 per cent flowering ranged from 47 days (IC-286827, IC-286828, IC-286998, IC-287157 and IC-287159) to 121 days (IC-287346) with a general mean of 86.54 days (non-adjusted mean). The best check for days to 50 per cent flowering was CSV17 (59.29 days). Out of 1700 germplasm, 1153 were flowered. Adjusted mean of 36 Germplasm lines were significantly superior over the best check CSV17 for earliness. The accession IC-286998 (39.90 days) was earliest to flower followed by IC-286992 and IC-286993 (42.90 days), IC-287000 (45.90 days), IC-286991 (46.90 days), IC-286827 and IC-286828 (49.82 days), IC-286990 (49.90 days), IC-287493 (51.07 days) and IC-286989 (51.9 days).

##### Plant height (cm)

Plant height ranged from 88 cm (IC-288089) to 470 cm (IC-286736) with general mean of 253.24 cm. The best check for plant height was CSV21F (263 cm). Out of 1153 germplasm lines, adjusted mean of 600 lines were significantly superior over the best check CSV21F. The accession IC-287324 having maximum plant height (441.73 cm) it was followed by IC-286736 (436.27 cm), IC-287054 (434.66 cm), IC-

287557 (431.01 cm), IC-287328 and IC-287332 (421.73 cm), IC 288148 (420.48 cm) and IC-288121 (417.00 cm).

### **Number of leaves**

The numbers of leaves per plant ranged from 6 leaves (IC-286811, IC-286993, IC-287133, IC-287157 and IC-287165) to 25 leaves (IC-286811) with a general mean of 14.02 leaves. The best check for number of leaves was CSV21F (12.13). Out of 1153 germplasm accessions, adjusted mean of 832 germplasm lines were significantly superior over the best check CSV21F. The accession IC-286811 (25.7) had maximum number of leaves followed by IC-286719 (24.54), IC-287316 (24.04), IC-286938 and IC-286939 (23.69), IC-288301 (23.58), IC-287081 (22.95 cm), IC-287054 (22.90) and IC-286666 (22.87).

### **Leaf length (cm)**

Among the 1700 germplasm lines, 1153 lines reached upto the 7<sup>th</sup> leaf stage. Leaf length in these genotypes ranged from 24 cm (IC-288202) to 115 cm (IC-286890, IC-287238, IC-287490 and IC-288231) with a general mean of 79.74 cm. The best check for leaf length was CSV27 (88.81 cm). While comparing the adjusted means, 288 germplasm lines were significantly superior over the best check CSV27. The accessions IC-287814 having maximum leaf length (115.4 cm) followed by IC-287490 (114.90 cm), IC-288182 (113.43 cm), IC-286890 (112.57 cm), IC-287059 (112.19 cm), IC-286984 (111.57 cm), IC-287792 and IC-287793 (111.40 cm) and IC-287238 (111.35 cm).

### **Leaf width (cm)**

Leaf width ranged from 4 to 13 cm with a general mean of 8.31 cm. The best check was CSV27 (8.28 cm). Out of 1153 accessions, adjusted means of 628 germplasm lines were significantly superior over the best check CSV27 on the basis of adjusted means. The accession IC-286982 (14.52 cm) was having maximum leaf width followed by IC-286900 (12.79 cm), IC-288297 (12.67 cm), IC-287537 (12.52 cm), IC-287054 (12.42 cm), IC-287919 (12.36 cm) and IC-288269 (12.35 cm).

### **Panicle length (cm)**

Panicle length ranged from 6 cm (IC-287531 and IC-287863) to 45 cm (IC-287950) with a general mean of 19.69 cm (non-adjusted means). The best check was

CSV27 (25.38 cm). Out of 1153 germplasm lines, adjusted means of 195 lines were significantly superior over the best check CSV27. The accession IC-287950 having maximum panicle length (43.42 cm) it was followed by IC-286922 (42.52 cm), IC-288160 (42.23 cm), IC-287253 (41.21 cm), IC-287866 (40.33 cm), IC-286852 (39.57 cm), IC-288161 (39.23 cm) and IC-288060 (36.56 cm).

#### **Panicle width (cm)**

Panicle width ranged from 3 cm (IC-287039, IC-287238 and IC-288079) to 19 cm (IC-287681 and IC-287144) with a general mean of 8.02 cm. The best check was CSV21F (9.33 cm). Out of 1153 germplasm lines, adjusted means of 324 lines were significantly superior over the best check CSV21F. The accession IC-287144 having maximum panicle width (19.93 cm) it was followed by IC-287145 (18.93 cm), IC-286921 (18.48 cm), IC-287681 (18.44 cm), IC-287019 (17.99 cm), IC-287169 (17.93 cm) and IC-287405 (17.65 cm), IC-287678 (17.44 cm).

#### **100-Seed weight (g)**

Out of 1700 germplasm lines the required quantity of 100 seed was available in 595 lines only. 100-seed weight ranged from 0.62 g (IC-288119) to 5.88 g (IC-287651) with general mean 2.92 g. The best checks were both CSV21F and CSV27 (3.73 g). Adjusted means of 86 germplasm lines were significantly superior over the best checks CSV21F and CSV27. The accessions IC-287651 having maximum 100-seed weight followed (6.12 g) it was by IC-287444 (5.17 g), IC-287529 (5.03 g), IC-288281 (4.95 g), IC-287454 (4.87 g), IC-287482 and IC-288006 (4.71 g), IC-288270 (4.63 g), IC-287769 (4.60 g) and IC-287743 (4.59 g).

#### **Grain yield per panicle (g)**

Out of 1700 germplasm lines only 595 reached upto maturity stage. Grain yield per panicle in these germplasm ranged from 2.77 g (IC-286709) to 103.67 g (IC-288008) with general mean 34.68 g. The best check was CSV27 (57.52 g). Adjusted means of 78 germplasm lines were significantly superior over the best check CSV27. Accession IC-287836 having maximum grain yield per panicle (111.65 g) it was followed by IC-287072 (118.25 g), IC-288215 (107.65 g), IC-288008 (104.35 g), IC-287078 (101.67 g), IC-287821 (99.76 g), IC-288009 (99.15 g), IC-287779 (98.57 g) and IC-288035 (98.54 g).

**Table 4.3 Summary of mean values for days to 50 % flowering, number of leaves, leaf length, leaf width and panicle length, panicle width, plant height, grain yield per panicle and 100 seed weight**

|                  | Days to 50%<br>flowering | Plant height<br>(cm) | Number of<br>leaves | Leaf length<br>(cm) | Leaf width<br>(cm) | Panicle<br>length (cm) | Panicle width<br>(cm) | 100-seed<br>weight (g) | Grain yield<br>per panicle<br>(g) |
|------------------|--------------------------|----------------------|---------------------|---------------------|--------------------|------------------------|-----------------------|------------------------|-----------------------------------|
| <b>Germplasm</b> |                          |                      |                     |                     |                    |                        |                       |                        |                                   |
| Mean             | 88.90                    | 261.11               | 14.54               | 79.89               | 8.39               | 19.06                  | 8.06                  | 2.75                   | 31.86                             |
| Minimum          | 47.00                    | 88.00                | 6.00                | 24.00               | 4.00               | 6.00                   | 3.00                  | 0.62                   | 2.77                              |
| Maximum          | 121.00                   | 470.00               | 25.00               | 115.00              | 13.00              | 45.00                  | 19.00                 | 5.88                   | 103.67                            |
| <b>Checks</b>    |                          |                      |                     |                     |                    |                        |                       |                        |                                   |
| CSV 17           | 59.29                    | 130.66               | 9.51                | 71.11               | 7.88               | 24.39                  | 6.57                  | 2.65                   | 33.49                             |
| CSV 20           | 76.04                    | 223.90               | 11.44               | 79.84               | 8.16               | 22.90                  | 7.52                  | 3.69                   | 55.44                             |
| CSV 21F          | 80.33                    | 263.11               | 12.13               | 77.60               | 7.17               | 20.12                  | 9.33                  | 3.73                   | 26.13                             |
| CSV 27           | 80.11                    | 228.22               | 11.91               | 88.81               | 8.28               | 25.38                  | 7.67                  | 3.73                   | 57.52                             |
| Mean             | 73.57                    | 210.06               | 11.20               | 78.90               | 7.85               | 23.12                  | 7.76                  | 3.42                   | 42.82                             |
| Minimum          | 59.29                    | 130.66               | 9.51                | 71.11               | 7.17               | 20.12                  | 6.57                  | 2.65                   | 26.13                             |
| Maximum          | 80.33                    | 263.11               | 12.13               | 88.81               | 8.28               | 25.38                  | 9.33                  | 3.73                   | 57.52                             |
| SEd              | 0.89                     | 5.45                 | 0.21                | 1.67                | 0.18               | 0.71                   | 0.33                  | 0.05                   | 2.63                              |
| CD 5%            | 1.76                     | 10.75                | 0.42                | 3.30                | 0.36               | 1.39                   | 0.65                  | 0.10                   | 5.18                              |

### 4.2.3 Variability analysis

The estimate of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ( $h^2$ ) and genetic gain (GG) are presented in table 4.4. It is apparent from the table that phenotypic coefficients of variation were invariably greater than the corresponding genotypic coefficient of variation though the trend of both GCV and PCV was same. The parameter-wise findings are as follows:

#### Genotypic Coefficient of Variation (GCV)

On the basis of standard deviation (SD) characters were classified in three categories greater than mean + SD i.e. high in between mean  $\pm$ SD i.e. medium and mean – SD i.e. lower.

GCV was high for Grain yield per panicle (43.75 %), 100-seed weight (29.96 %), panicle length (25.45 %), number of leaves (23.69 %) and panicle width (22.32 %). Medium (between 9.42 to 22.28 %) GCV was observed for Plant height (21.31 %), days to 50 per cent flowering (15.55 %), Leaf width (14.81 %) and Leaf length (11.40 %), (Table 4.4).

**Table 4.4 Variability parameters**

| Sr.N. | Character                   | GCV (%) | PCV (%) | $h^2$ (%) | GG (%) |
|-------|-----------------------------|---------|---------|-----------|--------|
| 1     | Days to 50 % flowering      | 15.55   | 16.50   | 88.89     | 30.21  |
| 2     | Plant height (cm)           | 21.31   | 24.18   | 77.64     | 38.67  |
| 3     | Number of leaves            | 23.69   | 24.99   | 89.89     | 46.28  |
| 4     | Leaf length (cm)            | 11.40   | 16.16   | 49.73     | 16.56  |
| 5     | Leaf width (cm)             | 14.81   | 18.97   | 61.00     | 23.83  |
| 6     | Panicle length (cm)         | 25.45   | 32.57   | 61.08     | 40.97  |
| 7     | Panicle width (cm)          | 22.32   | 31.58   | 49.96     | 32.50  |
| 8     | 100-seed weight (g)         | 29.96   | 31.49   | 90.53     | 58.72  |
| 9     | Grain yield per panicle (g) | 43.75   | 62.89   | 48.39     | 62.70  |

#### Phenotypic Coefficient of Variation (PCV)

The PCV was high for grains yield per panicle (62.89 %) and medium (between 14.51 to 43.11 %) PCV was observed for panicle length (32.57 %) followed by panicle width (31.62 %), 100-seed weight (31.49 %), number of leaves (24.99 %), plant height (24.18 %), leaf width (18.97 %), days to 50 per cent flowering (16.50 %), and leaf length (16.16 %), (Table 4.4)

### Heritability ( $h^2$ )

Heritability was high for 100-seed weight (90.53 %), number of leaves (89.89 %), days to 50 per cent flowering (88.89 %) and plant height (77.64 %). Medium (between 17.21 to 66.57 %) heritability was observed for panicle length (61.08 %), leaf width (61.00 %), panicle width (49.96 %), leaf length (49.72 %) and grain yield per panicle (48.39 %), (Table 4.4).

### Genetic Gain

Genetic gain was high for grain yield per panicle (62.70 %), 100-seed weight (58.72 %), number of leaves (46.28 %), panicle length (40.97 %) and plant height (38.67 %). Medium (between 7.65 to 35.91 %) genetic gain was observed for panicle width (32.50 %), days to 50 per cent flowering (30.21 %), leaf width (23.83 %) and leaf length (16.56 %), (Table 4.4).

#### 4.2.4 Correlation Coefficient Analysis

In order to improve complex characters like yield, it is essential to have comprehensive knowledge its correlation with other traits and correlation between them. Further the correlation is also influenced by environment therefore, in present study the correlation coefficients were worked out between nine characters at both genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) levels. Higher values of genotypic correlation coefficients than their corresponding phenotypic correlation coefficients may be due to masking effect of environment. The degree of association was quantified on the basis of value phenotypic and genotypic correlation coefficient.

A perusal of table 4.5 revealed that grain yield per panicle exhibited significantly positive correlation with 100-seed weight ( $r_g = 0.52$  and  $r_p = 0.47$ ) at both genotypic and phenotypic level. Whereas, it was significant negatively correlated with panicle length ( $r_g = -0.53$  and  $r_p = -0.21$ ), leaf length ( $r_g = -0.48$  and  $r_p = -0.17$ ), plant height ( $r_g = -0.40$  and  $r_p = -0.22$ ) at both genotypic and phenotypic level and number of leaves ( $r_g = -0.37$  and  $r_p = -0.22$ ) and panicle width ( $r_g = -0.39$  and  $r_p = -0.04$ ) at genotypic level. Days to 50 per cent flowering ( $r_g = -0.52$  and  $r_p = 0.35$ ) and leaf width ( $r_g = -0.08$  and  $r_p = 0.13$ ) were correlated significant negative and positive at genotypic and phenotypic level respectively.

100-Seed weight showed significantly positive correlation with leaf width ( $r_g = 0.20$  and  $r_p = 0.18$ ) and leaf length ( $r_g = 0.05$  and  $r_p = 0.07$ ). Panicle length ( $r_g = -$

0.51 and  $r_p = -0.36$ ) and panicle width ( $r_g = -0.21$  and  $r_p = -0.11$ ) exhibited significantly negative correlation with 100-seed weight at both genotypic and phenotypic level. Days to 50 per cent flowering ( $r_g = -0.23$  and  $r_p = 0.35$ ) was significant negatively correlated at genotypic level and significant positively correlated at genotypic level.

Panicle width showed significantly positive correlation with panicle length ( $r_g = 0.56$  and  $r_p = 0.52$ ) at both genotypic and phenotypic level and plant height ( $r_g = 0.03$  and  $r_p = 0.06$ ) at phenotypic level. Number of leaves ( $r_g = -0.16$  and  $r_p = -0.06$ ) at both genotypic and phenotypic level and leaf length ( $r_g = -0.23$  and  $r_p = 0.03$ ) at genotypic level showed significantly negative correlation with Panicle width. Days to 50 per cent flowering ( $r_g = -0.10$  and  $r_p = 0.35$ ) and leaf width ( $r_g = -0.10$  and  $r_p = 0.07$ ) showed significantly positive correlation at phenotypic level and significantly negative correlation at genotypic level. Panicle width showed significantly positive correlation with plant height ( $r_p = 0.06$ ) at phenotypic level.

Number of leaves ( $r_g = -0.16$  and  $r_p = -0.08$ ) at both genotypic and phenotypic level and leaf length ( $r_g = -0.18$ ), leaf width ( $r_g = -0.13$  and) and plant height ( $r_g = -0.11$ ) at genotypic level exhibited significantly negative correlation with panicle length. Panicle length showed significantly positive correlation with days to 50 per cent flowering ( $r_g = 0.16$  and  $r_p = 0.11$ ) at both genotypic and phenotypic level.

Leaf width showed significantly positive correlation with number of leaves ( $r_g = 0.64$  and  $0.53$ ), plant height ( $r_g = 0.36$  and  $r_p = 0.27$ ), 50 per cent flowering ( $r_g = 0.31$  and  $r_p = 0.35$ ) and leaf length ( $r_g = 0.31$  and  $r_p = 0.38$ ) at both genotypic and phenotypic level. Days to 50 per cent flowering ( $r_g = 0.56$  and  $r_p = 0.35$ ), number of leaves ( $r_g = 0.59$  and  $0.50$ ) and plant height ( $r_g = 0.46$  and  $r_p = 0.42$ ) exhibited significantly positive correlation with leaf length at both genotypic and phenotypic level.

Number of leaves showed significantly positive correlation with 50 per cent flowering ( $r_g = 0.72$  and  $r_p = 0.65$ ) and plant height ( $r_g = 0.57$  and  $r_p = 0.53$ ) at both genotypic and phenotypic level. Correlation between plant height and days to 50 per cent flowering was significant positive ( $r_g = 0.40$  and  $r_p = 0.35$ ) at both phenotypic and genotypic level.

**Table 4.5 Genotypic and phenotypic correlation coefficients between different characters in sorghum**

| Sr.N. | Characters             | G/P | Plant height | Number of leaves | Leaf length | Leaf width | Panicle length | Panicle width | 100-seed weight | Grain yield per panicle |
|-------|------------------------|-----|--------------|------------------|-------------|------------|----------------|---------------|-----------------|-------------------------|
| 1     | Days to 50 % flowering | G   | 0.40**       | 0.72**           | 0.56**      | 0.31**     | 0.16**         | -0.10**       | -0.23**         | -0.52**                 |
|       |                        | P   | 0.35**       | 0.65**           | 0.36**      | 0.35**     | 0.11**         | -0.07**       | -0.22**         | 0.37**                  |
| 2     | Plant height           | G   |              | 0.57**           | 0.46**      | 0.36**     | -0.11**        | 0.03          | 0.02            | -0.40**                 |
|       |                        | P   |              | 0.53**           | 0.42**      | 0.27**     | -0.04          | 0.06*         | 0.04            | -0.22**                 |
| 3     | Number of leaves       | G   |              |                  | 0.59**      | 0.64**     | -0.16**        | -0.16**       | -0.01           | -0.37**                 |
|       |                        | P   |              |                  | 0.50**      | 0.53**     | -0.08**        | -0.06*        | -0.01           | -0.22                   |
| 4     | Leaf length            | G   |              |                  |             | 0.31**     | -0.18**        | -0.23**       | 0.05*           | -0.48**                 |
|       |                        | P   |              |                  |             | 0.38**     | -0.02          | 0.03          | 0.07**          | -0.17**                 |
| 5     | Leaf width             | G   |              |                  |             |            | -0.13**        | -0.10**       | 0.20**          | -0.08**                 |
|       |                        | P   |              |                  |             |            | -0.02          | 0.07**        | 0.18**          | 0.13**                  |
| 6     | Panicle length         | G   |              |                  |             |            |                | 0.56**        | -0.51**         | -0.53**                 |
|       |                        | P   |              |                  |             |            |                | 0.52**        | -0.36**         | -0.21**                 |
| 7     | Panicle width          | G   |              |                  |             |            |                |               | -0.21**         | -0.39**                 |
|       |                        | P   |              |                  |             |            |                |               | -0.11**         | -0.04                   |
| 8     | 100-seed weight        | G   |              |                  |             |            |                |               |                 | 0.52**                  |
|       |                        | P   |              |                  |             |            |                |               |                 | 0.47**                  |

\*, \*\*significant at 5% and 1% level of significance respectively

G and P Genotypic and Phenotypic correlation coefficients, respectively



#### **4.2.5 Path Coefficient Analysis:**

In present study, path coefficients were calculated for grain yield per panicle at genotypic and phenotypic level using eight independent characters.

##### **Genotypic path coefficients for grain yield per panicle**

The residual effect ( $R = 0.5336$ ) indicated that 53.36 per cent variability of grain yield per panicle was explained by days to 50 per cent flowering, number of leaves, leaf width, panicle length, panicle width, plant height and 100-seed weight. The influence of characters can be judged by magnitude of direct effects, irrespective of its direction. The direct effect was maximum for leaf length (-0.48) followed by panicle length (-0.32), 100-seed weight (0.30), panicle width (-0.27), plant height (-0.16), number of leaves (-0.09), leaf width (-0.07) and days to 50 per cent flowering (-0.06). The indirect effect was also in the same order through these characters. Directions of direct effect and correlation coefficients were same for days to 50 per cent flowering, plant height, number of leaves, leaf length, panicle length, panicle width and 100-seed weight. Whereas, for leaf width the value was in opposite direction, (Table 4.6).

##### **Phenotypic path coefficients for grain yield per panicle**

The residual effect ( $R = 0.8000$ ) indicated that only 20 per cent variability of grain yield per panicle was explained by days to 50 per cent flowering, plant height, number of leaves, leaf length, leaf width, panicle length, panicle width and 100-seed weight characters. The direct effect was maximum for 100-seed weight (0.37) followed by leaf width (0.24 %), days to 50 per cent flowering (-0.18), plant height (-0.13), number of leaves and leaf length (-0.11), panicle length (-0.07) and panicle width (0.01). Indirect effect via, these characters was also in the same order. Direction of direct effect and correlation coefficients were same in all the cases except where, panicle width direct effect was positive and correlation coefficients was negative, (Table 4.7).

**Table 4.6 Genotypic path coefficients for grain yield per panicle**

| SN | Character              | Days to flowering | Plant height | Number of leaves | Leaf length  | Leaf width  | Panicle length | Panicle width | 100 Seed weight | r       |
|----|------------------------|-------------------|--------------|------------------|--------------|-------------|----------------|---------------|-----------------|---------|
| 1  | Days to 50 % flowering | <b>-0.06</b>      | -0.06        | -0.06            | -0.27        | 0.02        | -0.05          | 0.03          | -0.07           | -0.52** |
| 2  | Plant height           | -0.02             | <b>-0.16</b> | -0.05            | -0.22        | 0.02        | 0.04           | -0.01         | 0.01            | -0.40** |
| 3  | Number of leaves       | -0.04             | -0.09        | <b>-0.09</b>     | -0.28        | 0.04        | 0.05           | 0.04          | -0.00           | -0.37** |
| 4  | Leaf length            | -0.03             | -0.07        | -0.05            | <b>-0.48</b> | 0.02        | 0.06           | 0.06          | 0.02            | -0.48** |
| 5  | Leaf width             | -0.02             | -0.06        | -0.06            | -0.15        | <b>0.07</b> | 0.04           | 0.03          | 0.06            | -0.08** |
| 6  | Panicle length         | -0.01             | 0.02         | 0.01             | 0.08         | -0.01       | <b>-0.32</b>   | -0.15         | -0.16           | -0.53** |
| 7  | Panicle width          | 0.01              | -0.00        | 0.01             | 0.11         | -0.01       | -0.18          | <b>-0.27</b>  | -0.07           | -0.39** |
| 8  | 100 Seed weight        | 0.01              | -0.00        | 0.00             | -0.02        | 0.01        | 0.16           | 0.06          | <b>0.30</b>     | 0.52**  |

Residual effect = 0.5336

Bold value indicates direct effect

\*\* significant at 1% level of significance

**Table 4.7 Phenotypic path coefficients for grain yield per panicle**

| SN | Character             | Days to flowering | Plant height | Number of leaves | Leaf length  | Leaf width  | Panicle width | Panicle width | 100 Seed weight | R       |
|----|-----------------------|-------------------|--------------|------------------|--------------|-------------|---------------|---------------|-----------------|---------|
| 1  | Days to 50% flowering | <b>-0.18</b>      | -0.05        | -0.07            | -0.04        | 0.05        | -0.01         | -0.00         | -0.08           | -0.37** |
| 2  | Plant height          | -0.06             | <b>-0.13</b> | -0.06            | -0.04        | 0.07        | 0.00          | 0.00          | 0.02            | -0.22** |
| 3  | Number of leaves      | -0.12             | -0.07        | <b>-0.11</b>     | -0.05        | 0.13        | 0.01          | -0.00         | -0.00           | -0.22** |
| 4  | Leaf length           | -0.07             | -0.06        | -0.06            | <b>-0.11</b> | 0.09        | 0.00          | 0.00          | 0.03            | -0.17** |
| 5  | Leaf width            | -0.04             | -0.04        | -0.06            | -0.04        | <b>0.24</b> | 0.00          | 0.00          | 0.07            | 0.13**  |
| 6  | Panicle length        | -0.02             | 0.01         | 0.01             | 0.00         | -0.01       | <b>-0.07</b>  | 0.00          | -0.14           | -0.21** |
| 7  | Panicle width         | 0.01              | -0.01        | 0.01             | -0.00        | 0.02        | -0.04         | <b>0.01</b>   | -0.04           | -0.04   |
| 8  | 100 Seed weight       | 0.04              | -0.01        | 0.00             | -0.01        | 0.04        | 0.03          | -0.00         | <b>0.37</b>     | 0.47**  |

Residual effect = 0.8000

Bold value indicates direct effect

\*\* significant at 1% level of significance

#### 4.2.5 Multivariate analysis of variance:

MANOVA was carried out using 9 characters. Probability of Wilks lambda is 0.000 and has an associated F of 4.101, which was significant at  $p < 0.001$ . A multivariate analysis of variance wilks lambda using indicates that there was significant difference between genotypes over the nine dependent variables.

#### 4.2.6 Genetic Diversity:

Equilibrium distance was carried out using 9 characters viz., days to 50 % flowering, plant height, total number of leaves, leaf length, leaf width, panicle length, panicle width, 100 seed weight and grain weight having significant difference between genotype.

#### Group constellations

The 599 germplasm were grouped in 10 clusters. The number of germplasm in each cluster ranged from 37 to 137. (Table 4.8) Cluster- VII was the largest with 137 germplasm followed by cluster- III (69), Cluster- II (66), Cluster- V (55), Cluster- IV (52) Cluster- VIII (50), Cluster- X (49), Cluster- VI (46), cluster-I (38) and cluster- IX (37).

**Table 4.8: Cluster composition**

| Cluster | Number of germplasm | Germplasm  |
|---------|---------------------|--|
| I       | 38                  | CSV 17, IC-286797, IC-287519, IC-287571, IC-287580, IC-287581, IC-287592, IC-287593, IC-287594, IC-287601, IC-287602, IC-287609, IC-287679, IC-287866, IC-287873, IC-287959, IC-287960, IC-287962, IC-287973, IC-287977, IC-287980, IC-287981, IC-287982, IC-287985, IC-287986, IC-287989, IC-287992, IC-288001, IC-288012, IC-288052, IC-288058, IC-288089, IC-288090, IC-288091, IC-288095, IC-288097, IC-288099, IC-288201  |
| II      | 66                  | IC-286718, IC-286722, IC-286735, IC-286830, IC-286870, IC-286875, IC-286878, IC-286930, IC-286931, IC-286932, IC-286944, IC-286962, IC-287118, IC-287129, IC-287181, IC-287184, IC-287185, IC-287224, IC-287229, IC-287312, IC-287346, IC-287390, IC-287396, IC-287403, IC-287476, IC-287530, IC-287555, IC-287603, IC-287656, IC-287658, IC-287661, IC-287670, IC-287673, IC-287676, IC-287691, IC-287808, IC-287917, IC-287949, IC-288083, IC-288088, IC-288112, IC-288113, IC-288116, IC-288127, IC-288155, IC- |

|     |    |   |
|-----|----|---|
|     |    | 288161, IC-288162, IC-288166, IC-288167, IC-288169, IC-288188, IC-288196, IC-288207, IC-288214, IC-288223, IC-288224, IC-288230, IC-288249, IC-288251, IC-288252, IC-288264, IC-288283, IC-288307, IC-288336, IC-288345, IC-288359  |
| III | 69 | CSV 21F, IC-286700, IC-286703, IC-286704, IC-286708, IC-286729, IC-286744, IC-286770, IC-286778, IC-286791, IC-286819, IC-286820, IC-286861, IC-286911, IC-287013, IC-287028, IC-287070, IC-287071, IC-287090, IC-287105, IC-287133, IC-287134, IC-287142, IC-287290, IC-287431, IC-287439, IC-287443, IC-287528, IC-287532, IC-287537, IC-287539, IC-287551, IC-287560, IC-287574, IC-287584, IC-287681, IC-287706, IC-287747, IC-287780, IC-287804, IC-287807, IC-287817, IC-287833, IC-287926, IC-287930, IC-287948, IC-287951, IC-287952, IC-287964, IC-288030, IC-288034, IC-288066, IC-288101, IC-288109, IC-288114, IC-288130, IC-288273, IC-288274, IC-288326, IC-288327, IC-288329, IC-288334, IC-288337, IC-288341, IC-288346, IC-288348, IC-288352, IC-288355, IC-288361 |
| IV  | 52 | IC-286719, IC-286812, IC-286816, IC-286845, IC-286853, IC-286860, IC-286929, IC-286939, IC-286942, IC-287048, IC-287121, IC-287180, IC-287208, IC-287209, IC-287234, IC-287270, IC-287363, IC-287442, IC-287456, IC-287494, IC-287526, IC-287654, IC-287659, IC-287660, IC-287669, IC-287758, IC-288032, IC-288086, IC-288087, IC-288163, IC-288164, IC-288168, IC-288171, IC-288173, IC-288174, IC-288175, IC-288194, IC-288195, IC-288199, IC-288208, IC-288211, IC-288218, IC-288232, IC-288238, IC-288241, IC-288243, IC-288245, IC-288255, IC-288270, IC-288314, IC-288328, IC-288363  |
| V   | 55 | IC-286671, IC-286682, IC-286689, IC-286696, IC-286728, IC-286762, IC-286769, IC-286781, IC-286818, IC-286846, IC-286880, IC-286947, IC-286984, IC-287016, IC-287031, IC-287053, IC-287088, IC-287183, IC-287249, IC-287432, IC-287438, IC-287444, IC-287448, IC-287454, IC-287472, IC-287510, IC-287538, IC-287556, IC-287564, IC-287568, IC-287585, IC-287651, IC-287711, IC-287731, IC-287740, IC-287750, IC-287756, IC-287778, IC-287787, IC-287813, IC-287831, IC-287837, IC-287898, IC-288006, IC-288074, IC-288103, IC-288105, IC-288107, IC-288128, IC-288141, IC-288262, IC-288318, IC-288333, IC-288347, IC-288349   |
| VI  | 46 | IC-286668, IC-287054, IC-287169, IC-287257, IC-287269, IC-287327, IC-287380, IC-287466, IC-287470, IC-287471, IC-287477, IC-287548, IC-287549, IC-287558, IC-287561, IC-287562, IC-287588, IC-287677, IC-287684, IC-287686, IC-287693, IC-287696, IC-287699, IC-287714, IC-287739, IC-287764, IC-287769, IC-287793, IC-287800, IC-287877, IC-287937, IC-287941, IC-287942, IC-287944, IC-288125, IC-  |

|      |     |   |
|------|-----|---|
|      |     | 288133, IC-288135, IC-288149, IC-288219, IC-288253, IC-288281, IC-288282, IC-288284, IC-288296, IC-288305, IC-288319  |
| VII  | 137 | IC-286669, IC-286670, IC-286681, IC-286684, IC-286709, IC-286711, IC-286745, IC-286780, IC-286804, IC-286821, IC-286822, IC-286826, IC-286855, IC-286881, IC-286887, IC-286888, IC-286890, IC-286895, IC-286910, IC-286914, IC-286915, IC-286920, IC-286938, IC-286941, IC-286943, IC-286963, IC-286967, IC-286978, IC-286981, IC-286982, IC-286985, IC-286986, IC-286997, IC-287027, IC-287062, IC-287063, IC-287086, IC-287087, IC-287190, IC-287214, IC-287226, IC-287232, IC-287262, IC-287278, IC-287298, IC-287402, IC-287415, IC-287440, IC-287451, IC-287457, IC-287458, IC-287460, IC-287461, IC-287462, IC-287464, IC-287467, IC-287468, IC-287469, IC-287478, IC-287479, IC-287482, IC-287492, IC-287495, IC-287496, IC-287498, IC-287499, IC-287512, IC-287513, IC-287525, IC-287527, IC-287544, IC-287546, IC-287550, IC-287552, IC-287553, IC-287614, IC-287650, IC-287652, IC-287655, IC-287662, IC-287664, IC-287665, IC-287678, IC-287689, IC-287701, IC-287743, IC-287744, IC-287745, IC-287746, IC-287751, IC-287766, IC-287789, IC-287790, IC-287791, IC-287792, IC-287801, IC-287816, IC-287818, IC-287820, IC-287900, IC-287902, IC-287905, IC-287946, IC-287950, IC-287953, IC-288013, IC-288081, IC-288082, IC-288085, IC-288119, IC-288120, IC-288122, IC-288126, IC-288134, IC-288154, IC-288160, IC-288165, IC-288185, IC-288189, IC-288193, IC-288198, IC-288220, IC-288229, IC-288263, IC-288278, IC-288285, IC-288287, IC-288288, IC-288291, IC-288313, IC-288316, IC-288335, IC-288338, IC-288339, IC-288340, IC-288344, IC-288350 |
| VIII | 50  | IC-286701, IC-286712, IC-286779, IC-286959, IC-286990, IC-286991, IC-287004, IC-287015, IC-287025, IC-287045, IC-287046, IC-287130, IC-287152, IC-287271, IC-287422, IC-287424, IC-287434, IC-287435, IC-287436, IC-287524, IC-287529, IC-287534, IC-287547, IC-287575, IC-287576, IC-287590, IC-287612, IC-287680, IC-287827, IC-287881, IC-287908, IC-287928, IC-287957, IC-287997, IC-288015, IC-288019, IC-288025, IC-288026, IC-288027, IC-288037, IC-288062, IC-288110, IC-288321, IC-288322, IC-288330, IC-288351, IC-288353, IC-288356, IC-288364, IC-288367  |
| IX   | 37  | CSV 20, CSV 27, IC-286675, IC-286690, IC-286691, IC-286776, IC-287026, IC-287072, IC-287106, IC-287111, IC-287131, IC-287159, IC-287522, IC-287567, IC-287573, IC-287587, IC-287615, IC-287657, IC-287716, IC-287726, IC-287752, IC-287775, IC-287779, IC-287821, IC-287823, IC-287826, IC-287874, IC-287879, IC-287886, IC-287921, IC-288009, IC-288021, IC-288035, IC-288042, IC-288051, IC-  |

|   |    |   |
|---|----|---|
|   |    | 288077, IC-288215   |
| X | 49 | IC-286906, IC-287010, IC-287014, IC-287051, IC-287135, IC-287136, IC-287248, IC-287423, IC-287425, IC-287493, IC-287531, IC-287582, IC-287586, IC-287596, IC-287599, IC-287606, IC-287685, IC-287717, IC-287720, IC-287836, IC-287843, IC-287856, IC-287955, IC-287958, IC-287961, IC-287963, IC-287966, IC-287970, IC-287974, IC-287978, IC-287990, IC-287991, IC-287993, IC-287995, IC-287996, IC-288005, IC-288008, IC-288011, IC-288017, IC-288020, IC-288024, IC-288038, IC-288080, IC-288084, IC-288100, IC-288143, IC-288202, IC-288272, IC-288332 |

**Inter clusters distance:**

Inter cluster distance are given in table 4.9. Maximum inter cluster distance was between cluster- I and VI (240.654) and followed by between cluster- VI and X (200.500), cluster- I and VII (186.887), cluster- I and V (160.787), cluster- VI and VIII (155.903), cluster- I and II (145.435), cluster- VI and IX (138.568), cluster- I and III (129.086) and cluster- I and IV (99.029).

**Table 4.9: Inter cluster distance**

| Cluster | I | II      | III     | IV     | V       | VI      | VII     | VIII    | IX      | X       |
|---------|---|---------|---------|--------|---------|---------|---------|---------|---------|---------|
| I       |   | 145.435 | 129.086 | 99.029 | 160.787 | 240.654 | 186.887 | 86.782  | 111.042 | 40.527  |
| II      |   |         | 29.766  | 51.495 | 42.870  | 99.792  | 45.558  | 64.415  | 66.252  | 105.936 |
| III     |   |         |         | 49.644 | 40.802  | 112.980 | 59.882  | 43.174  | 46.272  | 89.084  |
| IV      |   |         |         |        | 82.731  | 151.113 | 96.659  | 38.040  | 65.069  | 62.345  |
| V       |   |         |         |        |         | 82.737  | 37.314  | 79.026  | 56.008  | 121.044 |
| VI      |   |         |         |        |         |         | 54.738  | 155.903 | 138.568 | 200.500 |
| VII     |   |         |         |        |         |         |         | 102.445 | 90.606  | 146.798 |
| VIII    |   |         |         |        |         |         |         |         | 45.971  | 47.839  |
| IX      |   |         |         |        |         |         |         |         |         | 73.834  |
| X       |   |         |         |        |         |         |         |         |         |         |

**Cluster means:**

The analysis of variance revealed significant difference between cluster means for plant height, grain weight, days to 50 % flowering, leaf length, total number of leaves, panicle length, leaf width, 100 seed weight and panicle width, (Table 4.10).

The cluster means of 9 characters are presented in the Table 4.11. Maximum plant height (cm) was in cluster VI (362.7) followed by cluster VII (308.1), V (284.4), II (263.6), III (251.9), IX (232.8), IV (212.4), VIII (209.2), X (164.4) and I (124.5). Days to 50 % flowering was minimum in cluster VIII (72) followed by I (74), IX (77), III (79), X (80), V (84), VII (94), VI (95), cluster II (100) and IV (104). The maximum leaf length (cm) was in cluster VI (87) followed by cluster VII (86), II (85), IV (83), V (81), IX (74), III (73), VIII (72), I (69) and X (68). Grain weight (g) was maximum in cluster IX (69.53) followed by cluster V (50.31), I (46.35), X (42.82), VIII (30.29), III (27.46), VI (27.38) VII (24.13), II (17.61) and IV (15.25). The maximum panicle length (cm) was in cluster II (23.98) followed by cluster I (22.80), IV (22.06), X (20.38), VI (20.19), IX (17.81), III (17.74), VII & VIII (17.38) and V (17.17). The total number of leaves maximum was in cluster VI (17.4) followed by cluster VII (16.1), II (15.7), IV (15.0), V (14.3), III (12.0), IX (11.6), X (11.5), VIII (10.7) and I (10.5). The leaf width maximum was in cluster VI (9.3) followed by cluster VII (8.6), IX & V (8.4), X (8.1), IV (8.1), II (8.1), I (8.1), III (8.0), and VIII (7.5). The maximum panicle width (cm) was in cluster II (9.055) followed by cluster IX (8.876), VI (8.469), VIII (8.352), VII (8.300), III (8.123), V (8.069), IV (7.987), I (7.743) and X (7.659). Similarly maximum 100 seed weight (g) was in cluster V (3.41) followed by cluster IX (3.08), I (3.05), VI (2.99), III (2.94), X (2.80), VIII (2.71), VII (2.68), II (2.22) and IV (2.00). Germplasm belong to cluster VI and IX having higher mean values for plant height and grain weight. Cluster VIII having lower value of days to 50 % flowering. For leaf length and total number of leaves both belonging to cluster VI. For panicle length, leaf width, 100 seed weight and panicle width belonging to cluster II, VI, V, and II, respectively.

**Table 4.10: Analysis of variance for cluster means**

| SN | Characters             | Cluster         | Error             | Probability |
|----|------------------------|-----------------|-------------------|-------------|
|    |                        | Mean Square [9] | Mean Square [589] |             |
| 1. | Days to 50% flowering  | 7370.052        | 104.569           | .000        |
| 2. | Plant height (cm)      | 248569.444      | 221.248           | .000        |
| 3. | Total number of Leaves | 356.980         | 6.771             | .000        |

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|    |                     |           |         |      |
|----|---------------------|-----------|---------|------|
| 4. | Leaf length (cm)    | 3205.999  | 118.076 | .000 |
| 5. | Leaf width (cm)     | 11.673    | 2.030   | .000 |
| 6. | Panicle length (cm) | 321.563   | 37.989  | .000 |
| 7. | Panicle width (cm)  | 10.351    | 6.356   | .104 |
| 8. | 100-Seed weight (g) | 9.442     | 0.615   | .000 |
| 9. | Grain weight (g)    | 13710.575 | 197.577 | .000 |

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**Table 4.11: Cluster mean for 9 characters**

| SN | Character                 | Cluster |       |       |       |       |       |       |       |       |       |
|----|---------------------------|---------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
|    |                           | I       | II    | III   | IV    | V     | VI    | VII   | VIII  | IX    | X     |
| 1. | Days to 50 %<br>flowering | 74      | 100   | 79    | 104   | 84    | 95    | 94    | 72    | 77    | 80    |
| 2. | Plant height (cm)         | 124.5   | 263.6 | 251.9 | 212.4 | 284.4 | 362.7 | 308.1 | 209.5 | 232.8 | 164.4 |
| 3. | Total number of<br>Leaves | 10.5    | 15.7  | 12.0  | 15.0  | 14.3  | 17.4  | 16.1  | 10.7  | 11.6  | 11.5  |
| 4. | Leaf length (cm)          | 69      | 85    | 73    | 83    | 81    | 87    | 86    | 72    | 74    | 68    |
| 5. | Leaf width (cm)           | 8.1     | 8.1   | 8.0   | 8.1   | 8.4   | 9.3   | 8.6   | 7.5   | 8.4   | 8.1   |
| 6. | Panicle length (cm)       | 22.80   | 23.98 | 17.74 | 22.06 | 17.17 | 20.19 | 19.72 | 17.38 | 17.81 | 20.38 |
| 7. | Panicle width (cm)        | 7.743   | 9.055 | 8.123 | 7.987 | 8.069 | 8.469 | 8.300 | 8.352 | 8.876 | 7.659 |
| 8. | 100-Seed weight (g)       | 3.05    | 2.22  | 2.94  | 2.00  | 3.41  | 2.99  | 2.68  | 2.71  | 3.08  | 2.80  |
| 9. | Grain weight(g)           | 46.35   | 17.61 | 27.46 | 15.25 | 50.31 | 27.38 | 24.13 | 30.29 | 69.53 | 42.82 |

## 5. DISCUSSION

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Sorghum is known by different names in different parts of the world. In Western Africa, it is called great millet, kafir corn or guinea corn, which represents its connection with corn or millet. In India it is called jowar, in China kaolian and in Spain milo.

Grain sorghum is mainly used as a principal food in tropical area and often used as raw material for alcoholic beverages, sweets and glucose industries. Broom sorghum is used as a syrup. Grass sorghum is grown for green feed and forage use. More than 35% of sorghum is grown for human consumption, while rest is used for animal feed, alcohol production and industrial products (Mamoudou *et al.*, 2006). The large diverse germplasm provides great opportunities for improvement of plant adaptation and other agronomic traits (Huang, 2004). Selection of genotypes meeting specific local food and industrial requirements from this great biodiversity is of high importance for food security.

Germplasm is the most important raw material for any crop improvement program. The major challenge facing sorghum research and development work is to provide technologies that will enable the agricultural sector to affect transformation of "subsistence farming" to a sustainable "market-oriented" enterprise successfully competing with rest of the world. Therefore, we are developing strategies for resolving the constraints which inhibit the increased use of improved technologies in a cost-effective manner. The higher scope for industrial utilization, livestock development through quality forage and enhanced utilization of grain by poultry, and potable alcohol industries, and sweet stalk juice by bio fuel industry will aid increased income to sorghum cultivators, industries and exporters. Therefore, sorghum can be called as industrial crop rather than poor man's crop. Significant scope for export of hybrid seed for international markets is a new opportunity especially for all the entrepreneurs. (Source: Directorate of Sorghum Research VISION 2030, January, 2011, New Delhi).

Variability is a pre requisite for any breeding programme aimed at improving the yield and other characters. Thus, it is imperative to have information on both genotypic and phenotypic coefficients of variation. The information on phenotypic coefficient of variation and heritability are help full in prediction of the possible genetic advance by selection of genotypes for a character. Besides, the knowledge of association, correlation and path coefficient analysis also assist in setting up selection indices. Looking to the importance

variability parameters viz., GCV, PCV,  $h^2$  and GG, genotypic and phenotypic correlation coefficients, path coefficients and genetic divergence were studied.

The 1700 germplasm lines were evaluated along with four checks in augmented RBD with 60 blocks. Out of 1700 lines, 16 entries did not germinate and 503 entries germinated but affected by shoot fly and caused dead heart. Observations were recorded for 17 qualitative and nine quantitative characters.

Majority of the accessions showed good early plant vigour (872), dark green leaf (1108), non-tan leaf sheath pigmentation (1089), drooping leaves (1153), green midrib colour (605), non senescence (1059), compact panicle density (618), elliptical panicle shape (402), straw glume colour (407),  $\frac{1}{2}$  glume coverage (493), presence of awns (1028), creamy straw seed (468), sub lenticular round but flat from other side grain shape (403), medium seed size (406), non-lustrous seed (1081), intermediate endosperm texture (516) and durra race (347).

In sorghum, early vigour is associated with good stand establishment and increased biomass accumulation early in the season which ultimately leads to increased grain yield. Germplasm lines were having 7.9 per cent very good vigour while, 52.7 per cent exhibited good and 39.4 per cent poor plant vigour.

Variation was observed for leaf colour in the evaluated sorghum germplasm. Leaf colour was dark green in CSV17 and CSV20, light green in CSV27 and CSV21F checks. Dark green leaves (96.1 %) were common while some of the germplasm had light green (3.9 %). Elangovan *et al.* (2007) also reported maximum frequency of dark green leaves.

Leaf sheath pigmentation was found tan type in all the four checks. About 94.4 per cent germplasm were having non-tan leaf sheath while 5.6 per cent germplasm had tan characters and can be used as source for resistance against foliar disease.

Erect leaf architecture reduces shading to the lower leaves, allows better light distribution to the lower canopy, and thus enables higher plant density (Fellner *et al.*, 2006; Tian *et al.*, 2011; Narayanan *et al.*, 2013). The architecture of sorghum hybrids ranges from flat to droopy. The architecture of sorghum has remained largely unchanged during the last 50 year (Assefa and Staggenborg, 2011). New germplasm with advantageous architecture characters are needed to improve sorghum canopy for increasing biomass and grain production. Whereas, in the present study leaf orientation was drooping type in all the four checks and all the 1153 germplasm accessions that reached upto this stage.

The check, CSV20 showed white and CSV17, CSV27 and CSV 21F showed green midrib colour. Leaf midrib colour among the sorghum germplasm displayed ample variation. Five different colours were observed *i.e.* green, white, yellow, dark green and colourless at frequency of 52.5, 21.8, 18.4, 6.6 and 0.7 per cent, respectively.

Stay green or non-senescence is an important trait associated with drought tolerance (Rosenow, 1977). It is indicated by maintenance of stem and upper green leaves when water is limiting during grain filling. Sorghum genotypes with the stay-green trait continue to fill their grains normally even under limited water or moisture stress conditions (Duncan *et al.*, 1981; Rosenow and Clark 1981, Borrell *et al.*, 2000). Delaying the onset of leaf senescence and reducing its rate (*i.e.* two components of the stay green trait) offer an effective strategy for increasing grain production, fodder quality and grain crop residues particularly under water limited conditions. In present investigation stay green trait was present in CSV20 and absent in CSV17, CSV27 and CSV21F. About 91.8 per cent germplasm lines were stay green and 8.2 per cent were senescence type. Stay green can be used in future breeding programme.

Panicle compactness and shape are important characters in determining grain yield and are useful for varietal identification. It was found semi-compact in CSV17 and CSV20, and loose in CSV27 and CSV21F. Majority of the germplasm in this study had compact (53.6 %), semi-compact (25.5 %), very loose (13.5 %), loose (6.5 %), and broom corn (0.9 %). Open panicles are preferred in high rainfall and humid areas to avoid mold and ergot diseases (Singh *et al.*, 1997).

Panicle shape was observed cylindrical in CSV17, elliptical in CSV20 and CSV27 and ovate in CSV21F. Whereas, out of 1153 germplasm lines, 34.9 per cent were elliptical, 25.2 per cent broom corn, 23.4 per cent cylindrical, 14.8 per cent oblong, 1.6 per cent ovate and 0.1 per cent round.

All the four checks were having straw glume colour. The germplasm also showed wide range of glume colours. The straw, light brown, reddish brown, brown, red, straw brown, dark red, light red, black and purple glume colour was observed in 35.3, 30.8, 11.1, 8.1, 4.8, 3.4, 2.5, 2.2, 1.0 and 0.8 per cent germplasm. Elangovan *et al.*, (2007) also observed different coloured glumes. Darker glumes contributed to grain mould resistance. The variability of glume colour available in the present study may be utilized for screening of germplasm for grain mold resistance in sorghum, (Audilakshmi *et al.*, 1999).

Coverage of seed by glume is directly related with threshability. Threshability becomes poor with increasing coverage. Generally in grain sorghum coverage is less and in fodder types it is maximum. In present investigation glume covering was  $\frac{1}{2}$  in all the four checks. Whereas, 42.8 per cent germplasm were having  $\frac{1}{2}$  covering, 36.2 per cent were  $\frac{3}{4}$  covering, 14.7 per cent were  $\frac{1}{4}$  covering and 6.3 per cent were covered fully.

Sorghum genotypes with awns are less eaten by birds but are low grain yielders. In present investigation awn was present in CSV21F and absent in CSV17, CSV20 and CSV27 checks. Whereas, 89.2 per cent germplasm were with awns and 10.8 per cent germplasm not having awns. Absence of awns in sorghum is associated with the ability to reduce evapotranspiration in dry lowland areas (Ayana and Bekele, 1998 a).

Variation was observed for grain colour in the evaluated germplasm. Grain colour was creamy straw in CSV17 and CSV20 and white in CSV27 and CSV21F checks. The majority of accessions produced creamy straw (40.6%) grain colour followed by chalky white, light yellow, white, light brown, reddish brown, yellow, white and red mixed, light brown, light red, red and brown grain colour at frequency of 20.8, 9.6, 8.5, 7.0, 3.8, 2.9, 2.5, 2.0, 1.5 and 0.7 per cent, respectively. Kernel colour determination is important because the information obtained helps in anticipating end product colour quality. White or light sorghums are more preferred for porridge making. Red coloured sorghums are generally preferred for brewing traditional beer (Hikeezi, 2010).

In all the four checks, grain shape was oval. The sub-lenticular round flat from other side, elliptical, oval, round and compactly flat but grain shape were observed in 35.0, 33.7, 16.3, 12.3 and 2.7 per cent germplasm, respectively.

Grain size was found small in CSV17, medium in CSV27 and CSV21F and bold in CSV20 checks. Whereas, 35.2 per cent germplasm were medium, 35.0 per cent germplasm were small and 29.8 per cent were bold grain type.

Endosperm texture was observed intermediate in all the four checks. Whereas, 44.8 per cent germplasm exhibited intermediate endosperm texture, 30.3 per cent completely corneous, 13.3 per cent mostly corneous, 11.6 per cent mostly starchy and 0.1 per cent compactly starchy floury endosperm texture. Grain mould resistance is either due to harder grains or higher levels of phenols in seed. Sorghum kernels with more corneous endosperm were more resistant to grain mold than those with floury endosperm (Ibrahim *et al.*, 1985; Jambunathan *et al.*, 1992; Mukuru 1992). Jambunathan *et al.* (1992) and Mukuru (1992)

concluded that grain mold resistance in sorghum cultivars with white pericarp is mostly due to kernel hardness and darker glumes. The variability of glume color in this study may be utilized in screening for mould resistance (Teshome *et al.* 1997, Kudadjie 2006 and Audilakshmi *et al.*, 1999).

Non-lustrous grains were observed in CSV17, CSV20 and CSV27 and lustrous in CSV21F. About 93.8 per cent germplasm were having non-lustrous and 6.2 per cent were having lustrous grain.

Three checks belonged to kafir race *viz.*, CSV17, CSV20 and CSV27 and CSV21F belonged to bicolor. Among germplasm lines 30.0 per cent were durra type, 28.7 per cent kafir, 17.9 per cent caudatum, 12.0 per cent bicolor and 11.4 per cent guinea type, (Table 4.1). Five basic and ten intermediate races are possible based on grain shape, glumes and panicles (Harlan & de Wet 1972; Harlan 1992).

Members of the race durra have moderate levels of drought resistance and very large panicles as in Yemen (Appa Rao *et al.*, 1993) and in Namibia (Appa Rao *et al.*, 1992). The race Kafir which is indigenous to Southern Africa (Harlan 1992, Appa Rao *et al.*, 1992) was not reach India along with other races. Sub-race roxburghii of race guinea with small corneous endosperm are extensively grown in the tribal inhabited areas of Andhra Pradesh, Bihar, Madhya Pradesh, and Orissa probably because of their grain mold resistance and strong preference for such grain where the whole grain is cooked like rice (Prasada Rao *et al.*, 1989).

In quantitative characters mean square due to germplasm was significant for all the nine characters. CSV17 was the best check for days to 50 per cent flowering. Total 36 germplasm lines were significantly superior over the best check CSV17 for early flowering (59.29 days). The accession IC-286998 (39.90 days) was earliest to flower followed by IC-286992 and IC-286993 (42.90 days), IC-287000 (45.90 days), IC-286991 (46.90 days), IC-286827 and IC-286828 (49.82 days), IC-286990 (49.90 days), IC-287493 (51.07 days) and IC-286989 (51.9 days). Therefore these genotypes can be used for inducing the earliness.

CSV21F was the best check for plant height and number of leaves. Total 600 germplasm lines were significantly superior over the best check CSV21F (263 cm) for plant height. The accession IC-287324 (441.73 cm) was having maximum plant height followed by IC-286736 (436.27 cm), IC-287054 (434.66 cm), IC-287557 (431.01 cm), IC-287328 and IC-287332 (421.73 cm), IC 288148 (420.48 cm) and IC-288121 (417.00 cm).

Comparatively, 832 germplasm lines were significantly superior over the best check CSV21F (12.13) for number of leaves per plant. The accession IC-286811 (25.7) had maximum number of leaves followed by IC-286719 (24.54), IC-287316 (24.04), IC-286938 and IC-286939 (23.69), IC-288301 (23.58), IC-287081 (22.95 cm), IC-287054 (22.90) and IC-286666 (22.87). Lines with more number of leaves along with plant height can be utilized for development of fodder varieties.

CSV27 was the best check for leaf length, leaf width, panicle length and grain yield per panicle. Total 288 germplasm lines were significantly superior over the best check CSV27 (88.81 cm) for leaf length. The accessions IC-287814 (115.4 cm) was having maximum leaf length followed by IC-287490 (114.90 cm), IC-288182 (113.43 cm), IC-286890 (112.57 cm), IC-287059 (112.19 cm), IC-286984 (111.57 cm), IC-287792 and IC-287793 (111.40 cm) and IC-287238 (111.35 cm).

In the germplasm 628 lines were significantly superior over the best check CSV27 (8.28 cm) for leaf width. The accession IC-286982 (14.52 cm) was having maximum leaf width followed by IC-286900 (12.79 cm), IC-288297 (12.67 cm), IC-287537 (12.52 cm), IC-287054 (12.42 cm), IC-287919 (12.36 cm) and IC-288269 (12.35 cm).

In the germplasm 195 lines were found significantly superior over the best check CSV27 (25.38 cm) for panicle length. The accession IC-287950 (43.42 cm) were having maximum panicle length followed by IC-286922 (42.52 cm), IC-288160 (42.23 cm), IC-287253 (41.21 cm), IC-287866 (40.33 cm), IC-286852 (39.57 cm), IC-288161 (39.23 cm) and IC-288060 (36.56 cm).

Seventy eight germplasm lines were significantly superior over the best check CSV27 (57.52 g) for grain yield per panicle. The accession IC-287836 (111.65 g) recorded maximum grain yield per panicle followed by IC-287072 (118.25 g), IC-288215 (107.65 g), IC-288008 (104.35 g), IC-287078 (101.67 g), IC-287821 (99.76 g), IC-288009 (99.15 g), IC-287779 (98.57 g) and IC-288035 (98.54 g).

Total 324 germplasm lines were significantly superior over the best check CSV21F (9.33 cm) for panicle width. The accession IC-287144 (19.93 cm) were having maximum panicle width followed by IC-287145 (18.93 cm), IC-286921 (18.48 cm), IC-287681 (18.44 cm), IC-287019 (17.99 cm), IC-287169 (17.93 cm), IC-287405 (17.65 cm) and IC-287678 (17.44 cm).

Overall, 87 germplasm lines were significantly superior over the best checks both CSV27 and CSV21F (3.73 g) for 100-seed weight. The accessions IC-287651 (6.12 g) were having maximum 100-seed weight followed by IC-287444 (5.17 g), IC-287529 (5.03 g), IC-288281 (4.95 g), IC-287454 (4.87 g), IC-287482 and IC-288006 (4.71 g), IC-288270 (4.63 g), IC-287769 (4.6 g) and IC-287743 (4.59 g). These accessions can be used for the development of bold seeded varieties.

Characters having different unit of measurements cannot be compared as the magnitude of variances is also affected by unit of measurements. However, if variance is converted into coefficients such character comparisons are possible. In present investigation variability parameters viz., GCV, PCV,  $h^2$ , and genetic gain (GG) were estimated.

In general, estimates of phenotypic coefficient of variation (PCV) were slightly greater than corresponding genotypic coefficient of variation (GCV) indicating the role of environment in the expression of characters. Similar findings were reported by Chung and Liang (1970), Median and Choudhary (1980) and Godbharle *et al.* (2010) in sorghum. The variability parameters were classified in three categories viz., high ( $>$  mean + SD), medium (mean  $\pm$  SD) and low ( $<$  mean – SD).

In present investigation, magnitude of GCV ranged from 11.40 to 43.75 per cent. GCV was high for (more than 22.28 %) grain yield per panicle (43.75 %), 100-seed weight (29.96 %), panicle length (25.45 %), number of leaves (23.69 %) and panicle width (22.32 %). Medium (between 9.42 to 22.28 %) GCV was observed for Plant height (21.31 %), days to 50 per cent flowering (15.55 %), Leaf width (14.81 %) and Leaf length (11.40 %). On account of skewed distribution of GCV estimates of distribution was un equal.

In present investigation, magnitude of PCV estimates ranged from 16.16 to 62.89 per cent with SD of 14.29. The PCV was high ( $>$  43.11%) for grain yield per panicle (62.69%) and medium for all other characters. Among medium PCV characters more PCV was for panicle length (32.57 %) followed by panicle width (31.62 %), 100-seed weight (31.49 %), number of leaves (24.99 %), plant height (24.18 %), leaf width (18.97 %), days to 50 per cent flowering (16.50 %) and leaf length (16.16 %).

High PCV for grain yield per panicle was also reported by Sharma *et al.* (2006) and Arun Kumar (2013).

In present investigation, magnitude of heritability ranged from 48.39 to 90.53 per cent. Heritability was high ( $>$  66.57 %) for 100-seed weight (90.53 %), number of leaves

(89.89 %), days to 50 per cent flowering (88.89 %) and plant height (77.64 %). Medium heritability was observed for panicle length (61.08 %), leaf width (61.00 %), panicle width (49.96 %), leaf length (49.72 %) and grain yield per panicle (48.39 %).

The ultimate aim of studying the variability and heritability of any trait is to have an idea about the feasibility of selection. The improvement in the mean performance of progeny of the selected families over the base population is known as genetic advance, and when expressed as per cent of mean is called genetic gain (Johnson *et al.* 1955).

In this investigation, magnitude of genetic gain ranged from 16.56 to 62.70 per cent. Genetic gain was high (35.91 %) for grain yield per panicle (62.70 %), 100-seed weight (58.72 %), number of leaves (46.28 %), panicle length (40.97 %) and plant height (38.67 %). Medium genetic gain was observed for panicle width (32.50 %), days to 50 per cent flowering (30.21 %), leaf width (23.83 %) and leaf length (16.56 %).

Using the variability parameters we can identify the characters having high response to selection whether it has any economic importance or not. Plant breeders are mainly interested in characters having economic importance. If these characters have less variability, improvement through direct selection is difficult. These characters can be improved by indirect selection. For indirect selection, identification of component character is essential. The genotypic and phenotypic correlation coefficients are helpful in identification of such characters.

In general, a close agreement existed between genotypic and phenotypic correlation coefficients. Grain yield per panicle exhibited positively significant correlation with 100-seed weight at both genotypic (0.52) and phenotypic (0.47) level. These findings were also supported by the results of Veerabathiran and Kennedy (2001) and Premalatha *et al.* (2006). Characters, with panicle length ( $r_g = -0.53$  and  $r_p = -0.21$ ), leaf length ( $r_g = -0.48$  and  $r_p = -0.17$ ), plant height ( $r_g = -0.40$  and  $r_p = -0.22$ ) were significant negatively correlated with grain yield per panicle. 100-Seed weight positively correlated with leaf width, leaf length and grain yield per panicle had significantly negative correlation with Panicle length and panicle width. Leaf width showed significantly positive correlation with number of leaves, plant height, 50 per cent flowering and leaf length at both genotypic and phenotypic level.

Direction and magnitude of correlation provide relationship between the characters. But path analysis is a better tool for identification of component characters. The variability explained by the path analysis is inversely proportionate to residual effect. The path analysis

for grain yield per panicle at genotypic and phenotypic level revealed that residual effect depends on combination of characters. In general residual effect decrease with increase in the number of characters in path analysis both genotypic and phenotypic level, but it is not always true.

In genotypic path analysis residual effect (0.5336) was observed when eight characters *viz.*, days to 50 per cent flowering, number of leaves, leaf length, leaf width, panicle length, panicle width, plant height and 100-seed weight were used. They explained 53.36 per cent variability of grain yield per panicle. The direct effect was maximum for leaf length (-0.48) followed by panicle length (-0.32), 100-seed weight (0.30), panicle width (-0.27), plant height (-0.16), number of leaves (-0.09), leaf width (-0.07) and days to 50 per cent flowering (-0.06). The indirect effect was also in the same order through these characters. Directions of direct effect and correlation coefficients were for all same except leaf width where it was in opposite direction.

In case of phenotypic path analysis residual effect 0.800 was observed when 8 characters was used. The direct effect was maximum for 100-seed weight. Direction of direct effect and correlation coefficients were same in the cases of 100-seed weight, leaf width, days to 50 per cent flowering, plant height, number of leaves, leaf length and panicle length. It was opposite in case of panicle width where direct effect was positive and correlation coefficients was negative.

Warkad *et al.* (2010) and, Chavan *et al.* (2010) also realized the importance of days to 50 per cent flowering, panicle length, plant height and number of leaves per panicle and 100-seed weight in improving the seed yield.

MANOVA was carried out using 9 characters. Wilks lambda is 0.000 and has an associated F of 4.101, which is significant at  $p < 0.001$ . Multivariate analysis of variance using wilks lambda indicates that there was significant difference between genotypes over the nine dependent variables.

Several methods have been advocated by various workers to estimate the genetic divergence in crop plants. Mahalanobis generalized distance estimated by  $D^2$  statistic (Rao, 1952) is a unique tool for discriminating population considering a set of parameters together rather than infusing from indices based on morphological similarities and phylogenic relationships. In present investigation ward method was used as only mean were available for germplasm lines.

Based on equilibrium distance, 599 germplasm were grouped into 10 clusters. Among them Cluster- VII was the largest with 137 germplasm followed by cluster- III (69), II (66), V (55), IV (52), VIII (50), X (49), VI (46), I (38) and IX (37). Maximum inter cluster distance was between cluster- I and VI (240.654) and followed by between cluster- VI and X (200.500), cluster- I and VII (186.887), cluster- I and V (160.787), cluster- VI and VIII (155.903), cluster- I and II (145.435), cluster- VI and IX (138.568), cluster- I and III (129.086) and cluster- I and IV (99.029).

The analysis of variance revealed significant difference between cluster means for plant height, grain weight, days to 50 % flowering, leaf length, total number of leaves, panicle length, leaf width, 100 seed weight and panicle width. Germplasm belong to cluster VI and IX having higher mean values for plant height and grain weight and cluster VIII having lower mean values for days to 50 % flowering. For higher mean value leaf length and total number of leaves both belonging to cluster VI. Higher mean values for panicle length, leaf width, 100 seed weight and panicle width belonging to cluster II, VI, V, and II, respectively.

Three lines (IC-286998, IC-286992 and IC-286993) which flowered in less than 45 days were identified for earliness. These lines can be utilized in the breeding programs for development of early flowering. Seven lines (IC-287324, IC-286736, IC-287054, IC-287557, IC-287328, IC-287332 and IC 288148) were identified for more than 420 cm plant height. Germplasm lines (IC-286811, IC-286719, IC-287316, IC-286938, IC-286939 and IC-288301) were identified for higher number of leaves per plant. Germplasm lines (IC-287814, IC-287490, IC-288182, IC-286890, IC-287059 and IC-286984) were identified for leaf length. Four lines (IC-287144, IC-287145, IC-286921 and IC-287681) were identified for panicle width. Germplasm lines (IC-287950, IC-286922, IC-288160, IC-287253 and IC-287866) were identified for more than 40.00 cm panicle length.

Ten lines (IC-287651, IC-287444, IC-287529, IC-288281, IC-287454, IC- 287482, IC-288006, IC-288270, IC-287769 and IC-287743) were identified for maximum 100-seed weight. High yielding germplasm lines (IC-287836, IC-287072, IC-288215, IC-288008 and IC-287078) with more than 100 g seed yield per panicle.

The 32 lines having productivity more than 100 q ha<sup>-1</sup> i.e. grain weight > 67.5 g. Out of these, five lines viz., IC-287567, IC-288009, IC-288107, IC-287556 and IC-287444 were having bold seeds with seed index more than 4 g. The five lines fall in two distinct clusters

i.e. IC-287567 and IC-288009 in cluster IX and IC-288107, IC-287556 and IC-287444 in cluster V leaving scope for hybridization to still improve the grain yield with bold seeded (Table 5.1).

**Table 5.1: Lines selected for grain purpose sorghum**

| ACC No.   | Cluster | Grain Weight (g) | 100 Seed Weight (g) |
|-----------|---------|------------------|---------------------|
| IC-287567 | IX      | 99.00            | 4.33                |
| IC-288009 | IX      | 98.47            | 4.36                |
| IC-288107 | V       | 91.73            | 4.04                |
| IC-287556 | V       | 86.77            | 4.41                |
| IC-287444 | V       | 83.21            | 5.34                |

There were 16 lines having plant height more than 400 cm having scope of selection of lines for high biomass or fodder purpose genotypes. But, there is great demand of dual purpose genotypes therefore, where tall genotypes with high grain yield are required. To identify such lines need grain as well as fodder yield but in present investigation no fodder yield was recorded therefore, lines were selected on the basis of grain yield and plant height assuming higher biomass in taller plants. The lines having productivity more than 80 q ha<sup>-1</sup> grain yield i.e. more than 54 g per plant gain yield and plant height more than 300 cm were identified. These eleven lines were belongs to three clusters *viz.*, IC-287731, IC-287831, IC-286769, IC-287454, IC-286682 and IC-287249 were in cluster V, IC-287464, IC-287469 and IC-287467 were in cluster VII and IC-287699 and IC-287257 were in cluster VI (Table 5.2). This distribution still leaves the scope of hybridization.

**Table 5.2: Lines selected for dual purpose sorghum**

| ACC No.   | Cluster | Plant height<br>(cm) | Grain weight<br>(g) | 100-seed<br>weight (g) |
|-----------|---------|----------------------|---------------------|------------------------|
| IC-287699 | VI      | 420                  | 65.75               | 2.89                   |
| IC-287257 | VI      | 340                  | 66.35               | 4.23                   |
| IC-287464 | VII     | 330                  | 62.39               | 2.96                   |
| IC-287469 | VII     | 330                  | 61.33               | 3.8                    |
| IC-287731 | V       | 325                  | 84.23               | 3.78                   |

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|           |     |     |       |      |
|-----------|-----|-----|-------|------|
| IC-287467 | VII | 320 | 63.33 | 3.17 |
| IC-287831 | V   | 309 | 55.04 | 2.85 |
| IC-286769 | V   | 305 | 80.54 | 2.38 |
| IC-287454 | V   | 305 | 58.68 | 4.76 |
| IC-286682 | V   | 302 | 54.28 | 2.25 |
| IC-287249 | V   | 300 | 61.2  | 3.23 |

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## 6. SUMMARY

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The present investigation was carried out to study the variability parameters, correlation coefficient, path coefficients, MANOVA and genetic divergence for grain yield per panicle and their component traits in Sorghum [*Sorghum bicolor* (L.) Moench].

The experimental material consisting of 1700 germplasm lines of sorghum along with four checks *i.e.* CSV20, CSV17, CSV27, and CSV21F provided by National Bureau of Plant Genetic Resources (NBPGR) through ICAR- Indian Institute of Millet Research (IIMR), Hyderabad were evaluated in augmented RBD with 60 replications. Observations were recorded for 26 characters *i.e.* 17 qualitative and nine quantitative characters. The important findings of the study were as follows.

1. No germination was observed in 44 germplasm lines. Early plant vigour observed only on 1656 germplasm.
2. The 7.9 per cent germplasm were having very good vigour, 52.7 per cent germplasm were having good and 39.4 per cent germplasm were having poor vigour.
3. On account of shoot fly dead hearts only 1153 lines were available for further observations.
4. Leaf colour was dark green in CSV17 and CSV20, light green in CSV27 and CSV21F checks. Dark green leaves (96.1 %) were common in germplasm while some of the germplasm had light green (3.9 %) leaves.
5. Leaf sheath pigmentation was found tan type in all the 4 checks and 5.6 per cent germplasm lines. Rest 94.4 per cent was non-tan type.
6. Leaf orientation was drooping type in all the 4 checks and germplasm.
7. The check CSV20 showed white and CSV17, CSV27 and CSV21F showed green midrib colour. The mid-rib colour of 52.5, 21.8, 18.4, 6.6 and 0.7 per cent germplasm were green, white, yellow, dark green and colourless, respectively.
8. Stay green was found in CSV20 and senescence in CSV17, CSV27 and CSV21F. The 91.8 per cent germplasm lines were stay-green and 8.2 per cent were senescence type.

9. Panicle was semi-compact in CSV17 and CSV20, and loose in CSV27 and CSV21F. In this study compact (53.6 %), semi-compact (25.5 %), very loose (13.5 %), loose (6.5) and broom corn (0.9 %) type of panicles were observed.
10. Panicle shape was cylindrical in CSV17, elliptical in CSV20 and CSV27 and ovate in CSV21F. Whereas, out of 1153 germplasm, 34.9 per cent germplasm lines were elliptical, 25.2 per cent broom corn, 23.4 per cent cylindrical, 14.8 per cent oblong, 1.6 per cent ovate and 0.1 per cent round.
11. Glume colour was straw in all the 4 checks. The straw, light brown, reddish brown, brown, red, straw brown, dark red, light red, black and purple glume colour was observed in 35.3, 30.8, 11.1, 8.1, 4.8, 3.4, 2.5, 2.2, 1.0 and 0.8 per cent germplasm lines, respectively.
12. Glume covering was  $\frac{1}{2}$  in all the 4 checks. Whereas,  $\frac{1}{2}$ ,  $\frac{3}{4}$ ,  $\frac{1}{4}$  and fully covered glume covering was observed in 42.8, 36.2, 14.7 and 6.3 per cent germplasm lines.
13. Awn was present in CSV21F and absent in CSV17, CSV20 and CSV27 checks. In germplasm lines 89.5 per cent were with awns and 10.8 per cent germplasm without awns.
14. Grain colour was creamy straw in CSV17 and CSV20 and white in CSV27 and CSV21F checks. The 39.9 per cent germplasm exhibited creamy straw grain colour while chalky white, light yellow, white, light brown, reddish brown, yellow, white and red mixed, light brown, light red, red and brown grain colour were at frequency of 40.6, 20.8, 9.6, 8.5, 7.0, 3.8, 2.9, 2.5, 2.0, 1.5 and 0.7 per cent, respectively.
15. Grain shape was oval in all the four checks. The sub-lenticular round flat from other side, elliptical, oval, round and compactly flat but grain shape were observed in 35.0, 33.7, 16.3, 12.3 and 2.7 per cent germplasm, respectively.
16. Grain size was found small in CSV17, medium in CSV27 and CSV21F, and bold in CSV20 checks. Whereas, 35.2 per cent germplasm were medium, 35.0 per cent germplasm were small and 29.8 per cent were bold grain type.
17. Endosperm texture was observed intermediate in all the four checks. 44.8 per cent germplasm exhibited intermediate endosperm texture, 30.3 per cent completely corneous, 13.3 per cent mostly corneous, 11.6 per cent mostly starchy and 0.1 per cent compactly starchy floury endosperm texture.

18. Non-lustrous grain was observed in CSV17, CSV20 and CSV27 and lustrous in CSV21F checks. In germplasm 93.8 per cent germplasm were having non-lustrous and 6.2 per cent were having lustrous grain.
19. Three checks belonged to kafir race *viz.*, CSV17, CSV20 & CSV27 and CSV21F were belongs to bicolor race. The 30.0 per cent germplasm lines were durra type, 28.7 per cent kafir, 17.9 per cent caudatum, 12.0 per cent bicolor and 11.4 per cent guinea type.
20. At the time of recording observations unequal number of lines available in different blocks even checks were damaged in some of the blocks therefore data were analysed using augmented CRD. The mean squares due to treatment, check, germplasm and checks were v/s germplasm highly significant for all the characters except for leaf length.
21. CSV17 was the best check for days to 50 per cent flowering. Thirty six germplasm lines were significantly superior over the best check CSV17 (59.29 days) for earliness.
22. CSV21F was the best check for plant height and number of leaves. Total 600 germplasm lines were significantly superior over the best check CSV21F (263 cm). Similarly 832 germplasm lines were significantly superior over the best check CSV21F (12.13) for number of leaves per plant.
23. CSV27 was the best check for leaf length, leaf width, panicle length and grain yield per panicle. The 288, 628, 195 and 78 germplasm lines were significantly superior over the best check CSV27 for leaf length, leaf width, panicle length and grain yield per panicle, respectively.
24. Panicle width of 324 germplasm lines were significantly more than the best check CSV21F (9.33 cm).
25. 100-Seed weight of 87 germplasm lines was significantly higher than the best checks CSV27 and CSV21F (3.73 g).
26. In present investigation, magnitude of GCV ranged from 11.40 to 43.75 per cent and PCV ranged from 16.16 to 62.89 per cent.

27. Heritability was high for 100-seed weight number of leaves days to 50 per cent flowering and plant height. Medium heritability was observed for panicle length, leaf width, panicle width, leaf length and grain yield per panicle.
28. In present investigation, magnitude of genetic gain ranged from 16.56 to 62.70 per cent. It was higher for for grain yield per panicle, 100-seed weight, number of leaves, panicle length and plant height characters.
29. Grain yield per panicle exhibited positively significant correlation with 100-seed weight at both genotypic and phenotypic level. Whereas, it was significant negatively correlated with panicle length, leaf length, plant height at both genotypic and phenotypic level with number of leaves and panicle width it significantly negative at genotypic level.
30. 100-Seed weight showed significantly positive correlation with leaf width and leaf length. Panicle length and panicle width exhibited significantly negative correlation with 100-seed weight at both genotypic and phenotypic level.
31. The residual effect 0.5336 at genotypic level and 0.8000 at phenotypic level indicated that 53.36 and 20 per cent variability of seed yield was explained by 8 characters.
32. In genotypic path analysis direct effect was maximum for leaf length followed by panicle length, 100-seed weight, panicle width, plant height, number of leaves, leaf width and days to 50 per cent flowering. Directions of direct effect and correlation coefficients were same for all the characters except leaf width in opposite direction.
33. In phenotypic path analysis direct effect was maximum for 100-seed weight. Direction of direct effect and correlation coefficients were same in the cases of 100-seed weight, leaf width, days to 50 per cent flowering, plant height, number of leaves, leaf length and panicle length. Direct effect of panicle width was positive and correlation coefficients were negative.
34. MANOVA was carried out using 9 characters. Wilks lambda was 0.000 and has an associated F of 4.101, which is significant as was  $p < 0.001$ . Thus indicate that there was significant difference between genotypes over all the 9 variables.
35. Based on equilibrium distance, 599 genotypes were grouped into ten clusters. Among them cluster- VII was the largest with 137 genotypes. The analysis of variance revealed significant difference between cluster means for plant height, grain weight,

days to 50 % flowering, leaf length, total number of leaves, panicle length, leaf width, 100 seed weight and panicle width. Maximum inter cluster distance was between cluster-I and VI and followed by between cluster-VI and X, cluster-I and VII, cluster-I and V, cluster- VI and VIII, cluster- I and II, cluster- VI and IX, cluster-I and III and cluster-I and IV.

36. Germplasm was belonging to cluster VI and IX having higher mean values for plant height and grain weight. Early days to 50 % flowering were in cluster VIII. High leaf length and total number of leaves in cluster VI. High panicle length, leaf width, 100 seed weight and panicle width in cluster II, VI, V, and II, respectively.

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