Character association and genetic divergence studies in *Sorghum bicolor* (L.) Moench

THESIS

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RAJMATA VIJAYARAJE SCINDIA KRISHI VISHWA VIDYALAYA

In partial fulfillment of the requirements for the Degree of

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In

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(PLANT BREEDING AND GENETICS)

by

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CERTIFICATE – I

This is to certify that the thesis entitled **“Character association and genetic divergence studies in Sorghum bicolor (L) Moench”** submitted in partial fulfillment of the requirement for the Degree of **Master of Science in Agriculture** in the Department of **Plant Breeding and Genetics** of Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior is a record of the bona-side research work carried out by **Mr. LOKENDRA SINGH RAJPUT** I.D. No. awaited under my guidance and supervision. The subject of the thesis has been approved by the Students’ Advisory Committee and the Director of Instruction.

No part of the thesis has been submitted for any other degree or diploma or has been published. All the assistance and help received during the course of this investigation have been acknowledged by the scholar.

Place - Indore

Date - Signature

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MEMBER OF STUDENTS’ ADVISORY COMMITTEE

Chairman - Shri V.P. Kataria __________________

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Member - Dr. S. Holkar __________________

CERTIFICATE – II

This is to certify that the thesis entitled **“Character association and genetic divergence studies in Sorghum bicolor (L) Moench”** submitted by **Mr. LOKENDRA SINGH RAJPUT** I.D. No. Awaited to the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior for the degree of **Master of Science in Agriculture** in the Department of **Plant Breeding and Genetics** has been accepted after evaluation by the External Examiner and approved by the Students’ Advisory Committee after an oral examination of the same.

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LIST OF SYMBOLS AND ABBREVIATIONS

% : per cent
< : less than
> : more than
ANOVA : analysis of variance
C.D. : critical difference
cm : centimeter
C.V. : co-efficient of variation
d.f. : degrees of freedom
et al. : and others
etc. : extra
g : gram
GCV : gennotypic co-efficient of variation
ha : hectare
kgha : kilogram per hectare
lit ha-1 : litre per hectare
m : meter
MSS : mean sum of squares
No. : number
RBD : randomized block design
viz. : namely

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I wish that my research would always be useful and serve good purposes for all humankind.

Place : Indore

Date 11-07-2017 Lokendra Singh Rajput

INTRODUCTION

Sorghum {*Sorghum bicolor* (L) Moench} is one of the most important crops which allow farmers to use one third less water than similar crops such as corn. It is physiologically very efficient plant characterized, by C4 photosynthetic pathway. Sorghum is well known for its drought tolerance. It is also known as “camel crop”. Sorghum has been, for centuries, one of the most important staple foods for millions of poor rural people in the semi-arid tropics of Asia and Africa. For some impoverished regions of the world, sorghum remains a principal source of energy, protein, vitamins and minerals. Sorghum grows in harsh environments and it is usually grown without application of any fertilizers or other inputs by a multitude of small and marginal farmers in many countries.

Grain sorghum is the fifth most important cereal crop grown in the world. In developed countries, and increasingly in developing countries such as India, the predominant use of sorghum is as fodder for poultry and cattle. An international effort is under way to improve sorghum farming. The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) has improved sorghum using traditional genetic improvement and integrated genetic and natural resources management practices. A new variety of sorghum from ICRISAT has now resulted in India producing 7 tonnes per hectare. In India, increases in sorghum productivity resulting from improved cultivars have freed up six million hectares of land, enabling farmers to diversify into high-income cash crops and boost their livelihoods. Sorghum is used primarily as poultry feed, and secondarily as cattle feed and in brewing applications.

In India, sorghum is cultivated in 5.3 million hectares with a production of 5 Million tonnes (Anonymous 2015). The major sorghum growing states are Andhra Pradesh, Gujarat, Karnataka, Madhya Pradesh, Maharashtra, Rajasthan and Tamil Nadu. Though sorghum cultivation is reported from more than 100 countries, only eight countries have over 1 million hectare area under sorghum, which together contribute more than 60 % of world sorghum production. In spite of its economic importance, sorghum cropped area around the world has declined over the last four decades at a rate of over 0.15 million hectare per year. However, in some countries including Brazil, Ethiopia, Sudan, Australia, Mexico, Nigeria, and Burkina Faso it is expanding, mainly because of new land brought under sorghum cultivation or diversion of a portion of area planted to other crops such as maize and wheat. Global sorghum production peaked during the mid-1980s, and thereafter it declined by about 13–15 %, but not steadily. In almost all the sorghum growing regions except Africa yield levels have been enhanced over the years as a result of improved cultivars, higher input use, better resources, and crop management.

Sorghum is important food grain in India since its relative importance for alternate uses such as poultry and cattle feed, livestock forage, starch, sugar, alcohol and other uses will increase. Some varieties of sorghum have been used for thatch, fencing, baskets, brushes, and brooms, and stalks have been used as fuel. Sorghum straw (stem fibres) can also be made into excellent wall board for house building, as well as biodegradable packaging. It is therefore of paramount importance that technological developments are extended to increase the productivity and sustainability of sorghum production. It is well established fact that the progress in improvement of a crop depends on the degree of variability in the desired character in the base material vis-a-vis germplasm collection.

The role of plant genetic resources in the improvement of cultivated plants has been well recognized. High priority has been given to the development of crop specific characterization and evaluation programmes to identify useful accessions and for detecting valuable genes. Assembly of germplasm representing the genetic diversity in a crop species is a pre-requisite for its effective study, conservation and utilization for any improvement programme. Therefore, characterization and evaluation of both exotic and indigenous collections will provide explicit information on useful traits, which can be utilized in the crop improvement programmes. To realize the various benefits of exotic collections, knowledge of their genetic diversity and their performance against local high yielding varieties is a pre-requisite. Therefore, it is necessary to evaluate their performance as well as study the nature and magnitude of variability in various agronomic and yield traits and the degree of inter-relationship among the various traits. This information would be of immense value in formulating suitable breeding programmes. The success of any plant hybridization programme mostly depends upon the selection of suitable genetically diverse parents. Mahalanobis (1936) D^2 statistics based on multivariate analysis of quantitative traits is a powerful tool for measuring divergence in a set of population using the concept of statistical distances utilizing multivariate measurement.

The study of relationships among quantitative traits is important for assessing the feasibility of joint selection of two or more traits and hence for evaluating the effect of selection for secondary traits on genetic gain for the primary trait under consideration. A positive genetic correlation between two desirable traits makes the job of the plant breeder easy for improving both traits simultaneously. Path coefficient analysis was performed to qualify the direct and indirect contributors of yield components and developmental traits of fodder yield.

Increasing the yield of a crop is primary objective of any breeding programme. The yield is a complex quantitative character which cannot be improved by simple selection procedures. As correlation coefficients measure the magnitude and direction of association among characters. Thus the knowledge of inter-relationship between yield and its attributing trait is essential.

Further, the genotypically diverse genotypes are required for creation of wide spectrum of genetic variability. Keeping these points the present investigation was planed with following objectives:

1. To estimate various parameters of genetic variability for traits in sorghum involved in the study.

2. To work out the interrelationship among yield and various yields contributing traits using correlation and path coefficient analysis.

3. To assess the extent of genetic divergence among sorghum genotypes using Mahalanobis D^2 analysis and identification of diverse genotypes for hybridization programme.

CHAPTER II

REVIEW OF LITERATURE

The literature relevant to the present study is reviewed under the following sub-heads

2.1 Genetic variation

2.2 Heritability in broad sense

2.3 Correlation coefficients studies

2.4 Path coefficient analysis

2.5 Genetic divergence

2.1 Genetic variation

Knowledge of the nature and magnitude of genotypic and phenotypic variability present in the crop species plays a vital role in formulating a successful breeding programme to evolve superior cultivars. Hence, the study of existing variability becomes highly essential. Johannsen (1903) gave the basic idea of variability, while developing the concept of pure lines. Vavilov (1951) reported that greater the variability, higher will be the chances of obtaining desirable genotypes which later proved to be the foundation for improvement of crop plants through selection.

Narkhede *et al.* (2000b) evaluated 168 sorghum genotypes for assessing the variability in 22 yield related traits. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits studied. High values of GCV and PCV were obtained for length and breadth of panicle and grain yield per plant. The range of variability was comparatively low for days to 50 per cent flowering and leaf length. Other characters like plant height, number of leaves per plant, leaf breadth and 1000 grain weight were moderately variable.

Chaudhary *et al.* (2001b) evaluated 100 sorghum germplasm lines. The highest PCV and GCV were recorded for ear head width followed by grain yield per plant, days to maturity, plant height and ear length.

Prabhakar (2001) estimated variability parameters in 48 rabi sorghum genotypes and reported higher PCV and GCV values for 1000 grain weight and grain yield per plant and low PCV and GCV values for days to 50 per cent flowering and days to maturity.

Tiwari *et al*. (2001b) estimated variability parameters in 10 sorghum cultivars. High variability was recorded for panicle width, leaf width, panicle length and test weight.

Veerabadhiran and Kennedy (2001b) estimated variability parameters in 75 sorghum genotypes. The results reported that 100 grain weight and grain yield exhibited high GCV and PCV estimates.

Manonmani *et al.* (2002) exhibited variability parameters in red grain sorghum. The result revealed that the magnitude of PCV and GCV were more or less equivalent for all the characters studied. Plant height and grain yield recorded high variability among all the traits studied.

Reddy (2002) studied genetic variability in sorghum genotypes. Lowest GCV and PCV were observed for days to 50% flowering

Prabhakar (2003) studied genetic variability in rabi sorghum. The result revealed that 1000 grain weight and grain yield exhibited high PCV and GCV.

Arunkumar *et al.* (2004) studied genetic variability in 138 genotypes of rabi sorghum. High PCV and GCV were observed for grain yield per plant, plant height, ear head length and number of leaves per plant.

Jhansi Rani (2004) reported that PCV and GCV were moderate for panicle width and low variability for days to 50 per cent flowering and number of leaves per plant.

Mallinath *et al.* (2004) estimated genetic variability parameters in 175 genotypes of sorghum. Grain yield per plant exhibited high PCV and GCV followed by plant height, number of leaves, panicle length and 1000 grain weigh.

Misal *et al.* (2008) reported high estimates of PCV and GCV for grain yield, days to 50% flowering and plant height at 50 % flowering.

Ali *et al*. (2009) observed significant differences among the 10 sorghum genotypes including one check (JS-2002) for flag leaf length, leaf area and grain yield per plant. Genotypic coefficient of variation was high for grain yield suggesting considerable scope for selection of this trait.

Elangovan *et al*. (2009) evaluated 86 sorghum accessions with two checks in augmented design. High estimates of variability were observed for grain yield per plant, 100 seed weight and ear head length.

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

Kumar *et al.* (2011) observed that the phenotypic coefficient of variation was greater than the corresponding genotypic coefficient of variation for all the traits studied. In general, genetic variability was high for fodder yield, panicle length, test weight and seed yield.

Ali *et al*. (2012) observed high heritability and genetic advance for grain yield per plant, 1000 grain weight and days to 50% flowering.

Jain and Patel (2012) reported that high heritability accompanied with high genetic advance as per cent of mean was observed for days to 50% flowering, plant height, number of leaves per plant, leaf length and fodder yield per plant suggested that these characters are under additive gene action and gives better scope for selection. Fodder yield was positively and significantly correlated with number of leaves per plant, leaf length, leaf width and panicle length.

Kalpande *et al*. (2014) reported that the phenotypic co-efficient of variation (PCV) was greater than genotypic co-efficient of variation (GCV) for most of the characters studied indicating influence of the environmental effect on the characters. The GCV values were close to PCV values for the characters like days to 50% flowering, days to physiological maturity and grain yield, indicating very little effect of environment on the genotype, on the phenotypic expression for these traits.

Kumar (2014) evaluated 102 land races of forage sorghum for days to 50 % flowering, plant height, number of leaves per plant, leaf length, leaf breadth and fodder yield per plant in augmented block design during 2010-11 and 2011-12 and revealed highly significant differences among the accessions for these traits.

Khandelwal *et al*. (2015) reported that significant variation were recorded among 224 sorghum genotypes for various morphological and yield traits. The Phenotypic Coefficients of Variation (PCV) were higher than the Genotypic Coefficients of Variation (GCV) for all the traits under investigation.

2.2 Heritability and Genetic advance:

Heritability in broad sense refers to the functioning of the whole genotypes as a unit used in contrast with the environmental effects. The narrow sense heritability includes only the average affects 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 result and affects for selecting the best individuals (Johanson *et al*. 1955).

Arunkumar *et al*. (2004) observed high heritability and genetic advance for ear head length and number of leaves per plant indicating that additive gene affects were operating for these traits and direct selection of these traits for superior genotype was possible.

Mallinath *et al.* (2004) observed high heritability and genetic advance for fodder yield per plant, grain yield per plant and number of leaves per plant.

Sharma *et al*. (2006) observed that maximum heritability was exhibited by panicle length.

Deeplakshmi and Ganeshmurti (2007) observed high heritability accompanied with high genetic advance as per percent of mean for the characters *viz*., days to 50% flowering, plant height, leaves per plant, leaf length, number of primary branches per panicle, 1000 grain weight and single plant yield thus suggesting that these characters are under additive gene action and thus give better scope for selection.

Misal *et al*. (2008) reported high heritability for grain yield days to 50% flowering.

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.

Kusalkar *et al.* (2009) observed high heritability in broad sense and the high heritability accompanied with high genetic advance for 1000 grain weight, grain yield, number of leaves per plant, leaf width, and peduncle length.

Chavan *et al.* (2010) observed high heritability coupled with high genetic advance for plant height and grain yield per panicle.

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 and test weight and fodder yield in both crosses.

Singh *et al.* (2011) reported high heritability coupled with high genetic advance for number of leaves per plant and leaf area.

Ali *et al*. (2012) observed high heritability and genetic advance for grain yield per plant, 1000 grain weight and days to 50% flowering.

Jain and Patel (2012) reported that high heritability accompanied with high genetic advance as percent of mean was observed for days to 50% flowering, plant height, number of leaves per plant, leaf length and fodder yield per plant suggested that these characters are under additive gene action and gives better scope for selection. Fodder yield was positively and significantly correlated with number of leaves per plant, leaf length, leaf width and panicle length.

2.3 Correlation studies

Association between yield and yield components as determined by correlation coefficient is useful for selecting desirable plant types. The efficiency of selection depends on the direction and magnitude of association between yield and its components. Thus correlation coefficient enables to identify characters or combination of characters which might be useful as indicator of high yield by way of evaluating the relative influence of various characters on grain yield and among themselves as well.

Kumaravadivel and Amirthadevarathinam (2000) reported that in F2 and F3 generations, leaf area index, dry matter production and harvest index along with grain yield were important for yield improvement.

Navale *et al*. (2000) reported that, ear girth exhibited highly significant and positive correlation with grain yield. The results suggest that, ear girth plays a major role in determining yield in sorghum.

Chaudhary *et al*. (2001a) studied path coefficient analysis in 23 sorghum genotypes and reported that number of leaves per plant had positive direct effect on seed yield per plant.

Iyanar *et al.* (2001) estimated the direct and indirect effects of the yield contributing characters viz., plant height, days to 50 per cent flowering, number of leaves, panicle length, panicle weight and test weight. Their results showed that the direct contribution of panicle weight was maximum (0.987) followed by panicle length, days to 50 per cent flowering and test weight.

Iyanar *et al*. (2001) reported that, seed yield had positive and significant correlation with panicle length and panicle width.

Prabhakar (2001) reported that, there was a strong correlation of days to 50 percent flowering and days to maturity with grain yield per plant.

Tiwari *et al*. (2001a) studied inter-relationships between yield and yield components in sorghum genotypes. Their study revealed that, there was significant positive correlation between seed yield and stem diameter, panicle length and panicle width. Test weight was significantly and negatively correlated with grain yield.

Veerabadhiran and Kennedy (2001a) estimated the direct and indirect effects on yield. Their results revealed a high direct effect of 100 grain weight on grain yield followed by days to 50 per cent flowering.

Manonmani *et al*. (2002) reported that plant height, number of leaves and leaf length had direct positive effect on grain yield per plant

Reddy (2002) reported that panicle breadth recorded maximum positive direct effect on yield followed by panicle length and 100 grain weight whereas, plant height exhibited low direct effect on yield.

Reddy (2002) reported that grain yield has significant positive correlation with plant height, panicle length, panicle breadth and 100 grain weight whereas, days to 50 per cent flowering recorded significant negative association with grain yield per plant.

Sunku *et al*. (2002) studied path coefficient analysis in grain sorghum genotypes and reported a high degree of direct positive effect of plant height, number of leaves, leaf length and leaf width on seed yield.

Veerabadhiran and Kennedy (2002) observed that, 100 grain weight exhibited significant and positive correlation with grain yield.

Prabhakar (2003) reported that, plant height and 1000 grain weight had positive and significant correlation with grain yield per plant. The results indicated that, these characters should be given due importance for improving the yield potential of the crop.

Arunkumar *et al.* (2004) reported highly significant positive correlation between grain yield per plant and plant height followed by days to 50 per cent flowering, number of leaves per plant, ear head diameter and test weight.

Jhansi Rani (2004) reported significant negative correlation of grain yield with days to 50 per cent flowering.

Mallinath *et al.* (2004) reported that, positive correlation was observed between days to 50 per cent flowering, plant height and number of leaves per plant with grain yield.

Patil *et al*. (2004) observed positive correlation between grain yield and yield components viz., ear mass/plant, grain mass/plant, ear length, ear diameter and 1000 grain mass.

Iyanar *et al*. (2005) studied genetic diversity, correlation coefficient analysis in 109 multicut fodder sorghum types. The results showed that, all the traits were positively correlated with green fodder yield per plant. Among these traits dry fodder yield exhibited high correlation coefficient with green cane yield per plant.

Premalatha *et al*. (2006) estimated correlation coefficient analysis in 49 genotypes of sorghum, the results indicated that, grain yield was significantly positively correlated with number of grains per panicle and 100-grain weight.

Arun *et al*. (2008) studied correlation coefficient analysis in sorghum. The studies indicated that, besides panicle weight, the number of grains per plant had significant positive correlation with grain yield.

Unche *et al*. (2008) studied sixteen genotypes of sweet sorghum, results showed that, green cane yield was positively correlated with total bio mass followed by plant height at physiological maturity.

Khandelwal *et al.* (2015) reported that high magnitude of genotypic and phenotypic coefficient of variations was observed for grain yield per plant, dry and fresh weight per plant and panicle length. The association of high heritability with high genetic advance and GCV was reported in case of fresh weight per plant and leaf area. Grain yield per plant was significantly and positively correlated with harvest index, 1000 seed weight, panicle length, fresh weight per plant and leaf area. Results from both correlation and path coefficient analysis indicated that 1000 seed weight, harvest index, dry weight per plant, panicle length and leaf area should be balanced for selecting high yielding genotypes.

2.4 Path coefficient analysis

Correlation coefficients estimate the degree of association among different characters, but path coefficient analysis is helpful in partitioning the correlation coefficient into direct and indirect effects. Path coefficient is a standard regression coefficient, helps in specifying the actual forces acting in the cause and effect system and indicates their relative importance instead of simply measuring the natural relationship. Path analysis gives additional information on the magnitude of direct and indirect effects of the characters on yield. Hence, the relative contribution of each component character towards yield can be assessed.

Kumaravadivel and Amirthadevarathinam (2000) reported that in F2 and F3 generations, leaf area index, dry matter production and harvest index along with grain yield were important for yield improvement.

Chaudhary *et al*. (2001a) studied path coefficient analysis in 23 sorghum genotypes and reported that number of leaves per plant had positive direct effect on seed yield per plant.

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Veerabadhiran and Kennedy (2001a) estimated the direct and indirect effects on yield. Their results revealed a high direct effect of 100 grain weight on grain yield followed by days to 50 per cent flowering.

Manonmani *et al.* (2002) reported that plant height, number of leaves and leaf length had direct positive effect on grain yield per plant.

Reddy (2002) reported that panicle breadth recorded maximum positive direct effect on yield followed by panicle length and 100 grain weight, whereas, plant height exhibited low direct effect on yield.

Sunku *et al.* (2002) studied path coefficient analysis in grain sorghum genotypes and reported a high degree of direct positive effect of plant height, number of leaves, leaf length and leaf width on seed yield.

Arunkumar *et al*. (2004) reported that panicle breadth had high positive direct effect on yield.

. Premalatha *et al*. (2006) studied genetic diversity analysis of sorghum. Their investigation revealed that, the direct contribution of 100-grain weight was high on grain yield followed by number of grains per panicle leaf area index, plant height and days to 50 per cent flowering.

Sharma *et al.* (2006) reported path analysis for grain yield indicated highest direct effect of days to 50% flowering followed by 100 seed weight.

Khapre *et al*. (2007) studied path analysis in Sorghum and revealed that, the maximum contribution of ear head weight, ear head girth and number of leaves to the grain yield.

Warkad *et al.* (2010) reported that the only character 1000 seed weight showed highly significant association with grain yield per plant at both genotypic and phenotypic level. This indicates that strong association of this trait with grain yield per plant could be fruitfully exploited for enhancing the yield potential in sorghum.

2.5 Genetic diversity

Genetic diversity is the basis for any crop improvement programme. Mahalanobis D^2 statistic is an effective tool for quantifying the degree of divergence at genetic level and provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936).

Multivariate analysis is a useful statistical method for analysis of the various factors and their inter relationships operating within the plant populations under natural and human selection. It has been used to classify biological populations and to identify factors influencing their genetic divergence (Anderson, 1959)

Ayana and Bekele (2000) through genetic diversity studies in 415 sorghum accessions reported that days to 50 per cent flowering, plant height panicle length, panicle width and 1000 seed weight contributed maximum for total variation.

Narkhede *et al*. (2000a) assessed the genetic divergence among 64 germplasm lines and grouped them into 19 clusters. Days to 50 per cent flowering contributed most to divergence, followed by plant height, 1000 grain weight, internodes length and panicle length.

Kadam *et al*. (2001) estimated genetic diversity in 64 genotypes of sorghum. The 64 genotypes were grouped into 13 clusters. The clustering pattern of the genotypes did not necessarily follow their geographic distribution.

Singh *et al*. (2001) investigated the genetic divergence in 46 genotypes of sorghum using multivariate analysis. The genotypes were divided into eight clusters indicating a wide range of genetic diversity among the strains.

Agarwal *et al*. (2002) studied genetic divergence in 41 sorghum genotypes. The genotypes were grouped into five non-overlapping clusters. The D^2 analysis indicated that plant height, number of leaves per plant and stem diameter were important sources of variation.

Asthana *et al*. (2002) studied genetic divergence in 52 exotic sorghum genotypes. The genotypes were grouped into 10 clusters. Grain yield contributed greater towards divergence. The clustering pattern of genotypes did not confirm the geographical origin.

Umakanth *et al*. (2002) estimated genetic diversity in 48 genotypes of sorghum using Mahalanobis D^2 statistics. The genotypes were grouped into five clusters. Plant height contributed maximum towards genetic divergence followed by panicle length and days to flowering.

Veerabadhiran and Kennedy (2002) estimated genetic divergence in 75 genotypes of sorghum. The genotypes were grouped into eight clusters. A critical examination of clustering pattern indicated that the geographical diversity need not necessarily be related to the genetic diversity.

Sridhar *et al*. (2003) estimated the genetic divergence among 88 sorghum germplasm lines. Clustering based on D^2 statistic grouped the genotypes into 23 clusters.

Umakanth *et al*. (2003) assessed the genetic divergence in 41 land race collections of rabi sorghum and grouped them into 14 clusters. They reported that genetic diversity was not necessarily parallel to geographical diversity.

Arunkumar and Biradar (2004) evaluated 138 genotypes of rabi sorghum to assess the genetic diversity using Mahalanobis D^2 statistic. Based on D^2 values, 138 genotypes were grouped into 13 clusters. Among the eight characters studied, plant height found to be the most important contributing character towards divergence followed by days to 50 per cent flowering, grain yield per plant, ear head length and ear head breadth.

Jhansi Rani (2004) observed high genetic divergence among 41 genotypes. They formed into seven clusters. Plant height contributed maximum (17.2%) to genetic divergence followed by grain yield/plant (14.88%).

Nirmala *et al.* (2004) studied genetic diversity in 26 genotypes of sorghum using Mahalanobis D^2 statistics and grouped them into 8 different clusters

Rohman *et al*. (2004) estimated genetic diversity in 35 sorghum genotypes using D^2 statistic. The genotypes were grouped into 4 clusters. The inter cluster distance in most cases was higher than the intra cluster distance, indicating wider genetic diversity between the genotypes of different clusters. Days to maturity and 1000 grain weight exhibited greatest contribution towards genetic diversity among the genotypes.

Khapre *et al.* (2007) estimated genetic diversity in 74 local land races. All genotypes were grouped into 9 clusters and sorghum possesses diverse and desirable gene combinations.

Singh *et al.* (2008) estimated genetic diversity among 32 genotype of forage sorghum. The leaves per plant (45.16) had the greater contribution towards genetic divergence.

Ganesamurthy *et al.* (2010) conducted an experiment on sixty three local land races of sorghum (*Sorghum bicolor* L.) collected from different parts of Tamil Nadu. The genotypes were grouped into 14 clusters indicating high genetic divergence among them. The study indicated no definite relationship between geographic and genetic diversity and suggested that the geographic diversity cannot be used as an index of genetic diversity.

CHAPTER-III

MATERIAL AND METHODS

The present investigation entitled **"Character association and genetic divergence studies in Sorghum bicolour (L) Moench"** was carried out during kharif 2016-17. A detailed account of the material employed and methods followed during the course of investigation is embodied in this chapter.

3.1. Site of the experiment

The experiment was carried out at Research Farm, College of Agriculture, Indore (M.P.). Indore is situated between latitude 22^{o}43' N and longitude 75°58' E and at an altitude of 555.7meters above the mean sea level.

3.2. Climate and weather conditions

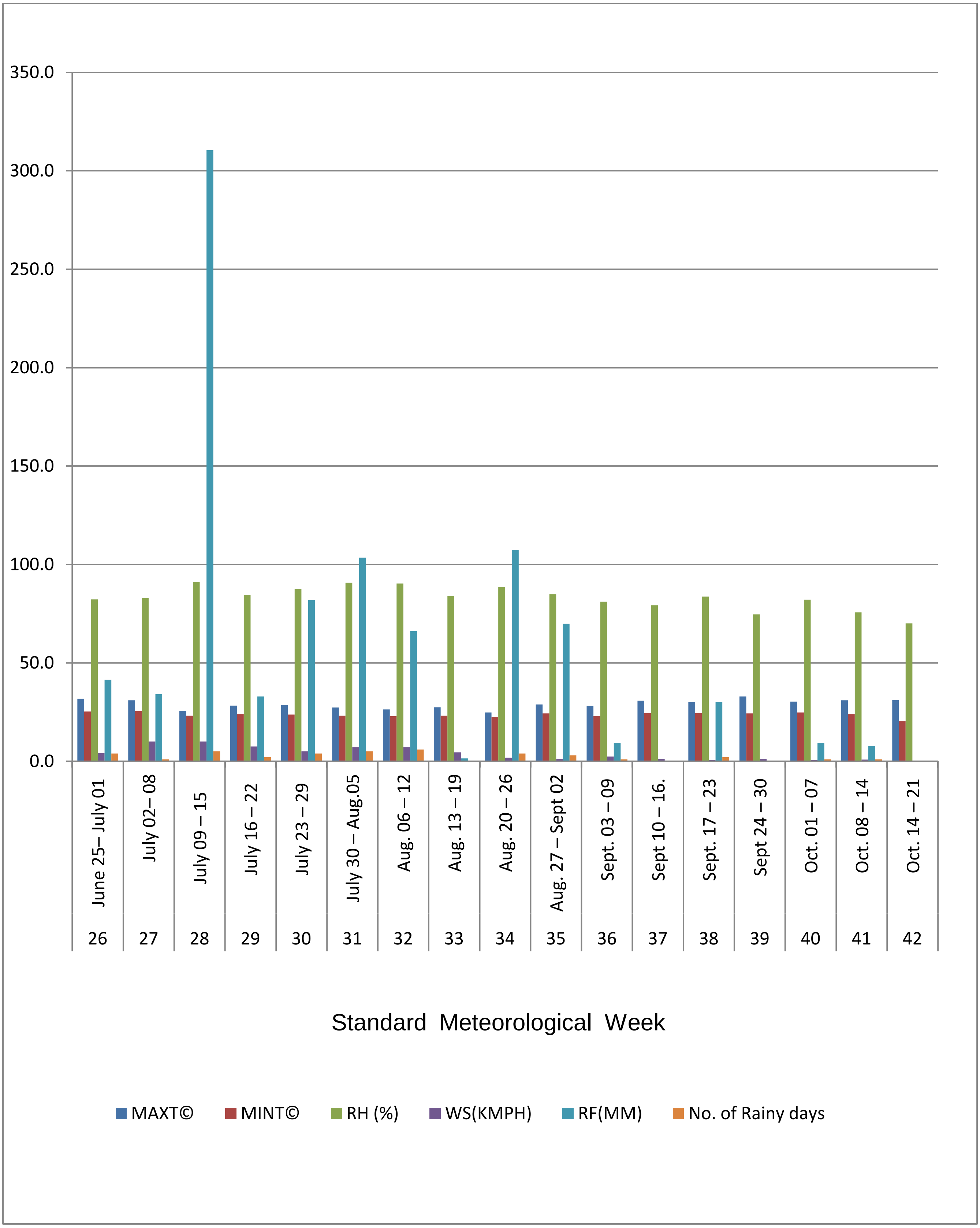
Indore belongs to Malwa plateau in western part of Madhya Pradesh. It has sub-tropical and semi arid climate having a temperature ranged from minimum 5.7ºC to maximum 43.5ºC in winter and summer respectively. In this area most of the rainfall is received during mid June to early October. The weekly maximum and minimum temperatures, rainfall and relative humidity during crop period are presented in Table 3.1. As per the meteorological data, 1011 mm annual rainfall was recorded in the rainy season of 2016.

3.3. Experimental material:

The experimental material used in the present study comprised of thirty genotypes including standard checks. The experiment was laid down in a randomized block design with three replications. The distance between rows was 45 cm and between plants was 12-15 cm. Sowing was done on 025/06/2016. All recommended package of practices were followed during the conduction of experiment to raise a good crop. The details are as under.

Table 3.1: meteorological data observed during crop growth in the year 2016 recorded at Indore.

Weather data Indore.2016-17							
SMW	**DATE**	**MAXT ©**	**MINT©**	**RH (%)**	**WS(KMPH)**	**RF(MM)**	**Rainy days**
26	June 25– July 01	31.7	25.3	82.2	4.2	41.4	4
27	July 02– 08	31.0	25.6	83.0	10.0	34.1	1
28	July 09 – 15	25.6	23.1	91.1	10.0	310.5	5
29	July 16 – 22	28.2	24.0	84.5	7.5	32.9	2
30	July 23 – 29	28.6	23.7	87.4	5.1	82.0	4
31	July 30 – Aug.05	27.4	23.1	90.7	7.2	103.5	5
32	Aug. 06 – 12	26.4	22.9	90.4	7.1	66.2	6
33	Aug. 13 – 19	27.4	23.1	84.1	4.5	1.4	0
34	Aug. 20 – 26	24.9	22.6	88.5	1.8	107.S4	4
35	Aug. 27 – Sept 02	28.9	24.3	84.9	1.1	69.9	3
36	Sept. 03 – 09	28.1	23.0	81.1	2.4	9.2	1
37	Sept 10 – 16.	30.7	24.5	79.2	1.2	0.0	0
38	Sept. 17 – 23	30.0	24.4	83.7	0.6	30.0	2
39	Sept 24 – 30	32.9	24.3	74.6	1.0	0.0	0
40	Oct. 01 – 07	30.3	24.9	82.1	0.6	9.3	1
41	Oct. 08 – 14	31.0	24.0	75.7	0.8	7.8	1
42	Oct. 14 – 21	31.1	20.4	70.1	0.1	0.0	0


350.0
300.0
250.0
200.0
150.0
100.0
50.0
0.0
June 25– July 01
July 02– 08
July 09 – 15
July 16 – 22
July 23 – 29
July 30 – Aug.05
Aug. 06 – 12
Aug. 13 – 19
Aug. 20 – 26
Aug. 27 – Sept 02
Sept. 03 – 09
Sept 10 – 16.
Sept. 17 – 23
Sept 24 – 30
Oct. 01 – 07
Oct. 08 – 14
Oct. 14 – 21
26
27
28
29
30
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32
33
34
35
36
37
38
39
40
41
42
Standard Meteorological Week
MAXT©
MINT©
RH (%)
WS(KMPH)
RF(MM)
No. of Rainy days

Table 3.2: list of genotypes

1	**SPV 1832**	**11**	**CSV 27**	**21**	**IV 16-9**
2	**SPV 2357**	**12**	**IV 16-4**	**22**	**CSV 30**
3	**SPV 2376**	**13**	**IV 16-5**	**23**	**CSV 20**
4	**SPV 2375**	**14**	**CSV 21**	**24**	**IV 16-10**
5	**IV 16-1**	**15**	**CSV 17**	**25**	**IV 16-11**
6	**IV 16-2**	**16**	**IV 16-6**	**26**	**1187**
7	**IV14-7**	**17**	**IV 14-9**	**27**	**1155**
8	**30-4-5-2-11-3**	**18**	**IV 14-8**	**28**	**1088**
9	**CSV-23**	**19**	**IV 16-7**	**29**	**JJ 1041**
10	**IV 16-3**	**20**	**IV 16-8**	**30**	**IV 16-12**

3.4. Observations recorded:

Observations were recorded on plot as well as single plant basis. Observations on plot basis were recorded for 50% flowering, plant height at maturity (cm), total number of leaves, leaf area (cm^2), length of panicle at maturity (cm), number of primary branches per panicle, number of secondary branches per panicle, number of grains per secondary branch, number of grains per panicle, flag leaf length (cm), grain yield per plant (g), fodder yield fresh per plant (g), fodder yield dry per plant (g) and 1000 seed weight (g) was used for statistical analysis. The following observations were recorded on three competitive plants of each hybrid and parent in each replication for all characters.

1. Days to 50% flowering:

Number of days taken from sowing to the flowering of fifty percent of the plant in the plot was recorded.

2. Plant height (cm):

Plant height in cm was measured form the base of the plant to the tip of panicle at maturity.

3. Leaf area (cm^2)

For this observation, five leaves were selected randomly from three tagged plant in each plot and calculate the leaf area.

4. Total number of leaves:

For this observation, leaves were counted from top to bottom of plant.

5. Length of panicle at maturity (cm)

Length of panicle at maturity was measured at maturity.

6. Number of primary branches per panicle:

Primary branches of each selected panicle were plunked and counted.

7. Number of secondary branch per panicle:

Secondary branches emerging out of each primary branch were counted and average was worked out.

8. Number of grains per secondary branch:

Average number of grain borne on three randomly selected primary branches recorded through normal counting.

9. Number of grains per panicle:

Number of grains per panicle was calculated by using the formula:

$$\text{Number of grains per panicle} = \frac{\text{Grain yield per panicle}}{\text{Weight of 1000 grains (g)}} \times 100$$

10. Flag leaf length (cm):

Length of the flag leaf of the plant was measured in cm.

11. 1000 grain weight:

One thousand well developed grains were counted and weighing with the help of digital balance to record this observation.

12. Grain yield per plant (g):

Grains obtained from all panicle of individual plants were weighted and recorded.

13. Fodder fresh weight per plant (g):

Fodder yield (fresh) of each selected plant was recorded after harvesting.

14. Fodder dry weight per plant (g):

Fodder yield (dry) of each selected plant was recorded after harvesting.

3.5. Statistical procedures:

The data collected on the quantitative characters were subjected for statistical analysis and following different statistical parameters were worked out.

3.5.1. Analysis of variance (ANOVA) and covariance:

The data on various characters were subjected to statistical analysis by using appropriate method of analysis of variance and covariance as described by Panse and Sukhatme (1954). The range and estimates of mean, phenotypic, genotypic and environmental variances and co-variances, standard error, coefficient of variation and critical difference were obtained for all the 14 traits. The significant differences between genotypes for the characters under study were tested by F- test.

Analysis of variance was done separately for each character for all treatments. The model of analysis of variance was given below.

Source	D.F	SS	MSS	Cal. F
Replication	r-1	RSS	RSS/(r-1)	RMSS/EMSS
Treatments	t-1	TSS	TSS/(t-1)	TMSS/EMSS
Error	(r-1)(t-1)	ESS	ESS/(r-1)(t-1)	
Total	(rt-1)	TSS		

Where,

t = Number of treatments (genotypes)

r = Number of replications

The standard error was calculated as,

$$SEm = \sqrt{EMSS/r}$$

The significance of treatments mean squares and replication mean squares were tested by comparing with error mean squares referring to ‘F’ table values at 5 and 1 per cent level of probabilities.

3.5.2. Estimation of genetic variability parameters:

3.5.2.1. Genotypic, phenotypic and environmental variance:

The Variance due to genotype, phenotype and environment were computed as follows.

$$\text{Genotypic variance } (\sigma g^2) = \frac{\text{MS due to genotypes – MS due to error}}{\text{r (replication)}}$$

Environmental variance (σe^2) = Error mean sum of squares

Phenotypic variance (σp^2) = $\sigma g^2 + \sigma e^2$ (MS due to error)

Where, ‘r’ is number of replications.

3.5.2.2. Genotypic and phenotypic coefficient of variation:

Genotypic and phenotypic coefficients of variance were estimated according to Burton and Devane (1953) based on estimate of genotypic and phenotypic variance.

Genotypic co-efficient of variation (GCV)

$$\text{GCV (\%)} = \frac{\sigma g}{\bar{X}} \times 100$$

Phenotypic co-efficient of variation (PCV)

$$\text{PCV (\%)} = \frac{\sigma p}{\bar{X}} \times 100$$

Where, $\bar{X}$ = General mean

σ g = Genotypic standard deviation

σ p = Phenotypic standard deviation

GCV and PCV were classified as suggested by Burton and Devane (1953)

0-10% : Low

10-20% : Moderate

20% and above : High

3.5.2.3. Heritability (h^2):

The broad sense heritability (h^2bs) was estimated by following the procedure suggested by Singh and Choudhary(1977) as indicated here below.

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where, h^2 (%) = Heritability (Broad sense)

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

3.5.2.4. Expected genetic advance:

Genetic advance for each character was predicted by the formula given by Robinson *et al*. (1949).

$$GA = h^2 \times \sigma_p \times k$$

Where, k = Selection differential (2.06) at 5 per cent selection intensity

h^2 = Heritability in broad sense

σ_p = Phenotypic standard deviation

3.5.2.5. Genetic advance as per cent of mean (GAM):

Genetic advance as percentage over mean was worked out as suggested by Robinson *et al*. (1949).

$$\text{Genetic advance over mean (GAM)} = \frac{GA}{\overline{X}} \times 100$$

Where, GA = Genetic advance

$\bar{X}$ = General mean

The genetic advance as per cent of mean was categorized as suggested by Robinson *et al*. (1949) and the same is given below.

0-10%	: Low
11-20%	: Moderate
21% and above	: High

3.5.3. Correlation coefficient analysis:

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

$$r_{xy} = \frac{\text{Cov.}_{x,y}}{\sqrt{V_x \times V_y}}$$

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

$\text{Cov}_{x,y}$ = Co-variance of character x and y,

V_x = Variance of character x, and

V_y = Variance of character y.

To test the significance of phenotypic and environmental correlation coefficient, the estimated values were compared with the tabulated values of Fisher and Yates (1938) at n-2 d.f. at two levels of probability, viz., 5% and 1%.

3.5.4. Path coefficient analysis:

The proportion of direct and indirect contributions of various characteristics to the total correlation coefficient with seed yield was estimated through path coefficient analysis as suggested by Wright (1921, 1934) and elaborated by Dewey and Lu (1959).

Path coefficient is a standardized partial regression, which measures the direct influence of one variable upon another and allows partition of correlation coefficient into components of direct and indirect effects.

To estimate various direct and indirect effects, the following set of simultaneous equations were formed and solved.

$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots + r_{1l}P_{ly}$

$r_{2y} = r_{2y}P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots + r_{2l}P_{ly}$

$r_{ly} = r_{l1}P_{1y} + r_{l2}P_{2y} + r_{l3}P_{3y} + \ldots + P_{ly}$

Where,

r_{1y} to r_{ly} = Coefficient of correlation between causal factor 1 to l and dependent character y,

r_{12} to $r_{l-1,l}$ = Coefficient of correlation among causal factors themselves, and

P_{1y} to P_{ly} = Direct effects of characters 1 to l on character y.

Residual effect, which measures the contribution of the characters not considered in the causal scheme, was obtained as:

Residual effect (P_{RY}) = $\sqrt{1 - R^2}$

Where,

$$R^2 = \sum_{iy} P_i^2 Y + 2 \sum_{\substack{i \neq j \\ i > j}} P_{iy}\, P_{jy}\, R_{ij}$$

3.5.5. Multivariate analysis:

3.5.5.1. Estimation of Wilk’s (Λ) criterion:

To test the significance of difference between lines, taking all the characters simultaneously, 'V' statistic was calculated which was based on Wilk’s (Λ) criterion (Wilks, 1932). The sum of squares and sum of products of error and error + variety were utilized for estimation of "Λ".

To calculate the value of "Λ" following relationship was used:

$$\text{"}\Lambda\text{"} = \frac{|E|}{|E+V|}$$

Where,

$|E|$ was the determinant of error sum of squares and sum of products matrix and $|E+V|$ was the determinant of the "error + variety' sum of squares and sum of products matrix.

χ^2 was used to test the significance of "Λ" as

$$\chi^2_{pq} = V = -m \log_e \Lambda$$

Where,

m = n - $\frac{p+q+1}{2}$ with pq degree of freedom.

Where,

n = total number of observations –1,

p = number of characters,

q = k – 1, and

k = number of lines

3.5.5.2. Genetic divergence (D^2 statistic):

Mahalanobis (1928) D^2 statistic was used for assessing the genetic divergence between different populations. The D^2 analysis was carried out using the data recorded on germplasms. Mahalanobis generalized distance (D^2) between any two populations is given by the formula

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

Where, D^2 = Square of generalized distance

λ^{ij} = Reciprocal of the common dispersal index

$\sigma^i = \mu i1 - \mu i2$

$\sigma^j = \mu j1 - \mu j2$

μ = General mean

Since the formula for computation requires inversion of higher order determinants, transformation of the original correlated unstandardised character mean (Xs) to standard uncorrelated variable (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated genotypes (Rao, 1952).

Clustering D^2 values:

All the n (n-1)/2D^2 values were clustered using Toucher's method (Rao, 1952).

Intra and inter-cluster distance:

The intra and inter-cluster distances were calculated by following the formula described by Singh and Choudhary (1977).

$$\text{Square of intra cluster distance} = \frac{\Sigma D_i^2}{N}$$

Where, ΣD_i^2 = Sum of distances between all possible combinations of the entries included in the cluster

N = Number of all possible combinations

$$\text{Square of inter-cluster distance} = \frac{\Sigma D_{ij}^2}{n_i n_j}$$

Where,

ΣD_{ij}^2 = Sum of distances between all possible combinations ($n_i n_j$) of the entries included in the cluster

n_i = Number of entries in the cluster i

n_j =Number of entries in the cluster j

3.5.5.3. Determination of population constellations:

Population constellations were determined by Tocher's method described by Rao (1952). A cluster or constellation may be explained as a group of populations or genotypes such that any two populations belonging to the same cluster showed, on the average, a smaller D^2 value than those belonging to different clusters.

Rao (1952) suggested that two closely related populations of low D^2 value be pooled together and then a third population of similar D^2 value be added to this group such that it did not increase the average D^2 value appreciably. This process is continued. Any population, which sharply increases the average D^2 value, should not be included in that group.

After formation of first cluster, the process is repeated to form second, third, etc., clusters using remaining populations until all populations are included in one or the other cluster. After cluster formation average intra and inter-cluster distances were calculated. The square root of corresponding average D^2 values represents the distance within and between groups.

3.5.5.4. Canonical analysis:

To visualize multidimensional picture of variability among genotypes canonical analysis was done. Canonical roots were estimated by transformation of correlated, unstandardized means into uncorrelated, standardized variables (Rao, 1952). From these uncorrelated standardized variables, matrix of variance and covariance (matrix A) was obtained by computing sums of squares and sums of products. From matrix A, matrix (A) was derived, where p is the number of characters. The column totals of matrix $(A)^P$ were obtained and each total was divided by the highest value among them to obtain the first approximation trial vectors. The canonical variants were determined by iteration. The vectors were then standardized by dividing them with correlated sum of squares of these vectors. The first root, $A_{1,}$ was calculated as the p^{th} root of the highest column total of the approximation.

The second root, $\lambda_{2\ ,}$ was obtained by transforming the original $(A)^p$ matrix to reduced matrix $(B)^p$. Each i × j^{th} element of $(B)^p$ was calculated as:

$(I, j)^{th}$ element of $(A)^p = \lambda_1 \times i^{th}$ element × j^{th} element of the vector.

Estimation of second and third canonical root was done following the same procedure as in the case of ‘A’ was followed. The utility of estimation of other roots depended on the proportions of the sum of squares accounted for by the first three roots.

CHAPTER-IV

RESULTS

The experimental results of the present study are reported in this chapter under the following headings:

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 coefficients of variation

4.1.4. Heritability

4.1.5. Genetic advance

4.2. Study of relationship of seed yield and its contributing traits:

4.2.1. Correlation coefficients estimate

4.2.2. Path analysis

4.3. Study of genetic divergence

4.3.1. D^2 analysis

4.3.2. Canonical analysis

4.1. Study of genetic variability:

4.1.1. Analysis of variance:

Analysis of variance showed highly significant differences among genotypes for all fourteen traits that were days to 50% flowering, plant height at maturity (cm), total number of leaves, leaf area (cm^2), length of panicle at maturity (cm), number of primary branches per panicle, number of secondary branches per panicle, number of grains per secondary branch, number of grains per panicle, flag leaf length (cm), grain yield per plant (g), fodder yield fresh per plant (g), fodder yield dry per plant (g) and 1000 seed weight (g) indicating the presence of considerable variability among genotypes for all traits (Table 4.1).

Table 4.1: ANOVA showing mean sum of squares for different traits in Sorghum

	Source of variation	**Replication**	**Treatment**	**Error**
	d.f	2	29	58
Mean sum of squares	Days to 50% flowering	5.82	15.52**	6.1
	Plant height at maturity (cm)	1428.50	4709.21**	275.5
	Total number of leaves	0.34	9.04**	2.15
	Leaf area (cm^2)	1528.0	8149.38**	1852.9
	Length of panicle at maturity (cm	7.63	24.65**	9.74
	Number of primary branches per panicle	63.24	189.03**	18.6
	Number of secondary branches per panicle	1873.50	26480.15**	11123.36
	Number of grains per secondary branch	3.24	3.07**	1.66
	Number of grains per panicle	142176.00	415034.86**	173674.30
	Flag leaf length (cm)	170.74	243.70**	40.12
	1000 Seed weight (g)	11.67	13.80**	5.19
	Grain yield per plant (g)	112.31	233.94**	95.00
	Fodder yield fresh per plant (g)	408.81	2332.35**	242.02
	Fodder yield dry per plant (g)	12.14	910.68**	54.65

*** *** Significant at 0.01 level of significance

4.1.2. Mean performance and range:

The mean values for fourteen characters and their range for thirty genotypes are presented in Appendix-I and Table 4.2.

4.1.2.1. Days to 50% flowering:

Days required for 50% flowering varied from 65.00 (IV 14-8) to 77.00 (IV 16-2) days around a grand mean of 71.56 days. Sixteen genotypes were below the grand mean. Genotype, IV 14-8 took minimum days to flowering (65.00 days) followed by genotype IV 16-10 (66.67), 3-3-10-10 (69.00) while genotype IV 16-2 took maximum days (77.00) followed by 1155-5-1-1 (75.67 days) and 1187-2-1-2 (75.33 days). Out of 30 genotypes, sixteen genotypes showed earliness for days to 50% flowering which ranged from 65.00 to 71.33 days.

4.1.2.2. Plant height at maturity:

This trait was ranged from 139.00 (CSV 21) to 300.00 (IV 16-8) cm around a grand mean of 245.26 cm. Out of 30 genotypes studied, thirteen genotypes exhibited more height than average which ranged from 139 to 241.67 cm.

4.1.2.3. Total number of leaves:

This trait was ranged from 7.67 (IV 16-12) to 14.33 (CSV 30) leaves around a grand mean of 10.61 leaves. Out of 30 genotypes studied, 14 genotypes exhibited more number of leaves than average which ranged from 10.67 to 14.33 leaves.

4.1.2.4. Leaf area:

Leaf area was ranged from 260.88 (30-4-5-2-1) to 465.28 (IV 16-12) cm^2 with grand mean of 370.69 cm^2. Out of 30 genotypes, 14 genotypes exhibited more leaf area which varied from 3.70 to 465.28 cm^2

4.1.2.5. Length of panicle at maturity:

It ranged from 16.67(IV 116-9) to 28.00 (CSV 23) cm with grand mean of 23.40 cm, in which 11 genotypes showed more length of panicle which varied from 33.43 to 28.00 cm.

4.1.2.6. Number of primary branches per panicle:

It ranged from 33.00 (CSV 20) to 67.67 (IV 14-9) primary branches per panicle with grand mean of 48.72 primary branches per panicle in which 12 genotypes showed more length of panicle plant which varied from 52.00 to 67.67 primary branches per panicle.

4.1.2.7. Number of secondary branches per panicle:

This trait was ranged from 212.33 (IV 14-7) to 598.33 (IV 14-9) with grand mean of 371.88 number of secondary branches per panicle. Out of which, 11 genotypes showed high number of secondary branches per panicle which ranged from 378.00 to 598.33 secondary branches per panicle.

4.1.2.8. Number of grains per secondary branch:

It ranged from 3.67 (IV16-4) to 7.33 (SPV 2357) number of grains per secondary branch around a grand mean of 5.41 number of grains per secondary branch. Out of 30 genotypes studied, 13 genotypes exhibited high value than average which varied from 15.80 to 7.33 number of grains per secondary branch.

4.1.2.9. Number of grains per panicle:

It ranged from 1646.33 (IV14-8) to 2838.00 (JJ1041) grains per panicle with a grand mean of 2211.03 grains per panicle. Out of 30 genotypes studied, 14 genotypes showed high grains per panicle which ranged from 2211.00 to 2838.00 grains per panicle.

4.1.2.10. Flag leaf length (cm)

It ranged from 24 (30-4-5-2) to 60.33 cm (IV16-5) with a grand mean of 41.58 cm. Out of 30 genotypes studied, 18 genotypes showed high length which ranged from 42.33 to 60.33 cm.

4.1.2.11. 1000 Seed weight (g):

It ranged from 22.33 (1088) to 32.00 g. (30-4-5-2-1) around a grand mean of 25.98 g. Out of 30 genotypes studied, 12 genotypes exhibited high value than average which varied from 26.00 to 32.00 g.

4.1.2.12. Grain yield per plant (g):

It ranged from 25.67(IV 16-2) to 62.67 g (IV 14-8) around a grand mean of 40.79 g. Out of 30 genotypes studied, 13 genotypes exhibited high value than average which varied from 41.67 to 62.67 g.

4.1.2.13 Fodder yield fresh per plant (g):

It ranged from 71.67(CSV 17) to 189.33 g (IV 16-1). around a grand mean of140.0 g. Out of 30 genotypes studied, 16 genotypes exhibited high value than average which varied from 141.67 to189.33 g.

4.1.2.14 Fodder yield dry per plant (g):

It ranged from 44.33(CSV 17) to 99.67 g (IV 16-1) around a grand mean of 68.00 g. Out of 30 genotypes studied, 16 genotypes exhibited high value than average which varied from 69 to 99.67 g.

4.1.3. Phenotype and genotype coefficient of variation:

The phenotypic and genotypic coefficients of variation were estimated from the corresponding variances and were used for the assessment of genetic variability among the characters studied. Phenotype coefficient of variation (PCV) and genotype coefficients of variation (GCV) were worked out and are presented in (Table 4.2).

The highest PCV value was observed for grain yield per plant (29.14%) followed by fodder yield dry per plant (27.12%), number of grains per secondary branch (26.97%), number of secondary branches per panicle (26.31%), flag leaf length (24.99%), number of grains per panicle (22.80%), fodder yield fresh per plant (21.88%), total number of leaves (19.87%), number of primary branches per panicle (17.82%), plant height at maturity (17.07%), leaf area (16.96%), length of panicle at maturity (16.39%) and 1000 seed weight (10.93%), while the least PCV was recorded for days to 50% flowering (4.25%).

The GCV values were lower than PCV values for all the characters under study. The highest GCV of 24.84% was recorded for fodder yield dry per plant, followed by number of secondary branches per panicle (24.72%), fodder yield fresh per plant (18.85%), grain yield per plant (16.68%), plant height at maturity (15.67%), number of primary branches per panicle (15.47%), total number of leaves (14.28%), number of grains per panicle (12.83%), number of grains per secondary branch (12.69%), leaf area (12.36%), flag leaf length(9.81%), length of panicle at maturity (9.53%) and

Table 4.2.Parameters of genetic variability for different traits in Sorghum (*Sorghum bicolor* (L.) Moench)

S.No.	Characters	Mean	Range		PCV (%)	GCV (%)	Heritability broad sense (%)	Genetic advance	Genetic advance as % of Mean
			Min	Max					
1	Days to 50% flowering	71.5667	65.00	77.00	4.25	2.47	33.9	2.13	2.98
2	Plant height at maturity (cm)	245.255	139	300	17.07	15.67	84.3	72.71	29.64
3	Total number of leaves	10.611	7.67	14.33	19.87	14.28	51.7	2.24	21.13
4	Leaf area (cm^2)	370.6977	260.88	465.28	16.96	12.36	53.1	68.78	18.56
5	Length of panicle at maturity (cm)	23.400	16.67	28	16.39	9.53	33.8	2.67	11.41
6	Number of primary branches per panicle	48.722	33	67.67	17.82	15.47	75.3	13.48	27.67
7	Number of secondary branches per panicle	371.8778	212.33	598.33	26.31	24.72	88.3	177.93	47.84
8	Number of grains per secondary branch	5.411	3.67	7.33	26.97	12.69	22.1	0.67	12.38
9	Number of grains per panicle	2211.033	1646.33	2838	22.80	12.83	31.7	328.77	14.86
10	Flag leaf length (cm)	41.577	24	60.33	24.99	9.81	62.8	13.47	32.40
11	1000 Seed weight (g)	25.988	22.33	32.00	10.93	6.52	35.6	2.08	8.00
12	Grain yield per plant (g)	40.788	25.67	62.67	29.14	16.68	32.8	8.03	19.72
13	Fodder yield fresh per plant (g)	140.01	71.67	189.33	21.88	18.85	74.2	46.85	33.46
14	Fodder yield dry per plant (g)	68.00	44.33	99.67	27.12	24.84	83.9	31.88	46.88

4.1.4. Heritability:

The estimates of heritability in broad sense were worked out for all the fourteen characters and are presented in (Table 4.2).The estimates of heritability ranged between number of secondary branches per panicle (88.3%) to number of grains per secondary branch (22.10%). High heritability was recorded for number of secondary branches per panicle (88.33%) followed by plant height at maturity (84.30%), fodder yield dry per plant (83.90%), number of primary branches per panicle (75.30%), fodder yield fresh per plant (74.20%), flag leaf length (62.80%), leaf area (53.10%), total number of leaves (51.70%), 1000 seed weight (35.60%), days to 50% flowering (33.90%), length of panicle at maturity (33.80%) and grain yield per plant (32.80%) while it was low for number of grains per panicle (31.70%) and number of grains per secondary branch (22.10%).

4.1.5. Genetic advance:

Genetic advance was estimated for all the characters under study and are presented in (Table 4.2).

Genetic advance as per cent of mean was found highest for number of secondary branches per panicle (47.84) followed by fodder yield dry per plant (46.88), fodder yield fresh per plant (33.46), flag leaf length (32.40), plant height at maturity (29.64), number of primary branches per panicle (27.67), total number of leaves (21.13), grain yield per plant (19.72), leaf area (18.56), number of grains per panicle (14.86), number of grains per secondary branch (12.38), length of panicle at maturity (11.41), while low for 1000 seed weight (8.00) and days to 50% flowering (2.98).

4.2. Study of relationship of seed yield and its contributing traits:

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 presented in Table 4.3 and 4.4 respectively.

Correlation coefficient with seed yield:

1. Seed yield per plant (g):

At phenotypic level, none of the characters had positive and significant correlation coefficient with seed yield per plant.

At genotypic level seed yield per plant showed positive correlation coefficient with fodder yield fresh per plant (0.463), fodder yield dry per plant (0.335) and number of primary branches per panicle (0.315), while days to 50% flowering (-0.632), number of grains per panicle (-0.510) and leaf area (-0.398) showed negative correlation coefficient with seed yield per plant.

Correlation coefficient among yield attributes:

Phenotypic and genotypic correlation coefficient among yield attributes were calculated and presented in Table 4.3 and 4.4 respectively.

2. Days to 50% flowering:

At phenotypic level, none of the characters had positive and significant correlation coefficient with days to 50% flowering.

At genotypic level, days to 50% flowering had negative correlation coefficient with grain yield per plant (-0.632).

3. Plant height (cm):

At phenotypic level, plant height had negative and significant correlation coefficient with fodder yield fresh per plant (-0.291).

At genotypic level, plant height showed positive correlation coefficient with 1000 seed weight (0.395) whereas fodder yield fresh per plant (-0.342) and fodder yield dry per plant (-0.300) showed negative correlation coefficient with plant height.

4. Total number of leaves:

At phenotypic level, total number of leaves had positive and significant correlation coefficient with fodder yield fresh per plant (0.385), and fodder yield dry per plant (0.291).

At genotypic level, total number of leaves had positive correlation with the fodder yield fresh per plant (0.491) and fodder yield dry per plant (0.466) whereas thousand seed weight (-0.445) and number of secondary branches per panicle (-0.294) showed negative correlation coefficient with total number of leaves.

5. Leaf area (cm^2):

At phenotypic level, leaf area exhibited negative and significant correlation coefficient with fodder yield dry per plant (-0.293).

At genotypic level, leaf area had positive correlation with number of secondary branch per panicle (0.307) whereas fodder yield dry per plant (-0.529), grain yield per plant (-0.398), fodder yield fresh per plant (-0.391) and 1000 seed weight (-0.355) showed negative correlation coefficient with leaf area.

6. Length of panicle at maturity (cm):

At phenotypic level, length of panicle at maturity had positive and significant correlation with flag leaf length (0.325).

At genotypic level, length of panicle at maturity had positive and significant correlation coefficient with flag leaf length (0.588), number of primary branches per panicle (0.383) and number of grains per secondary branches (0.343), whereas 1000 seed weight (-0.532) and number of grains per panicle (-0.320) showed negative correlation coefficient length of panicle at maturity .

7. Number of primary branches per plant:

At phenotypic level, number of primary branches per plant had positive and significant correlation coefficient with fodder yield dry per plant (0.305) and number of secondary branches per panicle (0.292).

At genotypic level, number of primary branches per plant showed positive correlation coefficient with fodder yield dry per plant (0.403), length of panicle at maturity (0.383), fodder yield fresh per plant (0.354), grain yield per plant (0.315) and number of secondary branches per panicle (0.298), whereas number of grains per panicle (-0.414) showed negative correlation coefficient with number of primary branches per panicle.

8. Number of secondary branches per panicle:

At phenotypic level, number of secondary branches per panicle exhibited positive and significant correlation coefficient with number of primary branches per panicle (0.292).

At genotypic level, number of secondary branches per panicle exhibited positive and significant correlation coefficient with leaf area (0.307), number of primary branches per panicle (0.298) and number of grains per secondary branches (0.283) whereas number of grains per panicle (-0.341), total number of leaves (-0.294) and 1000 seed weight (-0.294) showed negative correlation coefficient with number of secondary branches per panicle.

9. Number of grains per secondary branch:

At phenotypic level, none of the characters showed positive and significant correlation coefficient with number of grains per secondary branch.

At genotypic level, number of grains per secondary branch exhibited positive and significant correlation coefficient with length of panicle at maturity (0.343), flag leaf length (0.340) and number of secondary branches per panicle (0.283) whereas 1000 seed weight (-0.766) and days to 50% flowering (-0.275) showed negative correlation coefficient with number of grains per secondary branch.

10. Number of grains per panicle:

At phenotypic level, number of grains per panicle exhibited negative and significant correlation coefficient with fodder yield dry per plant (-0.298).

At genotypic level, number of grains per panicle showed positive correlation coefficient with flag leaf length (0.357) while fodder yield dry per plant (-0.584), grain yield per plant (-0.510), number of primary branches per panicle (-0.414), fodder yield fresh per plant (-0.354) and number of secondary branches per panicle (-0.341) showed negative correlation coefficient with number of grains per panicle.

11. Flag leaf length:

At phenotypic level, flag leaf length had positive and significant correlation coefficient with length of panicle at maturity (0.325).

At genotypic level, flag leaf length showed positive correlation coefficient with length of panicle at maturity (0.588), number of grains per panicle (0.357) and number of grains per secondary branch (0.340) whereas with 1000 seed weight (-0.321) and plant height at maturity (-0.265) showed negative correlation coefficient with flag leaf length.

12. 1000 seed weight:

At phenotypic level, none of characters showed positive and significant correlation coefficient with1000 seed weight.

At genotypic level, 1000 seed weight showed positive and significant correlation coefficient with plant height at maturity (0.395).

13. Fodder yield fresh per plant:

At phenotypic level, fodder yield fresh per plant had positive and significant correlation coefficient with fodder yield dry per plant (0.667) and total number of leaves (0.385) whereas it had negative and significant correlation coefficient with plant height at maturity (-0.291).

At genotypic level fodder yield fresh per plant had positive correlation coefficient with fodder yield dry per plant (0.789), total number of leaves (0.491) and number of primary branches per panicle (0.354) whereas leaf area (-0.391), number of grains per panicle (-0.354) and plant height at maturity (-0.342) showed negative correlation coefficient with fodder yield fresh per plant.

14. Fodder yield dry per plant:

At phenotypic level, fodder yield dry per plant had positive and significant correlation coefficient with length of fodder yield fresh (0.667), number of primary branches per panicle (0.305), and total number of leaves (0.291), whereas it had negative and significant correlation coefficient with number of grains per panicle (-0.298) and leaf area (-0.293).

At genotypic level, fodder yield dry per plant had positive correlation coefficient with fodder yield fresh per plant (0.789), total number of leaves (0.466), number of primary branches per panicle (0.403) and grain yield per plant (0.335) whereas it showed negative correlation coefficient with number of grains per panicle (-0.584), leaf area (-0.529) and plant height at maturity (-0.300) .

Table 4.3: Estimates of Phenotypic correlation coefficients for yield and its contributing traits in Sorghum

Characters	Plant Height at maturity (cm)	Total no. of leaves	Leaf area (cm^2)	Length of panicle at maturity (cm)	No. of primary branches per panicle	Number of secondary branches per panicle	No. of grains per secondary branch	No. of grains per panicle	Flag leaf length (cm)	1000 Seed weight (g)	Fodder yield fresh per plant (g)	Fodder yield Dry per plant (g)	Grain yield per plant (g)
Days to 50% flowering	**-0.054**	-0.001	-0.091	0.00	0.043	0.009	-0.173	0.047	-0.034	0.214	0.021	-0.041	-0.101
Plant height at maturity (cm)		**-0.127**	0.053	-0.139	0.064	0.042	-0.035	0.037	-0.151	0.239	-0.291*	-0.245	0.119
Total no. of leaves			**-0.102**	0.012	-0.075	-0.202	-0.084	0.094	0.063	-0.196	0.385*	0.291	0.013
Leaf area (cm^2)				**0.038**	-0.038	0.196	0.086	0.148	0.063	-0.044	-0.257	-0.293*	-0.174
Length of panicle at maturity (cm)					**0.233**	0.180	0.056	-0.051	0.325*	-0.090	0.035	-0.013	0.060
Number of primary branches per panicle						**0.292***	0.023	-0.150	0.089	0.042	0.175	0.305*	0.196
Number of secondary branches per panicle							**0.140**	-0.202	0.064	-0.147	0.013	0.081	0.162
Number of grains per secondary branch								**0.020**	0.143	-0.246	0.007	-0.007	0.082
Number of grains per panicle									**0.133**	0.094	-0.250	-0.298*	-0.161
Flag leaf length (cm)										**-0.080**	0.097	-0.056	-0.100
1000 seed weight (g)											**0.020**	-0.105	0.156
Fodder yield fresh per plant (g)												**0.667****	0.216
Fodder yield dry per plant (g)													**0.175**

Table 4.4: Estimates of Genotypic correlation coefficients for yield and its contributing traits in Sorghum

Characters	Plant height at maturity (cm)	Total number of leaves	Leaf area (cm^2)	Length of panicle at maturity (cm)	Number of primary branches per panicle	Number of secondary branches per panicle	Number of grains per second. branch	Number of grains per panicle	Flag leaf length (cm)	1000 Seed weight (g)	Fodder yield fresh per plant (g)	Fodder yield dry per plant (g)	Grain yield per plant (g)
Days to 50% flowering	**0.005**	-0.143	-0.050	0.107	0.128	-0.014	-0.274	0.137	0.136	0.273	-0.048	-0.059	-0.632
Plant height at maturity (cm)		**-0.114**	0.001	-0.205	0.050	0.076	-0.225	0.065	-0.265	0.395	-0.342	-0.300	0.275
Total no. of leaves			**-0.223**	-0.152	-0.078	-0.294	0.081	-0.006	0.160	-0.445	0.491	0.466	-0.078
Leaf area (cm^2)				**0.025**	-0.099	0.307	0.069	0.249	0.127	-0.355	-0.391	-0.529	-0.398
Length of panicle at maturity (cm)					**0.383**	0.265	0.343	-0.320	0.588	-0.532	0.111	0.018	0.122
Number of primary branches per panicle						**0.298**	-0.069	-0.414	0.175	-0.037	0.354	0.403	0.315
Number of secondary branches per panicle							**0.283**	-0.341	0.081	-0.294	-0.016	0.099	0.235
Number of grains per secondary branch								-**0.136**	0.340	-0.766	0.155	-0.135	0.079
Number of grains per panicle									**0.357**	0.251	-0.354	-0.584	-0.510
Flag leaf length (cm)										**-0.321**	0.061	-0.066	-0.098
1000 seed weight (g)											**-0.132**	-0.226	0.025
Fodder yield fresh per plant (g)												**0.789**	0.463
Fodder yield dry per plant (g)													**0.335**

4.2.2. Path analysis:

The phenotypic as well as genotypic correlation coefficient between seed yield and its components were further partitioned into direct and indirect effects. Phenotypic and genotypic path has been presented in Table 4.5 and Table 4.6 and is described as follows

` (a) Direct effects:

Phenotypic path analysis (Table 4.5) showed that 1000 seed weight registered the maximum positive direct effects of 0.216, followed by, number of secondary branches per panicle (0.180), fodder yield fresh per plant (0.165), number of grains per secondary branch (0.121), length of panicle at maturity (0.079), number of primary branches per panicle (0.075), total number of leaves (0.058) and plant height at maturity (0.014) whereas flag leaf length recorded the highest negative direct effect of -0.316, followed by leaf area (-0.170) and days to 50% flowering (-0.148) on grain yield per plant. The rest of characters *viz*. number of grains per panicle and fodder yield dry per plant had negligible negative direct effects on grain yield per plant.

Study of genotypic path analysis (Table 4.6) revealed that 1000 seed weight registered the maximum positive direct effects of 0.743, followed by length of panicle at maturity (0.739), number of secondary branches per panicle (0.341), fodder yield fresh per plant (0.252), plant height at maturity (0.236), number of grains per secondary branch (0.229), fodder yield dry per plant (0.164) and total number of leaves (0.144) while days to 50% flowering recorded the highest negative direct effect of -0.799, followed by flag leaf length (-0.276) and leaf area (-0.263) on grain yield per plant. The remaining characters *viz*., number of primary branches per panicle (-0.007) and number of grains per panicle (-0.127) recorded negligible negative direct effects on grain yield per plant.

(b) Indirect effect:

(1) Days to 50% flowering:

At phenotypic level, positive indirect effect was exerted through number of leaf area (0.051) and 1000 seed weight (0.046) on grain yield per plant, whereas number of grains per secondary branches per panicle (-0.021) and plant height at maturity (-0.006) exhibited negative indirect effect on grain yield per plant.

At genotypic level, days to 50% flowering recorded the positive indirect effect through 1000 seed weight (0.203), and length of panicle at maturity (0.079) on grain yield per plant, whereas number of grains per secondary branch (-0.063) and total number of leaves (-0.021) exhibited negative indirect effect on grain yield per plant.

(2) Total number of leaves:

At phenotypic level, positive indirect effect was recorded through leaf area (0.073) and fodder yield fresh per plant (0.064) on grain yield per plant, whereas negative indirect effect through 1000 seed weight (-0.042) and number of secondary branches per panicle (-0.036) on grain yield per plant.

At genotypic level, days of maturity recorded the positive indirect effect through fodder yield fresh per plant (0.124) and days to 50% flowering (0.114) on grain yield per plant, while negative indirect effect exerted through 1000 seed weight (-0.331) and length of panicle at maturity (-0.112) on grain yield per plant.

(3) Leaf area:

At phenotypic level, positive indirect effect was recorded through number of secondary branches per panicle (0.035) and days to 50% flowering (0.013) on grain yield per plant, whereas negative indirect effect through fodder yield fresh per plant (-0.043) and flag leaf length (-0.009) on grain yield per plant.

At genotypic level, positive indirect effect was recorded through length of panicle at maturity (0.187) and number of secondary branches per panicle (0.105) on grain yield per plant, whereas negative indirect effect through 1000 seed weight (-0.264) and leaf area (-0.263) on grain yield per plant.

(4) Plant height at maturity (cm):

At phenotypic level, this trait was recorded the positive indirect effect for flag leaf length (0.021) and number of secondary branches per panicle (0.008) on grain yield per plant, whereas the negative indirect effect exerted through fodder yield fresh per plant (-0.048), and length of panicle at maturity (-0.011) on grain yield per plant.

At genotypic level, positive indirect effect was exerted through 1000 seed weight (0.293) and flag leaf length (0.071) on grain yield per plant, whereas negative indirect effect through length of panicle at maturity (-0.152) and fodder yield fresh per plant (-0.086) on grain yield per plant.

(5) Length of panicle at maturity:

At phenotypic level, positive indirect effect was exerted through number of secondary branches per panicle (0.032) and number of primary branches per panicle (0.018) on grain yield per plant whereas flag leaf length (-0.044) and 1000 seed weight (-0.019) negative indirect effect on grain yield per plant.

.At genotypic level, lower branch height recorded the positive indirect effect through number of secondary branch per panicle (0.090) and number of grains per secondary branch (0.078)) on grain yield per plant, while negative indirect effect through 1000 seed weight (-0.395) and flag leaf length (-0.157) on grain yield per plant.

(6) Number of primary branches per panicle:

At phenotypic level, positive indirect effect was exerted through number of secondary branches per panicle (0.052) and fodder yield fresh (0.045) per plant, whereas the negative indirect effect exerted through flag leaf length

(-0.012), fodder yield dry per plant (-0.006), and 50% flowering (-0.006) on grain yield per plant.

.At genotypic level, this trait was recorded the positive indirect effect for length of panicle at maturity (0.283) and number of secondary branch per panicle (0.102) on grain yield per plant, whereas the negative indirect effect exerted through days to 50% flowering (-0.102), and number of grains per panicle (-0.052) on grain yield per plant.

(7). Number of secondary branches per panicle:

At phenotypic level, this trait was recorded the positive indirect effect for number of primary branches per panicle (0.022) and number of grains per secondary branch (0.017) on grain yield per plant whereas the negative indirect effect exerted through leaf area (-0.033), and 1000 seed weight (-0.032) on grain yield per plant.

At genotypic level, this trait was recorded the positive indirect effect for length of panicle at maturity (0.196) and number of grains per secondary branch (0.065) on grain yield per plant, while negative indirect effect through 1000 seed weight (-0.218) and leaf area (-0.081) on grain yield per plant.

(8) Number of grains per secondary branch:

At phenotypic level, this trait was recorded the positive indirect effect through days to 50% flowering (0.026) and number of secondary branches per panicle (0.025) on grain yield per plant, whereas the negative indirect effect exerted through flag leaf length (-0.091) and 1000 seed weight (-0.053) on grain yield per plant.

At genotypic level, number of grains per secondary branch recorded the substantial positive indirect effect through length of panicle at maturity (0.254) and days to 50% flowering (0.219) on grain yield per plant, whereas negative indirect effect through 1000 seed weight (-0.569) and flag leaf length (-0.091) on grain yield per plant.

(9) Number of grains per panicle:

At phenotypic level, positive indirect effect was exerted through 1000 seed weight (0.020) and fodder yield dry per plant (0.006) on grain yield per plant, whereas fodder yield fresh per plant (-0.041) and number of secondary branches per panicle (-0.036) exhibited negative indirect effect on grain yield per plant.

At genotypic level, number of grains per panicle was recorded the positive indirect effect through 1000 seed weight (0.186) and plant height at maturity (0.015) on grain yield per plant, whereas negative indirect effect through length of panicle at maturity (-0.237) and number of secondary branches per panicle (-0.117) on grain yield per plant.

(10) Flag leaf length:

At phenotypic level, this trait was recorded the positive indirect effect for length of panicle at maturity (0.026) and number of grains per secondary branch (0.017) on grain yield per plant, whereas the negative indirect effect exerted through 1000 seed weight (-0.017) and plant height at maturity (-0.016) on grain yield per plant .

At genotypic level, the positive indirect effect through length of panicle at maturity (0.435) and number of grains per secondary branch (0.078) on grain yield per plant, while negative indirect effect through 1000 seed weight (-0.238) and days to 50% flowering (-0.109) on grain yield per plant.

(11) 1000 seed weight:

At phenotypic level, the positive indirect effect through plant height through maturity (0.025) on grain yield per plant, while negative indirect effect through days to 50% flowering (-0.032) and number of secondary branches per panicle (-0.026) on grain yield per plant.

At genotypic level, the positive indirect effect plant height through maturity (0.093), leaf area (0.093) and flag leaf length (0.086) on grain yield per plant, whereas negative indirect effect through length of panicle at maturity (-0.393) and days to 50% flowering (-0.219) on grain yield per plant.

(12) Fodder yield fresh per plant:

At phenotypic level, this trait was recorded the positive indirect effect for leaf area (0.044) and total number of leaves (0.022) on grain yield per plant, whereas the negative indirect effect exerted through plant height at maturity (-0.030) and fodder yield dry per plant (-0.014) on grain yield per plant.

At genotypic level, substantial positive indirect effect through leaf area (0.103) and length of panicle at maturity (0.082) on seed yield per plant, while 1000 seed weight (-0.098) and plant height at maturity (-0.081) exhibited negative direct effect on grain yield per plant.

(13) Fodder yield dry per plant:

At phenotypic level, this trait was recorded the positive indirect effect for fodder yield fresh per plant (0.110) and leaf area (0.050) on grain yield per plant, whereas the negative indirect effect exerted through plant height at maturity (-0.025) and 1000 seed weight (-0.023) on grain yield per plant.

At genotypic level, substantial positive indirect effect through fodder yield fresh per plant (0.199) and leaf area (0.139) on grain yield per plant, while 1000 seed weight (-0.168) and number of grains per panicle (-0.074) exhibited negative direct effect on grain yield per plant.

Table 4.5: Phenotypic path analysis of various characters for yield and its contributing traits in sorghum

Characters	Days to 50% flowering	Plant height at maturity (cm)	Total number of leaves	Leaf area (cm^2)	Length of panicle at maturity (cm)	No. of primary branches per panicle	Number of secondary branches per panicle	No.of grains per secondary branch	No. of grains per panicle	Flag leaf length (cm)	1000 Seed weight (g)	Fodder yield fresh per plant (g)	Fodder yield dry per plant (g)	Phenotypic correlation with grain yield per plant (g)
Days to 50% flowering	**-0.148**	-0.006	0.000	0.051	0.000	0.003	0.002	-0.021	-0.003	0.005	0.046	0.004	0.001	-0.101
Plant height at maturity (cm)	0.008	**0.014**	-0.007	-0.009	-0.011	0.005	0.008	-0.004	-0.002	0.021	0.051	-0.048	0.005	0.119
Total number of leaves	0.000	-0.013	**0.058**	0.073	0.001	-0.006	-0.036	-0.010	-0.005	-0.008	-0.042	0.064	-0.006	0.013
Leaf area (cm^2)	0.013	0.005	-0.006	**-0.170**	0.0003	-0.003	0.035	0.010	-0.008	-0.009	-0.009	-0.043	0.006	-0.174
Length of panicle at maturity (cm	0.000	-0.014	0.001	-0.007	**0.079**	0.018	0.032	0.007	0.003	-0.044	-0.019	0.006	0.000	0.060
Number of primary branches per panicle	-0.006	0.007	-0.004	0.006	0.018	**0.075**	0.052	0.003	0.008	-0.012	0.009	0.045	-0.006	0.196
Number of secondary branches per panicle	-0.001	0.004	-0.012	-0.033	0.014	0.022	**0.180**	0.017	0.011	-0.009	-0.032	0.002	-0.002	0.162
Number of grains per secondary branch	0.026	-0.004	-0.005	-0.015	0.004	-0.002	0.025	**0.121**	-0.001	-0.091	-0.053	0.001	0.000	0.082
Number of grains per panicle	-0.007	0.004	0.006	-0.025	-0.004	-0.011	-0.036	0.002	**-0.056**	-0.018	0.020	-0.041	0.006	-0.161
Flag leaf length (cm)	0.005	-0.016	0.004	-0.011	0.026	0.007	0.012	0.017	-0.007	**-0.316**	-0.017	0.016	0.001	-0.100
1000 Seed weight	-0.032	0.025	-0.011	0.007	-0.007	0.003	-0.026	-0.030	-0.005	0.011	**0.216**	0.003	0.002	0.156
Fodder yield fresh per plant (g)	-0.003	-0.030	0.022	0.044	0.003	0.021	0.002	0.001	0.014	-0.013	0.004	**0.165**	-0.014	0.216
Fodder yield dry per plant (g)	0.006	-0.025	0.017	0.050	-0.001	0.023	0.015	-0.001	0.017	0.008	-0.023	0.110	**-0.021**	0.175

Residual value = 0.7957

Table 4.6: Genotypic path analysis of various characters for yield and its contributing traits in sorghum

Character	Days to 50% flowering	Plant height at maturity (cm)	Total number of leaves	Leaf area (cm^2)	Length of panicle at maturity (cm)	Number. of primary branches per panicle	Number of secondary branches per panicle	Number of grains per secondary branch	Number of grains per panicle	Flag leaf length (cm)	1000 Seed weight (g)	Fodder yield fresh per plant (g)	Fodder yield dry per plant (g)	Genotypic correlation with grain yield per plant (g)
Days to 50% flowering	**-0.799**	0.001	-0.021	0.013	0.079	-0.001	-0.005	-0.063	0.017	-0.036	0.203	-0.012	-0.010	-0.632
Plant height at maturity (cm)	-0.004	**0.236**	-0.016	0.00	-0.152	0.00	0.026	-0.051	0.008	0.071	0.293	-0.086	-0.049	0.275
Total number of leaves	0.114	-0.027	**0.144**	0.059	-0.112	0.001	-0.100	0.019	-0.001	-0.043	-0.331	0.124	0.077	-0.078
Leaf area (cm^2)	0.040	0.000	-0.032	**-0.263**	0.187	0.001	0.105	0.016	0.032	-0.034	-0.264	-0.099	-0.087	-0.398
Length of panicle at maturity (cm)	-0.086	-0.048	-0.022	-0.066	**0.739**	-0.003	0.090	0.078	-0.041	-0.157	-0.395	0.028	0.003	0.122
Number of primary branches per panicle	-0.102	0.012	-0.011	0.026	0.283	**-0.007**	0.102	-0.016	-0.052	-0.047	-0.028	0.089	0.066	0.315
Number of secondary branches per panicle	0.011	0.018	-0.042	-0.081	0.196	-0.002	**0.341**	0.065	-0.043	-0.022	-0.218	-0.004	0.016	0.235
Number of grains per secondary branch	0.219	-0.053	0.012	-0.018	0.254	0.000	0.097	**0.229**	-0.017	-0.091	-0.569	0.039	-0.022	0.079
Number of grains per panicle	-0.110	0.015	-0.001	-0.065	-0.237	0.003	-0.117	-0.031	**-0.127**	-0.095	0.186	-0.089	-0.096	-0.510
Flag leaf length (cm)	-0.109	-0.063	0.023	-0.033	0.435	-0.001	0.028	0.078	0.045	**-0.276**	-0.238	0.016	-0.011	-0.098
1000 Seed weight (g)	-0.219	0.093	-0.064	0.093	-0.393	0.000	-0.100	-0.175	0.032	0.086	**0.743**	-0.033	-0.037	0.025
Fodder yield fresh per plant (g)	0.039	-0.081	0.071	0.103	0.082	-0.002	-0.006	0.035	-0.045	0.016	-0.098	**0.252**	0.130	0.463
Fodder yield dry per plant (g)	0.047	-0.071	0.067	0.139	0.014	-0.003	0.034	-0.031	-0.074	0.018	-0.168	0.199	**0.164**	0.335

Residual value = -0.0014

Study of genetic divergence:

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

4.3.1. D^2 analysis:

Based on the estimates of genetic divergence, all the thirty genotypes of sorghum were grouped into 9 different clusters (Table 4.7). Generalized distance was estimated through Mahalanobis' D^2 – statistic. Among the nine clusters, clusters IV were largest including nine genotypes followed by cluster III including five genotypes. Clusters II were found to have four genotypes. Cluster VI and VII were found to have three genotypes each. Clusters I, had two genotypes and cluster VIII and IX were having one genotype each.

(i) The intra and inter-Cluster average distance:

The average distance within and between clusters and average inter and intra cluster D^2 values are presented in Table 4.8. In this table, the diagonal values are mean intra cluster and off the diagonal values are inter cluster distances.

The maximum inter-cluster distance of 6.645 was recorded between cluster V and cluster VIII followed by cluster I and VIII (6.505), cluster I and VI (6.097), cluster VI and VII (5.879), cluster V and VI (5.860), cluster I and V (5.828), and cluster V and IX (5.714).It suggested that if the diverse genotypes from these diverse groups are used in breeding programme, it is expected to produce a wide range of genetic variability in the population. The lowest inter-cluster distance of 3.270 was recorded between cluster II and IV. The highest (D = 2.287) intra cluster distance was found for cluster II, followed by, cluster III (2.816). The cluster VIII and IX both registered the lowest intra-cluster distance of 0.00 followed by cluster I recording 1.486

(ii) Cluster mean:

Clusters means of all 14 characters are presented in Table 4.9.

1. Days to 50% flowering:

The cluster mean was highest for days to 50% flowering cluster IX (77.0) and lowest for cluster V and VIII (71.00).

2. Plant height at maturity:

The cluster mean was highest for plant height at maturity cluster II (285) and lowest for cluster I (162).

3. Total number of leaves:

The cluster mean was highest for total number of leaves cluster I (12.33) and lowest for cluster VI (7.89).

4. Leaf area:

The cluster mean was highest for leaf area cluster VIII (414.83) and lowest for cluster V (263.43).

5. Length of panicle at maturity:

The cluster mean was highest for length of panicle at maturity cluster VII (25.56) and lowest for cluster II (20.33).

6. Number of primary branches per panicle:

The cluster mean was highest for number of primary branches per panicle cluster VII (59.89) and lowest for cluster VI (38.22).

7. Number of secondary branches per panicle:

The cluster mean was highest for number of secondary branches per panicle cluster VIII (535.00) and lowest for cluster IX (242.33).

8. Number of grains per secondary branch:

The cluster mean was highest for number of grains per secondary branch cluster VIII (7.00) and lowest for cluster II (4.00).

9. Number of grain per panicle (g):

The cluster mean was highest for number of grains per panicle cluster IV (2424.59) and lowest for cluster VII (1768.11).

10. Flag leaf length (cm):

Cluster mean was highest for flag leaf length cluster VIII (54.33) and lowest for cluster VI (33.33).

11. 1000 seed weight (g):

Cluster mean was highest for 1000 seed weight cluster V (30.50) and lowest for cluster VIII (22.33).

12. Grain yield per plant (g):

Cluster mean was highest for grain yield per plant cluster V (59.22) and lowest for cluster IX (25.67).

13. Fodder yield fresh per plant (g):

Cluster mean was highest for fodder yield fresh per plant cluster VII (172.44) and lowest for cluster VI (89.22).

14. Fodder yield dry per plant (g):

Cluster mean was highest for fodder yield dry per plant cluster I (96.00) and lowest for cluster VI (46.11).

(d) Cluster characteristics:

Cluster I was characterized by dwarf plant type that is lowest plant height (162.83), highest numbers of leaves (12.33) and highest fodder yield dry per plant (96.00).

Cluster II was characterized by lowest number of grains per secondary branch (4.00), lowest length of panicle at maturity (20.33) and highest plant height (285.00).

Cluster III was characterized by lowest earliness to 50% flowering (70.13).

Cluster IV was characterized by highest number of grains per panicle (2424.59).

Cluster V was characterized by lowest leaf area (263.43), highest 1000 seed weight (30.50) and highest grain yield per plant (59.22).

Cluster VI was characterized by lowest fodder yield fresh per plant (89.22), lowest flag leaf length (33.11), lowest primary branch (38.22) and lowest number of leaves (7.89).

Cluster VII was characterized by lowest number grains per panicle (1768.11), highest length of panicle (25.56), highest number of primary branches (59.89) and highest fodder yield fresh per plant (172.44).

Cluster VIII was characterized by lowest fodder yield dry per plant (51.00), lowest thousand seed weight (22.33), highest leaf area (414.83), highest number of secondary branches per panicle (535.00), highest number of grains per secondary branch (7.00) and highest flag leaf length (54.33)

Cluster IX was characterized by lowest grain yield (25.67) lowest number of secondary branches per panicle (248.33) and delayed 50% flowering (77.00).

Table 4.7: Clustering pattern of thirty genotypes on the basis of genetic divergence in sorghum:

Cluster	Genotypes	Number of genotypes
I	IV 16-3, CSV 21	2
II	IV 14-7, IV 16-4, CSV 27, IV 16-19	4
III	SPV 2357, SPV 2376, IV 16-6 CSV 30, IV 14-8	5
IV	IV 16-5, CSV 23, 1187-2-1-2, 1155-5-1-1-3, IV 16-8, IV 16-10, IV 16-11, 3-3-10-10, JJ 1041	9
V	SPV 3375, 30-4-5-2-11-3	2
VI	CSV 20, CSV 17, IV 16-12	3
VII	IV 16-1, IV 14-9, SPV 1862	3
VIII	1088	1
IX	IV 16-2	1

Table 4.8: Average intra and inter cluster D^2 values between the clusters in sorghum

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	1.486								
II	4.214	2.287							
III	4.083	3.926	2.816						
IV	4.441	3.270	3.088	2.408					
V	5.828	4.184	4.931	5.095	2.372				
VI	6.097	4.180	4.943	3.653	5.860	2.216			
VII	4.172	4.948	3.880	4.083	4.984	5.879	1.918		
VIII	6.505	5.563	4.479	4.108	6.645	4.449	4.156	0.00	
IX	4.998	3.797	5.009	3.958	5.714	5.156	4.993	5.698	0.00

Table 4.9. Clusters means of all 14 characters

Characters	**Cluster mean**								
	I	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**
Days to 50% flowering	72.17	72.50	70.13	71.44	71.00	71.33	71.67	71.00	77.00
Plant height at maturity (cm)	162.83	285.00	240.87	227.70	274.00	280.00	236.78	278.33	261.67
Total number of leaves	12.33	11.83	12.20	10.07	9.33	7.89	10.56	10.33	10.33
Leaf area (cm^2)	333.63	352.82	349.42	407.87	263.43	401.08	375.30	414.83	353.66
Length of panicle at maturity (cm)	22.17	20.33	23.87	24.93	22.00	22.00	25.56	21.67	24.33
Number of primary branches per panicle	43.33	47.50	42.87	49.44	58.17	38.22	59.89	58.67	56.33
Number of secondary branches per panicle	371.17	318.83	316.60	347.74	369.00	458.89	511.33	535.00	242.33
Number of grains per secondary branch	4.50	4.00	6.60	5.11	5.33	5.44	6.22	7.00	5.67
Number of grains per panicle	1816.33	2237.08	2267.73	2424.59	2170.33	2290.89	1768.11	2083.67	1988.67
Flag leaf length (cm)	33.33	37.17	45.07	46.74	36.17	33.11	41.89	54.33	34.33
1000 Seed weight	24.17	27.67	24.13	26.26	30.50	27.11	24.11	22.33	26.67
Grain yield per plant (g)	36.50	38.75	46.93	37.37	59.22	37.78	42.67	39.67	25.67
Fodder yield fresh per plant (g)	160.33	140.92	154.80	134.37	163.33	89.22	172.44	99.00	122.00
Fodder yield dry per plant (g)	96.00	69.92	68.73	58.33	81.00	46.11	91.56	51.00	73.67

Canonical root analysis:

How far the divergence between the genotypes arrived at D^2 values agrees with those determine by the use of canonical analysis method was also examined. These method dealt with the replacement of the measurements of a number of mutually correlated characters by relatively five measurement obtained as linear combinations of large number of such measurement. The divergence as determine by canonical analysis following the procedure given by Rao (1952), the standardized best linear functions (canonical vectors) were obtained and are presented in table 4.9. Of the total variation, the first root alone accounted for 28.62% and is the major axis of differentiation. Further first two roots together accounted for 67.26% of the diversity indicating that the difference for the straits in these accessions was nearly complete in the two phases. It was observed that the clusters were distinctly delineated to their position similar to their position in D^2 analysis.

From the coefficient of first canonical root it was found that primary axis was based on fodder yield dry per plant, fodder yield fresh per plant, flag leaf length, number of primary branches per panicle, total number of leaves and grain yield per plant .

From the coefficient of second canonical root it was found that secondary axis was based on number of secondary branches per panicle, fodder yield dry per plant , number of primary branches per panicle, fodder yield fresh per plant, length of panicle, total number of leaves and plant height .

From the coefficient of third canonical root it was found that tertiary axis was based on plant height, fodder yield dry per plant, total number of leaves, 1000 seed weight, fodder yield fresh per plant, grain yield and number of primary branches per panicle.

From the coefficient of fourth canonical root it was found that quatnory axis was based on number of primary branches per panicle, flag leaf length , length of panicle, days to 50% flowering, grain yield per plant, leaf area and total number of leaves.

With respect to the relative importance of different characters under study , it would be apparent from the absolute size of coefficients that fodder yield dry per plant (0.4746), fodder yield fresh per plant (0.3299), flag leaf length (0.2273), number of primary branches per panicle (0.2251), total number of leaves(0.0729), grain yield per plant (0.0131) , on secondary axis of differentiation , number of secondary branches per panicle(0.7089), fodder yield dry per plant (0.5549), number of primary branches per panicle (0.3494), fodder yield fresh per plant (0.1445), length of panicle (0.0592), total number of leaves (0.0242), plant height (0.0141), on tertiary axis of differentiation, plant height at maturity (0.6391), thousand seed weight (0.2754), fodder yield dry per plant (0.2555), total number of leaves(0.2037), fodder yield fresh per plant (0.1569), grain yield (0.0976), number of primary branches per panicle (0.0333) and on quatnory axis of differentiation, number of primary branches per panicle (0.5529), plant height at maturity (0.4336), flag leaf length (0.4286), length of panicle (0.2623), days to 50% flowering (0.1304), grain yield per plant (0.0136), leaf area (0.0490), total number of leaves (0.0048).

Table 4.10 Values of the four canonical vectors, which supply the best linear function of variates

Characters	**CANONICAL ROOT**			
	CR I	**CR II**	**CRIII**	**CRIV**
Days to 50% flowering	0.0016	-0.0086	-0.0203	0.1304
Plant height at maturity (cm)	-0.4414	0.0141	0.6391	0.4336
Total number of leaves	0.0729	0.0242	0.2037	0.0048
Leaf area (cm^2)	-0.0843	-0.0359	-0.3730	0.0490
Length of panicle at maturity (cm	-0.0390	0.0592	-0.1407	0.2623
Number of primary branches per panicle	0.2251	0.3494	0.0333	0.5529
Number of secondary branches per panicle	-0.5670	0.7089	-0.2427	-0.2199
Number of grains per secondary branch	0.0939	-0.0449	-0.1331	-0.1051
Number of grains per panicle	-0.1542	-0.1078	-0.0813	-0.0638
Flag leaf length (cm)	0.2273	-0.0038	-0.3622	0.4286
1000 Seed weight	-0.0245	-0.1590	0.2754	-0.2988
Grain yield per plant (g)	0.0131	0.0455	0.0976	0.0136
Fodder yield fresh per plant (g)	0.3299	0.1445	0.1569	-0.2480
Fodder yield dry per plant (g)	0.4746	0.5549	0.2555	-0.1413
Percentage of variation observed	**28.62**	**21.64**	**17.07**	**8.79**

CHAPTER V

DISCUSSION

Sorghum is an important cereal crop of semi-arid tropics of the world and it is utilized as food, feed, forage and for alternative uses. In India, though the crop is grown in kharif and rabi seasons, productivity of rabi sorghum (640 kg/ha) is much less compared to kharif sorghum (1060 kg/ha). The success of sorghum cultivation as a high valuable crop in sorghum growing areas will largely depend on the extent of improvement made in its yield. Plant breeding aims at genetic improvement of crop plants by making the genotypes argonomically adaptable and economically superior in their performances. The selections made in the field on phenotypic expression are less efficient. Studies on relative magnitude of heritable and non-heritable variability exhibited for various traits are therefore, likely to be useful in line selection. Partitioning the total observed variance into genotypic, phenotypic and environmental components will be helpful in making an efficient selection. Knowledge of nature and extent of character association and an understanding of direct and indirect forces that influence particular character are essential to formulate a fruitful breeding programme. An experiment was hence formulated to obtain information on these aspects and results are discussed in this chapter. Success in plant breeding programme depends largely on the extent of genetic variability available to a breeder. A detailed study of exotic collections is essential, to provide a greater opportunity for selection of parents with wide genetic divergence or better quality traits which are absent in land races. The importance of these exotic accessions depends on the existence of genetic diversity and how different they are from indigenous land races and varieties. The evaluation and characterization of exotic accessions will help us to identify and describe new and useful genetic traits. Therefore, the exotic accessions and some indigenous land races along with improved indigenous varieties were evaluated for qualitative and quantitative traits. In order to describe, establish diagnostic characteristics and identify genotypes with desired agronomic traits, it is essential to estimate the extent of morphological variation in collection. In the present investigation, 30 diverse genotypes of kharif sorghum were evaluated to assess their genetic potential with respect to yield and yield attributes. The results presented in the preceding chapter are discussed in the light of pertinent literature. The discussion is confined to the following heads,

5.1 Genetic variability

5.2 Heritability and Genetic advance

5.3 Correlation coefficient and path analysis

5.4 Genetic divergence

5.1 Genetic variability

A broad spectrum of genetic variability in the population is fundamental requisite for success of a crop improvement programme since it provides opportunity to breeders to making selection of desirable superior individuals from genetically diverse base population. Wide range of variability existing among the genotypes to be tested for all the characters is also necessary to isolate significantly superior genotypes.

Wide range of variability was observed in the experimental material for all the traits under study. The values of mean and range revealed that there is wide variability among genotypes for most of the characters. The variation was uniformly distributed on the both sides of the means for each character, indicating normal distribution in the population for all characters. The value of mean sum of squares due to genotypes was significant for all the traits. This suggests that the experimental material differed in the population significantly amongst themselves and the existence of genetic variability for all the traits under the study.

The total variance was partitioned into genotypic, phenotypic and environment components. The estimates of PCV and GCV were high in case of number of secondary branches per panicle, number of grains per secondary branch, number of grains per panicle, flag leaf length, grain yield per plant, fodder yield fresh per plant, and fodder yield dry per plant. This highlighted the presence of genetic variation in respect of these attributes. Similar results were obtained by Narkhede *et al*. (2000b), Lata Chaudhary *et al*. (2001b), Prabhakar (2001), Veerabhadiran and Kennedy (2001b), Manonmani *et al.* (2002), Prabhakar (2003), Arunkumar *et al.* (2004) and Mallinath *et al.* (2004).

Moderate estimates of PCV and GCV were exhibited by five characters *viz.,* plant height at maturity, total number of leaves, leaf area, length of panicle at maturity, number of primary branch per panicle, number secondary branch per panicle and these findings were in accordance with the reports given by Narkhede *et al.* (2000b), Prabhakar (2003) and Mallinath *et al*. (2004) for the traits in sorghum.

The magnitude of PCV and GCV were not equivalent for all the characters studied. This suggested that the genotype under study is influenced by the environment.

5.2. Heritability and Genetic advance:

The total variability present in the population was not transmitted as such, only its heritable portion was transmitted to the next generation. The knowledge of heritable proportion of genetic variability present in the population can be obtained by another genetic parameter that is heritability estimates.

Heritability estimate in broad sense is the ratio 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 helps the plant breeders in the selection of superior genotypes from the genetically variable population. Robinson *et al*. (1949) had classified heritability estimate in broad sense as high (above 70%), medium (50-70%) and low (below 50%).

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 abiotic factors hence their utility will be restricted. Thus, heritability estimate coupled with genetic advance would be more reliable and useful in formulating selection criteria.

Estimates of heritability value was high for number of secondary branches per panicle, plant height at maturity, fodder yield dry per plant, number of primary branches per panicle, fodder yield fresh per plant, flag leaf length and these characters may be used to construct selection indices so that the progress made through them would be high.

The estimates of heritability in broad sense were relatively moderate for leaf area, total number of leaves, 1000 seed weight, panicle length and days to 50% flowering. These characters may be used to construct selection indices but the progress made through these traits would be relatively slow.

Expected genetic advance:

The genetic gain that can be expected by selection for a character was estimate by another genetic parameters, genetic advance. It measures the genetic gain under selection. Since the genetic advance is affected by unit of measurement, genetic advance as percentage of mean was calculated which is free from unit and it will facilitate comparison of genetic gain for various characters.

In present investigation, the estimates of expected genetic advance expressed as percentage of mean were high for the number of secondary branches per panicle, fodder yield dry per plant, fodder yield fresh per plant, flag leaf length and plant height at maturity. The moderate value of expected genetic advance as percentage of mean was for number of primary branches per panicle, total number of leaves, grain yield per plant, leaf area, number of grains per panicle, number of grains per secondary branch and length of panicle at maturity. Low value of expected genetic advance as percentage of mean was for 1000 seed weight and days to 50% flowering.

Fodder yield dry per plant, fodder yield fresh per plant, number of secondary branches per panicle, plant height at maturity, flag leaf length showed high value of heritability coupled with high genetic advance as per cent of mean indicating lesser influence environmental factors on the expression of these characters and their was prevalence of additive gene action for expression of these characters and hence were amenable for simple selection and these findings were in accordance with the reports given by Jain and patel (2012), Deepalakhami and Ganeshmurthi (2007) and Mallinath *et al*. (2004) for the traits in sorghum.

High heritability with moderate genetic advance as per cent of mean was recorded for number of grains per panicle, leaf area, number of grains per panicle, number of grains per secondary branch and length of panicle at maturity indicating that these characters were governed by both additive and non-additive gene action. Hence, simple selection procedure can be practiced for further improvement in the later generations.

High heritability coupled with low genetic advance as per cent of mean was recorded for days to 50% flowering indicating prevalence of non-additive gene action. Hence there is a good chance of improvement of this trait through methods involving indirect selection.

5.3. Correlation coefficient and Path analysis:

Correlation coefficient studies:

Correlation coefficient is a statistical measure which is used to find out the degree and direction of relationships between two or more variables. Thus, it measures the mutual relationship between two or more variables. It provides better understanding of yield components which helps the plant breeder during selection (Johnson *et al.* 1955). For the selection purpose, phenotypic correlation coefficient is of little practical value unless genetic correlation coefficients between pair of characters are in the same directions when estimated separately. Genotypic correlation coefficients provide a measure of genetic association between characters and are generally used in selection of one character as a means of improving another. Genetic correlation coefficient may be accounted by linkage and pleiotropy. Environmental correlation coefficient indicated non-genetic values and arises due to the fact that several observations are affected by the same amount of environmental factors. Therefore, the knowledge of correlation coefficient is of great significance.

Correlation coefficient studies showed that for most of characters pairs, genotypic and phenotypic associations were in the same direction and the genotypic estimates were higher than the phenotypic ones, indicating an inherited association between the characters.

Grain yield per plant, the most important economic trait, exhibited positive association with fodder yield fresh per plant, number of primary branches per panicle, fodder yield dry per plant, plant height at maturity, number of secondary branches, 1000 seed weight, number of grains per secondary branches per panicle, length of panicle at maturity both at phenotypic and genotypic level and these findings were in accordance with the reports given by Reddy (2002), Prabhakar (2003), Patil *et al*. (2004), Iyanar *et al*. (2005), Premlata *et a*l. (2006) and Khandelwal *et al*. (2015) for the traits in sorghum.

Apart from showing correlation coefficients with grain yield, the inter–correlation coefficients of total number of leaves with fodder yield fresh per plant, total number of leaves with fodder yield dry per plant, length of panicle at maturity with flag leaf length, number of primary branches per panicle with number of secondary branches per panicle, number of primary branches per panicle with fodder yield dry per plant, fodder yield dry per plant with number of primary branches per panicle and fodder yield dry per plant with fodder yield fresh per plant were also found positive. Strong positive correlation of these characters with grain yield indicated that these characters should be given importance for improving the yield potential of the crop.

The estimates of genotypic correlation coefficient with yield showed similar trend to those of phenotypic correlation coefficient in direction. However, these were higher in magnitude. It suggested that these correlation coefficients were due to breeding values and therefore, more dependable.

Hence, on the basis of correlation coefficient studies, it is obvious, that the characters fodder yield fresh per plant, number of primary branches per panicle, fodder yield dry per plant, plant height at maturity, number of secondary branches, 1000 seed weight, number of grains per secondary branches per panicle, length of panicle at maturity were positively correlated with grain yield and also with one another indicating their utility in selection programme for improving yield potential of population.

Path coefficient:

Correlation coefficient provides information regarding the direction and strength of relationship between two or more variables. Path coefficient analysis, on the other hand, is an efficient statistical technique specially designed to quantify the inter-relationships of different components and their direct and indirect effects on the seed yield. Through this technique, yield-contributing components can be ranked and specific traits producing a given correlation coefficient can be revealed. These will in turn impair the true association existing between a component and seed yield and a change in any one component are likely to disturb the whole network of cause and effect. Thus, each component has two paths of action viz., (1) The direct influence on seed yield (2) Indirect effects through components which are not revealed from the correlation coefficient studies. The path analysis was first suggested by Wright (1921) provides an effective measure of direct and indirect causes of association and depicts the relative importance of each factor involved in contributing to the final product that is, grain yield. In order to obtain the such relations, the cause and effect of relationship between yield *per se*, thirteen yield components was studied in sorghum through path coefficient analysis and the results are discussed below.

As the result of this study, it revealed that 1000 seed weight registered the maximum positive direct effect followed by, number of secondary branches per panicle, fodder yield fresh per plant, number of grains per secondary branch, length of panicle at maturity, and plant height at maturity while the correlation coefficient of these traits with grain yield per plant was also positive. Therefore, a true relationship exists between grain yield per plant with 1000 seed weight, number of secondary branches per panicle, fodder yield fresh per plant, number of grains per secondary branch, length of panicle at maturity and plant height at maturity.

Fodder yield dry per plant had positive correlation coefficient with grain yield per plant, exhibited negative direct contribution. This negative direct contribution was converted into positive correlation coefficient mainly due to its positive indirect effects *via* 1000 seed weight, number of secondary branches per panicle, fodder yield fresh per plant, number of grains per secondary branch, length of panicle at maturity, number of primary branches per panicle, total number of leaves and plant height at maturity and these findings were in accordance with the reports given by Arun kumar et al. (2004) and Reddy (2002) for the traits in sorghum.

The result obtained from genotypic correlation coefficients and path analysis indicated that the characters namely number of secondary branches per panicle, fodder yield fresh per plant, number of grains per secondary branch, exhibited strong positive correlation coefficient and high magnitude of positive direct effects on grain yield. Hence, it is suggested that while exercising selection index more weightage should be given to number of secondary branches per panicle , fodder yield fresh per plant and number of grains per secondary branch, as an important components influencing seed yield of sorghum.

Correlation coefficient analysis at phenotypic and genotypic levels indicated that apart from number of secondary branches per panicle, fodder yield fresh per plant, plant height, number of grains per secondary branch other traits like 1000 seed weight, fodder yield dry per plant, length of panicle at maturity and number of primary branches per plant were positive correlated with seed yield per plant. It is therefore suggested that preference should also be given to these traits in selection programme to isolate superior strains with genetic potentiality for higher seed yield.

5.4. Genetic divergence:

Genetic divergence study is a vital tool for the evaluation of genotypes and selection of parents for the breeding programme. So, present study was aimed at analysis of genetic divergence among the 30 genotypes and to identify the superior and divergent lines for formulating the crossing programme.

Wilk's lambda criterion was used for simultaneous test of significance for differences in the mean values of the fourteen characters and the pooled effect was found significant indicating a wide spectrum of diversity among the genotypes.

D^2 analysis:

The multivariate analysis giving the D^2 value, the 30 genotypes were grouped into nine clusters.

The inter-cluster distances were greater than intra-cluster distances, revealing that considerable amount of genetic diversity existed among the genotypes. Average intra-cluster distance revealed that cluster VIII and IX, which contained one genotype each, had lowest intra-cluster distance followed by cluster I. It indicated that these genotypes were closely related in their evolutionary process and passed through similar evolutionary factors. Highest intra-cluster distance of 2.816 was observed for cluster III which comprises of five genotypes. This suggests that these five genotypes possess all most same genetic makeup with minute difference due to evolutionary channel.

Inter-cluster distance is the main criterion for selection of genotypes for hybridization programme using D^2 analysis. Genotypes belonging to the clusters with maximum inter-cluster distance are genetically more divergent and hybridization between genotypes of divergent clusters is likely to produce wide spectrum of genetic variability with desirable segregates. The maximum inter-cluster distance of 6.645 was recorded between cluster V and cluster VIII followed by cluster I and VIII (6.505), cluster I and VI (6.095),cluster VI and VII (5.879), cluster V and VI (5.860), cluster I and V (5.828), and cluster V and IX (5.714).It suggested that if the diverse genotypes from these diverse groups are used in breeding programme, it is expected to produce a wide range of genetic variability in the population. The lowest inter-cluster distance of 3.270 was recorded between cluster II and IV which indicates that the genotypes of these cluster are genetically less diverse and were almost with same genetic makeup.

Sometimes a breeder is asked to improve a particular trait of a variety which is otherwise suitable. For this a donor parent is required. Information about a range of suitable donors thus becomes inevitable. Estimates of cluster mean make this information readily available. Cluster means for the fourteen traits of all the nine clusters were worked out. It was found that Cluster III had lowest mean value for days to 50% flowering, so it can be used for earliness character. Cluster V had highest mean values for grain yield per plant and 1000 seed weight which suggests that genotypes of cluster V may be selected for high potential with bold seed. This may be explained on the basis that yield being a complex character, exhibits polygenic inheritance, therefore, similar genotypes could be produced by different gene combinations. Such combinations may have selective advantage when constant selection is practiced in the segregating population. Similar plant types are expected to be established in the future generations. The genotypes of cluster VIII may be selected for leaf area, number of secondary branches per panicle, number of grains per secondary branch, and flag leaf length, Cluster I for total number of leaves and fodder yield dry per plant, cluster II for plant height, Cluster VII for fodder yield fresh per plant, length of panicle and number of primary branches and cluster IV for number of grains per panicle. The characters contributing maximum to the D^2 values are to be given greater emphasis for deciding on the clusters for the purpose of further selections and choice of parents for hybridization. To improve any particular trait donor may be selected from these clusters for hybridization program to evolve high yielding strains.

The following genotypes of marked mean performance from the selected clusters may serve as parents for hybridization programmes.

Clusters	**Characters**	**Genotypes**
I	Total number of leaves	IV 16-3, CSV 21
	Fodder yield dry per plant	
II	Plant height	IV 14-7, IV 16-4, CSV 27, IV 16-9
III	Days to 50% flowering	SPV 2357, SPV 2376, IV 16-6, CSV 30, IV 14-8
IV	Number of grains per panicle	IV 16-5, CSV 23, 1187-2-1-2, 1155-5-1-1-3, IV 16-8, IV 16-10, IV 16-11, 3-3-10-10, JJ 1041
V	1000 seed weight Grain yield per plant	SPV 3375, 30-4-5-2-11-3
VII	Number of primary branches per panicle	IV 16-1, IV 14-9, SPV 1862
	Length of panicle,	
	Fodder yield fresh per plant	
VIII	Flag leaf length	1088
	Leaf area	
	Number of secondary branches per panicle	
	Number of grains per secondary branch	

Canonical analysis:

Mahalanobis (1936) generalised distance D^2 statistic, is a useful measure of genetic divergence among genotypes. It provides degree of divergence based on multiple variables. However, it does not provide any indication about the quantum of contribution of each character towards the total genetic divergence. Further, it is difficult to classify characters, by D^2 statistic, into major or secondary traits, based on their contribution to the genetic divergence. Canonical analysis is another useful technique to analyse genetic divergence based on multivariate analysis. It not only discerns the genetic divergence but also supplies information about relative contribution of the traits under study.

In the present study, canonical analysis was carried out to classify the thirty sorghum accessions and to verify the clustering pattern on the basis of D^2 values. Four roots were considered for this study.

The coefficient of canonical root -1 revealed that primary axis rotated around fodder yield dry per plant, fodder yield fresh per plant, flag leaf length, number of primary branches per panicle, total number of leaves and grain yield per plant . These traits thus, were primary responsible for variation between genotypes. It indicated that these yield components were the major traits for genetic divergence. Therefore, greater significance needs to be attached to these traits during selection.

The coefficient of canonical root II revealed that secondary axis was primary concerned with number of secondary branches per panicle, fodder yield dry per plant , number of primary branches per panicle, fodder yield fresh per plant, length of panicle, total number of leaves and plant height .

The coefficient of canonical root III revealed that tertiary axis was primary concerned with plant height, fodder yield dry per plant, total number of leaves, 1000 seed weight, fodder yield fresh per plant, grain yield and number of primary branches per panicle.

The coefficient of canonical root IV revealed that quatnory axis was primary concerned with number of primary branches per panicle, flag leaf length , length of panicle, days to 50% flowering, grain yield per plant, leaf area and total number of leaves.

CHAPTER – VI

SUMMARY, CONCLUSION AND SUGGESTIONS FOR FURTHER WORK

A field experiment was conducted with thirty sorghum genotypes, raised in randomized block design with three replications during kharif season of 2016-17 at research farm, College of Agriculture, Indore (M.P.).

The observations were recorded on days to 50% flowering, plant height at maturity (cm), total number of leaves, leaf area (cm^2), length of panicle at maturity (cm), number of primary branches per panicle, number of secondary branches per panicle, number of grains per secondary branch, number of grains per panicle, flag leaf length (cm), grain yield per plant (g), fodder yield fresh per plant (g), fodder yield dry per plant (g), 1000 seed weight (g) from three competitive plants selected randomly from in each replication for collecting the information on existing genetic variability, heritability, expected genetic advance, genetic divergence, inter relationship among traits and direct and indirect contribution of traits. The salient findings of the present investigation entitled **"**Character association and genetic divergence studies in *Sorghum bicolor* (L) Moench***"*** are listed below:

1. The analysis of variance revealed highly significant differences among genotypes for all the characters at univariate as well as at multivariate level. Estimates of population mean were high and range was wide for most of the traits. Trend of variability at genotypic level was similar to that observed at phenotypic level for most of the characters. The highest GCV of 24.84% was recorded for fodder yield dry per plant, followed by number of secondary branches per panicle, fodder yield fresh per plant, grain yield per plant, plant height at maturity, number of primary branches per panicle, total number of leaves, number of grains per panicle, number of grains per secondary branch, leaf area, flag leaf length, length of panicle at maturity and 1000 seed weight while the least GCV was recorded for days to 50% flowering.

.2. The estimates of heritability in broad sense for most of the traits were high. High heritability was recorded for no of secondary branches per panicle followed by plant height at maturity, fodder yield dry per plant, number of primary branches per panicle, fodder yield fresh per plant, flag leaf length, leaf area, total number. of leaves, 1000 seed weight, days to 50% flowering, length of panicle at maturity, and number of grains per panicle while it was low for grain yield per plant and number of grains per secondary branch.

3. The estimated genetic advance as per cent of mean was found highest for number of secondary branches per panicle followed by fodder yield dry per plant, fodder yield fresh per plant, flag leaf length and plant height at maturity.

4. High value of heritability coupled with high genetic advance as per cent of mean has been reported for fodder yield dry per plant, fodder yield fresh per plant, number of secondary branches per panicle, plant height at maturity and flag leaf length.

5. The characters *viz*., fodder yield fresh per plant, number of primary branches per panicle, fodder yield dry per plant, plant height at maturity, number of secondary branches, 1000 seed weight, number of grains per secondary branches and length of panicle at maturity recorded positive correlation coefficient with seed yield both at genotypic and phenotypic level while leaf area, number of grains per panicle and days to 50% flowering, showed negative correlation coefficient with seed yield.

6. Path coefficient analysis revealed a higher and positive direct effect for 1000 seed weight, length of panicle at maturity, number of secondary branches per panicle and fodder yield fresh per plant on yield.

7. The thirty genotypes of sorghum were grouped into nine clusters based on D^2 values. Among the nine clusters, clusters IV were largest including nine genotypes followed by cluster III including five genotypes. Clusters II were found to have four genotypes. Cluster VI and VII were found to have three genotypes each. Clusters I, had two genotypes and cluster VIII and IX were having one genotype each.

8. The maximum inter-cluster distance of 6.645 was recorded between cluster V and cluster VIII followed by cluster I and VIII (6.505), cluster I and VI (6.095), cluster VI and VII (5.879), cluster I and V (5.828), cluster V and VI (5.860), cluster I and V (5.828) and cluster V and IX (5.714). The highest (D = 2.287) intra cluster distance was found for cluster II, followed by, cluster III (2.816).

9. The genotypes IV 16-3, CSV 21 for total number of leaves, and fodder yield dry per plant; IV 14-7, IV 16-4, CSV 27, IV 16-19 for plant height; SPV 2357, SPV 2376, IV 16-6 CSV 30, IV 14-8 for earliness 50% flowering ; IV 16-5, CSV 23, 1187-2-1-2, 1155-5-1-1-3, IV 16-8, IV 16-10, IV 16-11, 3-3-10-10, JJ 1041 for number of grains per panicle; SPV 3375, 30-4-5-2-11-3 for 1000 seed weight and grain yield per plant; IV 16-1, IV 14-9, SPV 1862 for length of panicle number of primary branches per panicle, fodder yield fresh per plant; 1088 for leaf area, number of secondary branches per panicle, number of grains per secondary branch and flag leaf may serve as potential for hybridization programme in the improvement of potentiality of the yield contributing traits in sorghum.

Conclusion:

1. The analysis of variance revealed highly significant differences among genotypes for all the characters studied indicating the existence of sufficient genetic variability in the experimental population. The studied traits had high phenotypic and genotypic coefficient of variation values further suggested that the high existence of genetic variability was present in population for these traits.

2. Fodder yield dry per plant, fodder yield fresh per plant, number of secondary branches per panicle, plant height at maturity and flag leaf length have high values of heritability coupled with high genetic advance as per cent of mean indicating lesser influence of environment on the expression of these characters and prevalence of more additive gene action in their inheritance.

3. The characters *viz*., fodder yield fresh per plant, number of primary branches per panicle, fodder yield dry per plant, plant height at maturity, number of secondary branches, 1000 seed weight, number of grains per secondary branches and length of panicle at maturity recorded positive correlation coefficient with grain yield both at genotypic and phenotypic level. The magnitude of phenotypic correlation coefficient was higher than genotypic correlation coefficient indicating that the genotype under study is influenced by the environment.

4. Path coefficient analysis revealed a higher and positive direct effect for 1000 seed weight, length of panicle at maturity, number of secondary branches per panicle and fodder yield fresh per plant on yield, should be given due weightage in selection of parents for hybridization for yield improvement.

5. The highest inter cluster distance was observed between cluster I and IX (7.911) indicating wide diversity between genotypes in these clusters. A cross between these two cluster’s genotypes is expected to give a heterotic hybrid and wide spectrum of variability. Therefore, these genotypes may be used as parents for hybridization.

6. The genotypes IV 16-3, CSV 21 for total number of leaves, and fodder yield dry per plant; IV 14-7, IV 16-4, CSV 27, IV 16-19 for plant height; SPV 2357, SPV 2376, IV 16-6 CSV 30, IV 14-8 for earliness 50% flowering ; IV 16-5, CSV 23, 1187-2-1-2, 1155-5-1-1-3, IV 16-8, IV 16-10, IV 16-11, 3-3-10-10, JJ 1041 for number of grains per panicle; SPV 3375, 30-4-5-2-11-3 for 1000 seed weight and grain yield per plant; IV 16-1, IV 14-9, SPV 1862 for length of panicle number of primary branches per panicle, fodder yield fresh per plant; 1088 for leaf area, number of secondary branches per panicle, number of grains per secondary branch and flag leaf may serve as potential for hybridization programme in the improvement of potentiality of the yield contributing traits in sorghum.

Suggestions for further work:

The following suggestions have been made for further study:-

- The genetic variability reported for different characters in relation to yield should be exploited for future genetic improvement of sorghum.
- Characters showing high heritability with high genetic advance should be utilized in direct selection.
- A better crop ideotype should be developed using findings from association analysis.
- The promising diverse genotypes identified can be tested for combining ability and inheritance of yield and its contributing traits for further use in breeding programme.
- The genotypes may be tested for genetic diversity study one or two more years so as to drive some concrete conclusions regarding diversity spectrum.
- Genotypes from the different clusters, identified for a specific character may be used as a parent for breeding programme with an objective to improve the specific character.

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APPENDIX

Mean performance of yield and its components of 30 genotypes of sorghum

S.No..	Genotypes	Days to 50% flowering	Plant height at maturity (cm)	Total no. of leaves	Leaf area (cm^2)	Length of panicle at maturity (cm)	No. of primary branches per panicle	Number of secondary branches per panicle	No.of grains per secondary branch	No. of grains per panicle	Flag leaf length (cm)	1000 Seed weight (g)	Grain yield per plant (g)	Fodder yield fresh per plant (g)	Fodder yield dry per plant (g)
1.	1088	71.00	278.33	10.33	414.83	21.67	58.67	535.00	7.00	2083.67	54.33	22.33	39.67	99.00	51.00
2.	SPV 2357	71.33	234.33	10.67	337.72	26.33	43.0	347.67	7.33	2198.67	46.33	24.67	44.33	118.33	48.67
3.	SPV 2376	72.00	247.33	10.33	328.92	27.0	41.33	314.33	6.00	2070.00	43.67	23.00	53.00	164.67	42.00
4.	SPV 3375	71.00	263.67	10.67	265.97	25.33	59.67	459.67	5.67	2212.00	48.33	29.00	58.33	162.00	94.67
5.	IV 16-1	72.33	250.0	11.00	341.57	27.0	56.33	434.33	6.33	1703.33	42.67	24.67	42.00	189.33	99.67
6.	IV 16-2	77.00	261.67	10.33	353.66	24.33	56.33	242.33	5.67	1988.67	34.33	26.67	45.67	122.00	73.67
7.	IV 14-7	70.67	298.33	11.67	376.80	19.0	49.67	212.33	4.0	2709.00	42.33	28.00	23.33	122.33	70.00
8.	IV 16-3	72.33	168.67	13.67	343.93	20.67	43.33	334.67	4.00	1707.00	27.00	24.00	39.67	151.67	98.67

9.	IV 16-4	74.00	270.00	12.67	343.97	22.33	52.0	333.67	3.67	2385.67	27.67	26.67	38.67	131.67	56.00
10.	IV 16-5	72.00	231.67	10.67	358.92	25.33	48.33	378.00	3.67	2652.33	60.33	25.67	41.67	121.67	62.67
11.	IV 16-6	71.00	191.0	12.00	275.02	21.33	37.67	272.00	6.67	2636.63	54.33	20.00	38.33	165.33	84.67
12.	CSV 27	72.33	271.67	12.33	352.16	23.33	45.67	260.33	4.00	1843.00	51.33	30.00	37.67	180.00	80.33
13.	CSV 21	72.00	139.0	11.00	323.32	23.67	43.33	407.67	5.00	1925.67	39.67	24.33	33.33	159.00	93.33
14.	CSV 20	71.00	268.33	8.33	367.0	18.33	33.0	370.67	6.00	2126.67	35.67	28.00	27.33	96.00	45.33
15.	CSV 17	71.00	291.67	7.67	370.96	25.33	42.67	420.0	5.00	2128.67	34.00	25.33	41.67	71.67	35.67
16.	CSV 23	70.67	265.0	10.00	442.55	28.0	55.67	313.33	5.00	2165.67	42.33	26.00	40.33	110.00	55.67
17.	CSV 30	71.33	286.67	14.33	411.42	21.0	37.33	324.00	6.67	2787.00	42.67	24.33	36.33	169.00	63.33
18.	1187 -2-1-2	75.33	205.0	8.00	411.25	24.33	48.33	306.00	5.00	2072.00	51.00	28.00	43.33	131.67	58.00
19.	1155 -5-1-1-3	75.67	239.33	11.00	433.89	25.67	47.67	416.00	5.33	2688.33	55.00	27.33	38.67	143.33	44.33
20.	IV 16-8	71.67	199.33	10.33	434.46	22.67	60.3	400.00	5.00	2578.00	40.67	26.33	41.67	169.33	69.00
21.	IV 16-9	72.00	300.00	10.67	338.35	16.67	42.67	369.00	4.33	2010.67	27.33	26.00	45.33	141.67	73.00

22.	IV 16-10	66.67	241.61	9.33	419.66	24.0	48.3	293.67	5.00	2487.67	42.33	24.67	36.33	126.67	75.00
23.	IV 16-11	71.00	215.00	10.33	431.97	23.0	42.67	312.67	6.67	2688.67	40.33	25.67	33.00	128.33	55.00
24.	3-3-10-10	69.00	239.0	9.0	392.70	26.33	52.67	415.00	5.00	1687.67	44.33	26.00	34.67	151.67	55.00
25.	IV 14-8	65.00	245.0	13.67	394.0	23.67	45.00	325.00	6.33	1646.33	38.33	24.67	62.67	156.67	75.00
26.	IV 14-9	71.67	280.0	11.0	367.56	27.33	67.67	598.33	5.67	1767.67	42.33	23.67	46.00	165.00	96.00
27.	30-4-5-2-11-3	71.00	284.33	8.0	260.88	18.67	56.67	278.33	5.00	2128.67	24.00	32.00	59.67	164.67	67.00
28.	IV 16-12	72.00	280.0	7.67	465.28	22.33	39.00	586.00	5.33	2581.00	29.67	28.00	44.33	100.00	57.33
29.	SPV 1862	71.00	180.0	9.67	416.77	22.33	55.67	501.33	6.67	1833.33	40.67	24.00	40.00	163.00	79.00
30.	JJ 1041	71.00	213.33	12.0	345.41	25.0	41.00	295.00	5.33	2838.00	44.33	26.67	26.67	116.67	50.33
	General mean	71.567	245.2556	10.6111	370.6977	23.4000	48.7222	371.8778	5.4111	2211.0334	41.5778	25.9889	40.7889	140.0111	68.000
	SE (m)	2.01	13.55	1.19	35.146	2.549	3.5225	27.3663	1.0514	340.2688	5.1719	1.861	7.958	12.7021	6.036
	CV (%)	3.453	6.76	13.81	11.61	13.34	8.85	9.01	23.79	18.84	15.23	8.77	23.89	11.11	10.87

VITA

The author of this thesis **Mr. Lokendra Singh Rajput s/o Shri Kalyan Singh Rajput** was born on 15 June 1992 At Chandi ji ward Teh-Hatta Dist-Damoh (M.P).

He acquired his High School level education in 2008 with 82 per cent mark from CBSE Board. After that he passed Higher Secondary in 2010 scoring 76.70 per cent marks.

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During all the period of his education, from schooling to post graduation he was very sincere and honest towards his studies.