"Evaluation and Identification of *Kharif* Sorghum [*Sorghum bicolor (L.)* Moench] Landraces for Desirable Traits"

THESIS

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Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior

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In

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(GENETICS AND PLANT BREEDING)

BY

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CERTIFICATE – I

This is to certify that the thesis entitled **"Evaluation and Identification of *Kharif* Sorghum [*Sorghum bicolor (L.)* Moench] Landraces for Desirable Traits''** submitted in partial fulfillment of the requirements for the **"DEGREE OF MASTER OF SCIENCE IN AGRICULTURE (GENETICS AND PLANT BREEDING)"** of the Rajmata Vijayaraje Scindia Krishi Vishwa Vidhyalaya , Gwalior, is a record of the bonafide research work carried out by **DEEPAK NAGAR**, I.D.No. 18121604, under my guidance and supervision. The subject of the thesis has been approved by the student's advisory committee and the Director of Instructions, R.V.S.K.V.V Gwalior (M.P.).

No part of the thesis has been submitted for any other degree or diploma (certificate awarded etc.) or has been published. All the assistance and help received during the course of investigation have been published. All the assistance and help received during the course of investigation have been duly acknowledged by him.

Place: Indore (**Dr. M. K. SAXENA**)

Date: Chairman of Advisory Committee

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Chairman - (Dr. M. K. Saxena) …….

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Member - (Dr. Usha Saxena) …….

Member - (Dr. S. Holkar) …….

CERTIFICATE – II

This is to certify that the thesis entitled **"Evaluation and Identification of *Kharif* Sorghum [*Sorghum bicolor (L.)* Moench] Landraces for Desirable Traits''** submitted by **DEEPAK NAGAR**, I.D.No. 18121604 to the Rajmata Vijayaraje Scindia Krishi Vishwa Vidhyalaya, Gwalior, in partial fulfillment of the requirements for the **"DEGREE OF MASTER OF SCIENCE IN AGRICULTURE (GENETICS AND PLANT BREEDING)"** has been accepted after evaluation by the external examiner and approved by the student's advisory committee after oral examination on the same.

Place: Indore (**Dr. M. K. SAXENA**)

Date: Chairman of Advisory Committee

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Member (Dr. S. Holkar) …….

Head of the Department/Section …….

Dean of the college …….

Director Instruction …….

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Place : Indore ***(Deepak Nagar)***

Date:.

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LIST OF SYMBOL AND ABBREVIATION:

S. No	Symbol	Abbreviation
1	**CD**	Critical Difference
2	**i.e.**	That is (in reference to)
3	***et al.***	Allied (and other)
4	**RBD**	Randomized block Design
5	**D.F.**	Degree of freedom
6	**S. V.**	Source of variance
7	**SE(m)±**	Standard error of mean
8	**SMW**	Standard meteorological week
9	**RH**	Relative humidity
10	**%**	Percent
11	**G**	Gram
12	**C. V.**	Coefficient of variance
13	**MSS**	Mean sum of square
14	**ESS**	Error sum of square
15	**S.S**	Sum of square
16	**Fig.**	Figures
17	**DTF50%**	Days to 50% flowering
18	**DTM**	Days to maturity
19	**PH**	Plant height (cm)
20	**LA**	Leaf area (cm^2)
21	**BRIX**	Brix at physiological maturity (%)
22	**FLL**	Flag leaf length (cm)
23	**CL**	Cob length (cm)
24	**CW**	Cob Width (cm)
25	**NPBPP**	Number of primary branches per panicle
26	**NGPPB**	Number of grains per primary branch
27	**SW**	100 seed weight (g)
28	**GYPP**	Grain yield/plant (g)
29	**FW**	Green fodder yield per plant (g)
30	**DW**	Dry fodder yield per plant (g)
31	**HI**	Harvest index %
32	**GA**	Genetics Advance
33	**PCV**	Phenotypic Correlation Coefficient
34	**GCV**	Genotypic Correlation Coefficient
35	**^oC**	Degree of centigrade

CHAPTER – I
INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] also known as Jowar has originated and domesticated in Africa about 5000 – 8000 years ago (De Candolle 1884). It is one of the major cereal crops of the semiarid tropics. Presently sorghum is a major staple food crop of rural India (Anglani, 1998), This crop requires less water and nutrient and hence is widely cultivated in the semi-arid tropics in Sub-Saharan Africa and India (Rooney *et al*., 2000). It is grown mostly by marginal and poor farmers, and sorghum has a significant impact on food security. Ethiopia is a center of origin. Sorghum is the king of millets and is one of the important food crops in dry lands of tropical Africa, India and China. High diversity in sorghum is distributed throughout India.

It is a traditionally important cereal crop of India cultivated under approximately 5.14 million ha with a production of 4.73 million tonnes with productivity of 920 kg/ha, Fourth Advance Estimate, Directorate of Economics and Statistics (2019-20). The major sorghum growing states in India are Maharashtra, Karnataka, Madhya Pradesh, Andhra Pradesh, Telangana, Tamilnadu, Rajasthan and Gujarat. In the state of Madhya Pradesh, sorghum is important as a food crop, feed crop, and fodder crop for rainfed farming. In view of the multiple usage of this crop, is presently grown under approximately 0.22 million ha with a production of 0.36 million tonnes and productivity 1641 kg/ha in Madhya Pradesh, Fourth Advance Estimate, Directorate of Economics and Statistics (2019-20).

Landraces have more genetic diversity, wider adaptability and high degree of resistance to biotic and a biotic stresses and even respond to selection for high yield. In the present world of research, great studies in sorghum improvement have been made by transforming the local landraces into more productive forms through hybridization to evolve highly adapted hybrids.

Crop improvement depends on the magnitude of genetic variability and the extent of transmission of traits in successive generation. Yield, being a complex polygenic trait is highly influenced by the environmental factors.

It is therefore essential to partition the variability into its heritable and non heritable components, which will enhance the precision of selection. The knowledge of genetic variability among the germplasm lines for the characters of economic importance is useful when the degree and direction of relationship among yield and yield contributing traits are known to the breeder.

In present study analysis will be done to determine the variability among the experimental material for quantitative traits in sorghum germplasm accessions from various sources and to evaluate germplasm for certain useful agro morphological traits. The identified accessions may prove to be an important gene pool for different traits in the backdrop of the above information.

The present investigation was undertaken with the following objectives:

1. To study parameters of genetic variability for yield and its component traits in sorghum genotype

2. To estimate the extent of genetic diversity among genotypes by using Mahalanobis D^2 analysis

3. To study the nature and magnitude of relationship of seed yield with other traits and amongst themselves for genetic improvement in sorghum

CHAPTER – II
REVIEW OF LITERATURE

The information on genetic architecture of the economic traits is insufficient for any crop improvement programme. A thorough understanding of the extent of variation, genetic architecture of the plant and heritability of characters, among the germplasm lines would help in developing sound plant improvement programmes. A brief review of available information on the above aspects in sorghum is presented in this section under the following headings.

Parameters of genetic variability

Correlation coefficient studies

Genetic Diversity

Parameters of genetic variability:

Genetic variation:

Possibility of achieving improvement in any crop plants depends heavily on the magnitude of genetic variability. The phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and phenotypic components. The genotypic component being the heritable part of the total variability, it's magnitude on yield and it's component characters influences the selection strategies to be adopted by the breeders.

The genetic variability in relation to environmental variability was first studied by Fisher (1918). Next to Fisher, several workers discovered many techniques for the estimation of components of variance (Wright, 1921; Lush, 1949; Robinson *et al.,* 1951 and Weber and Moorthy, 1952).

Rao and Patile (1996) obtained the highest genotypic and phenotypic coefficients of variation for number of grains per panicle followed by grain yield per plant.

Narvaria (1998) reported that the characters *viz.,* plant height, area of flag leaf, number of grains per panicle, length of last internode and grain yield per panicle possessing high genotypic coefficients of variation indicated relatively higher genetic variation for these traits in the experimental material.

Prabhakar (2001) reported that PCV was higher than the GCV for all the characters studied, which provides the extent of variability present in the population. He observed high GCV for 1000 grain weight and grain yield per plant, whereas, low GCV values were recorded for days to 50% flowering

Chaudhary *et al.,* (2001) recorded high phenotypic and genotypic coefficients of variation for grain yield per plant (35.35 and 32.32), number of primaries per panicle (30.06 and 29.52), plant height (28.49 and 26.45) and ear length (25.91 and 19.39).

Kenga *et al.,* (2006) collected data on grain yield, days to anthesis, plant height, inflorescence length, threshing percentage and seed mass and subjected to statistical genetic analyses. Genetic variance was essentially attributed to additive gene effects, with dominance variance for grain yield being negligible. However, the reverse was observed for threshability. Genetic variance components were much higher for plant height and grain yield than for days to anthesis, seed mass and threshability

Bello *et al.,* (2007) evaluated thirty landraces for one year a cross two environments, to obtain information on genetic and morphological diversity. High estimates of genotypic and phenotypic variances were observed for flag leaf length, panicle length and panicle width.

Khapre *et al,.* (2007) observed high G.C.V. values for leaf area (cm^2), number of grains per earhead, number of primaries per earhead and grain yield per plant.

Ali *et al.,* (2009) observed genotypic coefficient of variation was the highest for excised leaf weight loss followed by grain yield suggesting considerable scope for selection of these traits.

Chavan *et al., (*2010) observed that genotypic and phenotypic coefficients of variation were greatest for number of grains per panicle, followed by plant height, grain yield per panicle, number of primary branches per panicle, harvest index, number of days to maturity, number of days to 50% flowering, test weight, panicle length and panicle width. The values of genetic and phenotypic variation were highest for harvest index and lowest for number of days to maturity.

Godbharle *et al.,* (2010) studied the genetic variability in 20 B lines and 16 R lines of *kharif* sorghum (*sorghum bicolor* (L) Moench). The genotypic variance was lower than the phenotypic variance for all the characters. High genotypic and phenotypic variance were observed for the characters panicle length, fodder yield, 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.

Zou GuiHua *et al.,* (2011) evaluated seven stalk yield related traits including heading date (HD), plant height (PH), harvested stem length (HSL), number of nodes (NN), stem diameter (SD), panicle length (PL) and panicle neck length (PNL), along with sugar concentration (SC) of stalk juice in a sweet sorghum population. Significant differences among genotypes were observed for all measured traits. A large proportion of the phenotypic variance for PH, HSL, PL and SC was attributed by genotypic variance. Moderate proportion of phenotypic variances for HD, NN and PNL were explained by genotypic variances.

Jain and Patel (2012) studied the variability parameters and character association in single cut sorghum varieties under the arid and semi arid condition of Gujarat. Genotypic coefficient of variation (GCV) was maximum for green fodder yield followed by dry fodder yield and their per day productivity.

Singh *et al.,* (2013) studied the variability parameters of multicut forage sorghum variety SSG 59-3 and its 15 mutants derived from gamma irradiation for green fodder yield per plant per day and their component traits. Out of 41 significant characters, magnitude of GCV ranged from 0.71 to 42.42 per cent, PCV ranged from 0.73 to 47.70 per cent.

Swamy *et al.,* (2018) determined high genotypic and phenotypic variance for the characters *viz.,* stover weight, panicle length, panicle weight and grain yield.

Subhashini *et al.,* (2019) studied variability and association for nine morphological traits. Based on the variability parameters, high GCV for flag leaf width, panicle weight and grain yield exhibiting lower environmental influence and high PCV was observed for the traits *viz.,* flag leaf length, flag leaf width, panicle length, panicle weight, number of primaries, 100 seed weight and grain yield per plant.

Heritability and Expected genetic advance:

Heritability in broad sense refers to the functioning of the whole genotype as a unit used in contrast with environmental effects. The narrow sense heritability includes only the average effects of genes transmitted adaptively from parent to progeny (Lush,1949).

The heritability estimates along with genetic advance are more useful than the heritability value alone in predicting the resultant effect for selecting the best individual (Johnson *et al.,* 1955). According to Ramanujan and Tirumalachar (1967) heritability is more reliable if accompanied by high genetic advance.

Kukadia *et al.,* (1983) observed high heritability in broad sense for number of primary branches per panicle (97.99%), grain yield per plant (95.35%), 1000 grain weight (94.64%), plant height (88.43%) and days to 50 per cent flowering (85.36%) whereas moderate for panicle length (68.83%) and low for area of flag leaf (48.27%).

Veerabadhiran and Kennedy (2001) reported high heritability estimates coupled with high genetic advances for 100 grain weight and grain yield.

Deepalakshmi and Ganesamurthy (2007) observed high heritability accompanied with high GA as per cent of mean for the characters days to fifty per cent flowering, plant height, leaves per plant, leaf length, earhead weight, number of primaries per panicle, 100 grain weight, grain mould score and single plant yield thus suggesting that these characters are under additive gene action and thus gives better scope for selection

Ali *et al.,* (2009) reported high estimates of broad sense heritability for flag leaf length , leaf area and grain yield per plant. They also reported high estimate of genetic advance along with high estimates of broad sense heritability for flag leaf length , leaf area and grain yield per plant indicated the most appropriate condition for selection against these traits except for relative dry weight

Jain *et al.,* (2010) reported that plant height, stem girth, and dry & green fodder yield responded positively to selection because of high board sense heritability and high genetic advance.

Godbharle *et al.,* (2010) observed high heritability estimates coupled with high genetic advances for the characters panicle length, fodder yield, primary branches per panicle, grains per primary branches, harvest index, grain yield and plant height.

Kumar *et al., (*2011) reported high estimates of heritability for plant height, test weight, seed yield, days to maturity and high estimates of genetic advance for plant height and test weight. The seed yield showed a positive and significant correlation with days to maturity in Sb x Sl, and test weight and fodder yield in both crosses.

Tomar *et al.,* (2012) assessed genetic variability and heritability of 52 sweet sorghum genotypes. The observations were recorded for 17 quantitative traits. 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

Idris *et al.,* (2015) exhibited high heritability for dry weight, days to 50% flowering and days to maturity.

Jimmy *et al.,* (2017) studied genetic variability, heritability and genetic advance as well as association between yield and yield related traits in selected sorghum varieties. All the traits evaluated exhibited high genotypic and phenotypic components of variance than environmental variance, showing that characters in the population was genetically controlled and can be exploited in breeding programs.

Chaudhary *et al.,* (2017) studied variability parameters on thirty-four sorghum genotypes. The highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for a number of leaves per plant, leaf stem ratio and green fodder yield indicating that these characters could be used as a selection for crop improvement.

Swamy *et al.,* (2018) high magnitude of heritability coupled with high magnitude of genetic advance over mean was obtained for the characters viz., days to 50 per cent flowering, plant height, panicle length, panicle girth, panicle weight, stover weight, grain yield and 1000-grain weight.

Al-Naggar *et al.,* (2018) studied genetic variability, heritability, genetic advance and strength of association of yield related traits among sorghum lines under different environments in Egypt. Grain yield per plant and plant height traits showed high heritability associated with high genetic advance from selection.

Wadikar *et al*., (2018) carried out the high estimates of heritability and expected genetic advance for green cane yield, total biomass, total soluble sugar, non-reducing sugar, reducing sugar and juice yield.

Singh *et. al.,* (2019) estimated high heritability coupled with high genetic advance were for plant height, leaf area, stem girth and green fodder yield, which indicates that preponderance of additive gene effects for these attributes and hence may prove useful for effective selection.

Endalemaw and Semahegn (2020) showed high heritability (H%) with high genetic advance as percentage of mean (GAM%) were grain filling rate, plant height, grain yield, panicle weight, panicle exertion and stay green.

Correlation coefficient studies:

Grain yield is a complex trait, which is influenced by a number of contributing characters. The estimates of the inter relationship between grain yield and other yield attributes and among themselves would facilitate effective selection schemes to improve the yield.

Jayprakash *et al.,* (1997) studied correlation in 65 genotypes grain sorghum and observed that grain yield was significantly and positively correlated with panicle weight, panicle length and dry fodder yield. Plant height also had a positive, significant association with grain yield at genotypic level.

Can *et al.,* (1998) worked out correlation between characters of 13 local germplasm lines of sorghum and found that harvest index 19 and its yield components like total fodder yield, plant height, 100 seed weight, leaves per plant , number of internodes had a high positive correlation with grain yield.

Soltani *et al.,* (2001) reported that grain yield had significant negative correlation with physiological traits related to development and vegetative growth. However, there was significant positive correlation between growth rate, grain filling rate and harvest index.

Sunku *et al.,* (2002) studied correlation in grain sorghum and found that correlation coefficients were significant and high among dry matter yield, green fodder yield, leaf length, plant height , number of leaves, dry matter

content and leaf width. node number per plant, panicle weight and kernel number per panicle correlated positively and significantly with seed yield per plant.

Deepalakshmi and Ganesamurthy (2007) reported that seed yield positively and significantly correlated with days to maturity, number of leaves per plant, earhead weight and number of primaries per panicle but there was negative significant correlation with grainmould score.

Godbharle *et al.,* (2010) observed positive and significant correlation between grain yield and harvest index, total biomass, fodder yield and leaf area index both at phenotypic and genotypic level, while the characters field grade score, threshed grade score and days to 50% flowering exhibited negative correlation with grain yield.

Jain *et al.,* (2010) estimated that plant height, stem girth and leaf length were positively and significantly associated with green fodder and dry fodder yield per plant. Leaf breath was positively and significantly associated with plant height, number of leaves per plant and leaf length

Shinde *et al.,* (2011) reported that plant height, number of leaves per plant, number of internodes per plant, panicle length, panicle breadth, number of primaries per panicle, test weight, number of grains per panicle and fodder yield per plant had positive association with grain yield per plant. On the other hand, days to 50% flowering had negative association with grain yield per plant.

El Naim *et al.,* (2012) Revealed that grain yield per hectare had high significant positive correlation with number of grain per panicle and number of panicles per unit area.

Patil *et al.,* (2014) carried out investigation to study the correlation and path analysis in dual purpose sorghum (Sorghum bicolor L.) with the set of thirty seven genotypes of sorghum grown in Randomized Block Design with four replications. The correlation analysis suggested that the magnitude of

genotypic correlations was higher as compared to their corresponding phenotypic correlations indicating the inherent relationship among the characters studied. Grain yield per plant exhibited significant positive association with thousand grain weight, stem girth, leaf length, panicle length, panicle diameter, panicle weight and protein per cent in grain at both genotypic and phenotypic levels.

Arunah *et al.,* (2015) determined mutual association between characters of two sorghum varieties (ICSV III and SAMSORG 14) using correlation coefficient of two years experiment. The percent contribution of growth and yield components to yield. In both years and the average over the years, a positive and highly significant correlation was observed between sorghum yield and plant height, leaf area index and total dry matter. Likewise, sorghum yield also had a positive and highly significant interaction with panicle weight and 1000- grain weight. In improving sorghum yield emphasis on breeding should be on its height, leaf area index and panicle length.

Endalemaw and Semahegn (2020) showed the positive associations among grain yield with panicle weight, panicle width and grain filling rate indicate that selecting positively associated panicle related traits would have a positive effect on grain yield.

Genetic Diversity

Genetic divergence or D^2 statistics analysis is a potential tool for the selection of genetically divergent parents in hybridization programme. It separates the genotypes into different clusters and assess the relative contribution of different traits to the total divergence, both at the inter and intra cluster levels. Hence, it permits the selection of parents for hybridization. On the basis of clustering pattern, it helps in the assessment of the nature and magnitude of diversity between genotypes to isolate diverse parents. Intercrossing between genetically divergent parents is expected to produce superior hybrids and desirable recombinants.

Mehndiratta *et al.,* (1971) studied genetic divergence with respect to fodder yield and its components in thirty genotypes of sorghum {Sorghum vulgare Pers.) The thirty varieties were grouped into seven clusters or groups on the basis of D^2 values. The maximum distance based on D values was between groups VI and VII (22.40), followed by that between II and VI (17.59) and V and VI (17.12). The distance between groups II and V was the shortest (4.72). The intra-cluster variation was almost parallel in all the groups.

Joshi and Vashi (1992) classified Eighty-nine sorghum genotypes into nine clusters using D^2 statistic. A comparison of the culturing pattern of parents vis-a-vis their hybrids, the magnitude of heterosis in crosses involving parents in the same cluster with those in different clusters and the D^2 values between parents with heterosis exhibited in their cross combinations revealed absence of any relationship between topological distance and genetic diversity.

Biradar *et al.,* (1996) studied a representative group of 67 maintainer lines of sotghum using Mahalanobis D^2 statistic. The 67 genotypes were grouped into 20 clusters. Results showed that 50 % flowering contributed most to divergence followed by plant height, panicle length, number of primaries and ear weight. There were no indications of relationship between geographical diversity and genetic diversity

Barhate *et al.,* (2000) studied genetic diversity of 50 sorghum genotypes under light and medium soil types and found substantial genetic diversity among them. The fifty genotypes were grouped into thirteen and sixteen clusters under light and medium soil conditions respectively. Plant height, panicle length, flag leaf area, panicle breadth, 1000 grain weight and fodder yield per plant appeared to be very potent in contributing towards divergence. He concluded that genotypes from extreme divergent groups with better values for yield and its components may yield superior segregants if used in breeding programme.

Narkhede *et al.,* (2000) assessed the genetic divergence among 64 Rahuri sorghum local germplasm (RSLG) collected from different geographic

origin, and grouped them into 19 clusters, according to Tocher's method. Among the 13 quantitative characters studied, days to 50 per cent flowering contributed most to genetic divergence, followed by plant height, 1000 grain weight, intenode length and panicle length. Based on D 2 values and pet se performance, divergent pairs for hybridization programme and 15 other genotypes have been suggested to obtain superior types to secure yield improvement in rabi sorghum.

Rahman *el al.,* (2004) studied genetic divergence of 35 sorghum {*Sorghum bicolor* (L.) Moench) genotypes using D^2 and principle component analysis for nine characters. The genotypes under study were grouped into nine clusters. The cluster I contained maximum genotypes and cluster III contained minimum. The intercluster distances in most of the cases were higher than intra cluster distance indicating wider genetic diversity among the genotypes of different groups. Days to maturity, number of tillers per plant and 1000 grain weight showed maximum contribution towards divergence among the genotypes.

Arunkumar and Biradar (2004) applied D^2 statistics to assess the genetic diversity available among 138 genotypes comprising of 91 exotic and 47 local collections of rabi sorghum Based on D^2 values 138 genotypes were grouped into 13 clusters. Among the clusters, cluster I was the largest with 67 genotypes followed by cluster II with 57 genotypes. Cluster III had 4 genotypes, while cluster 4-13 were solitary clusters with a single genotype. This revealed the presence of divergent genotypes within different clusters.

Ganesamurthy *et al.,* (2010) evaluated sixty three local land races of sorghum for their genetic diversity based on nine characters. The genotypes were grouped into 14 clusters indicating high genetic divergence among them. Based on the inter cluster distance and cluster mean for various characters it could be seen that the clusters VI, X, XII were the most divergent from the other clusters. Days to flowering, plant height, ear head length and grain weight contributed highly towards the genetic divergence among the genotypes studied.

Mahajan and Wadikar (2012) assessed genetic divergence among twenty four sorghum genotypes using Mahalnobis D^2 statistic. The genotypes were grouped in to eight clusters, which revealed wide diversity in the experimental material. The maximum inter cluster distance was observed between clusters VII and VIII followed clusters II and VI.

Jain and Patel (2013) applied Mahalanobis D2 statistics revealed considerable genetic diversity among the 108 genotype of sorghum. The genotypes grouped into 11 clusters. Cluster 1 contains maximum twenty three genotypes, followed by seventeen in cluster II and fourteen in cluster III. The average inter-cluster values were maximum between cluster V and cluster XI (54.42) followed by III and VI (49.29). At intra cluster level maximum value was recorded for cluster IV (22.12), followed by cluster VII (21.39) and cluster III (20.01).

Shinde *et al*., (2013) studied genetic diversity among 46 genotypes of Sweet Sorghum and revealed that the clustering pattern based on D^2 statistics grouped 46 genotypes into 11 clusters, out of which cluster I shows the highest intra cluster value (13.79) followed by cluster II (13.64) while maximum inter cluster distance (i.e. 34.72) was observed between cluster V and cluster IX.

Khadakabhavi *et al*., (2014) assessed genetic divergence in 121 germplasm lines of Rabi sorghum using Mahalanobis D^2 analysis. All the genotypes were grouped into 13 clusters where, cluster-I was the largest with 68 genotypes followed by cluster-XIII with 38 genotypes. Whereas, cluster-II, to cluster-XII consisted of two genotypes in each clusters. The intra cluster distance was maximum in cluster-XIII and cluster-I followed by cluster-XII and cluster-XI whereas inter cluster distance was maximum between cluster-X and cluster-XI.

Sujatha and Pushpavalli (2015) used Mahalanobis D^2 statistics to assess the divergence among the forty-five rabi sorghum landraces, thirteen advanced breeding lines and four popular cultivars. The sixty-two genotypes were grouped into fifteen clusters where cluster I was the largest comprising

of forty-one genotypes followed by cluster III with seven genotypes and cluster XI with two 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.

Doijad, *et al.,* (2016) carried out D^2 analysis to assess the diversity among sixty-one genotypes of sorghum. The genotypes were grouped into fifteen clusters, where cluster I comprised maximum of forty-seven genotypes, while the rest of the clusters had one genotype each. Inter-cluster distance was maximum between the clusters XV and XIV followed by XV and IX which indicated that genotypes included in these clusters may give heterotic response and thus better segregants.

Damor *et al*., (2017) carried out D^2 analysis in sixty genotypes of forage sorghum and revealed considerable genetic diversity among the genotypes. The genotypes grouped into 5 clusters. Cluster I contains forty genotypes followed by sixteen in cluster II, while cluster III and V were contain solitary genotype and cluster IV had only two genotypes.

Hari Vara Prasad *et al.,* (2018) applied D^2 statistics to assess the diversity among 41 B-lines and 43 R-lines of sorghum identified from minicore collection. The genotypes were grouped into 13 clusters, where cluster III comprised maximum of 14 genotypes followed by cluster IV with 7 genotypes each among R-lines whereas B-lines grouped into 6 clusters with cluster I with 22 genotypes followed by cluster II with 9 genotypes. Inter-cluster distance was maximum between the clusters IX and X with 648.07 among R-lines and in B-lines maximum intercluster distance was between I and VI with 1136.00.

Swamy *et al*., (2018) applied Mahalanobis D^2 statistics to assess the divergence among one hundred and twenty-two rabi sorghum genotypes. All the genotypes were grouped into nine clusters and cluster I was largest with 88 genotypes, followed by cluster IV, II and V (17, 10 and 2 genotypes respectively) and remaining clusters (III, VI, VII, VIII and IX) were solitary in nature.

Yuvaraja *et al*., (2019) evaluated sorghum germplasm for forage traits during the Rabi to study the divergence using multivariate (D2) analysis. Resul revealed four distinct cluster indicates that the germplasm had variation between group of cluster. The intra-cluster distances in all the four clusters were registered low, indicating that the genotypes within the same cluster were closely related for its forage value. The highest inter-cluster distance was observed between cluster I (14 genotypes) and cluster IV (2 genotypes) and the lowest between the cluster II (25 genotypes) and III (85 genotypes).

CHAPTER III

MATERIALS AND METHODS

The present investigation entitled **"Evaluation and Identification of *Kharif* Sorghum [*Sorghum bicolor (L.)* Moench] Landraces for Desirable Traits"** was carried out during *kharif* of 2019-2020 at All India Coordinated Research Project on Sorghum, College of Agriculture farm, Indore - (M.P.) 452001.

Indore is situated in Malwa plateau in western part of Madhya Pradesh. Indore is situated between latitude 22º43' N and longitude 75º53' E and at an altitude of 562 meters above the mean sea level. It has semi-humid and subtropical climate having a temperature range of 23º to 42ºC and 7º to 29ºC in summer and winter seasons, respectively. In this area most of the rainfall is received during mid June to early October. The rainfall in the year 2019-20 was 1565.40 mm. The south-western monsoon is responsible for the major part of the precipitation. The soil of the area are medium deep and shallow black soil mostly derived from Deccan trap. The weather prevailed during the crop season were recorded from the meteorological observatory of College of Agriculture, Indore and have been presented in Table 3.1.

Experimental method

Single row of each of 60 landraces were sown in kharif season during 2019-20 in randomized block design with three replications at All India Coordinated Research Project on Sorghum, College of Agriculture farm, Indore - (M.P.) 452001.

Experimental material:

The experimental material used in the present study comprised of 60 sorghum landraces. The lines here been listed in Table 3.2.1

Table3.1: Meteorological observations recorded during crop period 26 SMW to 47 SMW (June to November 2019-20)

Standard week no.	Temperature		RH (%)	Rainfall (mm)	No. of rainy days	Wind Velocity (Km/hr)	Wind direction
	Max. (^{0}C)	Min. (^{0}C)					
26th	31.57	23.64	77.3	145.1	4	1.82	SW-23
27th	26.78	22.42	82.22	121.8	4	2.58	SW-23
28th	31.35	24.71	77.93	0	0	2.79	SW-23
29th	32.85	24.85	75.02	52.3	3	1.09	SW-23
30th	26.42	22.42	83.21	83.3	5	2.77	SW-23
31st	27.07	23.28	81.29	66.7	3	1.42	SW-23
32nd	26.78	22.57	80.94	144.5	4	1.54	SW-23
33rd	27.14	22.14	81.16	66	5	2	WN-32
34th	26.42	22	82.04	103	4	1.47	SW-23
35th	27.21	22.71	79.45	111	2	0.29	WN-32
36th	26.85	22.85	83.83	125	7	0.25	SW-23
37th	26	21.28	85.27	145	5	1.46	WN-32
38th	29.14	22	84.45	59	4	0.11	NE-05
39th	28.57	21.42	81.8	52	5	0.37	SW-23
40th	29.78	20	80.84	125	3	0.22	NE-05
41st	29.92	19.57	75.19	27	2	0.04	NE-05
42nd	28.85	18.42	80.99	4	1	0.11	NE-05
43rd	28.57	19.21	81.03	5.1	1	0.12	NE-05
44th	30.85	19.85	77.74	0	0	0.09	SE-14
45th	31.42	18	76.62	0	0	0.18	SE-14
46th	30.64	15.21	74.6	0	0	0.11	SE-14
47th	30.85	15.35	78.41	0	0	0.04	SW-23
Total				1435.8	62		

Source: Meteorological observatory, College of Agriculture, Indore (M.P.)

Table 3.2: List of landraces included in study

S.N.	Landraces	S.N.	Landraces	S.N.	Landraces
1	Pop-8	**21**	Gird-20	**41**	E202
2	Pop-13	**22**	Gird-21	**42**	ELG31
3	Pop-14	**23**	Gird-23	**43**	E184
4	Pop-17	**24**	Gird-30	**44**	NCC1
5	Pop-18	**25**	Gird-31	**45**	E284
6	Pop-27	**26**	Gird-33-2	**46**	ERN36
7	Pop-31	**27**	Gird-35	**47**	1746
8	Pop-35	**28**	Gird-41	**48**	1572
9	Pop-1	**29**	Gird-45	**49**	1939
10	Pop-51	**30**	Gird-48	**50**	MO1567
11	Pop-37	**31**	GGUB13	**51**	1863
12	Pop-62	**32**	GGUB20	**52**	E68
13	KMJ-1	**33**	GGUB59	**53**	SOR1936
14	Khargoan	**34**	E248	**54**	3774
15	Gird-1	**35**	E102	**55**	6137
16	Gird-5	**36**	E246	**56**	SOR13
17	Gird-8	**37**	E207	**57**	SEB12025
18	Gird-10	**38**	EC6	**58**	3788
19	Gird-11	**39**	EG31	**59**	KHARGOAN3
20	Gird-3	**40**	EGN9	**60**	SOR6914

Experiment details

Crop : Sorghum [*Sorghum bicolor* (L.) Moench]

Season : *Kharif* (2019-20)

Sowing date : 27 & 28 June (2019-20)

Experimental Design : RBD (Randomized Block Design)

Number of genotypes : 60

Replications : 3

Plots size Gross : (3.00 m x 0.90 m)

Spacing : 45 cm X 15 cm.

Observations recorded

Fifteen biometrical observations were recorded on five randomly selected plants in each replication. The mean values were used for statistical analysis and listed below.

Days to 50% flowering

Number of days from sowing to 50 per cent flowering of panicle in a row was recorded and average number of days to 50 per cent flowering was worked out.

Days to maturity

Maturity was taken when a black- layer appears immediately above the point of kernel attachment in the floret near the base of the kernel.The number of days required from sowing till the date when seed matured physiologically was recorded.

Cob length (cm)

Length of the panicle from its base to tip.

Cob width (cm)

Width of panicle in natural position at the widest part.

Plant height (cm)

The plant height of the randomly selected plants from each row was recorded by measuring to the base of the plant near ground up to the panicle at physiological maturity.

Leaf area (cm2)

Area of the fourth leaf from the flag leaf, computed as (leaf length x leaf width x 0.747) suggested by Stickler *et al.,* (1961).

Flag leaf length (cm)

The average length of flag leaf from randomly selected plants per row is measured.

Number of primary branches/panicle

Primary branches of ea ch randomly selected panicle in per row were counted and averaged out.

Number of grains/primary branch

Average number of grains borne on randomly selected primary branches were recorded.

100 seed weight (g)

The weight of 100 randomly selected seeds for each landrace was recorded with the help of electronic top pan balance in grams and averaged out.

Grain yield per plant (g)

Ear head from randomly selected plants in a row was harvested, dried and threshed. The grain was thoroughly sun dried before weighing and finely grain weight (g) per plant was recorded.

Brix at physiological maturity (%)

Brix at physiological maturity was measured by hand refractometer/brixmeter.

Green fodder yield per plant (g)

Weight of the randomly selected green plants in each row at the time of harvesting was recorded.

Dry fodder yield per plant (g)

Dry weight of the randomly selected plants in each row excluding grain weight.

Harvest index %

It was calculated as proportion of grain yield to biological yield and expressed in percentage, where biological yield was determined as above ground biomass (leaves, stem and panicle) measured in grams.

HI% = Economic yield (grain) / Biological yield (grain + straw) x 100

Statistical analysis:

Analysis of variance (ANOVA):

The mean values of above mentioned characters in replication were taken for analysis of variance. The analysis of variance was carried out as per Panse and Sukhatme (1954).

Table 3.4. Skeleton of ANOVA for randomized block design

S. NO.	Source of Variation	D.F.	Sum of square	Mean Sum of square	F value
1.	Replications	(r-1)	SSr	MSr=SSr /(r-1)	MSr/MSe
2.	Treatments	(t-1)	SSt	MSt=SSt /(t-1)	MSt/MSe
3.	Error	(r-1)(t-1)	SSe	MSe =SSe/(r-1)(t-1)	
	Total	(rt-1)	TSS		

Where,

D.F. = Degrees of freedom

r= Number of replications

t= Number of treatments

MSr= Replication mean sum of square

MSt= Treatment mean sum of square

MSe= Error mean sum of square

The significance of differences among genotypes means was tested by the F test.

If, **Fcal > Ftab**

Then variance is significant. Wherever, the F test was found to be significant,

Critical Difference (C.D.) was calculated for a particular character.

C.D. (0.05) = SE_d ×'t'

Where,

't' = table value of 't' at error degree of freedom and 5% level of probability.

SE_d = Standard error of the difference between two treatment means.

Standard error of difference: $SE_d = \sqrt{2} \times MSe/r$

Where,

MSe = error mean square

r = number of replication

Analysis of genetic parameters

Mean and Range

The mean value for each character will be worked out by dividing sum of all observations by number of observations

$$\bar{x} = \sum xi / N$$

where,

$\bar{x}$ = Mean of the character.

$\sum xi$= summation of all observations,

N = number of observations

Range

The lowest and highest values from mean of each character will be recorded as range.

Range = maximum- minimum

Estimation of components of variation

The phenotypic, genotypic and environmental variances will be calculated by utilizing the respective mean squares values from the variance table

Genotypic variance = (Mg - Me) / r

Phenotypic variance = (Mg -Me)Me/ r

Environmental variance s =Me

Where,

Mg = Mean sum of Genotypes

Me = Mean sum of Environmental

r = Number of replications

g= Number of genotyps

Phenotypic & genotypic coefficients of variation:

The phenotypic and genotypic coefficients of variation in per cent were computed by the following formulae given by Burton (1952).

Phenotypic Coefficient of Variation (PCV) % = $\frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$

Genotypic Coefficient of Variation (GCV) % = $\frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$

The coefficient of variation were categorized as proposed by Sivasubramanian and Madhava Menon (1973)

Percent of variability	Category
<10	Low
10-20	Moderate
>20	High

Heritability (Board sense):

Heritability in broad sense was estimated as the ratio of genotypic to the phenotypic variance and was expressed in percentage. Heritability in per cent in broad sense was estimated by the following formula given by Singh and Choudhary (1977):

Heritability h^2 (Bs) % = $\frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$

The broad sense heritability estimates were categorized as low, moderate and high by Johnson et al. (1955a)

Low - <50%

Moderate - 50-70%

High - >70%

Genetic advance:

The estimates of expected genetic advance from selection, G(s), was obtained by the formula suggested by Johnson *et al.,* (1955a)

$G(s) = k \times h^2 \times \sigma p$

Where,

k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity,

h^2 = Heritability in broad sense, and

σ_p = Phenotypic standard deviation

Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al*., (1955).

$$\text{Genetic advance as percentage of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

The following classification was utilized in the study.

GA Percent value	**Category**
<10	Low
10-20	Moderate
>20	High

Correlations coefficients analysis:

Phenotypic and genotypic correlation coefficient between characters was computed utilizing respective components of variance and co-variance, by following formula suggested by Miller *et al.,* (1958).

$$r_{xy} = \frac{\text{Covariance x, y}}{\sqrt{(\text{Variance x}) \times (\text{Variance y})}}$$

Where,

r_{xy} = Correlation coefficient between character x and y,

The phenotypic correlation coefficients were tested for their significant with tabulated r values at g-2 degrees of freedom, where g is the number of genotypes (Singh and Chaudhary, 2001). The genotype correlation coefficient was tested with the following formula.

$$t = r_{gxy}/SE(r_{gxy})$$

Where,

$$SE\ (r_{gxy}) = [\{1-(r_{gxy})^2\}/\{2(g-2)(h_x)^2(h_y)^2\}]^{1/2}$$

r_{gxy} = genotypic correlation coefficient between character x and y

SE (r_{gxy}) = Standard error of genotypic correlation coefficient between character x and y

$(h_x)^2$ = Heritability for character x

$(h_y)^2$ = Heritability for character y

The calculated absolute t value was tested against tabulated t value at g-2 d.f. for genotypic correlation coefficients where g is the number of genotypes.

3.4.3 Genetic divergence

D² analysis

The analysis of divergence was carried out by D² statistic proposed by Mahalanobis (1936) as described by Rao (1952). Analysis of variance for the individual character studied was worked out as per RBD analysis, to test the significance of differences among genotypes. The characters exhibiting

significant differences were only used for further analysis of D^2 statistic. The analysis of covariance for character pairs based on plot average was carried out.

Wilk's criteria:

After testing differences among populations for fifteen characters, a simultaneous test of significance of difference between the mean value of number of correlated variables with regard to pooled effect of fifteen characters considered together was carried out using Wilk's criteria 'A' (Wilks, 1932) which was estimated using the relationship.

$$A = \frac{(E)}{(E + V)}$$

Where,

(E) = the determinant of experimental error sum of squares and sum of products matrix and

(E + V) = The determinant of experimental error sum of squares and sum of products plus population sum of squares and product matrix

The significance of Wilk's criteria (A) was tested by X^2as

$$X^2_{pq} = V = - m.\log_e(A)$$

Where,

$m = n - (p+q+1) / 2$

$n = N1+ ..... + N_{k-1}$(Total no. Of observations-1)

p= No. of significant characters

q= k-1 (No. of genotypes -1)

K= No. of genotypes

Mahalanobis's generalized distance (D^2):

The generalized distance between any two populations in defined as:

$$D^2 = \sum\sum \lambda ij\ \sigma i\ \sigma j$$

Where,

λij= Reciprocal matrix to the common dispersion matrix

σi= Difference between mean value of the two populations for the i^{th}character

σj= Difference between mean value of the two populations for the j^{th}character.

This quantity is estimated by D^2statistic (Majumdar and Rao, 1958) as :

$$D^2 = \sum\sum Sij\ di\ dj$$

Where,

Sij, di, dj are the sample estimates of λij, di and dj respectively.

Computation of D^2values:

For each combination, mean deviation i.e.

$$Yi^{-1} - Y\ i^{-2}$$ where,

i=1,2.....p was computed and the $D^2$was calculated as sum of squares of these deviation i.e.

$$\sum (Yi^{-1} - Y\ i^{-2})^{2}$$

Determination of population constellation:

No rules can be laid down for the finding the clusters, because cluster is not well defined term. The only criteria appears to be that, any two groups belonging to same cluster should be at least, on an average show a smaller D^2value than those belonging to two different clusters.

The simple method suggested by Tocher (Rao, 1952) for cluster formation is to start with two closely related groups and find third group which has a smaller average D^2value from the first two. Similarly, the fourth group is chosen to have smaller average D^2values from the first three and so on. While proceeding further from cluster formation, it at any stage, the average D^2value of the group appears to be high than those already listed, then this group does not fit in that format group and taken outside of that cluster.

The genotypes included in first cluster are then omitted and the rest are treated similarly to form next cluster.

Average intra-cluster distances:

The intra-cluster distances were calculated as,

$$\sum Di^2 / n$$

Where,

$\sum Di^2$= Sum of distances between all possible combinations

n = Number of genotypes included in a cluster

Average inter-cluster distances:

The procedure followed for calculating inter-cluster distances was first to measure the distance between cluster-I and cluster-II, between cluster-I and cluster-III, and between cluster-I and cluster-IV and so on. Likewise the clusters were taken one by one and the distances between other cluster were calculated. The average inter-cluster distances were calculated as,

$$\sum Di^2 / ninj$$

Where,

ni= Number of genotypes in cluster ‘i’

nj= Number of genotypes in cluster ‘j’

Cluster diagram:

The intra and inter-cluster distances (D values) were obtained by taking square root of average D^2values of respective groups.

With the help of D^2values between the clusters, a diagram showing the relationship between different populations was drawn.

CHAPTER-IV

RESULTS

The results obtained in present investigation entitled **"Evaluation and Identification of *Kharif* Sorghum [*Sorghum bicolor (L.)* Moench] Landraces for Desirable Traits"** are presented under following aspects.

4.1 Study of genetic variability:

4.1.1 Analysis of variance

4.1.2 Mean performance and range

4.1.3 Phenotypic and genotypic coefficient of variation (PCV and GCV)

4.1.4 Heritability in broad sense

4.1.5 Genetic advance

4.2 Study of association analysis

4.2.1 Correlation coefficient estimate

4.3. Genetic Divergence

4.3.1 D^2 analysis

4.1 Study of genetic variability:

4.1.1 Analysis of variance:

The analysis of variance was carried out for all the fifteen traits under study and are presented in Table 4.1. This analysis revealed that the landraces differ significantly for all the traits *viz.,* days to 50% flowering, days to maturity, plant height (cm), leaf area (cm^2), brix (%), flag leaf length (cm), cob Length (cm), cob width (cm), number of primary branches per panicle, number of grains per primary branch, 100-seed weight (g), grain yield per plant (g), green fodder yield per plant (g), dry fodder yield per plant and harvest index %, which revealed that there was considerable genetic variability amongst the material under study.

4.1.2 Mean performance and range of different characters studied.

1. Days to 50% flowering:

Days to 50% flowering varied from 59.00 days (Pop-18 & Pop-27) to 119.00 days (E102) with an overall mean performance is 91.62 days. The landraces namely Pop-18, Pop-27, and SOR13 were earliest in days to 50% flowering and landraces E102, ERN36 and 1746 were late in flowering.

2. Days to maturity:

Days to maturity ranged from 97.00 days (Pop-18) to 149.00 days (E102) with an overall mean performance is 125.48 days. The landraces *viz.,* Pop-18, SOR13, and Pop-17 showed earliness in maturity whereas, E102, 1939 and E248 showed late maturity.

3. Plant height (cm):

Plant height (cm) ranged from 195.66 cm (SOR13) to 365.00 cm (Gird-21) with an overall mean performance is 289.36 cm. The tallest plant was observed in Gird-21, E207 and Gird-5. The significantly lowest plant height was recorded for landraces SOR13, 1746, and Pop-18.

4. Leaf area (cm):

Leaf area (cm) varied from 193.26 cm (Pop-18) to 551.42 cm (Gird-20) with an overall mean performance is 404.17 cm. The highest value of leaf area was observed in Gird-20, Pop-51 and 6137. The significantly lowest leaf area was recorded in landraces Pop-18, SOR13, E246.

5. Brix %:

Brix % varied from 3.33% (GGUB13) to 16.66% (3774) with an overall mean performance is 8.03 %. The highest brix value was observed in 3774, Pop-31 and Khargoan. The significantly lowest value was recorded for landraces GGUB13, Pop-37, Gird-41, Gird-30.

6. Flag leaf length (cm):

Flag leaf length (cm) ranged from 21.33 cm (GGUB20) to 65.00 cm (Pop-31) with an overall mean performance is 38.01 cm. The largest flag leaf was observed in Pop-31, SOR6914 and Gird-45. The significantly lowest flag leaf length was recorded in landraces GGUB220, 1572 and E246.

Table 4.1(a) Analysis of variance for fifteen characters in sixty lines of sorghum landraces

S. No.	Source of Variations	d.f.	Mean sum of square							
			DTF50%	DTM	PH	LA	BRIX	FLL	CL	CW
1	Replication	2	0.27	0.28	204.02	1090.1	1.47	8.51	0.21	0.75
2	Treatments	59	742.39**	399.96**	4667.81**	15360.44**	21.07**	157.19**	63.69**	13.51**
3	Error	118	1.49	1.58	323.97	797.83	0.82	6.23	0.84	0.33

Table 4.1(a) Analysis of variance for fifteen characters in sixty lines of sorghum landraces

S. No.	Source of Variations	d.f.	Mean sum of square						
			NPBPP	NGPPB	SW	GYPP	FW	DW	HI
1	Replication	2	1.83	4.85	0.02	10.33	17.20	120.08	7.39
2	Treatments	59	489.00**	258.18**	0.48**	500.23**	50554.17**	12053.64**	293.40**
3	Error	118	3.70	4.22	0.009	9.59	174.04	84.27	6.28

****Significant at 1% probability level**

***Significant at 5% probability level**

7. Cob length (cm):

Cob length (cm) varied from 10.00 cm (EG-31) to 30.33 (SOR6914) with an overall mean performance is 20.28 cm. The largest flag leaf was observed in SOR6914, Khargoan and Gird-20. The significantly lowest flag leaf length was recorded in landraces E68 followed by E248.

8. Cob width (cm):

Cob width (cm) varied from 2.66 cm (NCC1) to 12.33 (MO1567) with an overall mean performance is 6.89 cm. The largest flag leaf was observed in MO1567 followed by Gird-5 and Gird-20. The significantly lowest flag leaf length was recorded in landraces NCC1, followed by Pop-13 and Pop-31.

9. Number of primary branches per panicle:

Number of primary branches per panicle ranged from 38.33 branches (E284) to 92.33 branches (Pop-27) with an overall mean performance is 68.14 branches. The highest number of primary branches per panicle was observed in Pop-27, Gird-35 and Gird-8. The significantly lowest flag leaf length was recorded in landraces E284, 1863 and SOR-13.

10. Number of grains per primary branch:

Number of grains per primary branch varied from 16.00 grains (Pop-17) to 65.66 grains (SOR1936) with an overall mean performance is 27.83 grains. The highest number of grains per primary branch was observed in SOR1936, 3788 and E207. The significantly lowest flag leaf length was recorded in landraces Pop-17, Pop-18 and Pop-27.

11. 100-seed weight (g):

100-seed weight (g) ranged from 1.40 g (Khargoan) to 3.20 (1863) with an overall mean performance is 2.13 g. The highest value was observed in landraces 1863, 3774 and E68. The significantly lowest flag leaf length was recorded in landraces Khargoan, Pop-17 and Pop-37.

12. Grain yield per plant (g):

Grain yield per plant (g) varied from 15.76 g (Pop-18) to 76.18 g (SOR1936) with an overall mean performance is 39.60 g . The highest value

was recorded in the landraces SOR1936, 3774, 3788 and E207 ; while the lowest value was recorded in Pop-18, Pop-17 and NCC1.

13. Green fodder yield per plant (g):

Green fodder per plant (g) varied from 141.66 g (Pop-18) to 806.66 g (SOR1936) with an overall mean performance is 344.15 g. The highest value was observed in landraces SOR1936, SOR6914 and EC6 . The significantly lowest value was recorded in landraces Pop-18, Khargoan3 and Pop-13.

14. Dry fodder yield per plant (g) :

Dry fodder yield per plant (g) varied from 67.33 g (Pop-18) to 333.65 g (SOR1936) with an overall mean performance is 169.36 g. The highest value was observed in landraces SOR1936, EC6 and SOR6914 . The significantly lowest value was recorded in landraces Pop-18, Gird-10 and Pop-13.

15. Harvest index (%):

Harvest index (%) varied from 11.39% (EC6) to 58.85% (GGUB20) with an overall mean performance of 25.50%. The highest value was observed in landraces GGUB20, Gird-10 and Khargoan-3 . The significantly lowest flag leaf length was recorded in landraces EC6, E202 and Gird-11.

4.1.3 Phenotypic and genotypic coefficient of variation (PCV and GCV):

The phenotypic and genotypic coefficients of variation were estimated from the corresponding variances and were used for the assessment of genetic variability for characters under studied. Phenotypic coefficient of variation (PCV) and genotypic coefficients of variation (GCV) were worked out for all the characters under study and have been presented in (Table 4.2).

The GCV and PCV was categorized as low (<10%), moderate (10-20%) and high (>20%), Sivasubramanian and Madhava Menon (1973). The estimated GCV and PCV helped in getting a clear understanding of the existence of genetic variability presented amongst the experimental material. The GCV values were lower than PCV values for all the characters under study.

The highest PCV was recorded for harvest index (39.59%), followed by, green fodder yield per plant (37.84%), dry fodder yield per

plant (37.68%), Brix (34.23%), number of grain per primary branch (33.87%), grain yield per plant (33.22%), co b width(31.54%), and cob length (23.01%). The moderate PCV was observed for 100-seed weight (19.25%), flag leaf length (19.78%), number of primary branches per panicle (18.87%), leaf area (18.60%), days to 50% flowering (17.20%), and plant height (14.55%). However, the low PCV was showed for days to maturity (9.23%)

The highest GCV was recorded for harvest index (38.35%), followed by, green fodder yield per plant (37.65%), dry fodder yield per plant (37.29%), number of grain per primary branch (33.05%), Brix (32.32%), grain yield per plant (32.29%), cob width(30.40%), and cob length (22.56%). The moderate GCV was observed for 100-seed weight (18.71%), number of primary branches per panicle (18.66%), flag leaf length (18.65%), leaf area (17.23%), days to 50% flowering (17.15%), and plant height (13.15%). However, the low GCV was showed for days to maturity (9.18%).

4.1.4 Heritability in broad sense:

In the present investigation broad sense heritability, which is ratio of total genotypic variance to total phenotypic variance, have been estimated and classified as high (>70%), medium (50-70%) and low (<50%) Johnson et al.(1955a). The heritability estimate for different traits was worked out and are presented in table- 4.2.In present investigation high heritability was recorded for the character *viz*., days to 50% flowering (99.40%), green fodder yield per plant (98.90%), days to maturity(98.8%), dry fodder yield per plant (97.90%), number of primary branches per panicle (97.70%) cob length (96.10%), number of grain per primary branch (95.20%), 100-seed weight (94.50%), grain yield per plant (94.40%), harvest index(93.80%), cob width(92.90%), Brix (89.10%), flag leaf length (88.80%), leaf area (85.80%), and plant height (81.70%).

Table 4.2. Estimates of various parameters of genetic variability for different traits in sorghum landraces

S. No	Characters	Mean	Range		PCV (%)	GCV (%)	Heritability (Broad sense) (%)	GA	GA as % of mean
			Mini.	Maxi.					
1	**DTF50%**	91.62	59	119	17.2	17.15	99.4	32.27	35.22
2	**DTM**	125.48	97	149	9.23	9.18	98.8	23.59	18.8
3	**PH**	289.36	195.66	365	14.55	13.15	81.7	70.85	24.49
4	**LA**	404.17	193.26	551.42	18.6	17.23	85.8	133	32.9
5	**BRIX**	8.03	3.33	16.66	34.23	32.32	89.1	5.05	68.88
6	**FLL**	38.01	21.33	65	19.78	18.65	88.8	13.78	36.25
7	**CL**	20.28	10	30.33	23.01	22.56	96.1	9.24	45.56
8	**CW**	6.89	2.66	12.33	31.54	30.4	92.9	4.16	60.37
9	**NPBPP**	68.14	38.33	92.33	18.87	18.66	97.7	25.9	38.01
10	**NGPPB**	27.83	16	65.66	33.87	33.05	95.2	18.49	66.45
11	**SW**	2.13	1.4	3.2	19.25	18.71	94.5	0.8	37.49
12	**GYPP**	39.6	15.76	76.18	33.22	32.29	94.4	25.6	64.65
13	**FW**	344.15	141.66	806.66	37.84	37.65	98.9	265.58	77.16
14	**DW**	169.36	67.33	333.66	37.68	37.29	97.9	128.76	76.03
15	**HI**	25.5	11.39	58.85	39.59	38.35	93.8	19.52	76.54

4.1.5 Genetic advance:

Genetic advance was estimated for all the characters under study and are presented in (Table 4.2). The genetic advance as percentage of mean was categorized and classified into three major classes i.e., High (> 20%), Medium (10-20%), Low (<10%) Johnson *et al.,* (1955a).

High genetic advance as percentage of mean was estimated for green fodder yield per plant (77.16%), harvest index(76.54%), dry fodder yield per plant (76.03%), Brix (68.88%), number of grain per primary branch (66.45%), grain yield per plant (64.65%), cob width(60.37%), cob length (45.56%), number of primary branches per panicle (38.01%), 100-seed weight (37.49%), flag leaf length (36.25%), days to 50% flowering (35.22%), leaf area (32.90%), and plant height (24.49%). However, moderate genetic advance as percentage of mean was recorded for days to maturity (18.80%).

4.2 Study of association analysis

4.2.1 Correlation coefficient estimate:

Estimates of phenotypic and genotypic correlation coefficient between seed yield and its contributing characters and among themselves were calculated and have been presented in Table 4.3.(phenotypic and genotypic correlation coefficient). In general, the genotypic correlation coefficients were slightly higher in magnitude than the corresponding phenotypic correlation coefficients.

Table 4.3: Phenotypic and genotypic correlation coefficient of various characters of Sorghum landraces:

Characters		DTF 50%	DTM	PH	LA	BRIX	FLL	CL	CW	NPBPP	NGPPB	SW	FW	DW	HI
GYPP	P	0.017	0.009	0.076	0.194**	0.107	-0.066	0.226**	0.152*	0.064	0.809**	0.272**	0.509**	0.432**	0.400**
	G	0.015	0.008	0.089	0.213	0.112	-0.067	0.246	0.165	0.058	0.816	0.270	0.530	0.449	0.378
DTF50%	P		0.887**	0.285**	0.173*	-0.665**	-0.246**	-0.403**	0.406**	-0.023	-0.094	0.219**	0.179*	0.204**	-0.164*
	G		0.888	0.32	0.182	-0.704	-0.264	-0.414	0.424	-0.024	-0.097	0.226	0.181	0.208	-0.172
DTM	P			0.287**	0.250**	-0.625***	-0.253**	-0.330**	0.293**	0.055	-0.101	0.170*	0.227**	0.257**	-0.239**
	G			0.322	0.27	-0.665	-0.27	-0.341	0.306	0.055	-0.103	0.176	0.23	0.262	-0.249
PH	P				0.255***	-0.127	0.088	-0.126	0.222**	0.246**	-0.135	0.074	0.158*	0.299**	-0.202
	G				0.316	-0.159	0.118	-0.141	0.244	0.277	-0.149	0.075	0.178	0.337	-0.219
LA	P					0.006	0.297**	0.114	0.067	0.227**	0.093	-0.052	0.292**	0.233**	-0.087
	G					0.009	0.321	0.123	0.091	0.243	0.117	-0.063	0.316	0.249	-0.093
BRIX	P						0.352**	0.421**	-0.290**	0.018	0.185*	-0.128	-0.078	-0.065	0.085
	G						0.39	0.454	-0.327	0.012	0.198	-0.133	-0.079	-0.072	0.091
FLL	P							0.251**	-0.051	0.077	0.091	-0.301**	0.188*	0.248**	-0.338**
	G							0.27	-0.038	0.081	0.108	-0.322	0.196	0.27	-0.373
CL	P								0.208**	-0.027	0.271**	0.027	0.133	0.100	0.130
	G								0.21	-0.031	0.29	0.036	0.137	0.103	0.143
CW	P									0.168*	-0.036	0.193**	0.408**	0.412**	-0.249**
	G									0.182	-0.044	0.21	0.431	0.43	-0.265
NPBPP	P										-0.279**	-0.436**	0.282**	0.274**	-0.239**
	G										-0.29	-0.452	0.287	0.28	-0.254
NGPPB	P											0.013	0.414**	0.296**	0.362**
	G											0.023	0.428	0.307	0.35
SW	P												-0.042	0.033	0.239**
	G												-0.043	0.034	0.240
FW	P													0.893**	-0.443**
	G													0.912	-0.462
DW	P														-0.579**
	G														-0.587**

*** * Significant at 1 % probability level**

*** Significant at 5% probability level**

Correlation coefficient with seed yield:

1. Grain yield per plant (g):

At phenotypic level, grain yield per plant had showed significant positive correlation with no. of grains per primary branch (0.809), green fodder yield per plant (0.509), dry fodder yield per plant (0.432), harvest index (0.400) ,cob length (0.226) and 100-seed weight (0.272). it showed negative association with flag leaf length (-0.066).

At genotypic level, grain yield per plant had showed significant positive correlation with number of grains per primary branch (0.816), green fodder yield per plant (0.530), dry fodder yield per plant (0.449) , harvest index(0.378) ,cob length(0.246), 100-seed weight (0.270) and leaf area (0.213).

Correlation coefficient amongst different characters:

Phenotypic and genotypic correlation coefficients amongst different characters have been presented in Table 4.3.(genotypic correlation coefficient) & Table 4.5.(phenotypic correlation coefficient).

2. Days to 50% flowering:

At phenotypic level, days to 50 % flowering had showed significant positive correlation with days to maturity(0.887), cob width(0.406), plant height(0.285), 100-seed weight(0.219) and dry fodder yield per plant(0.204). Days to 50 % flowering exhibited negative association with brix %(-0.665), cob length (-0.403) and flag leaf length (-0.246).

At genotypic level, days to 50 % flowering had showed significant positive correlation with days to maturity (0.888), cob width(0.424), plant height(0.320), 100-seed weight(0.226) and dry fodder yield per plant(0.208). Days to 50 % flowering exhibited negative association with brix %(-0.704), cob length (-0.414) and flag leaf length (-0.264).

3. Days to maturity:

At phenotypic level, days to maturity had showed significant positive correlation with cob width (0.293), plant height (0.287), dry fodder yield per plant(0.257), leaf area(0.250), and green fodder yield per plant(0.227). Days to maturity exhibited negative association with brix (-0.625), cob length (-0.330), flag leaf length (-0.253) and harvest index (-0.239).

At genotypic level, days to maturity had showed significant positive correlation with plant height(0.322), cob width (0.306), leaf area(0.270), dry fodder yield per plant(0.262), and green fodder yield per plant(0.227). Days to maturity exhibited highly negative association with brix (-0.665) , cob length (-0.341) , flag leaf length (-0.270) and harvest index (-0.249).

4. Plant height:

At phenotypic level, plant height had showed significant positive correlation with dry fodder yield per plant(0.299), leaf area(0.255), number of primary branches per panicle(0.246), and cob width(0.222).

At genotypic level, plant height had showed significant positive correlation with dry fodder yield per plant(0.337), leaf area(0.316), number of primary branches per panicle(0.277), and cob width(0.244). It exhibited negative association with harvest index (-0.219).

5. Leaf area:

At phenotypic level, leaf area had exhibited positive and significant correlation with flag leaf length(0.297), green fodder yield per plant(0.292), dry fodder yield per plant(0.233), and number of primary branches per panicle(0.227).

At genotypic level, leaf area had showed positive and significant correlation with flag leaf length(0.321), green fodder yield per plant(0.316), dry fodder yield per plant(0.239), and number of primary branches per panicle(0.243).

6. Brix:

At phenotypic level, brix had exhibited positive and significant correlation with cob length(0.421), flag leaf length(0.352), and it had positive and significant correlation with no. of grains per primary branch(0.185). Brix exhibited significant and negative association with cob width (-0.290).

At genotypic level, brix had exhibited positive and significant correlation with cob length(0.454), flag leaf length(0.390). Brix exhibited negative association with cob width (-0.327).

7. Flag leaf length:

At phenotypic level, flag leaf length had showed significant positive correlation with cob length(0.251), and dry fodder yield per plant(0.248). Flag leaf length exhibited negative association with harvest index (-0.338) and 100-seed weight (-0.301).

At genotypic level, flag leaf length had exhibited significant positive correlation with cob length(0.270), and dry fodder yield per plant(0.270). Flag leaf length exhibited negative association with harvest index (-0.373) and 100-seed weight (-0.322).

8. Cob length:

At phenotypic level, cob length had showed positive and significant with number of grains per primary branch (0.271), and cob width(0.208).

At genotypic level, cob length had showed positive and significant with number. of grains per primary branch (0.290), and cob width(0.210).

9. Cob width:

At phenotypic level, cob width had showed significant positive with only green fodder yield per plant (0.408). Cob width exhibited negative association with harvest index (-0.249).

At genotypic level, cob width had showed significant positive green fodder yield per plant (0.431) dry fodder yield per plant (0.430) and 100-seed weight(0.210). Cob width exhibited negative association with harvest index (-0.265).

10. Number of primary branches per panicle:

At phenotypic level, number of primary branches per panicle had showed positive and significant with green fodder yield per plant (0.282), and dry fodder yield per plant (0.274). it exhibited negative association with 100-seed weight (-0.436), number of grains per primary branch (-0.279) and harvest index(-0.239).

At genotypic level, number of primary branches per panicle had showed significant positive with green fodder yield per plant (0.287), and dry fodder yield per plant(0.280). it exhibited negative association with 100-seed weight (-0.452), number of grains per primary branch (-0.290) and harvest index(-0.254).

11. Number of grains per primary branch:

At phenotypic level, number of grains per primary branch had showed significant positive with green fodder yield per plant(0.414) , harvest index (0.362) and dry fodder yield per plant(0.296).

At genotypic level, number of grains per primary branch had showed significant positive with green fodder yield per plant (0.428) , harvest index (0.350) and dry fodder yield per plant(0.307).

12. 100-seed weight:

At phenotypic level, 100-seed weight had showed significant positive with only harvest index (0.239).

At genotypic level, 100-seed weight had showed significant positive with only harvest index (0.240).

13. Green fodder yield per plant:

At phenotypic level, green fodder yield per plant had showed significant positive with only dry fodder yield per plant(0.893). it exhibited negative association with harvest index (-0.443).

At genotypic level, green fodder yield per plant had showed significant positive with only dry fodder yield per plant (0.912). it exhibited negative association with harvest index (-0.462)

14. Dry fodder yield per plant:

At phenotypic level, dry fodder yield per plant had showed significant negative association with harvest index (-0.579)

At genotypic level, dry fodder yield per plant had showed significant negative association with harvest index (-0.587)

4.3 Genetic divergence:

The analysis of variance (Table 4.1) revealed highly significant differences among genotypes for all the fifteen characters under investigation. From the estimates of variances and co-variances, Mahalanobis' D^2 - statistic, which utilizes Wilk's criterion, a simultaneous test for all the fifteen characters was done, which also showed highly significant differences among landraces of sorghum. These differences suggest the existence of considerable divergence among the experimental material under study.

4.3.1 D^2 analysis:

1. **Wilk's criterion of D^2**

Significance was tested according to Wilk's criterion at 885 degrees of freedom. V(stat) is distributed as χ^2 with pq degrees of freedom where, p is no. of characters and q is degrees of freedom for genotype [V(stat) = 5792.81, at 885 degrees of freedom and χ^2 = 918.93 at 5% and χ^2 = 948.84

at 1%] which is highly significant . The significance of V(Stat) shows that the difference between the means in respect of the pooled effect of ‘p’ characters between different genotypes are significant . Hence further analysis can be made to estimate D^2 values.

2. Group constellation

Sixty landraces, included in study were grouped into fourteen clusters. The clustering pattern of the landraces has been presented in table

Among the fourteen clusters, cluster I was the largest including 25 landraces followed by cluster II had 17 landraces, cluster II had 5 landraces, cluster XII and XI had 2 landraces,, and rest of clusters III, IV, V, VII, VIII, IX, X, XII, and XIV had 1 landrace each.

1. Contribution of various characters:

The contribution of each character towards genetic divergence is presented in Table 4.5. The contribution of days to 50% flowering was maximum (37.57%) , followed by dry fodder yield per plant (19.89 %), green fodder yield per plant (12.82%) , number of primary branches per panicle(8.47%), days to maturity (8.47%), and minimum for cob length (3.95%), number of grains per primary branch (2.94%), 100-seed weight (2.49%), harvest index (1.47), flag leaf length(1.02%), cob width(0.68) and leaf area(0.23%). The characters plant height, brix at physiological maturity, grain yield per plant had zero contribution towards genetic divergence.

Table 4.4: Clustering pattern of sixty landraces of Sorghum on the basis of genetic divergence

Cluster Number	Constituent landraces	Number of Landraces
I	Gird-1, Gird-5, Gird-3, Gird-21, Gird-23, Gird-30, Gird-33-2, Gird-35, Gird-41, Gird-45, Gird-48 GGUB13,GGUB59,E248,E102,E246,E207,EG31, EGN9,E202,ELG31,1572,MO1567,E68,3788	25
II	Pop-8, Pop-13, Pop-14, Pop-17, Pop-31,Pop-37 Pop-35, Pop-1, Pop-51, Pop-62, KMJ1, Khargoan, Gird31,GGUB20, 6137, SEB12025, Khargoan3	17
III	NCC1	1
IV	Gird-10	1
V	E284	1
VI	Gird-8, Gird-11, Gird-20, EC6, E184	5
VII	1746	1
VIII	Pop-18	1
IX	SOR13	1
X	1863	1
XI	SOR1936, SOR6914	2
II	3774	1
XIII	Pop-27, 1939	2
XIV	ERN36	1

Table 4.5 Contribution towards divergence (%)

Characters	Times ranked	Percent contribution (%)
Days to 50% flowering	665	37.57%
Days to maturity	150	8.47%
Plant height (cm)	0	0.00%
Leaf area (cm^2)	4	0.23%
Brix at (%)	0	0.00%
Flag leaf length (cm)	18	1.02%
Cob length (cm)	70	3.95%
Cob Width (cm)	12	0.68%
Number of primary branches per panicle	150	8.47%
Number of grains per primary branch	52	2.94%
100 seed weight (g)	44	2.49%
Grain yield per plant (g)	0	0%
Green fodder yield per plant (g)	227	12.82%
Dry fodder yield per plant (g)	352	19.89%
Harvest index %	26	1.47%

2. The intra and inter-Cluster average distance:

The average distance within and between clusters and average inter and intra cluster D values have been presented in Table 4.6. In this table, the diagonal values are mean intra cluster and off the diagonal values are inter cluster distances.

The maximum intra clusters was found in cluster VI (15.43), followed by cluster XIII (14.47), cluster II (12.92), cluster XI (12.53) and cluster I (12.10). The cluster III, IV, V, VII, VIII, IX, X, XII, and XIV were being solitary recorded no intra cluster distance.

The highest (D=46.03) inter cluster distance was observed between cluster XIV and XI followed by cluster XI and III (43.29), cluster XI and VIII (43.06), cluster XI and IV (42.28), cluster XIV and XIII (42.06) indicating wide diversity between landraces in these clusters and the lower cluster distance of (D = 11.01) was observed between cluster VII and III followed by cluster V and III (11.02) and cluster IX and VIII (11.49) indicating lower diversity between landraces in these clusters.

3. Cluster mean:

Clusters means of all 15 characters have been presented in Table 4.7.

1. Days to 50% flowering:

The cluster mean was the highest for days to 50% flowering exhibited by cluster XIV (112.00) and lowest by cluster VIII (59.00).

2. Days to maturity:

The cluster mean was the highest for days to maturity in cluster V (140.33) and lowest by cluster VIII (97.00).

3. Plant height (cm):

The cluster mean was the highest for plant height in cluster IV (345.00) and lowest by cluster IX (195.67).

4. Leaf area (cm^2):

The cluster mean was the highest for leaf area observed in cluster XII (473.35) and lowest by cluster VIII (193.26).

5. Brix (%):

The cluster mean was the highest for brix at physiological maturity in cluster XII (16.67) and lowest by cluster III (5.50).

6. Flag leaf length (cm) :

The cluster mean was the highest for flag leaf length in cluster XI (47.17) and lowest by cluster V (28.67).

7. Cob length (cm):

The cluster mean was the highest for cob length in cluster XI (27.33) and lowest by cluster XIV (13.33).

8. Cob width (cm):

The cluster mean was the highest for cob width in cluster XIV (9.33) and lowest by cluster III (2.67).

9. Number of primary branches per panicle:

The cluster mean was the highest for number of primary branches per panicle in cluster XIII (85.33) and lowest by cluster V (38.33).

10. Number of grains per primary branch:

The cluster mean was the highest for number of grains per primary branch in cluster XI (55.33) and lowest by cluster VIII (16.00).

11. 100-seed weight:

The cluster mean was the highest for 100-seed weight in cluster X (3.20) and lowest by cluster VIII (1.63).

12. Grain yield per plant (g):

Cluster mean was the highest for seed yield per plant in cluster XI (65.40) and lowest by cluster VIII (15.77).

13. Green fodder yield per plant (g):

Cluster mean was the highest for green fodder yield per plant in cluster XI (728.33) and lowest by cluster VIII (141.67).

14. Dry fodder yield per plant (g):

Cluster mean was the highest for dry fodder yield per plant in cluster XI (307.00) and lowest by cluster VIII (67.33).

15. Harvest index (%):

Cluster mean was the highest for harvest index in cluster IV (53.21) and lowest by cluster VI (15.36).

6. Cluster characteristics:

The cluster XI was characterized for high value of number of grains per primary branch, grain yield per plant, cob length and flag leaf length.

The cluster XII was characterized for high value of brix and leaf area.

The cluster XIII was characterized for high value of number of primary branches per panicle.

The cluster VIII was characterized for early days to 50 % flowering, early days to maturity and low value of leaf area, grain yield per plant, fresh weight, dry weight, 100-seed weight and number of grains per primary branch.

The cluster V was characterized for delayed days to maturity, low value of flag leaf length and number of primary branches per panicle.

The cluster XIV was characterized for delayed days to 50 % flowering, high value of cob width and low value of cob length.

The cluster III was characterized for low value brix and cob width.

The cluster IV was characterized for tall type plant and high harvest index.

The cluster VI was characterized for low value of harvest index.

The cluster IX was characterized for short type of plant.

The cluster X was characterized for high value of 100-seed weight.

Table 4.6 Cluster means for 15 characters under study in sorghum landraces.

Traits	DTF50%	DTM	PH	LA	BRIX	FLL	CL	CW	NPBPP	NGPPB	SW	GYPP	FW	DW	HI
I	104.35	134.1	301.27	413.09	6.3	36.71	18.79	7.97	70.05	26.69	2.24	40.81	367.9	185.8	22.76
II	77.31	114.7	280.27	415.9	10.37	40.98	21.8	5.27	70.96	27.94	1.87	37.22	280.6	133.3	29.63
III	105.67	131	296.33	344.84	5.5	37.33	15.67	2.67	53.33	20.33	1.93	20.98	162	93.33	22.58
IV	99	131	345	420.65	6.67	31.67	23.33	4.33	60.67	27.33	2.5	41.44	155.3	78	53.21
V	104.67	140.3	331.67	312.28	8	28.67	12.67	4.67	38.33	31.67	2.17	26.29	214	111	23.74
VI	94.4	130.4	329.33	435.17	7.37	37.53	20.13	8.8	76.6	26.73	2.09	42.95	522.9	280.8	15.36
VII	111	135.7	210	375.67	7.17	33	17.67	8.33	44.67	17	2.9	22.05	228.3	88.33	24.96
VIII	59	97	220	193.26	8.67	36.33	20.67	7.33	56.67	16	1.63	15.77	141.7	67.33	23.41
IX	59.67	97.67	195.67	284.78	8.67	34.67	19	4.33	43.33	35	2.53	38.07	155	103.3	36.86
X	75	113	265	430.45	8.67	42.67	27	6.67	40	25.67	3.2	32.84	262	117	28.14
XI	83.67	117.3	232	365.93	8.67	47.17	27.33	7.83	57.5	55.33	2.07	65.4	728.3	307	21.03
XII	72	110	300	473.35	16.67	38.33	25.67	6.67	55.67	42.67	3.17	75.17	386.7	194	38.74
XIII	68.67	130.5	250.5	393.31	9.08	34.5	23.17	5.33	85.33	22.67	1.85	35.53	349.2	147.8	23.64
XIV	112	123.3	290	323.21	6	33	13.33	9.33	69.67	22.33	2.03	33.96	209.3	85.33	39.82

Table 4.7 Average inter and intra (in bold) cluster D2 values between the clusters in sorghum

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	**12.1**													
II	20.4	**12.92**												
III	19.36	21.58	**0**											
IV	21.01	18.92	13.88	**0**										
V	19.02	21.77	11.02	15.35	**0**									
VI	18.9	24.99	31.62	30.45	29.53	**15.43**								
VII	18.43	24.31	11.01	17.4	12.72	30.83	**0**							
VIII	29.73	17.64	24.43	23.39	26.88	35.73	28.25	**0**						
IX	30.1	18.04	25.48	22.62	25.22	35.67	27.92	11.5	**0**					
X	24.65	17.03	23.88	20.59	21.61	30.11	22.84	18.9	12.78	**0**				
XI	30.74	33.33	43.29	42.28	39.92	23.16	41.44	43.1	40.11	33.77	**12.5**			
XII	25.12	19.48	31.39	28.31	28.56	25.36	30.24	26.1	21.27	14.95	24.1	**0**		
XIII	29.01	21.34	34.21	29.25	30.82	27.99	36.16	27.1	27.25	25.57	35.4	25.16	**14.5**	
XIV	21.64	28.14	15.57	21.47	23	33.02	16.36	31.2	34.17	32.85	46	37.48	42.1	**0**

CHAPTER- V

DISCUSSION

The biometrical techniques applied in the analysis of the data in present investigation revealed conclusive findings. The merits of findings are discussed under the following heads in the light of available literatures.

5.1 Genetic variability

5.1.1 Phenotypic and Genotypic co-efficient of variation

5.1.2 Heritability and genetic advance:

5.2 Correlation coefficient

5.3 Genetic Divergence

5.1 Genetic Variability:

A broad spectrum of variability is fundamental for success of a plant breeding programme since it provides an opportunity to the plant breeder to practices the useful selections. Wide range of variability for traits is also necessary to isolate significantly superior varieties for commercial cultivation, to be used as parents in hybridization for combination breeding to develop high yielding hybrid varieties, and to create useful genetic diversity for further selection.

Results of analysis of variance indicated that the mean sums of squares due to landraces were highly significant for all the traits, suggesting presence of sufficient greater variation among the landraces for these traits. Maximum variability was observed for green fodder yield per plant and lowest for 100-seed wieght. These result were in agreement with the finding of Chavan *et al.,* (2010), Swamy *et al.,* (2018) and Subhashini *et al.,* (2019).

The magnitude of variability in decreasing order for different traits were green fodder yield per plant, leaf area, dry fodder yield per plant, plant height, days to 50 % flowering, grain yield per plant, number of primary branches per panicle, days to maturity, harvest index, number of grains per primary branches, flag leaf length, cob length, brix, cob width and 100-seed weight.

5.1.1 Phenotypic and Genotypic co-efficient of variation:

Genetic variability in experimental materials with which the breeder is working is the basis for any successful breeding programme. It is therefore, essential to know the genetic component of variation before variability can be utilized for further genetic improvement in crop plants. Genotypic and phenotypic coefficients of variation are important in this respect.

In present study, higher estimates of phenotypic and genotypic coefficients of variation were observed for harvest index, followed by, green fodder yield per plant, dry fodder yield per plant, Brix, number of grain per primary branch, grain yield per plant, cob width and cob length indicating more variability and scope for selection in improving the characters.

The result were in accordance with the findings of Rao and Patil (1996) and Narvaria (1998) for number of grain per primary branch and grain yield per plant, Chaudhary *et al.,* (2001) and Bello *et al.,* (2007) for cob width and cob length, Chavan *et al.,* (2010) for harvest index, Godbharle *et al.,* (2010) and Jain and Patel (2012) for green fodder yield per plant and dry fodder yield per plant and Zou GuiHua *et al.,* (2011) for brix.

The PCV and GCV were moderate for 100-seed weight, flag leaf length, number of primary branches per panicle, leaf area, days to 50% flowering, and plant height. The PCV and GCV were low for days to maturity.

PCV and GCV estimates showed wide differences in respect of for brix followed by, plant height, leaf area harvest index, cob width and flag leaf length. This might have been due to larger influence of environmental factors

for the expression of these traits. Grain yield per plant, number of grain per primary branch, 100-seed weight, cob length, dry fodder yield per plant, number of primary branches per panicle , green fodder yield per plant, days to maturity and days to 50% flowering showed low differences between PCV and GCV, indicating the greater role of genetic factors influencing the expression of these characters. This indicated the utility of these characters in the selection programme.

5.1.2 Heritability and genetic advance:

Heritability provides the information about the degree of inheritance of a particular character. Broad sense heritability, which is the proportion of genotypic variance to the phenotypic variance and is expressed in percentage. It is an index of transmission of a character from parents to their off-springs. It is a useful estimate since selections have to make on the phenotypic values of the characters, which are the results of breeding values and their interplay with environmental values. Traits with high heritability and high desirable correlation would yield correlated response and thus ease the task of the plant breeder.

Estimates of heritability value was high for all characters *viz.,* days to 50% flowering (99.40%), green fodder yield per plant (98.90%), days to maturity(98.8%), dry fodder yield per plant (97.90%), number of primary branches per panicle (97.70%), cob length (96.10%), number of grain per primary branch (95.20%), 100-seed weight (94.50%), grain yield per plant (94.40%), harvest index(93.80%)cob width(92.90%), Brix (89.10%), flag leaf length (88.80%), leaf area (85.80%), and plant height (81.70%) and these characters may be used to construct selection indices so that the progress made through them would be rewarding. These results were in consonance with the finding of Idris *et al*., (2015) for days to 50% flowering and days to maturity, Chaudhary *et al*., (2017) for green fodder yield, Kukadia *et al.,* (1983) for number of primary branches per panicle, grain yield per plant and plant height, Godbharle *et al.,* (2010) for panicle length,grains per primary branches and harvest index, Ali *et al.*, (2009) for flag leaf length , leaf area

and grain yield per plant. Swamy *et al.,* (2018) for cob width, Deepalakshmi and Ganesamurthy (2007) for 100 grain weight, Jain *et al.,* (2010) for dry fodder yield per plant

The estimates of heritability are influenced by various factors such as sample size, sampling methods, effects of linkage, method of estimation and population density *etc.,* and other biotic and a-biotic factors hence their utility will be restricted. Thus, heritability values coupled with genetic advance as percent of mean would be more reliable and useful in formulating selection criteria. Genetic advance is the product of selection intensity, heritability estimate and phenotypic standard deviation.

Green fodder yield per plant (77.16%), harvest index(76.54%), dry fodder yield per plant (76.03%), Brix (68.88%), number of grain per primary branch (66.45%), grain yield per plant (64.65%), cob width(60.37%), cob length (45.56%), Number of primary branches per panicle (38.01%), 100-seed weight (37.49%), flag leaf length (36.25%), days to 50% flowering (35.22%), leaf area (32.90%), and plant height (24.49%). showed high value of heritability together with high genetic advance as per cent of mean indicating lesser influence for environmental factors on the expression of these character and prevalence of additive gene action in their inheritance, hence, are amenable for simple selection. These results were in accordance with the findings of Singh *et al.,* (2019) for plant height, leaf area and green fodder yield, Swamy *et al.,* (2018) for cob length, cob width and grain yield per plant, Veerabadhiran and Kennedy (2001) for 100-seed weight, Jain *et al.*, (2010) for dry fodder yield per plant and harvest index, Godbharle *et al.*, (2010) for no. of primary branches per panicle, no. of grains per primary branches, Ali *et al.,* (2009) for flag leaf length, Wadikar *et al*., (2018) for brix and Kumar *et al.,(*2011) for days to maturity.

5.2 Correlation coefficient studies:

Correlation coefficient showed the relationship between two attributes and the strength of relationship is measured in terms magnitude of correlation coefficients, whose limits range from minus unity to plus unity.

If an increase in one variable results in the increase of other variable, the relationship is said to be positive and if it results in the decrease of other variable the association is regarded as negative. The two variables are said to be uncorrelated if the increase or decrease of one variable does not affected the other variable

Information about correlations is of great significance to a plant breeder because all the phenotypic traits are the result of interplay of several genetic factors among themselves and their individual and combined interactions with the environmental factors.

Knowledge of correlation helps a plant breeder to determine the methodology to improve a particular trait which is not readily amenable to direct selection and so indirect selection becomes inevitable. It also provides Information about the correlated response to directional selection to predict genetic advance and thus can be used as selection index for operating more efficient selection programe. Correlation could be at phenotypic, genotypic or environmental levels. Phenotypic correlation is between values directly measured on individuals and includes genetic and non-genetic effects. Genotypic correlation is between breeding values and accounts for only genetic causes, which could be due to pleiotropy, linkage or gene frequency disequilibrium. Environmental correlation is the relationship between non-genetic values and arises due to the fact that several observations are affected by the same amount of environment. Therefore, the knowledge of correlations is of great significance.

Grain yield per plant, the most important economic trait, exhibited significant positive association with no. of grains per primary branch (0.809), green fodder yield per plant (0.509), dry fodder yield per plant (0.432), harvest index (0.400), cob length (0.226), leaf area (0.194) and cob width (0.152). both at phenotypic and genotypic level. These results suggested that the characters no. of grains per primary branch, green fodder yield per plant, dry fodder yield per plant, harvest index, cob length, leaf area and cob width. were positively correlated with seed yield. These results indicated that

simultaneous improvement in seed yield through these traits could be achieved within a short period by simple selection procedures and also among themselves indicating their utility in selection programme for improving yield potential of population. These result were in consonance with the finding of Can *et al.,* (1998), Godbharle *et al.,* (2010) and Arunah *et al.,* (2015) for leaf area index and fodder yield, Jayprakash *et al.,* (1997) for panicle length and dry fodder yield, Sunku *et al.,* (2002) for dry matter yield and green fodder yield, Shinde *et al.,* (2011) for panicle width and number of primary branches per panicle, Deepalakshmi and Ganesamurthy (2007) for number of primary branches per panicle.

5.3 Genetic divergence :

The concept of genetic distance is very important while differentiating a well defined population. Several measures of genetic distance have been proposed over the past two decades to suit various objectives (Jacquard, 1974) in which Mahalnobis generalized distance (Mahalanobis,1936) occupied a unique place, several plant breeders used this technique of D for selection of divergent parents and their further exploitation in hybridization programmes. This phenomenon helps breeders in genetic interpretation of the material under investigation. In the present study attempts has been made to utilize this useful technique (D^2statistics) to know the genetic diversity among the promising and newly developed genotypes.

A set of 60 landraces of kharif sorghum landraces was evaluated in three replications. Analysis indicated wide genetic diversity among the landraces studied. Further, these landraces were grouped into fourteen clusters, on the basis of inter cluster distance.

5.3.1 Genetic divergence

Critical choice of diverse parents for creation of wide genetic diversity in the experimental population for improvement in yield and other quality attributes. Genetically divers parents are expected to produce high heterotic effects. Multivariate (D^2 statistic) analysis is useful tool to measure the genetic

variability quantitatively among the set of landraces (Mahalanobis, 1936). Sixty landraces of sorghum under study were therefore assessed for genetic diversity for a set of fifteen characters.

5.3.2 Diversity based on set of fifteen characters

Analysis of variance revealed highly significant differences among the landraces for all the characters under study. The estimates of D values ranged from 11.01 to 46.03 indicating the existence of genetic diversity among the landraces under investigation. Minimum D values was observed between the clusters III and VII (11.01) whereas, maximum distance was observed between landraces the clusters XI and XIV (46.03).

5.3.3 Cluster formation

Cluster formation helps in selection of superior parents. Parents selected from different clusters having large distance will be useful for better exploitation of heterosis in hybridization programme. The theoretical concept behind this grouping is that the landraces grouped into the same cluster presumably are less diverse from each other, than those belonging to different clusters (Rao, 1952). Thus, crossing between the landraces belonging to same cluster, will not give expected desirable heterotic response and desirable segretgants in further generations. Therefore, selection of parents from diverse clusters is perquisite for fruitful effects. Greater inter cluster distance implies greater diversity

The crosses involving extreme divergence have also been reported to exhibit decrease in heterosis (Moll and Stuber, 1974). Therefore, one should be judicious enough in selection and should consider genetic divergence as well as persent performance and inter cluster means for the character subjected to be improved.

Landraces were grouped into fourteen clusters. The cluster I was largest comprising of 25 landraces, followed by, cluster II (17 landraces),

cluster VI (5 landraces), cluster XI and XIII (each of 2 landraces) and cluster III, IV, V, VII, VIII, IX, X, XII and XIV (solitary clusters).

Such high amount of diversity was also observed by Mehendiratta *et al.*, (1971), Mahajan and Wadikar (2012), Jain and Patel (2013), Doijad, *et al.,*(2016), Damor *et al*., (2017), Hari Vara Prasad *et al* (2018) and Yuvaraja *et al*., (2019).

5.3.4 Intra and inter intercluster distance

Average intra and inter cluster statistical distance (Table 4.7) clearly showed that the intra cluster distance ranged from 0.00 (cluster III, IV, V, VII, VIII, IX, X, XII and XIV) to 15.43 (cluster VI). Maximum intra cluster distance was recorded by VI (15.43), followed by cluster (14.47), cluster II (12.92), cluster XI (12.53) and cluster I (12.10). Solitary clusters are III, IV, V, VII, VIII, IX, X, XII, and XIV had zero intra cluster distance. clusters III and VII (11.01)clusters XI and XIV (46.03).

The inter cluster distance ranged from 11.01 (cluster III and cluster VII) to 46.03 (between cluster XI and cluster XIV), followed by, 43.29 (cluster III and XI), 43.06 (cluster VIII and XI), 42.06 (cluster XIII and XIV), 41.44 (cluster VII and XI) and 40.11 (cluster IX and XI), Inter cluster distance suggested that these clusters were more interogenous. Crosses between landraces from these clusters are likely to exhibit more heterosis and more divergent segregation in subsequent generations. Cluster VI is more genetically diverse as intra cluster distance (15.43) was maximum.

Genetic divergence was assessed by Joshi and Vashi (1992) classified Eighty-nine sorghum genotypes into nine clusters using D^2 statistic. Arunkumar and Biradar (2004). applied D^2 statistics to assess the genetic diversity available among 138 genotypes were grouped into 13 clusters. Ganesamurthy *et al*. (2010) evaluated sixty three local land races of sorghum for their genetic diversity based on nine characters.

The 54 genotypes were grouped into 8 clusters. Khadakabhavi *et al*. (2014) assessed genetic divergence in 121 germplasm lines of Rabi sorghum using Mahalanobis D^2 analysis. All the genotypes were grouped into 13 clusters

5.3.5 Contribution of character to divergence

In present study, it was observed that Days to 50% flowering (37.57) followed by dry fodder yield per plant (19.89), green fodder yield per plant (12.82), Number of primary branches/panicle (8.47), days to maturity (8.47), contributed maximum to divergence. Narkhede *et al.,* (2000) studied 13 characters and reported that days to 50 per cent flowering contributed maximum to genetic divergence, Barhate *et al.,* (2000) for fodder yield per plant, Biradar *et al.,* (1996) for Number of primary branches/panicle and Rahman *el al.,* (2004) for days to maturity.

Chapter – VI

SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FURTHER WORK

Summary

The present investigation entitled — **"Evaluation and Identification of *Kharif* Sorghum [*Sorghum bicolor (L.)* Moench] Landraces for Desirable Traits"** was carried out during *kharif* of 2019-2020 at All India Coordinated Research Project on Sorghum, College of Agriculture farm, Indore - (M.P.) 452001. The experimental material consists of sixty landraces of sorghum. These landraces lines were sown in Randomized Complete Block Design with three replications.

The aim of this study was to study the genetic variability, correlation coefficients and genetic divergence for yield and yield attributing traits *viz.,* days to 50% flowering, days to maturity, plant height (cm), leaf area (cm^2), brix (%), flag leaf length (cm), cob Length (cm), cob width (cm), number of primary branches per panicle, number of grains per primary branch, 100-seed weight (g), grain yield per plant (g), green fodder yield per plant (g), dry fodder yield per plant and harvest index %,

A significant amount of variation for most of the characters was examined. Results of analysis of variance revealed that the mean sum of square due to landraces were highly significant for all the characters under study. The result revealed that maximum variation was exhibited in green fodder yield per plant, followed by, leaf area, dry fodder yield per plant, plant height, days to 50 % flowering, grain yield per plant, number of primary branches per panicle, days to maturity, harvest index, number of grains per primary branches, flag leaf length, cob length, brix, cob width and 100-seed weight.

The moderate to high PCV and GCV showed by harvest index followed by green fodder yield per plant, dry fodder yield per plant, Brix, number of

grain per primary branch, grain yield per plant, cob width, cob length, 100-seed weight, flag leaf length, number of primary branches per panicle, leaf area, days to 50% flowering and plant height is indicating the existence of sufficient genetic variability for these characters.

The estimate of heritability in board sense for all characters was high, *viz.,* days to 50% flowering, green fodder yield per plant, days to maturity, dry fodder yield per plant, number of primary branches per panicle, cob length, number of grain per primary branch, 100-seed weight, grain yield per plant, harvest index, cob width, Brix, flag leaf length, leaf area and plant height.

The estimate of the expected genetic advance as percentage of mean was high for all traits except days to maturity. It was observed for days to 50% flowering, green fodder yield per plant, dry fodder yield per plant, number of primary branches per panicle, cob length, number of grain per primary branch, 100-seed weight, grain yield per plant, harvest index, cob width, Brix, flag leaf length, leaf area and plant height.

High heritability together with high genetic advance as percentage of mean were observed for the characters namely, days to 50% flowering, green fodder yield per plant, days to maturity, dry fodder yield per plant, number of primary branches per panicle, cob length, number of grain per primary branch, 100-seed weight, grain yield per plant, harvest index, cob width, brix, flag leaf length, leaf area and plant height It indicates that the heritability is most likely due to additive gene effect and selection would be effective for on *per se* performance.

High heritability together with moderate genetic advance and low PCV and GCV exhibited for days to maturity. Selection for such traits may not be rewarding because the high heritability is being showed due to favorable influence of environment rather than landraces.

The characters, *viz.,* number of grains per primary branch, green fodder yield per plant, dry fodder yield per plant, harvest index, cob length, and 100-seed weight showed significant and positive correlation association with grain yield

per plant both at genotypic and phenotypic level. Thus, a simple selection based on these traits can be used for selecting the high yielding landrace lines in the segregating generation of sorghum.

On the basis of D^2 values, the sixty landraces of sorghum were grouped into fourteen clusters out of which five were polygenotypic and nine was monogenotypic. Similarly, the highest inter Cluster distance was recorded between landraces of Cluster XIV and XI, followed by, Cluster XI and III, Cluster XI and VIII, Cluster XI and IV, Cluster XIV and XIII whereas, least inter cluster distance was observed between Cluster VII and III, followed by, Cluster V and III and Cluster IX and VIII. While, highest intra Cluster value was observed for Cluster VI followed by Cluster XIII, Cluster II, Cluster XI and Cluster I indicating that the hybridization within cluster or between the distant clusters will lead to select the desirable recombinants and broadening genetic base for the future sorghum genotypes following the diallele selective mating system design.

However, the highest contribution towards divergence was exhibited due to days to 50% flowering, flag leaf area, followed by, dry fodder yield, green fodder yield, number of primary branches per panicle and days to maturity. Thus, these characters must be considered for selecting the genotypes for yield and other quality traits in segregating generation of sorghum.

Conclusions

- The results of analysis of variance indicated that the mean sums of squares due to sorghum were highly significant for all the traits under study.

- Least difference between GCV and PCV for the traits days to 50% flowering, days to maturity, green fodder yield per plant, number of primary branches per panicle, dry fodder yield per plant and cob length indicates the lowest environmental influence on these characters..

- Days to 50% flowering, green fodder yield per plant, days to maturity, dry fodder yield per plant, number of primary branches per panicle, cob length, number of grain per primary branch, 100-seed weight, grain yield per plant, harvest index, cob width, brix, flag leaf length, leaf area and plant height have high heritability together with high genetic advance as percentage of mean indication lesser influence of environment on the expression of these characters and prevalence of more additive gene action in their inheritance. therefore, are amenable for simple selection. Hence, there are good chances of improvement of these traits through direct selection in the material

- Based on the results from correlation it is concluded that number of grains per primary branch, green fodder yield per plant, dry fodder yield per plant, harvest index, cob length, and 100-seed weight showed positive correlation with grain yield Therefore, they seem to be primary yield contributing character and thus can be used as direct selection to improve genetic yield potential of sorghum.

- The landraces of cluster cluster XIV and XI showed higher (D=46.03) inter cluster distance followed by cluster XI and III (D=43.29), cluster XI and VIII (D=43.06), cluster XI and IV (D=42.28), cluster XIV and XIII (D=42.06) Hence, landraces of these clusters may be crossed to broaden the genetic base of sorghum. Intra cluster distance has been found the highest of cluster VI (D=15.43) and cluster XIII (D=14.47) hence, the hybridization among the landraces of cluster VI and cluster XIII may also result superior recombinants.

Suggestions for further work

The following suggestions have been made for further study:

- The genetic variability exist in the population can be exploited further.

- The traits showing additive gene action for their expression and can

be improved through simple selection procedure.

- The traits showing strong association with grain and fodder yield can be exploited further for improvement in production and productivity of sorghum via indirect selection.

- The genotypes found divergent on the basis of D^2-statistics analysis can be used as parents in hybridization programme to create and enhance genetic variability and broaden genetic base of population.

- The results of this study suggested further hybridization programme should be planned involving the diverse landraces viz. ERN36,SOR1936, SOR6914, NCC1, PoP-18, Gird-10, 3774, Pop-27, 1939, Gird-8 and Gird-11 present in Cluster XIV and XI, Cluster XI and III, Cluster XI and VIII, Cluster XI and IV, Cluster XIV and III , Cluster VI and Cluster XIII on the basis of their greater inter and intra-cluster distances and higher cluster mean values for the grain yield and others attributing character.

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APPENDIX-1

Table 1.Mean performance for yield and its components of 60 landraces of sorghum

S.N.	Landraces	DTF50%	DTM	PH	LA	BRIX	FLL	CL	CW	NPBPP	NGPPB	SW	GYPP	FW	DW	HI
1	Pop-8	77.33	116.33	285	442.14	9.33	42.66	20.66	5.66	63.33	36.66	1.93	46.07	362.33	131.33	35.11
2	Pop-13	82	119	289	380.76	8.16	40.33	19.66	4	60.33	20.67	2.03	25.34	151.33	68	37.35
3	Pop-14	74.66	112.66	289.33	430.72	13.67	42.67	27	6.66	86	22	1.6	30.22	322.33	151.66	19.9
4	Pop-17	68.66	106.66	255	304.88	10.33	43.33	19	4.33	71.66	16	1.5	18.69	250	131	14.29
5	Pop-18	59	97	220	193.26	8.67	36.33	20.66	7.33	56.66	16	1.63	15.76	141.66	67.33	23.4
6	Pop-27	59	119	261	322.88	10.33	37.33	20	4.33	92.33	16.33	1.7	25.6	321.67	135	18.97
7	Pop-31	73	111	299	434.26	15.33	65	20.66	5.33	88	23.33	1.56	32.09	266.66	186	17.24
8	Pop-35	81.33	117.33	310	397.33	10.33	42	20	4	80	28.33	1.6	36.18	359	167.33	21.21
9	Pop-1	78.33	116.33	285	345.13	11.33	42.67	19.66	4.33	62	41	1.9	48.21	300.33	154	31.31
10	Pop-51	76.67	114.66	278.33	547.35	12.16	48	23.33	4.5	54	29	1.93	30.27	330.33	170	17.8
11	Pop-37	87	123.66	239	505.69	4.67	35.67	16.66	5.33	77.66	24.33	1.5	32.21	345	93.67	34.5
12	Pop-62	71.33	108.66	241.67	356.55	13	40.67	24.33	6.5	67.33	26	2.1	36.76	251.33	121.66	30.19
13	KMJ-1	71.33	109.33	275	410.99	8	36.67	20	5.66	76.67	24.33	1.66	31.06	266.66	120.33	25.77
14	Khargoan	80	118	267.33	386.52	14.66	42.67	30.33	6.33	70	34.66	1.4	34.15	310	142.66	24.04
15	Gird-1	97	129	320	360.75	7.5	33	25	10.33	68.67	16.33	2.85	31.94	403.33	218.33	14.16
16	Gird-5	98.33	130.33	351.66	317.46	6.33	42	23.33	11.33	70.33	32	2.1	47.26	421.67	226	20.97
17	Gird-8	93	132.33	326.66	407	7.33	33.33	13.66	6.66	88	25.66	2.16	51.97	533.33	320	16.24
18	Gird-10	99	131	345	420.64	6.67	31.67	23.33	4.33	60.67	27.33	2.5	41.43	155.33	78	53.2
19	Gird-11	87	124	323.33	309.64	7	31	14.33	8.33	79.67	27	2.33	50.12	614	305.33	16.41
20	Gird-3	104.33	134.33	293.33	465.7	7	43.33	19	6.66	59.67	28.33	2.06	34.88	316	203.66	17.2
21	Gird-20	90	125.33	333.33	551.42	7	45.33	30	11.33	85	22	2.03	38.06	473.67	233	16.36
22	Gird-21	100	130	365	427.83	6.33	42	21.33	8.67	74	20.33	2.1	31.58	364.67	182	17.36
23	Gird-23	104	134	345	469.68	7.66	45.33	20.66	8.66	74.67	19	2.56	36.44	490.67	246	14.89
24	Gird-30	98	130	296.66	384.56	5.33	43	26	8.66	65.33	24.66	2.63	42.41	403.33	280.66	15.11
25	Gird-31	95	127	313.33	433.38	7.16	34	17.33	5.33	60.67	16.66	2.43	26.84	191.33	89.66	30.25
26	Gird-33-2	98	130	330	418.34	7.33	32	18.66	8.33	67.67	20.33	2.5	34.36	340.33	171.66	20.02
27	Gird-35	96.33	128.33	335	370.61	5.67	35.33	17.66	8.33	89.33	21.33	2	38.38	256.67	153.33	25.04
28	Gird-41	104.66	134.66	303.33	448.93	5.33	37	21	10.33	80.33	22	2.53	44.64	350	157.66	28.32
29	Gird-45	106.66	136.66	295	407.49	6	46.33	15	7	82.33	29.66	1.83	44.76	421	198.33	22.56
30	Gird-48	103	133	295	440.3	5.33	42.33	16	7.66	69.67	21.33	2.03	31.87	451	223.66	14.25

S.N.	Landraces	DTF50%	DTM	PH	LA	BRIX	FLL	CL	CW	NPBPP	NGPPB	SW	GYPP	FW	DW	HI
32	GGUB20	73.33	111.33	234.33	337.19	9.16	21.33	26	4.66	64.33	35.33	2.36	53.76	208.67	91.33	58.85
33	GGUB59	105.66	135.66	290	407.74	6.33	40.33	21	9.33	60.67	30	1.96	35.81	263.33	136.33	26.3
34	E248	111.33	141.33	250	443.5	6	39.67	15	6	49.33	42	2.33	48.32	284.33	149	32.45
35	E102	119	149	253.33	414.89	6.33	36.67	19.33	5.66	72	19	2.6	35.52	348	179.66	19.79
36	E246	105	135	281.67	286.01	6.83	23.33	15.33	4.66	71.67	23.33	2.22	37.1	376.33	183.33	20.31
37	E207	105	135	361.66	503.2	6	40.33	19.67	5.33	74	46.33	1.96	70.02	482	219.66	31.91
38	EC6	104.33	134.33	345	518	7.33	45.33	21.33	11	68.67	28.33	1.73	33.72	600	295.66	11.39
39	EG31	103.33	133.33	266.67	431.66	5.83	38.66	10	6.33	85	22.33	2.13	40.45	367	181.66	20.95
40	EGN9	106	136	295	455.84	5.67	41.67	14.33	6.33	52.67	28.33	1.9	28.29	354	181.33	15.6
41	E202	99	134.33	330	483.45	7.33	38.67	15	6.66	71	17	2.1	25.89	354	183.33	14.14
42	ELG31	110.33	133.33	248.33	372.96	6.83	32	21	10	69.6	26	2.03	36.86	446.66	196.33	20.09
43	E184	88.33	136	318.33	389.78	8.16	32.67	21.33	6.67	61.66	30.67	2.16	40.88	393.33	250	16.35
44	NCC1	105.66	131	296.33	344.84	5.5	37.33	15.66	2.66	53.33	20.33	1.93	20.98	162	93.33	22.57
45	E284	104.66	140.33	331.66	312.28	8	28.67	12.67	4.66	38.33	31.67	2.16	26.29	214	111	23.73
46	ERN36	112	123.33	290	323.2	6	33	13.33	9.33	69.67	22.33	2.03	33.96	209.33	85.33	39.81
47	1746	111	135.66	210	375.67	7.16	33	17.66	8.33	44.67	17	2.9	22.05	228.33	88.33	24.96
48	1572	110.66	134.66	250	451.03	7.33	22.67	16.33	8.66	81.67	25	2.16	44.19	387.33	151.66	29.12
49	1939	78.33	142	240	463.73	7.83	31.67	26.33	6.33	78.33	29	2	45.45	376.67	160.66	28.3
50	MO1567	109	130.33	301.33	314.62	6.17	26.67	24	12.33	68.67	32.33	2.4	53.75	280	146	36.83
51	1863	75	113	265	430.44	8.67	42.67	27	6.67	40	25.67	3.2	32.83	262	117	28.13
52	E68	98.66	128.66	330	313.26	5.83	32	12.67	6.66	52	25.33	3	41.8	235.67	136	30.74
53	SOR1936	82.33	116.33	225	385.04	8.66	42.67	24.66	8	53.33	65.67	2.16	76.18	806.67	333.66	22.84
54	3774	72	110	300	473.35	16.66	38.33	25.66	6.66	55.67	42.67	3.16	75.16	386.67	194	38.73
55	6137	70	108	340.66	537.24	11	42.67	19	6.33	83.33	35.67	1.96	60.75	421.67	187	32.5
56	SOR13	59.66	97.66	195.66	284.77	8.66	34.67	19	4.33	43.33	35	2.53	38.07	155	103.33	36.86
57	SEB12025	75.33	113.33	295.33	433.51	8.83	32.33	21	5.33	81.66	25.67	2.06	43.39	280	158.33	27.39
58	3788	104.66	134.66	280.33	466.69	7.83	31	23	7.6	65	46.67	2.33	70.56	442.33	171.33	41.21
59	Khargoan3	79	117	267.33	386.52	9.67	44	26	5.33	59.33	35.33	2.23	46.68	152.33	101.66	46
60	SOR6914	85	118.33	239	346.81	8.66	51.66	30	7.66	61.67	45	1.96	54.61	650	280.33	19.2
	Mean	**91.62**	**125.48**	**289.36**	**404.17**	**8.03**	**38.01**	**20.28**	**6.89**	**68.14**	**27.83**	**2.13**	**39.6**	**344.15**	**169.36**	**25.5**
	Minimum	**59**	**97**	**195.66**	**193.26**	**3.33**	**21.33**	**10**	**2.66**	**38.33**	**16**	**1.4**	**15.76**	**141.66**	**67.33**	**11.39**
	Maximum	**119**	**149**	**365**	**551.42**	**16.66**	**65**	**30.33**	**12.33**	**92.33**	**65.66**	**3.2**	**76.18**	**806.66**	**333.66**	**58.85**
	C.D. (at 5%)	**1.97**	**2.03**	**29.1**	**45.67**	**1.46**	**4.03**	**1.49**	**0.93**	**3.11**	**3.32**	**0.15**	**5**	**21.33**	**14.84**	**4.05**

VITA

The author of this thesis ***Mr. Deepak Nagar*** *S/O* ***Mr. Sobharam Nagar*** *was born on June 26, 1995 at Dhar district of Madhya Pradesh. I completed my* ***High School*** *Certificate Examination from Archana Vidyapeeth High School, Rajod with* ***80.00 %*** *in the year 2011 and* ***higher Secondary School*** *Certificate Examination from Shakti Vidhyapeeth, Rajod, in the year 2013 with* ***82.60%.***

Gradually, I joined College of Horticulture, Mandsaur in the year 2014 and successfully completed my ***B.Sc (Hort.)*** *degree in the year 2018 with an OGPA of* ***7.85*** *out of 10.00 point scales. Subsequently to graduation I joined the Genetics and Plant Breeding Section at College of Agriculture, Indore (M.P.) for master's degree in the year 2018-2019. For partial fulfillment of master's degree I was allotted a topic* ***"Evaluation and Identification of Kharif Sorghum [Sorghum bicolor (L.) Moench] Landraces for Desirable Traits"*** *which has been successfully completed by me and presented in the form of this thesis.*

I have completed my ***M.Sc. (Ag)*** *course with an OGPA of* ***7.24*** *out of 10.00 point of scale.*

Deepak Nagar