Genetic Analysis of Fodder Yield and its Components in Advanced Lines of Sorghum

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(GENETICS AND PLANT BREEDING)

By

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2018

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*This is to certify that the thesis entitled "**Genetic Analysis of Fodder Yield and its Components in Advanced Lines of Sorghum**" submitted in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE IN AGRICULTURE** (**Genetics and Plant Breeding)** of Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur is a record of the bonafide research work carried out by **Mr. GNYAN PRAKASH GUPTA** under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of Instructions.*

All the assistance and help received during the course of the investigation has been acknowledged by him.

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The matter embodied in the thesis has not been submitted for the award of any other degree/diploma. Due credit has been made to all the assistance and help.

I, undertake the complete responsibility that any act of misinterpretation, mistakes and errors of fact are entirely of my own.

I, also abide myself with the decision taken by my advisor for the publication of material extracted from the thesis work and subsequent improvement, on mutually beneficial basis, provided the due credit is given, thereof.

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Abstract

The present investigation of sorghum (*Sorghum bicolor* L. Moench) consisted of 31 genotypes along with checks to estimate the genetic variability, heritability, genetic advance, correlation coefficient path analysis and principal components for fodder yield and its components. It is revealed that mean sum of squares due to genotypes were indicating the presence of sufficient amount of genetic variability amongst the genotype. The high heritability coupled with high genetic advance as percent of mean was recorded for yield and quality attributing traits.

The correlation coefficient was studied fifteen traits, *viz.,* days to 50% flowering, plant height, no. of leaves/plant and other all traits showed significant positive correlation with green fodder yield/plant. Dry matter yield/plant has highest positive direct effect on green fodder yield/plant followed by green fodder yield/plant/day, dry matter yield/plant/day, crude protein yield/plant, stem girth, penultimate leaf area, crude protein yield/plant/day, days to 50% flowering, plant height, no. of leaves/plant, no. of internode/plant, internodal length, brix's value and leaf stem ratio.

All the genotypes grouped into six clusters for fodder sorghum. It were revealed that cluster III had maximum intra cluster value followed by cluster I, cluster II, while D^2 value was maximum in between cluster II and III followed by cluster II and VI. Total divergence was found highest for green fodder yield/plant followed by dry matter yield/plant/day, green fodder yield/plant/day. On the basis of Principle component analysis IS 17248 had the highest PC score followed by IS 15957, CSH 22 SS, IS 13705, IS25301, IS 13553, IS 18542, ICSV 93046 and SSG 59-3 in PC1 indicated that these genotypes possesses high values of phonological and quality traits. The PC2 was mainly related with quality attributing trait while, PC3 for yield contributing traits. These findings suggested that the simultaneous selection for these traits is possible for improvement of sorghum genotypes.

Keywords: sorghum, variability, heritability, genetic advance, correlation coefficient path analysis and principal components

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LIST OF SYMBOLS

et al.,	-	And Others
cm	-	Centimeter
©	-	Copyright
℃	-	Degrees Celsius
e.g.	-	For example
g	-	Gram
ha	-	Hectare
h^2 (b)	-	Heritability in broad sense
Hrs	-	Hours
Max.	-	Maximum
ml	-	Milliliter
Min.	-	Minimum
viz.,	-	Namely
/	-	Oblique
%	-	Percentage
±	-	Plus or Minus
σ	-	Sigma
√	-	Square root
∑	-	Summation
i.e.,	-	That is
v/v	-	Volume by volume

LIST of ABBREVIATIONS

% - Percentage
$\sqrt{\quad}$ - Square root
Σ - Summation
σ - Standard deviation (Sigma)
‘t’ test - Student ‘t’ test
cm - Centimeter
m - Meter
mm - Millimeter
ml - Milliliter
df - Degree of freedom
et al. - And others
g - Gram
SE - Standard Error
CD - Critical Difference
SV - Sources of Variations
SS - Sums of Squares
MSS - Mean Sums of Squares
i.e. - That is
viz., - Namely
Min - Minimum
Max - Maximum
No. - Number
PCV - Phenotypic Coefficient of Variation
GCV - Genotypic Coefficient of Variation
SN - Serial Number
Wt. - Weight
CV - Coefficient of Variation
Mor. - Morning
Eve. - Evening
^{0}C - Degree Celsius

DFF - Days to 50% flowering

PH - Plant height

NLP - Number of leaves/plant

PLA - Penultimate Leaf area

SG - Stem girth

LS - Leaf stem ratio

INL - Internodal length

NIP - Number of internode /plant

GFYP - Green fodder yield /plant

GFYPD - Green fodder yield /plant /day

DMYP - Dry matter yield /plant

DMYPD - Dry matter yield /plant /day

CPYP - Crude Protein yield /plant

CPYPD - Crude Protein yield /plant /day

M.P. - Madhya Pradesh

H_2SO_4 - Sulfuric acid

K_2SO_4 - Potassium sulfate

$CuSO_4$ - Copper sulfate

INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] is the world's fifth most important cereal, after wheat, rice, maize, and barley (Ritter *et al.* 2007; Motlhaodi *et al.* 2014). It is a major food crop in Sub-Saharan Africa and South Asia and is the staple food for the most under privileged people in the world (Bibi *et al.* 2010). Besides being an important food, feed and forage crop, it provides raw material for the production of starch, fiber, dextrose syrup, bio-fuels, alcohol, and other products. Sorghum was domesticated in African continent, particularly in Ethiopia, from where it was introduced to other regions of the world with diverse agro climatic conditions (Li *et al.,* 2010). Therefore a wide diversity is found within and among the sorghum cultivars. (Kong *et al*., 2000; Hart *et al.,* 2001).

The history of forage crops can be traced back to about 1300 BC when alfalfa has been traced to be cultivated in areas of modern Turkey. Relatively widespread use of forage crops, however, appeared much later, around the beginning of the Christian era, when several species were cultivated in different continents, mainly in the countries of Mediterranean Europe. Little happened between the fifth and twelfth centuries, but the thirteenth to nineteenth centuries witnessed great advances in forage crops.

Sorghum diverged from a common ancestor with maize ~12 MYA and with rice ~50 MYA (Swigonova *et al.,*2004). Taxonomically sorghum [*Sorghum bicolor* (L.) Moench] is included in the family *poaceae* that comes under order *poales*. Genus *sorghum* and species *bicolor*, with chromosome no. 2n=20, a C_4 plant. *Sorghum bicolor* commonly called as sorghum and also known as great millet, durra, jwari or millo. Sorghum is classified on the basis of relative height and grain/stover productivity and with or without sugar in stem. Crop can be used as fodder, dual purpose, grain and sweet stalk. Unlike other countries, there are two distinct sorghum growing season in India, *kharif* (rainy season – June to October) and *rabi* (post rainy season – October to February). Single-cut and multi-cut sorghum varieties/ hybrids are also cultivated for green fodder (forage). Forage sorghum are commonly grown in areas where rainfall is insufficient for production and sorghum may be utilized as silage, green chop, pasture, dry hay or fodder (Dahlberg *et al.,* 2011).

The importance of sorghum as a forage crop is growing in many regions of the world due to its high productivity and ability to utilize water efficiently even under drought conditions. Even in the time of drought it rolls its leaves to reduce water loss and if the drought is continues, it will go into dormancy rather than dying. Although sorghum has an ability to tolerate many of environmental stress, as it is affected by drought stress at the post flowering stage of growth (Kebede *et al.,* 2001; Tuinstra *et al.,* 1997). Hence due to these above properties sorghum make it as “Camel crop”.

Sorghum is more palatable and digestible than maize and pearl millet.l quality. It produces a tonnage of dry matter having digestible nutrients 50 percent, crude protein 10%, fat 2.5% and nitrogen free extracts 45% (Azam *et al.,* 2010). Along with forage quality sorghum fodder is also palatable and has high animal intake. Plant morphology, anatomical components, digestibility, protein, mineral, cellulose and lignin contents, and anti-nutritional factors like hydrocyanic acid in sorghum determine animal performance *i.e.* milk and meat production, (Hanna 1993). The farmers have a preference for sorghum as it can be utilized for different purposes like fresh fodder, hay and silage and grows well in hot and dry climate (Singh and Sukhchain, 2010). It has quick growth habit, quick recovery or regeneration after cutting or grazing and has ability to provide highly palatable and nutritious fodder for cattle. The green fodder is the cheapest sources of feed for milch, meat and draft animals.

The cultivated area under forage sorghum in india is about 2.3 m ha, which produce 833 m tonnes (390 mt green and 443 mt dry), where as the annual forage requirement is 1594 million tonnes (1025 mt green and 569 mt dry), to support existing livestock population. This present feed and fodder resources of the country can meet only 48% of requirement, with vast deficit of 52% (61.1% green & 21.9% dry fodder) (Anonymous, 2014). There is a large gap between requirement and availability of feed at the national level. It is matter of prime concern to bridge this gap. In 19th Livestock Census, the total livestock population in the country is 512.05 million, in which 37.28% were cattle, 26.40% goats, 21.23% buffaloes, 12.71% sheep and 2.01% pigs.

Improvement of sorghum is much emphasized owing to its importance as food and fodder crop. It is necessary to improve the fodder sorghum yield with nutritionally superior qualities in order to obtain better animal performance.

Estimation of genetic variability, correlation, genetic divergence, path analysis and principal component analysis are the tools which are effectively used by plant breeders for achieving desired improvement. Hence, the present investigations were carried out with the following objectives.

Objectives of Investigation:

1. To estimate various parameters of genetic variability.
2. To estimate the extent of association and determine direct and indirect effect.
3. To estimate the genetic divergence using D^2 statistics.
4. To rank the genotypes based on Principal Component Analysis.
5. To identify superior lines for forage yield and quality traits.

REVIEW OF LITERATURE

Crop improvement depends on the magnitude of genetic variability, heritability, genetic advance, inter-relationship between various characters and their direct and indirect effect on yield is of almost importance to achieve a dynamic crop improvement programme. It is only possible when we pass on the knowledge of previous work done in the concern field. In sorghum substantial contribution has been made to the literature regarding its genetics and breeding in recent years.

The available, relevant literature related to various quantitative and qualitative parameters of present investigation **"Genetic Analysis of fodder Yield and its Component in Advanced Lines of Sorghum"** has been reviewed under the following heads:

2.1 Genetic parameters

2.1.1 Genetic variability

2.1.2 Heritability and Genetic advance

2.2 Correlation coefficient analysis

2.3 Path coefficient analysis

2.4 Genetic divergence

2.5 Principal Component of Analysis

2.1 Genetic parameters

The development of an effective plant breeding programme is dependent upon the existence of genetic variability. The efficiency of selection largely depends upon magnitude of genetic variability present in the plant population. Thus the success of genetic improvement in any character depends on the nature of variability present in the gene pool for that character. Hence, an insight into the magnitude of variability present in the gene pool of a crop species is of great importance to plant breeder for starting a judicious plant breeding programme. Various parameters of genetic variability are mean, range, standard deviation, coefficient of variation, heritability and genetic advance. Related literature available for genetic variability on sorghum is as follows:

2.1.1 Genetic variability

Availability of genetic variability for the component characters is a major asset for initiating a fulfill crop improvement programme. In fact, plant breeding has been amply defined as the purposeful management of variability. Since, whole breeding pursuit relates to the creation and management of genetic variability, the proper information on this aspect in the material is a pre-requisite before embarking on any breeding method. Number of workers has reported the existence of very high to low genetic variability with respect to fodder yield and its components in sorghum.

Kumar and Sahib (2003) reported a wide range of variation for leaf number/plant, leaf length, leaf width, days to 50% flowering, plant height, dry leaf weight/plant, dry stem weight/plant, leaf stem ratio and dry fodder yield/plant, among the characters, the range was higher for leaf width, dry leaf weight/plant, dry stem weight/plant, leaf stem ratio and dry fodder yield/plant. Higher differences in PCV and GCV were observed for dry leaf weight /plant, leaf number /plant, days to 50% flowering, plant height, number of leaves, leaf length, leaf width, leaf stem ratio, and brix’s values indicating considerable variability in 88 lines of sorghum.

Bini and Sumabai (2005) observed genetic variability using 50 accessions of fodder sorghum revealed that all the characters studied was significantly differed from each other. High PCV reported for green fodder yield, leaf weight/plant and leaf area index. High GCV were reported for leaf weight/plant, green fodder yield, leaf area index and number of leaves/plant.

Kishore and Singh (2005) studied 30 genetically diverse strains of fodder sorghum and 11 hybrids of sorghum and sudan grass grown under both irrigated and rain-fed conditions for two years and reported sufficient genetic variability among the genotypes for all the characters studied The mean square values obtained in both the environments (irrigated and rain-fed) differed significantly, especially for days to 50% flowering, plant height and flag leaf area. High estimates of PCV and GCV were also recorded for green fodder and dry matter yield.

Warkad *et al.*, (2008) estimated range for genotypic and phenotypic coefficients of variation in 63 landraces and improved sorghum variety. The collection of landraces showed considerable amount of variability for all the traits studies *viz*. plant height, days to 50% flowering, number of nodes, number of leaves/plant, flag leaf area, leaf stem ratio crude protein and brix's value.

Kumar *et al.,* (2009) observed phenotypic and genotypic coefficients of variation in 68 sweet sorghum genotypes. The analysis of genetic parameters revealed considerable amount of variability for all the traits and high GCV, PCV were observed for plant height, stem girth and green fodder yield indicating that selection could be effective for improving these characters.

Patel *et al.,* (2013) observed high PCV for green fodder yield than dry fodder yield. High GCV was observed for green fodder yield and it's per day productivity, leaf breadth, plant height, stem girth, tillers/plant, crude protein and brix's value.

Ammanullah *et al.*, (2014) assessed ten sorghum varieties for growth character and fodder productivity. Significant variation for plant height, leaf area and fresh fodder yield were observed in the material studies.

Aminon *et al.*, (2015) studies 10 qualitative and 14 quantitative agro morphological traits. High variability among both qualitative and quantitative traits was observed. Days to 50% flowering and plant height were traits that exhibited broader variability.

Khandelwal *et al.,* (2015) evaluated 224 genotypes of Sorghum to study genetic parameters and recorded significant variation for various morphological and yield traits. High magnitude of GCV and PCV was observed for harvest index, grain yield/plant, dry and fresh weight/plant, panicle length and days to 50% flowering.

Gedam *et al.,* (2015) evaluated twenty five genotypes of sorghum for genetic studies and result of study revealed that the magnitudes of phenotypic coefficient of variation were greater than genotypic coefficient of variations for the characters viz. plant height, no. of leaves /plant, leaf breadth, green and dry fodder yield these characters show importance for crop improvement program in fodder sorghum.

Malik *et al.*, (2015) observed genetic parameters for twelve characters and revealed significant variability for all the traits. The GCV and PCV were high for leaf breadth, leaves/plant, leaf area, leaf stem ratio and green fodder yield and moderate was observed for leaf length, inter node length, stem girth and protein content and low for days to 50% flowering.

Singh *et al.,* (2016) observed GCV and PCV the estimates were high for plant height, leaves/plant, leaf area, stem girth, leaf stem ratio and green fodder yield.

Rana *et al*., (2016) studied magnitude of GCV, PCV, heritability and genetic advance as percentage of mean recorded high for various characters i.e. leaf-stem ratio, no. of leaves/plant, green fodder yield/plant, stem girth and dry matter yield/plant.

Vendruscolo *et al.*, (2016) evaluated agro-morphological traits *i.e.* flowering date, stem girth, number of stems, plant height and no. of leaves, green mass production and dry matter production.

Wuhaib *et al.,* (2017) experiments were carried out during spring and fall seasons of 2013, for seven traits days to 50% anthesis, plant height, leaf area, panicle length, panicle weight and crop growth rate. These traits were showed higher genotypic and phenotypic variances than environmental variance.

2.1.2 Heritability and Genetic advance

Heritability in broad sense is the ratio of genotypic variance to total variance (phenotypic variance). It is calculated from total genetic variance which is consists of additive, dominance and epistatic variances. It is a good index of the transmission of characters from parents to their off spring. The estimates of broad sense heritability help the plant breeder in selection of elite genotypes from homozygous populations.

While, the genetic advance is the deviation in the characters of selected population over the base population the estimation of heritability along with genetic advance is more applicable than the heritability value alone. Genetic variations for important traits can be used for improvement of crop in relation to heritability and genetic advance.

Shreenivasa *et al.*, (2000) conducted experiment on sorghum for the variability components in forage sorghum and reported higher amount of heritability for plant height, stem girth, no. of leaves, total leaf area, green forage yield, dry fodder yield, 100 seed weight, and grain yield. High heritability supported with high genetic advance for characters plant height, dry forage yield and stem diameter.

Singh, (2004) found high heritability for characters days to 50% flowering, leaf stem ratio, green fodder yield/plant/day, crude protein (%), stem girth and brix’s value.

Bini and Sumabai (2005) studied heritability for 50 accessions of fodder sorghum and revealed that plant height at harvest, leaf weight/plant and green fodder yield had high heritability coupled with high genetic advance.

Bello *et al.,* (2007) studies genetic and morphological characters and observed plant height, days to 50% flowering, number of nodes/plant, panicle length, no. of leaves/plant and days to maturity to high broad sense heritability.

Warkad *et al.,* (2008) estimated high heritability coupled with high genetic advance was observed for stem girth and dry matter yield/plant indicating the presence of additive gene effects.

Jain *et al.,* (2008) reported heritability and genetic advance were carried out in 48 genotypes of dual sorghum for yield and their contributing traits. Characters such as grain yield/plant, dry fodder yield/plant and plant height responded positively to selection because of high broad sense heritability and high genetic advance.

Kumar *et al.,* (2010) revealed significant variation for all the traits except cane yield and sucrose (%). Internodal length, tillers/plant, plant height, and TSS (%) recorded high estimates of genetic advance as percentage of mean, whereas moderate values were observed for stem girth.

Raveendran *et al.,* (2012) studied open and self pollinated F_2 populations of inter-specific cross of fodder sorghum (*Sorghum bicolor)* and found that heritability of fodder traits were higher in open-pollinated population than in the self-pollinated populations. High genetic advance was reported for characters brix's value and number of leaves/plant.

Patel *et al.,* (2013) reported high heritability along with higher genetic advance for days to 50% flowering, flag leaf area, stem girth, panicle length, panicle weight and 100 seed weight in sorghum land races.

Kumar and Reddy (2013) observed heritability coupled with genetic advance the parameters like grain yield and green fodder yield, tillers/plant, leaf stem ratio, internodal length indicating the dominance of the non-additive gene action; signifying that hybridization breeding should be effective.

Jain and Patel (2014) investigated 144 genotypes of forage sorghum and reported highly significant differences among genotypes for all characters. High genetic advance and high heritability was recorded for traits like plant height, stem girth, internodal length, number of leaves/plant, green forage yield and dry matter yield gave a positive response to the selection.

Dainel and Dikera (2014) studied the yield components of four local varieties of sorghum; Banina, Kadaga, Naga red and Kapala. High heritability accompanied with high genetic advance (GA) was observed for days to 50% flowering, weight of grains/panicle and days to maturity.

Khandelwal *et al.*, (2015) evaluated 224 genotypes of Sorghum to study genetic parameters and character association among yield components. Estimates of heritability varied from moderate for panicle width to higher for days to 50% flowering. The association of high heritability with high genetic advance and GCV was reported in case of fresh weight/plant and leaf area.

Gedam *et al.*, (2015) estimates the High heritability in conjugation with higher values of genetic advance and genotypic coefficient of variation for the characters *viz.* plant height, no. of leaves/plant, leaf breadth, green and dry matter yield indicated preponderance of additive genetic variance for these characters.

Malik *et al.*, (2015) observed genetic parameters for twelve characters in genetically diverse forage sorghum lines during *kharif* 2009 and find out heritability (broad sense) was high for all traits *viz.* days to 50% flowering, plant height, leaf breadth, leaf length, internodal length, stem girth, leaves/plant, leaf area, leaf stem ratio, protein content and green fodder yield. The genetic advance as percent of mean were high for plant height, leaf breadth, leaf length, inter node length, stem girth, leaves/plant, leaf area, leaf stem ratio and green fodder yield.

Dubey *et al.*, (2016) Carried out involving thirty genotypes of dual purpose sorghum characters like days to 50% flowering, days to maturity and panicle length, plant height, no. of leaves/plant, no. of grains/panicle showed higher heritability. Higher genetic advance recorded for panicle length, flag leaf area and grain yield/panicle.

Rana *et al.,* (2016) studied yield and its attributing characters in diverse genotypes of forage sorghum, the magnitude of GCV, PCV, heritability and genetic advance as percentage of mean were recorded high for various characters i.e. leaf-stem ratio, no. of leaves/plant, green fodder yield/plant, stem girth and dry matter yield/plant.

Wuhaib *et al.*, (2017) observed seven traits *viz.,* days to 50% anthesis, plant height, leaf area, panicle length, panicle weight, crop growth rate, and grain yield/plant. The genotypes exhibited varying degrees of heritability for most traits. Such traits were responded positively to selection due to high broad sense heritability estimates.

2.2 Correlation coefficient analysis

Correlation coefficient is a statistical measure to find out the degree and direction of relationship between two or more variables. A positive value of correlation shows that the changes of two variables are in same direction, whereas in negative correlation movements of two variables are in opposite direction. It measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. There are three types of correlation *viz.,* phenotypic, genotypic and environmental. Phenotypic correlation is the observable correlation between two variables. It includes both genotypic and environmental effects. Genotypic correlation on the other hand measures the inherent association between two variables. It may be either due to pleotropic action of genes or linkage, more likely both or developmentally induced relationships.

Board *et al.*, (2007) studied 49 sorghum types and revealed high positive and significant association among the inter-character correlations; stem girth, stem weight, leaf weight, dry matter yield and crude protein yield were significantly and positively associated with one another.

Warkad *et al.*, (2008) carried out estimation of 64 genotypes for correlation studies and showed that selection could be practised for days to 50% flowering, days to maturity and plant height as these characters manifested positive significant correlation with dry fodder yield.

Jadhav *et al.*, (2009) carried out studies using 62 diverse genotypes of forage sorghum. Correlation studies revealed that green fodder yield per plant had positive and significant association with days to 50% flowering, plant height leaves/plant, leaf length, leaf width, crude protein content and dry matter yield/plant.

Singh *et al.,* (2009) reported that genotypic correlations were of higher magnitude as compared to their corresponding phenotypic correlations for most of the character combinations. Green fodder yield was found to be positive and significantly correlated with green fodder yield/day, days to 50% flowering, leaf length, no. of nodes/plant and plant height. It indicates that any selection based on these characters will enhance performance and improvement in forage sorghum.

Iyanar *et al.*, (2010) showed that all the traits except HCN, crude protein and total soluble solids had significant and positive correlations with green fodder yield/plant. High correlation coefficient was exhibited by dry fodder yield/plant with green fodder yield followed by plant height, no. of leaves and leaf length.

Kumar and Singh (2012) studied different character combinations and observed the green fodder yield had positive and significant association with leaf breadth, no. of leaves/plant and leaf area at genotypic and phenotypic level.

Patel *et al.,* (2013) observed all the characters under study had significant positive correlation with green fodder yield/day, green fodder yield/plant, number of leaves/plant, plant height, dry matter yield/plant, penultimate leaf area and leaf length on green fodder yield.

Kumar and Reddy (2013) reported higher magnitude of genotypic than phenotypic correlation days to 50% flowering, panicle length, internodal length and test weight had positive direct influence on yield at both genotypic and phenotypic level. It showed the importance of these characters to increase the yield of sorghum.

Jain and Patel (2014) investigated 144 genotypes of forage sorghum and reported highly significant differences among genotypes for all characters. The traits like plant height and green forage yield gave a positive response to the selection. Leaf length and plant height were significantly and positively associated with green forage yield/plant.

Prakash *et al.,* (2014) observed that characters plant height, number of tillers, leaf length, crude protein yield, number of leaves/plant and stem diameter were significantly and positively correlated with green fodder yield/plant, while days to 50% flowering showed negative association with green fodder yield/plant indicating that these characters may be considered as selection indices in sorghum breeding programme.

Diwakar *et al.*, (2016) observed that the green fodder yield I cut was significant and positively correlated with dry fodder yield I cut both at genotypic and phenotype level. The phenotypic correlation of green fodder yield Ist cut was also significant with dry fodder yield /day, leaf stem ratio and leaf breadth in positive direction and with protein% in negative direction. The green fodder yield IInd cut was significant and positively correlated with dry fodder yield/day IInd cut at both genotypic and phenotypic level. The phenotypic correlation of green fodder yield II cut was positively correlated with leaf stem ratio.

Singh *et al.*, (2016) observed green fodder yield exhibits significant and positive correlation with leaf area, plant height, leaves/plant, leaf breadth and stem girth at genotypic and phenotypic level.

Dubey *et al.,* (2016) an investigation was carried out on dual purpose sorghum the characters like flag leaf area, panicle length, number of grains /panicle, thousand grain weight showed highly significant positive correlation with grain yield /panicle.

Vendruscolo *et al.*, (2016) evaluated agro-morphological traits *i.e*. flowering date, stem diameter, plant height, no. of leaves, green mass production, and dry matter production. Highest genotypic correlation was found between the traits green mass production and dry matter production.

2.3 Path coefficient analysis

The path coefficient analysis is a standardized partial regression coefficient which splits the correlation coefficient into the measure of direct and indirect effects. Path analysis measures the cause of association of two variables. It is based on all possible simple correlation among various characters. It helps in determining yield contributing characters and is useful in indirect selection. Path analysis is an extension of the regression model, used to test the fit of the correlation matrix against two or more causal models which are being compared. The concept of path analysis was developed by Wright (1921).

Chand (2000) observed character association and path analysis in 16 sorghum genotypes for green fodder yield among yield components. The characters green fodder yield/plant, days to 50% flowering, no. of leaves, leaf stem ratio and plant height was significantly and positively associated with green fodder yield.

Kishore and Singh (2005) studied genetically diverse strains of fodder sorghum and hybrids of sorghum and sudan grass grown under both irrigated and rained conditions for two years and reported significant and positive direct effect for plant height, no. of leaves/plant and penultimate leaf area with green fodder yield.

Board *et al.*, (2007) reported path analysis in fodder sorghum and revealed that the component traits namely plant height, internodal length, dry matter yield, leaf stem ratio and brix's value had negative direct association with green fodder yield, while rest of the characters had positive direct effect crude protein percent, stem girth and tillers/plant with green fodder yield.

Warkad *et al.*, (2008) carried out estimation of 63 genotypes landraces along with control (SPV 669). Path coefficient analysis revealed that the no. of leaves/plant was the main negative contributor with green fodder yield, while positive direct effect shown by days to 50% flowering, leaf breadth, internodal length, dry fodder yield and concluded that dry fodder as economic yield could be increased by improving plant height, days to 50% flowering and maturity and might be considered as the important yield contributing components.

Jadhav *et al.*, (2009) carried out investigation using 60 diverse genotypes of forage sorghum. Path coefficient analysis revealed that dry matter yield/plant exhibited highest positive direct effect on green fodder yield/plant indicated that direct selection of this trait would be effective in improving green fodder yield. While, dry matter (%) showed high magnitude of negative and direct effect on green fodder yield /plant.

Sankarapandian (2010) carried out path analysis in dual purpose sorghum and revealed that the components traits namely plant height; stem girth, number of leaves/plant, showed positive direct effects on green fodder yield. Further he reported that while focusing the traits, plant height, number of leaves/plant, internodal length, tillers/plant and crude protein yield would improve the yield and duality for fodder sorghum.

Kumar and Singh (2012) studied different character combinations and observed the Path coefficient analysis showed that leaf length, leaf breadth, leaves/plant and leaf area were the most important characters controlling directly green fodder yield. High indirect positive contribution of leaf length, leaf breadth, leaves/plant and stems girth via leaf area and leaf stem ratio, total soluble solids and protein content via leaves/plant. This indicates that, effectiveness of selection for high fodder yield could be enhanced by inclusion of leaf length, leaf breadth, leaves/plant, stem girth, and leaf area as a selection criterion along with the leaf stem ratio.

Singh *et al.,* (2013) studied path analysis and had direct effects with green fodder yield per plant via days to 50% flowering, penultimate leaf area, stem girth and internodal length. It concluded that green forage yield/plant and days to milking were effective parameters for enhancement of the green fodder yield.

Gedam *et al.*, (2015) evaluated twenty five genotypes of sorghum for revealed that the positive and significant association of no. of leaves /plant, leaf breadth and dry fodder yield with green fodder yield indicate the importance of these characters during selection for crop improvement program in forage sorghum.

Vendruscolo *et al.*, (2016) were evaluated thirty-four biomass sorghum genotypes and two forage sorghum genotypes morpho-agronomic traits *i.e.* flowering date, stem diameter, no. of stems, plant height, no. of leaves, green mass production, and dry matter production. The path analysis demonstrated that green mass production and number of leaves can assist in the selection of dry matter production.

Rana *et al.,* (2016) studied yield and its attributing characters in forty diverse genotypes of in forage sorghum, the results of path coefficient analysis revealed high positive direct effect of dry matter yield/plant, stem girth and days to 50% flowering.

Dubey *et al.,* (2016) an investigation was carried out on dual purpose sorghum. Path coefficient analysis revealed that flag leaf area, thousand grain weight, no. of grains/panicle and no. of leaves/plant, days to maturity, showed high positive direct effect on yield.

Singh *et al.,* (2016) observed genotypic and phenotypic path coefficient exhibits high positive and direct effect of leaves/plant, stem girth, leaf breadth and leaf stem ratio on green fodder yield.

2.4 Genetic divergence

Anthropologists adapted Karl Pearson, (1901) coefficient of racial likeness (CRL) for the purpose of discriminating any two populations having unknown origin. Mahalanobis, (1936) after identifying that CRL was a test of divergence between two samples rather than a measure of actual magnitude of divergence between them developed the D^2 statistics, which actually provides a measure of magnitude of divergence between two groups under consideration. Mahalanobis (1936) first used this technique in the form of generalized distance, which considers the variation produced by any character and their co-joint effect that it bears on other characters. Mahalanobis also pointed out that D^2 would remain constant when samples were drawn from two different populations irrespective of size of the representative samples which indicated that D^2 supplied measure of actual magnitude of divergence between two groups under comparison.

Agrawal *et al.*, (2002) studied genetic divergence using cluster analysis among 41 genotypes along with 25 tillering and 16 non-tillering types with 14 component characters in sorghum. The genotypes were grouped into five non-overlapping clusters. Six genotypes were included in cluster 1, twelve in cluster 2, eight in cluster 3, eight in cluster 4 and seven in cluster 5. Maximum and minimum inter cluster distances were observed between clusters 1 and 4, and 2 and 4, respectively.

Yadav *et al.*, (2003) recorded the observations on 16 characters related to fodder yield and head dimensions. Pooled analyses of data were done using hierarchical cluster analysis. The hierarchical cluster analysis resulted in formation of five clusters having 3 to 24 genotypes. The clustering pattern of genotypes revealed that geographical diversity did not necessarily represent genetic diversity. Maximum distance was observed between cluster 2 and cluster 4 and minimum distance between cluster 1 and cluster 5.

Bhatt and Singh (2005) classified 40 genotypes of sorghum on the basis of D^2 analysis in 8 clusters. The maximum numbers of genotypes (28) were included in clusters I and cluster VI, VII and VIII consisted of single genotype each. Maximum inter cluster distance was observed between clusters VI and VII. The genotypes belonging to these clusters were genetically most divergent The average cluster means for different characters showed that genotypes included in clusters III, IV and V were early flowering, cluster X had highest mean value for plant height, days to maturity, 100 grain weight and grain yield/panicle, cluster VIII had maximum value for penultimate leaf area, no. of leaves**/**plant and number of nodes/plant.

Mohanraj *et al.*, (2006) studied 55 sorghum accessions from ICRISAT. Multivariate analysis grouped the accessions in to 21 clusters. Clusters II and V were the largest and consisted of 10 accessions each followed by cluster I (8 accessions) and cluster IV (5 accessions). The largest inter cluster distances were observed between cluster XII and XVth followed by VI and XVIII indicating that the crosses between accessions of these different clusters could give heterotic response and better seggregnts after hybridization.

Kumar *et al.*, (2010) evaluated genetic diversity by using D^2 analysis in *rabi* sorghum genotypes (60) for six yield attributing characters. Maximum inter-cluster distance was observed between II and VI (1262.59), while lowest divergence was noticed between clusters I and V (188.87). Among the six characters studied, grain yield contributed maximum towards total genetic divergence (93.84%) followed by plant height (4.92%), followed by plant height, panicle length, days to 50 % flowering and dry fodder yield. Cluster IV exhibited highest means for seed yield followed by fodder yield, panicle length and days to 50 % flowering. Cluster II exhibited lowest mean for seed yield, fodder yield, panicle length and plant height. The genotypes from clusters IV and II, which exhibited high and low cluster means for majority of the characters, are suggested as parents for hybridization programme to achieve novel recombinants.

Sameer *et al.*, (2010) evaluated 60 sorghum genotypes for six yield and its attributing characters to study the genetic diversity. Maximum inter cluster distance was observed between cluster II and VI while, lowest divergence was noticed between clusters I and V. Cluster IV exhibited highest means for seed yield followed by fodder yield, panicle length and days to maturity. Cluster II exhibited lowest mean for seed yield, fodder yield, panicle length and plant height The genotypes from clusters VI and II, which had high and low cluster means for majority of the characters, were suggested as parents for hybridization programmed to obtain better combinations.

Yadav and Pahuja (2011) characterized 90 sorghum genotypes on the basis of plant height, leaf length, leaf breadth, stem girth, no. of tillers, no. of leaves/plant, 100 grain weight and three visual fodder quality parameters. The genotypes wore plotted on the rescaled distance, resulted in formation of 10 clusters consisting 1 to 26 genotypes out of 10 clusters, clusters V was the largest comprising 26 genotypes followed by cluster IV consisting 15 genotypes, cluster VII with 13 genotypes, whereas cluster VI, I, II, III, VIII, IX and X contained 12, 9, 6, 5, 1, 1 and 1 genotypes, respectively. Cluster VI exhibited maximum intra cluster distance (42.78), while maximum inter cluster distance was observed between cluster III and VII (317.89).

Singh *et al.*, (2013) studied a set of 40 genotypes of sorghum was used for estimating genetic diversity. On the basis of D^2 estimates, 40 genotypes were grouped into seven clusters. The generalized intra-cluster distance ranged between 0.00 for cluster IV (with only one genotype) to 5.06 for cluster VII (with 14 genotypes). The highest inter-cluster D^2 value (5.87) was observed between clusters VII and II and lowest D^2 value (2.93) between clusters I and II. Desirable genotypes (with high mean value) from the clusters having inter-cluster distance more than the average inter-cluster distance may be selected for crop improvement.

Chikuta *et al.*, (2015) studied cluster analysis and grouped the genotypes into 3 clusters with cluster I retaining majority of the forage genotypes characterized with high biomass, cluster II containing a mixture of the forage and grain sorghums characterized with high grain yield while cluster III contained only the grain sorghums.

Sinha and Kumaravadivel (2016) observations were recorded by using hierarchical cluster analysis; the accessions were grouped under 6 clusters. Cluster I contained maximum number of accessions and cluster VI contained the minimum. The maximum inter cluster distance was observed between cluster VI and cluster IV. Cluster III had the highest mean value for hundred-seed weight and yield. Hence, the selection of parents must be based on the wider inter cluster distance and superior mean performance for yield and its components.

2.5 Principal Component of Analysis

PCA is a well-known method of dimension reduction (Massay, 1965; Jolliffie, 1986). Principal component analysis is intended to derive a small number of linear combinations (principal components) of a set of variables that retain many of the existing information in the original variables. Thus, this analysis may also be seen as an attempt of evidencing the approximate linear dependences existing between variables. Often a small number of principal components may be used to replace the original variables, to draw graphical representations, regression analysis, cluster analysis, factor analysis, among others traits. A brief reviews has been summarized below:

Bhanupriya *et al.*, (2014) studied forty nine germplasm and principal component analysis (PCA) indicated that five components (PC1 to PC5) accounted for about 75 % of the total variation. Out of total principal components retained PC1, PC2 and PC3 with values of 25.9%, 17.1% and 13.3% respectively contributed more to the total variation. The first principal component had high positive loading for 9 characters out of 16 *viz.,* weight of grains/spike, number of grains/spike, number of spikelets/spike, spike length, plant height, days to heading, days to flowering, grain protein content and yield/plant which contributed more to the diversity.

Chikuta *et al.* (2015) studied PCs and they reported the first four principle components explained 89% of the total variations observed in the genotypes.

Sinha and Kumaravadivel (2016) observations were recorded on 14 quantitative traits, out of which 9 diverse traits were selected for genetic diversity analysis. The principle component analysis revealed that the panicle width, stem girth, and leaf breadth contributed maximum towards divergence.

Jain and Patel (2016) were evaluated by performing analysis for PCs the Eigen value was maximum (3.844) in PC-1 followed by PC-II (1.455) and least for PC-III (1.076). First three PC scored 70.89% variation and variance percentage was maximum in PC-I (42.72%) followed by PC-II (16.17%) and PC-III (11.97%). The total variation was mainly due to variation in the fodder yield and their contributing traits *i.e.,* green fodder yield, dry fodder yield, stem girth, leaf width, no. of leaves/plant, leaf length, and days to 50% flowering.

MATERIAL AND METHODS

This chapter deals with the procedure employed for data collection the techniques of data analysis of experimental material used and other details to this study are presented under following sub headings.

3.1 Experimental site and location

The experiment was carried out at Seed Breeding Farm, Department of Genetics and Plant Breeding, College of Agriculture, Jabalpur (Madhya Pradesh) during K*harif* 2016. Jabalpur is situated at 411.78 meters above the mean sea level at 23.9^{o}N altitude and 79.58^{o}E longitude. The experimental area occupied was quite uniform in respect of topography and fertility.

3.2 Climate and Weather

The climate of Jabalpur is typically semi-humid and subtropical with severe winter and summer season. Jabalpur traditionally comes under rice - wheat crop zone of Madhya Pradesh and classified as "Kymore plateau and Satpura hills agro-climatic zone". The maximum temperature during the month of May and June reaches up to 33ºC, whereas minimum temperature goes below 5.5ºC in the month of December or January. The average rainfall in this region is 1070.15 mm which is mostly received during monsoon season between last - June to entire august with little occasional showers in other seasons.

According to National Bureau of Soil Science and Land Use Planning of the ICAR, this area belongs to agro-ecological sub-region number 10.1 as (sub-humid dry eco-region). The data related to weekly maximum and minimum temperature, relative humidity, wind velocity, rainfall, number of rainy days, sunshine hours and evaporation during entries crop growing period of experiment, recorded at metrological observatory Krishi Nagar, J.N.K.V.V., Jabalpur have been presented in Appendix-2.

3.3 Experimental material and methods

Table 3.1. List of entries and checks used in the experiment

S. No.	Name of entry	S. No.	Name of entry
1	IS 3717	17	ICSH 28001
2	IS 13553	18	ICSR 14006
3	IS 13705	19	ICSR 93022
4	IS 15957	20	ICSR 93025
5	IS 17248	21	ICSR 93026
6	IS 17349	22	S 35
7	IS 18542	23	NTJ 2
8	IS 25234	24	ICSR 93034
9	IS 25301	25	ICSV 93046
10	IS 25302	26	ICSV 25306
11	IS 25340	27	ICSV 25308
12	ICSV 25335	28	ICSV 25316
13	ICSSH 28	29	ICSV 12006
14	CSH 22 SS	30	SSG 59-3 (C)
15	ICSV 93046	31	MP Chari (C)
16	ICSH 14002		

Experimental material consisted of 31 genotypes including 2 checks, were obtained from International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad (Telangana), and All India Co-ordinate Sorghum improvement project Indore. The experiment was conducted under Randomized Complete Block Design (RCBD), using three replications during *Kharif, 2016*.

Experimental details:

Number of accession	29 + 2 checks
Experimental design	Randomized Complete Block Design
Replication	3
Season	*Kharif* 2016
Row to row spacing	60 cm
Plant to plant distance	15 cm
Row Length	2m
Sowing date	30-06-16
Plot size	2 X 1.6 m^2

3.4. Observations recorded for fodder and allied traits

Five competitive plants were randomly selected and tagged in each plot per replication for recording observations on the following characters. However, days to 50 percent flowering were recorded on plot basis.

A. Morphological traits

3.4. a.1 Days to 50 % flowering

It was measured in days at which 50% of the plants of plot attended flowering stage from date of sowing in each treatment.

3.4. a.2 Plant height (cm)

It was measured in centimeter (cm) by meter scale from the base of plants to the ligules of top most fully opened leaf of the plants

3.4. a.3 Number of leaves per plant

Numbers of fully opened leaves per plant were recorded at 50 percent flowering.

3.4. a.4 Penultimate leaf area (cm^2)

Average area of the second leaf from top was calculated by using the formula given by Stickler *et al.* (1961).

Leaf Area = Leaf Length X Leaf Breath X 0.747

where, 0.747 is constant for calculating leaf area in sorghum.

3.4. a.5 Stem girth (mm)

Stem girth was measured by vernier caliper's scale from fourth node of the plant from bottom.

3.4. a.6 Inter nodal length (cm)

It was measure in centimeter (cm) by meter scale from the between 3rd and 4th nodes of plant at 50 percent flowering.

3.4. a.7 No. of Inter node/plant

Inter node were counted for each randomly selected five plants at the days to fifty percent flowering.

B. Agronomical traits

3.4. b.1 Leaf stem ratio

Leaf stem ratio was calculated by using the following formula

$$\textbf{Leaf stem ratio} = \frac{\text{Weight of fresh green leaves per plant (g)}}{\text{Weight of } \textbf{fresh} \text{ green stem per plant (g)}}$$

3.4. b.2 Green fodder yield/plant (g)

Green fodder yield/plant was recorded in grams by weighing whole fresh plant after harvesting at 50% flowering.

3.4. b.3 Green fodder yield/plant/Day (g)

It was calculated by using the following formula

$$\text{Green fodder yield/plant/day (g)} = \frac{\text{Green fodder yield/plant (g)}}{\text{Numbers of days to harvest}}$$

3.4. b.4 Dry matter yield/plant (g)

Dry matter yield was recorded in grams by weighing whole plant after drying it with sunrays and then in hot air oven at 65°C till constant weight for dry matter not obtained.

$$\text{Dry matter yield/plant (g)} = \frac{\text{Dm\% X green fodder/plant (g)}}{100}$$

3.4. b.5 Dry matter yield/plant/day (g)

It was calculated by using follows formula

$$\text{Dry matter yield/plant/day (g)} = \frac{\text{Dry matter yield/plant (g)}}{\text{Numbers of days to harvest}}$$

C. Biochemical traits

3.4. c.1 Crude protein yield/plant (g)

Crude protein content of sorghum will be determined by using Microkjeldal method by (AOAC, 1995). Total nitrogen will be estimated by using Kel-plus (digestion and distillation unit) process by the application of Con. (H_2SO_4), Catalyst mix (K_2SO_4 **:** $CuSo_4$ **.**5 H_2O) in 5:1 ratio, 40% NaOH etc. Crude protein value will be obtained by multiplying the total nitrogen by the conversion factor.

Crude protein percent = Percent Nitrogen content X 6.25

Where, 6.25 is constant factor

$$\text{Crude protien yield/plant (g)} = \frac{\text{CP\% X Dry matter yield/plant (g)}}{\text{Numbers of days to harvest}}$$

3.4. c.2 Crude protein yield/plant/day (g)

It was calculated by using follows formula

$$\text{Crude protein yield/plant/day (g)} = \frac{\text{Crude protein yield/plant (g)}}{\text{Numbers of days to harvest}}$$

3.4. c.3 Brix's values (%)

Take the third node from bottom at physiological maturity and note the sugar contents % using Brix's meter for three plants.

3.5 Statistical analysis

The mean value of the recorded data were subjected to analysis of variance (ANOVA) using the statistical analysis procedures.

3.5.1 Mean

It was calculated by using the following formula

Mean $$(\overline{X}) = \frac{\sum_{i=1}^{n} X_i}{n}$$

where,

$\sum X_i$ = sum of all observations

n = Number of observations

3.5.2 Range

Range is the difference between the minimum and the maximum values of a series of observation and thus provides the information about the dispersion present in the genotypes.

3.5.3Analysis of variance

The data on fodder and grain component traits were statically analyzed on the basis of modal for randomized complete block design. In order to test the significance of treatments critical difference was computed (Fisher 1918)

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

where,

Y_{ij} = Performance of i^{th} genotype in j^{th} block

μ = General mean

b_j = j^{th} block effect

t_j = i^{th} genotypes effect

e_{ij} = Random error which are supposed to be normally independently and identically distributed with mean zero and variance $\sigma^2_{e.}$

Table 3.2. Skeleton of ANOVA for Randomized Complete Block Design

Source of variation	**Df**	**Sum of square**	**Mean sum of**	**Expected MSS**	**F value**
Replication	(r-1)	RSS	M_1	$\sigma^2 e + g\sigma^2 r$	RMS/EMS
Genotypes	(g-1)	TSS	M_2	$\sigma^2 e + r\sigma^2 g$	TMS/EMS
Error	(r-1)(g-1)	ESS	M_3	$\sigma^2 e$	
Total	(rg-1)				

1. Genotypic variance $(\sigma^2 g) = \frac{M_2 - M_3}{r}$

2. Phenotypic variance $(\sigma^2 g) = \frac{M_2 - M_3 + M_3}{r}$

3. Genotypic variance $(\sigma^2 g) = M_3$

where,

r = Number of replications

g = Number of genotypes

df = Degrees of freedom

RSS = Replication sum of squares

TSS = Treatment sum of squares

ESS = Error sum of squares

M_1 = Mean square due to replications

M_2 = Mean square due to genotypes

M_3 = Mean square due to error

A significant value of F-test indicates that the test entries differ significantly among themselves, which requires computing the critical difference (CD).

$$\text{Coefficient of variation (CV)} = \frac{\sqrt{EMS}}{G.M.} \text{ X } 100$$

$$\text{Standerd error of any treatment mean } = \sqrt{\frac{EMS}{b}}$$

$$\text{Standard error of difference SE (between any two check means) (d)}$$

$$= \sqrt{\frac{2\text{EMS}}{\text{b}}}$$

Critical difference (CD) = $t_{(0.01)} \times S.E_{(d)}$

where,

G.M. = General mean

$t_{(0.01)}$ = t-value at 1% probability level at error d.f.

b = number of blocks

3.5.4 Coefficient of variation:

The coefficients of variation at genotypic and phenotypic levels were calculated as per the formula proposed by Burton, (1952). The phenotypic and genotypic variances were also estimated according to the method.

3.5.4.1 Genotypic coefficient of variation (GCV):

$\sigma^2_g = MS_g - MS_e \;/\; r$ ……….. (b)

GCV % = $\sigma_g / \bar{X} \times 100$

3.5.4.2 Phenotypic coefficient of variation (PCV):

$\sigma^2_p = \sigma^2_g + \sigma^2_e$ …….. (a)

PCV % = $(\sigma_p / \bar{X}) \times 100$

where, $\sigma_p = \sqrt{\sigma^2 p}$

where,

MS_g = Mean square due to genotypes or accessions

MS_e = Error mean square

b = Number of blocks

σ^2_p = Phenotypic variance

σ_p = Phenotypic standard deviation

σ^2_g = Genotypic variance

σ_g = Genotypic standard deviation

σ^2_e = Environmental variance

$\overline{X}$ = General mean

3.5.5 Heritability

It was calculated in broad sense by the formula proposed by Hanson *et al*., (1956).

$$\text{Heritability } (h^2\ \%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

where,

h^2 (bs) = heritability in broad sense

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The range of heritability was categorized as low (below 50%), moderate (50%-70%) and high (above 70 per cent) as given by Johnson et al. (1955).

3.5.6 Genetic advance (GA):

Genetic advance is calculated by the formula suggested by Johnson *et al.,* (1955).

$$GA = h^2(\text{bs}) \text{ x } \boldsymbol{\sigma p} \text{ x K}$$

Where,

GA = Genetic advance

σ_p = Phenotypic standard deviation

h^2 (bs) = Heritability in broad sense of the character

K= Selection intensity at 5% level of significance *i.e.,* 2.06

3.5.6.1 Genetic advance as percent of mean

It was calculated by the following formula

$$\text{GA as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \text{X} \quad 100$$

GA was categorized as

< 25 per cent = low

25-35 per cent = moderate

> 35 per cent = high

3.5.7 ESTIMATION OF CORRELATION COEFFICIENTS:

All correlation coefficients were calculated at genotypic and phenotypic levels using the formula suggested by Miller *et al.,* (1958).

$$r\, \boldsymbol{X_i X_j} = \frac{\text{Cov } X_i X_j}{\sqrt{(\text{Var } X_i) \cdot (\text{Var } X_j)}}$$

where,

$r\ x_i x_j$ = Coefficient of correlation between characters x_i and x_j

Cov (xi xj) = Covariance between characters $_{xi}$ and $_{xj}$

Var (xi) = Variance of character xi

Var (xj) = Variance of character xj

Genotypic and phenotypic correlation coefficients were compared by substituting the corresponding variance and covariance for all the observed characteristics.

$$\text{Genotypic r(XiYi)} = \frac{\text{Genotypic cov XiYi}}{\sqrt{\sigma_g^2\ (Xi)\ \sigma_g^2\ (Yi)}}$$

$$\text{Phenotypic r (XjYj)} = \frac{\text{Phenotypic cov XiYi}}{\sqrt{\sigma_p^2\ (Xi)\ \sigma_p^2\ (Yi)}}$$

where,

σ^2g (x_i) = Genotypic variance of character x_i

σ^2g (y_i) = Genotypic variance of character y_i

σ^2p (x_i) = Phenotypic variance of character x_i

σ^2p (y_i) = Phenotypic variance of character y_i

Testing of correlation coefficient for significance:

In order to test the significance of correlation coefficient, t-value was computed and compared with the tabulated value of ‘t’ at (n-2) degree of freedom at 5% and 1% level of probability.

$$'t_c' = \frac{r}{\sqrt{1-r^2}}\sqrt{n-2}$$

where,

t_c = Calculated value of t

r = Estimated value of correlation coefficient

n = Number of paired observations

3.5.8 Path coefficient analysis:

Path coefficients are standardized partial regression coefficient and such as provide the means to direct influence of one character upon another character. It also permits partitioning of correlation coefficient into direct and indirect effects via other character. For the path coefficient analysis the method originally proposed by Wright, (1921), which was further modified by Dewey and Lu, (1959). The cause and effect relationship is well defined in path coefficient analysis. It is possible to represent the whole system of variables in the form of a diagram known as path diagram.

Path coefficient analysis can be defined as the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect. In other words; it is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects, *i.e.*, it measures the direct and indirect contribution of various independent characters on a dependent character.

Wright (1921) proposed the original technique in which analysis was carried out by modified method devised by Dewey and Lu, (1959). Following set of simultaneously equations were formed and solved for estimating direct and indirect effects. Genotypic path coefficients were calculated separately for yield and yield components. The dependent variable was yield per plant. The unexplained variation in the dependent variable was obtained as residual factor from the following equation.

$$r_1Y = P_1Y + r_{12}\,P_2Y + r_{13}\,P_3\,Y + \ldots\ldots\ldots\ldots\ldots + r_1i\,P_1Y.$$

$$r_2Y = r_{21}\,P_1Y + P_2\,Y + r_{23}\,P_3Y + \ldots\ldots\ldots\ldots\ldots + r_{21}\,Y\,p_2Y.$$

$$r_kY = r_{k1}\,P_1Y + r_{k2}\,P_2Y + r_{k3}P_3Y + \ldots\ldots\ldots\ldots + r_k\,P_kY.$$

where,

r_1Y to r_kY = Coefficient of correlation between causal factors 1 to 'k' and independent character Y.

P_1Y to P_kY = Direct effect of characters 1 to k on character Y.

r_{12} to $r_{k-1,1}$ = Coefficient of correlation among causal factors.

The above equations were written in a matrix form as under-

$$\overset{A}{\begin{bmatrix} r_1Y \\ r_2Y \\ . \\ . \\ r_kY \end{bmatrix}} = \overset{C}{\begin{bmatrix} r_{11} & r_{12} & r_{13}\ldots\ldots\ldots\ldots r_{1k} \\ r_{21} & 1_{22} & r_{23}\ldots\ldots\ldots\ldots r_{2k} \\ . \quad . & & . \qquad\qquad . \\ . \quad . & & . \qquad\qquad . \\ r_{k1} & r_{k2} & r_{k3}\ldots\ldots\ldots\ldots 1 \end{bmatrix}} \overset{B}{\begin{bmatrix} P_1Y \\ P_2Y \\ \\ \\ P_kY \end{bmatrix}}$$

Then, $B = [C]^{-1}.A$

where,

$$[C_k]^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13}\ldots\ldots\ldots C_{1k} \\ C_{21} & C_{22} & C_{23}\ldots\ldots\ldots C_{2k} \\ . & . & . \qquad\qquad . \\ . & . & . \qquad\qquad . \\ C_{k1} & C_{k2} & C_{k3}\ldots\ldots\ldots C_{3k} \end{bmatrix}$$

Then the direct effects were calculated as follows-

$$P_1Y = \sum^{k} C_{1k}\, r_ky$$

$$i=1$$

$$P_2Y = \sum_{i=1}^{k} C_{2k}\, r_{ky}$$

$$P_kY = \sum_{i=1}^{k} C_{ki} r_k y$$

Residual effect:

Residual effect was obtained as per formula given below:

$$R = \sqrt{1 - E_{di} r_{ji}}$$

where,

d_i = Direct effect of character

j_{ij}= Correlation coefficient of i^{th} character with j^{th} character

Later the path coefficients were rated based on the scales given below (Lenka and Mishra, 1973).

0.0-0.09 = Negligible

0.1-0.19 = Low

0.2-0.29 = Moderate

0.3-0.99 = High

>1.00 = Very high

3.5.9 Genetic divergence

Mahalanobis, (1936) defines D^2 analysis as follows:

$$D^2P= b_1d_1+b_2d_2+\text{--------------}\ b_pd_p$$

A resource for group distance based on multiple characters with X_1, X_2, X_3…………X_p as the multiple measurements available on each individual and d_1, d_2 ………..d_p as $\bar{x}^1{}_{1.}$ $\bar{x}^2{}_2$ .... $\bar{x}^1{}_p$. $\bar{x}^2{}_p$ respectively is the difference in the means of two populations. The 'P' values are to be estimated that the ratio of variance between the populations to the variance within the populations is maximized. Taking variance and covariance under consideration, the D^2 value may be estimated by this formula.

$$D^2 = \sum_{i=0}^{1} Wij \sum \left(\bar{x}_i^{\,2} - \bar{x}_j^{\,1}\right)\left(\bar{x}_j^{\,1} - \bar{x}_i^{\,2}\right)$$

where,

W_{ij} is the inverse of estimated variance and covariance matrix

3.5.9.1 Step to estimate D^2 value

3.5.9.1.1 Collection of data

Data were collected considering “V” population and “P” characters and measured on each individual.

3.5.9.1.2 Test of significance

According to Wilk’s criteria a simultaneous test of difference between mean values of number of correlated variance is done.

Using pivotal condensation method, the determinant of error and error variety matrix will be calculated.

$$A = \left|\frac{W}{S}\right| = \left|\frac{\text{Determinant of errormatrix}}{\text{Determinant of error } + \text{ variety matrix}}\right|$$

$$\mathrm{V(State)} = -\mathrm{m}\log e = -\left[n\frac{(p+g+1)}{2}\right]\log e$$

where,

M = n – (p+q+1)/2

P = number of variance or character

Q = degree of freedom for population

N = degree of freedom for error + variety

E = constant (2.7183)

V (state) is distributed as X^2 with Pq degree of freedom.

The tabulated value of X^2 for Pq degree of freedom at 5% level is compared with the X^2 value for testing the significance.

3.5.9.1.3 Transformation of correlated values

Transformation was done by using pivotal consideration method. The correlated variables were first transformed into uncorrelated once and D^2 values were calculated.

3.5.9.2 Computation of D^2 values

The D^2 value obtained for a pair of population was taken as the calculated value of X^2 and tested against the tabulated value of X^2 at “P” degree of freedom, where “P” was considered as the number of characters.

3.5.9.3 Contribution of individual characters towards divergence

In all combination, each character was ranked on the basis of di = Yij – Yik values and rank 1 was given to the highest mean difference where “P” was considered as the number of characters.

3.5.9.4 Grouping of genotypes into various clusters by Tocher’s method

Populations are grouped in order to their relative genetic distance from each other, in the first step grouping of different varieties into distinct clusters. The two populations having the least distance from each other from the first two populations is added, then comes the fourth population and soon. There is disrupt increase in the average D^2 at certain stage by adding a particular population, and then this population is not added in the cluster.

Similarly, second cluster is formed. The process is continues till all the populations are included into one or other cluster.

3.5.9.5 Average intra cluster distance

The formula was used for measuring the intra cluster distance as follows:

$$\sum {Di^2}/{n}$$

Where,

$\sum Di^2/n$ is the sum of distance between all possible contributions (n) of the population included in the cluster.

3.5.9.6 Average inter cluster distance

First of all, the distance clusters were measured. The clusters were taken one by one and their distances from other cluster were calculated.

3.6 Principal component analysis

PCA is a well-known method of dimension reduction (Massay, 1965; Jolliffie, 1986), which seeks linear combinations of the columns of $\boldsymbol{X}$ with maximal variance, or equivalently, high information. It is routinely applied in chemo metrics with the goal of providing the most compact representation of the data. The original p variables $\boldsymbol{X} = [\mathbf{x}1 \ldots \mathbf{x}p]$ are transformed in a new predictor set $\mathbf{T} = [\mathbf{t}1 \ldots \mathbf{t}k]$, with $k \leq \min(n - 1, p)$. The new variables $\mathbf{t}j$, called *scores*, are a weighted average of the original $\boldsymbol{X}$ variables. The *principal components* are the eigenvectors, $\mathbf{u}j$ from the Eigen decomposition of $\boldsymbol{X}'\boldsymbol{X}$ (and of the sample covariance matrix $\mathbf{S}$, up to a constant). PCA sequentially maximizes the variance of a linear combination of the original predictor variables

$$\mathbf{U}j = \arg\max \mathrm{Var}(\boldsymbol{X}\mathbf{u}),$$

$$\mathbf{u}=1$$

Subject to the constraint that $\mathbf{u}'$ i $\mathbf{S}\mathbf{u}j = 0$ for all $1 \leq i < j$. This ensures that $\mathbf{t}j = \boldsymbol{X}\mathbf{u}j$ is un correlated with all the previous linear combinations $\mathbf{t}i = \boldsymbol{X}\mathbf{u}i$. The principal components are ordered in terms of the amount of variation of the original data they account for. The first principal component direction has the property that $\mathbf{t}1 = \boldsymbol{X}\mathbf{u}1$ has the largest sample variance among all normalized linear combinations of the columns of $\boldsymbol{X}$. Each subsequent component gives combinations with the largest possible variance which is un correlated with those that have been taken earlier.

There are various standard approaches to find the principal components, *e.g.* taking the singular value decomposition of $\boldsymbol{X}$. In chemo metrics it is common to estimate the principal components using the nonlinear iterative partial least-squares (NIPALS) algorithm (World, 1966). This is because the number of required components is usually much less than the total possible number (k _ p). In fact, the NIPALS algorithm does not calculate all the principal components at once, but it first calculates $\mathbf{t}1$ and $\mathbf{u}1$ from the $\boldsymbol{X}$ matrix. Then the outer product **t**1**u_**1 is subtracted from ***X*** and the residual ***X***2 is calculated. In turn, this residual can be used to calculate **t**2 and **u**2.

RESULTS

The result of the present study has been organized according to the objectives for conveniences of interpretation are presented under following headings.

4.1 Analysis of Variance

4.2 Parameter of Genetic Variability

4.2.1 Range and mean performance for different characters
4.2.2 Genotypic and Phenotypic coefficient of variation
4.2.3 Heritability (%)
4.2.4 Genetic advance as percentage of mean

4.3 Correlation Coefficient Analysis

4.4 Path Coefficient Analysis

4.5 Genetic Divergence

4.6 Principal Component Analysis

4.1 Analysis of variance

Analysis of variance refers to the observable differences in individuals for a particular trait. To know the extent of variation of observed characters among the genotypes in Sorghum, analysis of variance was performed and is presented in Table 4.1. Analysis of variance indicated that the mean sum of squares due to genotypes were significant for all the characters which revealed that there is considerable genetic variability among the material under study, which can be exploited through selection. The variability was observed for all the traits are presented under following headings.

.4.2 Parameter of genetic variability for fodder and allied traits

The parameter of genetic variability *viz*., mean, range, genotypic and phenotypic coefficient of variation (%) heritability (%) and genetic advance as percentage of mean for all the traits under study were analyzed for different traits and results are presented in Table 4.2.

Table4.1. Mean squares for fodder and allied traits in sorghum *(Kharif* 2016)

Source of Variation	**Degree of freedom**	**Mean square**						
		Days to 50 % flowering	**Plant height (cm)**	**No. of leaves/plant**	**Penultimate leaf area(cm^2)**	**Stem girth (mm)**	**Inter nodal length (cm)**	**No. of Inter nodes/Plant**
Replication	2	284.74	57.32	1.58	3421.25	0.59	0.61	1.96
Genotypes	30	371.34**	3051.06**	9.77**	13258.21**	37.31**	8.97**	10.40**
Error	60	125.00	419.87	2.95	1489.22	4.72	3.15	2.31

Source of Variation	**Degree of freedom**	**Mean square**							
		Leaf stem Ratio	**Brix's value (%)**	**Crude protein yield /plant (g)**	**Crude protein yield /plant/day (g)**	**Dry matter yield /plant/day (g)**	**Dry matter yield/plant (g)**	**Green fodder yield/ plant/day (g)**	**Green fodder yield/plant (g)**
Replication	2	0.00	1.13	0.577	0.00	0.00	55.54	0.06	1881.81
Genotypes	61	0.004**	6.99**	42.94**	0.004**	0.26**	4863.89**	5.74**	89958.73**
Error	122	0.001	2.94	0.00	138.54	0.01	2.31	0.54	4892.81

*Significant at probability level of 0.05 and **significant at probability level of 0.01.

4.2.1. Mean performance for different characters studied for fodder and allied traits

The mean performance of 31 diverse genotypes of Sorghum has been presented in Appendix-1. The value of mean and range for genotype are depicted in Table 4.2.

4.2.1.1 Days to 50% flowering

Genetic variability among accessions for days to 50% flowering ranged from 91.00 to 130.00 days with a mean value of 106.32 days. The genotypes IS 25301 required maximum days to 50% flowering (130.00), however ICSV 12006 took minimum 91.00 days to 50% flowering.

4.2.1.2 Plant height (cm)

Plant height recorded a minimum value of 142.00 cm and a maximum of 282.66 cm with a mean of 213.64 cm. The genotypes IS 17248 recorded maximum plant height (282.66 cm), whereas the minimum was (142.00 cm) recorded for genotype ICSH 14002.

4.2.1.3 Number of leaves/plant

The trait, number of leaves/plant varied from a minimum of 10.00 to maximum of 17.66 with a mean value of 13.29. The maximum number of leaves/plant (17.66) was recorded in ICSV 25335 genotype, and the number of leaves were minimum (10.00) in genotype ICSR 14006 and ICS 14002.

4.2.1.4 Penultimate leaf area (cm^2)

Penultimate leaf area ranged from 181.66 to 430.66 cm^2 the average being 274.80 cm^2. Genotype IS 17248 (430.66 cm^2) showed maximum leaf area, while the minimum was observed in genotype ICSR 93026 (181.66 cm^2).

4.2.1.5 Stem girth (mm)

Stem girth variability ranged between from 12.71 to 26.50 cm and the average was calculated to be 18.96 cm. Genotype IS 17248 (26.50) recorded highest stem girth, while it was lowest in ICSV 12006 (12.71 cm).

4.2.1.6 Inter nodal length (cm)

Variability for the trait inter nodal length ranged from 11.36 to 19.72 cm with a mean of 16.16 cm. Genotype CSH 22 SS (19.72) recorded maximum inter nodal length, while genotype ICSV 25335 expressed minimum (11.36 cm) inter nodal length.

4.2.1.7 No. of Internodes/plant

Internode/plant exhibited variability ranged from 9.66 to 17.66 with a mean of 13.41. The maximum number of Internodes/plant was recorded in ICSV 25335 (17.66). However, ICSH 14002 and ICSR 14006 recorded the lowest (9.66) on. of internodes/plant.

4.2.1.8 Leaf stem ratio

The range of leaf stem ratio varied from 0.36 to 0.54 with mean performance of 0.43. Genotype IS 17248 had maximum leaf stem ratio (0.54), while genotypes ICSV 93046 recorded minimum (0.36) leaf stem ratio.

4.2.1.9 Brix's value (%)

The trait brix's value ranged from 8.60 % to 14.93 % with a mean of 11.81 %. Genotype IS 17248 showed maximum value (14.93%), whereas genotypes ICSV 25308 showed minimum value of 8.60%.

4.2.1.10 Crude protein yield/plant (g)

This trait showed wide variation, ranging between 4.21 g to 20.08 g with a mean value of 10.49 g. Genotype IS 17248 showed maximum (20.07 g), whereas genotypes ICSV 12006 recorded minimum of 4.21 g crude protein yield/plant.

4.2.1.11 Crude protein yield/plant/day (g)

It ranged from 0.04 to 0.22 g with an average of 0.10 g. Maximum (0.22 g) crude protein yield/plant/day observed for genotype IS 17248, whereas genotypes ICSV 12006 and ICSH14002 had minimum of 0.04 g.

Table 4.2. Mean, Range, Variance, Heritability and GA as percentage of mean for 15 different traits in fodder Sorghum

S.N.	Characters	Mean	Range		Coefficient of variance (%)		Heritability broad sense (%)	Genetic advance as (%)of mean At k = 5%
			Min.	Max.	GCV (%)	PCV (%)		
1	Days to 50% flowering	106.32	91.00	130.00	8.52	13.54	40.20	11.05
2	Plant height (cm)	213.64	142.00	282.66	13.86	16.86	67.60	23.48
3	Number of leaves/plant	13.29	10.00	17.66	11.34	17.19	43.60	15.43
4	Penultimate leaf area (cm^2)	274.80	181.66	430.66	22.79	26.77	72.50	39.97
5	Stem girth (mm)	18.96	12.71	26.50	17.38	20.82	69.70	29.89
6	Inter nodal length (cm)	16.16	11.36	19.72	8.61	13.96	38.10	10.94
7	No. of Inter nodes/Plant	13.41	9.66	17.66	12.23	16.67	53.80	18.49
8	Leaf stem Ratio	0.43	0.36	0.54	7.85	10.92	51.60	11.62
9	Brix’s value (%)	11.81	8.60	14.93	9.83	17.55	32.40	11.34
10	Crude protein yield/plant (g)	10.49	4.21	20.08	35.06	37.93	85.40	66.78
11	Crude protein yield/plant/day (g)	0.10	0.04	0.22	37.02	41.62	79.10	67.85
12	Dry matter yield/plant/day (g)	0.96	0.49	1.75	30.48	32.44	88.30	59.01
13	Dry matter yield/plant (g)	109.03	50.94	201.34	36.43	37.90	92.40	72.12
14	Green fodder yield/plant/day (g)	4.25	2.07	7.85	31.84	36.24	77.22	57.65
15	Green fodder yield/plant (g)	450.84	201.67	839.67	38.13	41.17	85.80	72.76

4.2.1.12 Dry matter yield/plant/day (g)

The character dry matter yield/plant/day ranged from 0.49 g to 1.75 g with a mean performance of 0.96 g. Genotype CSH 22 SS showed highest value (1.75 g), whereas minimum value was recorded genotype ICS 14002 (0.49 g).

4.2.1.13 Dry matter yield/plant (g)

Dry matter yield/plant varied from 50.94 g to 201.34 g with mean value of 109.03 g. Genotype IS 17248 showed the highest dry matter yield (201.34g) while, genotype ICSH 14002 (50.94 g) had lowest.

4.2.1.14 Green fodder yield/plant/day (g)

The trait green fodder yield/plant/day ranged from 2.07 g to 7.85 g with mean of 4.25 g. Among all the genotypes CSH 22 SS recorded maximum (7.85 g) green fodder yield/plant/day whereas genotype ICSH 14002 had minimum of 2.07 g.

4.2.1.15 Green fodder yield/plant (g)

The character green fodder yield/plant ranged from 201.67g to 839.67 g with a mean value of 450.84 g/plant. Among all the genotypes IS 17248 (839.67) recorded maximum green fodder yield followed by IS 15957 (820.00), while genotype ICSV 12006 yielded minimum green fodder yield of 201.67 g. The green fodder yield for checks SSG59-3 and MP Chari was 444.00 and 377.00 g respectively.

4.2.2 Genotypic and phenotypic coefficient of variation

Genetic variability is the raw material for plant breeding on which selection acts to evolve superior genotypes. Thus, larger the amount of variation present for a character in the breeding materials, greater will be the scope for its improvement through selection. The phenotypic and genotypic coefficients of variation were computed to assess the existing variability in the material.

The estimation of phenotypic and genotypic coefficients of variation is of prime importance to get an idea about the relative extent of heritable and non heritable variation for all the characters studied.

The phenotypic coefficient of variation showed higher magnitudes than corresponding genotypic coefficient of variation. On the basis of overall results it was observed that highest PCV and GCV values 41.62% for crude protein yield/plant/day and 38.13% were for green fodder yield/plant respectively.

4.2.2.1 Genotypic coefficient of variation for fodder and allied traits

It is evident from the table 4.2 that genotypic coefficient of variation varied from 7.85% (leaf stem ratio) to 38.13% (green fodder yield/plant). The high magnitude (>30%) of genotypic coefficient of variation was recorded for the trait green fodder yield/plant (38.13%), crude protein yield/plant/day (37.02%), dry matter yield/plant (36.43%), crude protein yield/plant (35.06%), green fodder yield plant/day (31.84%) and dry matter yield/plant/day (30.48%).

The moderate (15%-30%) estimate of genotypic coefficient of variation was observed in penultimate leaf area (22.79%) and stem girth (17.38%).

The character exhibited low magnitude (<15%) of genotypic coefficient of variation were observed in plant height (13.86%), no. of internodes/plant (12.23%), no. of leaves/plant (11.34%), brix’s value (9.83%), internodal length (8.61%), days to 50% flowering (8.52%) and leaf stem ratio (7.85%).

4.2.2.2 Phenotypic coefficient of variation for fodder and allied traits

Phenotypic coefficient of variation showed the similar trends for all traits studied and the high magnitude (>30%) of phenotypic was recorded in crude protein yield/plant/day (41.62%), green fodder yield/plant (41.17%), crude protein yield/plant (37.93%), dry matter yield/plant (37.90%), green fodder yield/plant/day (36.24%) and dry matter yield/plant/day (32.44%).

The moderate (15%-30%) estimate of phenotypic coefficient of variation were observed in penultimate leaf area (26.77%), stem girth

(20.82%), brix's value (17.55%), no. of leaves/plant (17.19%), plant height (16.86%), and no. of internodes/plant (16.67%).

The characters exhibited low magnitude (<15%) of phenotypic coefficient of variation were observed in, intermodal length (13.96%), days to 50% flowering (13.54%) and leaf stem ratio (10.92%).

4.2.3.1 Heritability and genetic advance for fodder and allied traits

The estimate of broad sense heritability and genetic advance for all characters of 31 genotypes of fodder Sorghum is depicted in Table 4.2.

In order to measure relative magnitude of phenotypic and genotypic variability and to judge the masking influence of environment, heritability in broad sense for each trait was estimated. Heritability estimates provides the assessment of amount of transmissible genetic variability to total variability, it happens to be the most important basic factor that determines the genetic improvement attained through selection is not only dependent on heritability but also on the amount of genetic variation present in the breeding population and the extent of selection pressure applied by the breeder. Thus, heritability provides clear picture regarding the effectiveness of selection for improving the plant characters.

In general, high magnitude of heritability (>70%) was obtained for most of the characters. The heritability estimates ranged from 32.40% (brix's value) to 92.40% (dry matter yield/plant).

The highest heritability (>70%) was recorded for dry matter yield/plant (92.40%), dry matter yield/plant/day (88.30%), green fodder yield/plant (85.80%), green fodder yield/plant/day (77.22%), crude protein yield/plant (85.40%), crude protein yield/plant/day (79.10%) and penultimate leaf area (72.50%). The moderate range of heritability (50-70) estimate was observed for, stem girth (69.70%), plant height (67.60%), no. of internodes/plant (53.80%) and leaf stem ratio (51.60%).

The low value of heritability (<50%) was recorded for number of leaves/plant (43.60%), days to 50% flowering (40.20%), inter nodal length (38.10%) and brix's value (32.40%).

Genetic advance as percentage of mean

The parameter of genetic advance as percentage of mean (GA) is more reliable index for understanding the effectiveness of selection in improving the traits because its estimate is derived by involvement of heritability, phenotypic standard deviation and intensity of selection.

Thus genetic advance as percentage of mean along with heritability provides clear picture regarding the effectiveness of selection for improving the plant character. Genetic advance as percentage of mean were estimated for all the characters under study. The value of genetic advance as percentage of mean were classified into three groups *viz.,*

High = >50 percent

Medium = 30-50 percent

Low = < 30 percent

The estimate of genetic advance as percentage mean was high for most of the characters. The highest genetic advance as percentage of mean was observed in green fodder yield/plant (72.76%), dry matter yield/plant (72.12%), crude protein yield/plant/day (67.85%), crude protein yield/plant (66.78%), dry matter yield/plant/day (59.01%) and green fodder yield/plant/day (57.65 %).

The character recorded moderate range of genetic advance was obtained in penultimate leaf area (39.97%).

Low estimates of genetic advance as percentage of mean were obtained in Stem girth (29.89%), plant height (23.48%), no. of internodes/plant (18.49%), no. of leaves/plant (15.43%), leaf stem ratio (11.62%), brix's value (11.34%), days to 50% flowering (11.05%) and inter nodal length (10.94%).

4.3 Correlation coefficient analysis

The correlation coefficient analysis is the index of association between two variables. Phenotypic and genotypic correlations among forage yield and quality attributing traits were estimated. The result revealed higher estimate of phenotypic correlation coefficient than genotypic correlation coefficient for almost all the character studied results are presented in Table 4.3. (a) and 4.3. (b).

4.3.1 Phenotypic correlation coefficient for fodder yield and allied traits

4.3.1.1 Days to 50% flowering

Days to 50 percent flowering showed highly significant positive correlations with stem girth (0.545), green fodder yield/plant (0.524), dry matter yield/plant (0.511), penultimate leaf area (0.504), plant height (0.444), no. of internodes/plant (0.426), no. of leaves/plant (0.373), green fodder yield/plant/day (0.248), leaf stem ratio (0.218) and crude protein yield/plant (0.211).

4.3.1.2 Plant height (cm)

Plant height showed strong positive correlation with penultimate leaf area (0.802), no. of internodes/plant (0.739), green fodder yield/plant (0.723), dry matter yield/plant (0.722), stem girth (0.721), green fodder yield/plant/day (0.665), crude protein yield/plant (0.663), dry matter yield/plant/day (0.656), no. of leaves/plant (0.642), crude protein yield/plant/day (0.560), Inter nodal length (0.552) and with leaf stem ratio (0.357).

4.3.1.3 Number of leaves/plant

Number of leaves/plant showed highly significant positive correlation with no. of internodes/plant (0.833), stem girth (0.632), green fodder yield/plant (0.608), dry matter yield/plant (0.557), penultimate leaf area (0.554), crude protein yield/plant (0.484), green fodder yield/plant/day (0.458) and crude protein yield/plant/day (0.439).

Table 4.3. (a) Estimation of phenotypic correlation coefficients among fodder yield and its contributing traits in Sorghum.

SN	Characters	Plant height	No. of leaves /plant	Penultimate leaf area	Stem girth	Inter nodal length	No. of inter node /plant	Leaf stem ratio	Brix's value	Crude protein yield /plant	Crude protein yield/ plant/day	Dry matter yield/ plant/day	Dry matter yield/ plant	Green fodder yield/plant /day	Green fodder yield /plant
1	**Days to 50 % flowering**	0.444**	0.373**	0.504**	0.545**	0.115	0.426**	0.218*	0.074	0.211*	-0.027	0.188	0.511**	0.248**	0.524**
2	**Plant height**		0.642**	0.802**	0.721**	0.552***	0.739**	0.357**	0.044	0.663**	0.560**	0.656**	0.722**	0.665**	0.723**
3	**No. of leaves/Plant**			0.554**	0.632**	0.008	0.833**	0.279**	-0.012	0.484**	0.439**	0.505**	0.557**	0.458**	0.608**
4	**Penultimate leaf area**				0.739**	0.416**	0.640**	0.440**	0.232*	0.719**	0.616**	0.705**	0.809**	0.747**	0.812**
5	**Stem girth**					0.325**	0.589**	0.381**	0.195	0.749**	0.585**	0.751**	0.842**	0.750**	0.873**
6	**Inter nodal length**						-0.011	0.181	0.134	0.499**	0.434**	0.469**	0.438**	0.452**	0.397**
7	**No. of inter node /plant**							0.340**	-0.033	0.438**	0.376**	0.444**	0.525**	0.479**	0.572**
8	**Leaf stem ratio**								0.224*	0.351**	0.343**	0.312**	0.408**	0.368**	0.415**
9	**Brix's value**									0.317**	0.343**	0.297**	0.287**	0.306**	0.281**
10	**Crude protein yield/plant**										0.925**	0.954**	0.892**	0.919**	0.887**
11	**Crude protein yield/plant/day**											0.890**	0.743**	0.828**	0.743***
12	**Dry matter yield/plant /day**												0.903**	0.953**	0.912**
13	**Dry matter yield /plant**													0.897**	0.977**
14	**Green fodder yield/plant /day**														0.911**

Table 4.3. (b) Estimation of genotypic correlation coefficients among fodder yield and its contributing traits in Sorghum.

SN	Characters	Plant height	No. of leaves /plant	Penultimate leaf area	Stem girth	Inter nodal length	No. of inter node /plant	Leaf stem ratio	Brix's value	Crude protein yield /plant	Crude protein yield/ plant/day	Dry matter yield/ plant/day	Dry matter yield/ plant	Green fodder yield/plant /day	Green fodder yield /plant
1	**Days to 50 % flowering**	0.763	0.668	0.777	0.967	0.270	0.821	0.415	-0.125	0.686	0.461	0.684	0.845	0.809	0.832
2	**Plant height**		0.679	0.860	0.696	0.799	0.786	0.342	0.085	0.820	0.777	0.798	0.805	0.838	0.780
3	**No. of leaves/Plant**			0.620	0.733	0.155	0.942	0.248	0.138	0.754	0.758	0.748	0.787	0.753	0.778
4	**Penultimate leaf area**				0.853	0.779	0.659	0.552	0.323	0.911	0.844	0.871	0.911	0.931	0.898
5	**Stem girth**					0.533	0.626	0.350	0.435	0.899	0.785	0.890	0.961	0.919	0.954
6	**Inter nodal length**						0.178	0.370	0.331	0.824	0.821	0.796	0.657	0.783	0.640
7	**No. of inter node /plant**							0.327	-0.114	0.580	0.552	0.583	0.689	0.642	0.666
8	**Leaf stem ratio**								0.547	0.512	0.572	0.416	0.528	0.490	0.493
9	**Brix's value**									0.663	0.730	0.648	0.522	0.641	0.529
10	**Crude protein yield/plant**										0.954	0.985	0.969	0.962	0.961
11	**Crude protein yield/plant/day**											0.9222	0.860	0.852	0.848
12	**Dry matter yield/plant /day**												0.972	0.971	0.966
13	**Dry matter yield /plant**													0.984	1.008
14	**Green fodder yield/plant /day**														0.978

4.3.1.4 Penultimate leaf area (cm^2)

Correlation coefficient of this trait was highly significant and positive with green fodder yield/plant (0.812), dry matter yield/plant (0.809), green fodder yield/plant/day (0.747), stem girth (0.739), crude protein yield/plant (0.719), dry matter yield/plant/day (0.705), no. of internodes/plant (0.640), crude protein yield/plant/day (0.616), leaf stem ratio (0.440) and inter nodal length (0.416) and with brix value (0.232).

4.3.1.5 Stem girth (mm)

Positive correlation of stem girth with green fodder yield/plant (0.873), dry matter yield/plant (0.842), dry matter yield/plant/day (0.751), green fodder yield/plant/day (0.750), crude protein yield/plant (0.749), no. of internodes/plant (0.589), crude protein yield/plant/day (0.585), leaf stem ratio (0.381) and inter nodal length (0.325).

4.3.1.6 Inter nodal length (cm)

Inter nodal length expressed highly significant and positive correlation with crude protein yield/plant (0.499), dry matter yield/plant/day (0.469), green fodder yield/plant/day (0.452), dry matter yield/plant (0.438), crude protein yield/plant/day (0.434) and green fodder yield/plan (0.397).

4.3.1.7 No. of Internodes/plant

No. of Internodes per plant exhibited highly significance positive correlation green fodder yield/plant (0.572), dry matter yield/plant (0.525), green fodder yield/plant/day (0.479), dry matter yield/plant/day (0.444), crude protein yield/plant (0.438), crude protein yield/plant/day (0.376) and leaf stem ratio (0.340).

4.3.1.8 Leaf stem ratio

Leaf stem ratio expressed highly significant and positive correlation with green fodder yield/plant (0.415), dry matter yield/plant (0.408), green fodder yield/plant/day (0.368), crude protein yield/plant (0.351), crude protein yield/plant/day (0.343) and dry matter yield/plant/day (0.312) and with brix value (0.224).

4.3.1.9 Brix's value (%)

Brix's value exhibited highly significant and positive correlation with crude protein yield/plant/day (0.343), crude protein yield/plant (0.317), green fodder yield/plant/day (0.306), dry matter yield/plant/day (0.297), dry matter yield/plant (0.287) and green fodder yield/plant (0.281).

4.3.1.10 Crude protein yield/plant (g)

Crude protein yield/plant showed strong positive correlation with dry matter yield/plant/day (0.954), crude protein yield/plant/day (0.925), green fodder yield/plant/day (0.919), dry matter yield/plant (0.892) and green fodder yield/plant (0.887).

4.3.1.11 Crude protein yield/plant/day (g)

Crude protein yield/plant/day showed strong positive correlation with dry matter yield/plant/day (0.890), green fodder yield/plant/day (0.828), dry matter yield/plant and green fodder yield/plant (0.743).

4.3.1.12 Dry matter yield/plant/day (g)

Correlation coefficient of this trait showed highly positive association with green fodder yield/plant/day (0.953), green fodder yield/plant (0.912) and dry matter yield/plant (0.903).

4.3.1.13 Dry matter yield/plant (g)

The trait dry matter yield/plant showed highly significant and positively correlated with green fodder yield/plant (0.977) and green fodder yield/plant/day (0.897).

4.3.1.14 Green fodder yield/plant/day (g)

Green fodder yield/plant/day expressed strong positive correlation with green fodder yield/plant (0.911).

4.4 Path coefficient analysis

It is a standardized partial regression coefficient, which splits the correlation coefficient into the measure of direct and indirect effects. It measures the direct and indirect contribution of various independent characters on a dependent character for a replicated data; it is of three type's phenotypic, genotypic and environmental path coefficient.

Phenotypic path coefficient was worked out from all possible phenotypic correlation coefficient among the various characters under study constitute the genotypic path coefficient. Environmental path coefficients were worked out from all possible environmental correlation coefficient among various characters under study. Direct effect is the straightway effect of an independent character on a dependent one. Indirect effect is the effect of an independent character on the dependent one via other independent characters. Residual effect is the measure of the direct of other possible independent characters, which were not included in the study on the dependent character.

In general, the phenotypic direct as well as indirect effects were higher in magnitude as compared to the genotypic direct and indirect effects. The estimates of path coefficient for yield traits on green fodder yield per plant and its contributing traits. The results obtained from the present investigation for direct and indirect effects are presented as under following headings, Table 4.4. (a) and 4.4. (b).

Genotypic path analysis for fodder yield and its contributing traits.

4.4.1 Direct Effects

The genotypic path coefficient analysis of different morphological and its yield contributing traits on green fodder yield/plant revealed that crude protein yield/plant (0.5689), dry matter yield/plant/day (0.5341) and no. of leaves/plant (0.3113) recorded high estimates of positive direct effect. The moderate estimate of positive direct effect was recorded for green fodder yield/plant/day (0.2396), inter nodal length (0.2075), days to 50%

flowering (0.1548) and for leaf stem ratio (0.1687). While the dry matter yield/plant (0.0175) showed low value of positive direct effect on green fodder yield/plant.

On other hand the analysis of different morphological and its yield contributing traits on green fodder yield/plant revealed that high negative direct effect was exhibited by plant height (-0.4748) and crude protein yield/plant/day (-0.3803). The moderate negative direct effect was estimated for brix's value (-0.1956), While low value of negative direct effect was expressed by stem girth (-0.0571), no. of internodes/plant (-0.0414) and penultimate leaf area (-0.0244), and remaining other traits recorded either negligible positive or negative direct effect on green fodder yield/plant.

4.4.2 Indirect Effects

4.4.2.1 Days to 50% flowering

Days to 50% flowering had high positive indirect effect on green fodder yield/plant via crude protein yield/plant (0.3902) and dry matter yield/plant/day (0.3652) where as plant height had high and negative indirect effect (0.3620).

4.4.2.2 Plant height (cm)

This character expressed high negative indirect effect with all the traits such as penultimate leaf area (-0.4082), green fodder yield/plant/day (-0.3980), crude protein yield/plant (-0.3895), dry matter yield/plant (-0.3820), inter nodal length (-0.3791), dry matter yield/plant/day (-0.3789), no. of internodes/plant (-0.3729), crude protein yield/plant/day (-0.3692), days to 50% flowering (-0.3620), stem girth (-0.3303), no. of leaves/plant (-0.3223) and leaf stem ratio (-0.1624).

Table 4.4. (a) Estimation of genotypic path analysis among fodder yield and its contributing traits in Sorghum

S. N	Characters	Days to 50 % flowering	Plant height (cm)	No. of leaves/plant	Penultimate leaf area (cm^2)	Stem girth (mm)	Inter nodal length (cm)	No. of internodes/plant	Leaf stem ratio	Brix's value %	Crude protein yield/Plant (g)	Crude protein Yield/Plant /day (g)	Dry matter yield/plant/ day (g)	Dry matter yield/Plant (g)	Green fodder yield/plant /day (g)	Genotypic corre. Of yield with independent Character (r_{yi})
1	**Days to 50 % flowering**	**0.1548**	-0.3620	0.2079	-0.0189	-0.0552	0.0560	-0.0340	0.0701	0.0245	0.3902	-0.1755	0.3652	0.0148	0.1938	0.8318
2	**Plant height (cm)**	0.1181	**-0.4748**	0.2113	-0.0209	-0.0397	0.1656	-0.0325	0.0577	-0.0167	0.4667	-0.2957	0.4262	0.0141	0.2008	0.7801
3	**No. of leaves /plant**	0.1034	-0.3223	**0.3113**	-0.0151	-0.0418	0.0322	-0.0390	0.0418	-0.0269	0.4289	-0.2884	0.3994	0.0138	0.1803	0.7775
4	**Penultimate leaf area (cm^2)**	0.1203	-0.4082	0.1928	**-0.0244**	-0.0487	0.1616	-0.0272	0.0931	-0.0631	0.5182	-0.3210	0.4654	0.0159	0.2231	0.8976
5	**Stem girth (mm)**	0.1497	-0.3303	0.2281	-0.0208	**-0.0571**	0.1106	-0.0259	0.0591	-0.0851	0.5116	-0.2986	0.4754	0.0168	0.2201	0.9536
6	**Inter nodal length(cm)**	0.0418	-0.3791	0.0483	-0.0190	-0.0304	**0.2075**	-0.0074	0.0624	-0.0648	0.4688	-0.3122	0.4253	0.0115	0.1876	0.6401
7	**No. of internodes/plant**	0.1272	-0.3729	0.2931	-0.0160	-0.0357	0.0370	**-0.0414**	0.0551	0.0223	0.3297	-0.2100	0.3114	0.0121	0.1539	0.6658
8	**Leaf stem ratio**	0.0643	-0.1624	0.0772	-0.0134	-0.0200	0.0767	-0.0135	**0.1687**	-0.1070	0.2911	-0.2174	0.2224	0.0092	0.1174	0.4932
9	**Brix's value %**	-0.0194	-0.0405	0.0428	-0.0079	-0.0248	0.0687	0.0047	0.0923	**-0.1956**	0.3773	-0.2776	0.3462	0.0091	0.1536	0.5290
10	**Crude protein yield/plant (g)**	0.1062	-0.3895	0.2346	-0.0222	-0.0513	0.1710	-0.0240	0.0863	-0.1297	**0.5689**	-0.3628	0.5261	0.0170	0.2305	0.9610
11	**Crude protein yield/plant/day (g)**	0.0714	-0.3692	0.2360	-0.0206	-0.0448	0.1703	-0.0228	0.0965	-0.1428	0.5428	**-0.3803**	0.4925	0.0151	0.2042	0.8482
12	**Dry matter Yield/ plant/day (g)**	0.1059	-0.3789	0.2328	-0.0212	-0.0508	0.1652	-0.0241	0.0703	-0.1268	0.5604	-0.3507	**0.5341**	0.0170	0.2327	0.9657
13	**Dry matter yield/Plant (g)**	0.1309	-0.3820	0.2451	-0.0222	-0.0549	0.1362	-0.0285	0.0891	-0.1020	0.5513	-0.3272	0.5192	**0.0175**	0.2358	1.0083
14	**Green fodder yield/plant/day (g)**	0.1252	-0.3980	0.2342	-0.0227	-0.0524	0.1625	-0.0266	0.0827	-0.1254	0.5473	-0.3241	0.5187	0.0172	**0.2396**	**0.9782**

Table 4.4. (b) Estimation of phenotypic path analysis among fodder yield and its contributing traits in Sorghum

S. N	Characters	Days to 50 % flowering	Plant height (cm)	No. of leaves/ plant	Penultimate leaf area (cm^2)	Stem girth (mm)	Inter nodal length (cm)	No. of internodes/plant	Leaf stem ratio	Brix's value %	Crude protein yield/ Plant (g)	Crude protein Yield/plant/day (g)	Dry matter yield/Plant /day (g)	Dry matter yield/ Plant (g)	Green fodder yield/plant /day (g)	Phenotypic corre. Of yield with independent Character (r_{yi})
1	**Days to 50 % flowering**	**0.1712**	-0.0283	0.0261	0.0162	0.0493	-0.0015	-0.0022	0.0075	-0.0003	-0.0088	0.0002	0.0679	0.1892	0.0378	0.5244
2	**Plant height (cm)**	0.0760	**-0.0638**	0.0450	0.0258	0.0653	-0.0073	-0.0038	0.0123	-0.0002	-0.0277	-0.0042	0.2370	0.2673	0.1013	0.7233
3	**No. of leaves/plant**	0.0639	-0.0409	**0.0701**	0.0178	0.0572	-0.0001	-0.0043	0.0096	0.0000	-0.0202	-0.0033	0.1824	0.2062	0.0697	0.6083
4	**Penultimate leaf area (cm^2)**	0.0863	-0.0512	0.0388	**0.0321**	0.0669	-0.0055	-0.0033	0.0152	-0.0009	-0.0300	-0.0046	0.2547	0.2997	0.1136	0.8121
5	**Stem girth (mm)**	0.0932	-0.0459	0.0443	0.0237	**0.0906**	-0.0043	-0.0030	0.0132	-0.0007	-0.0312	-0.0043	0.2715	0.3118	0.1141	0.8730
6	**Inter nodal length(cm)**	0.0198	-0.0352	0.0006	0.0134	0.0294	**-0.0132**	0.0001	0.0063	-0.0005	-0.0208	-0.0032	0.1698	0.1623	0.0688	0.3975
7	**No. of internodes/plant**	0.0729	-0.0471	0.0584	0.0206	0.0534	0.0002	**-0.0051**	0.0117	0.0001	-0.0183	-0.0028	0.1603	0.1944	0.0730	0.5717
8	**Leaf stem ratio**	0.0373	-0.0228	0.0196	0.0141	0.0345	-0.0024	-0.0017	**0.0345**	-0.0008	-0.0146	-0.0025	0.1128	0.1512	0.0560	0.4151
9	**Brix's value %**	0.0126	-0.0028	-0.0008	0.0075	0.0176	-0.0018	0.0002	0.0077	**-0.0037**	-0.0132	-0.0025	0.1076	0.1063	0.0466	0.2814
10	**Crude protein yield/plant (g)**	0.0362	-0.0423	0.0339	0.0231	0.0678	0.0066	0.0022	0.0121	-0.0012	**-0.0417**	-0.0069	0.3448	0.3304	0.1399	0.8873
11	**Crude protein yield/plant/day (g)**	-0.0046	-0.0357	0.0308	0.0198	0.0530	-0.0057	-0.0019	0.0118	-0.0013	-0.0386	**-0.0074**	0.3217	0.2753	0.1260	0.7433
12	**Dry matter Yield/plant /day (g)**	0.0322	-0.0418	0.0354	0.0226	0.0681	-0.0062	-0.0023	0.0108	-0.0011	-0.0398	-0.0066	**0.3614**	0.3345	0.1450	0.9122
13	**Dry matter yield/plant (g)**	0.0875	-0.0460	0.0390	0.0260	0.0763	-0.0058	-0.0027	0.0141	-0.0010	-0.0372	-0.0055	0.3264	**0.3703**	0.1364	0.9778
14	**Green fodder yield/plant/day (g)**	0.0425	-0.0424	0.0321	0.0240	0.0679	-0.0060	-0.0024	0.0127	-0.0011	-0.0383	-0.0061	0.3444	0.3320	**0.1522**	**0.9114**

4.4.2.3 Number of leaves/plant

Positive indirect effect of no. of leaves/plant on green fodder yield/plant was found to be high for no. of internodes/plant (0.2931), followed by dry matter yield/plant/day (0.2451), crude protein yield/plant/day (0.2360), crude protein yield/plant (0.2346), green fodder yield/plant/day (0.2342), dry matter yield/plant/day (0.2328), stem girth (0.2281), plant height (0.2113), days to 50% flowering (0.2079), penultimate leaf area (0.1928), and some also low value of positive indirect effect was recorded for leaf stem ratio (0.0772), inter nodal length (0.0483) and brix value (0.0428).

4.4.2.4 Penultimate leaf area (cm^2)

Penultimate leaf area had exhibited low magnitude of negative indirect effect on green fodder yield/plant. The negative indirect effects were shown by green fodder yield/plant/day (-0.0227), dry matter yield/plant (-0.0222), crude protein yield/plant (-0.0222), dry matter yield/plant/day (-0.0212), plant height (-0.0209), stem girth (-0.0208) and crude protein yield/plant/day (-0.0206). And remaining traits had exhibited negligible negative indirect effect on green fodder yield/plant.

4.4.2.5 Stem girth (mm)

The observation was obtained low value of negative indirect effect of stem girth on green fodder yield/plant. These indirect effects were expressed by days to 50% flowering (-0.0552), dry matter yield/plant (-0.0549), green fodder yield/plant/day (-0.0524), crude protein yield/plant (-0.0513), dry matter yield/plant/day (-0.0508), penultimate leaf area (-0.0487), crude protein yield/plant/day (-0.0448), no. of leaves/plant (-0.0418), plant height (-0.0397), no. of internodes/plant (-0.0357), inter nodal length (-0.0304), brix value (-0.0248) and leaf stem ratio (-0.0200).

4.4.2.6 Inter nodal length (cm)

The trait inter nodal length indicated positive indirect effect on green fodder yield/plant such effects were observed via crude protein yield/plant (0.1710), crude protein yield/plant/day (0.1703), plant height (0.1656), dry matter yield/plant/day (0.1652), penultimate leaf area (0.1616), dry matter yield/plant (0.1362) whereas stem girth (0.1106), leaf stem ratio (0.0767), brix value (0.0687), days to 50% flowering (0.0560) and no. of internodes/plant (0.0370) had very low or negligible contribution.

4.4.2.7 No. of internodes/plant

No. of internodes/plant had low positive indirect effect on green fodder yield/plant were recorded via brix value (0.0047), while remaining characters had negative indirect effect which is very low in magnitude *i.e.*, no. of leaves/plant (-0.0390), days to 50% flowering (-0.0340), plant height (-0.0325), dry matter yield/plant (-0.0285), penultimate leaf area (0.0272), green fodder yield/plant/day (-0.0266), stem girth (-0.0259), dry matter yield/plant/day (-0.0241), crude protein yield/plant (-0.0240), crude protein yield/plant/day (-0.0228) and leaf stem ratio (-0.0135). The remaining traits had exhibited negligible negative indirect effect on green fodder yield/plant.

4.4.2.8 Leaf stem ratio

Leaf stem ratio had low positive indirect effect on green fodder yield/plant was exhibited via crude protein yield/plant/day (0.0965), penultimate leaf area (0.0931), brix value (0.0923), dry matter yield/plant (0.0891), crude protein yield/plant (0.0863), green fodder yield/plant/day (0.0827), dry matter yield/plant/day (0.0703), days to 50% flowering (0.0701), inter nodal length (0.0624), stem girth (0.0591), plant height (0.0577), no. of internodes/plant (0.0551) and no. of leaves/plant (0.0418).

4.4.2.9 Brix’s value (%)

Brix’s value had showed low magnitude of positive indirect effect on green fodder yield/plant. These low positive indirect effects were obtained for days to 50% flowering (0.0245) and no. of internodes/plant (0.0223). On other hand negative indirect effect on green fodder yield/plant exhibited via crude protein yield/plant/day (-0.1428), crude protein yield/plant (-0.1297), dry matter yield/plant (-0.1268), green fodder yield/plant/day (-0.1254), leaf stem ratio (-0.1070), dry matter yield/plant (-0.1020), stem girth (-0.0851), internodal length (-0.0648), penultimate leaf area (-0.0631), no. of leaves/plant (-0.0269), and plant height (-0.0167).

4.4.2.10 Crude protein yield/plant (g)

Crude protein yield/plant expressed high and effective positive indirect effect on green fodder yield/plant. These positive indirect effects were shown via dry matter yield/plant/day (0.5604), dry matter yield/plant (0.5513), green fodder yield/plant/day (0.5473), crude protein yield/plant/day (0.5428), penultimate leaf area (0.5182), stem girth (0.5116), internodal length (0.4688), plant height (0.4667), no. of leaves/plant (0.4289), days to 50% flowering (0.3902), brix value (0.3773), no. of internodes/plant (0.3297) and leaf stem ratio (0.2911).

4.4.2.11 Crude protein yield/plant/day (g)

Crude protein yield/plant/day had shown negative indirect effect on green fodder yield/plant. The negative indirect effects were shown via crude protein yield/plant (-0.3628), dry matter yield/plant/day (-0.3507), dry matter yield/plant (-0.3272), green fodder yield/plant/day (-0.3241), penultimate leaf area (-0.3210), inter nodal length (-0.3122), stem girth (-0.2986), plant height (-0.2957), no. of leaves/plant (-0.2884), brix value (-0.2776), leaf stem ratio (-0.2174), no. of internodes/plant (-0.2100) and days to 50% flowering (-0.1755).

4.4.2.12 Dry matter yield/plant/day (g)

Dry matter yield/plant/day had exhibited high and effective positive indirect effect on green fodder yield/plant. The positive indirect effects were manifested by crude protein yield/plant (0.5261), dry matter yield/plant (0.5192), green fodder yield/plant/day (0.5187), crude protein yield/plant/day (0.4925), stem girth (0.4754), penultimate leaf area (0.4654), plant height (0.4262), inter nodal length (0.4253), no. of leaves/plant (0.3994), days to 50% flowering (0.3652), brix value (0.3462), no. of internodes/plant (0.3114) and leaf stem ratio (0.2224).

4.4.2.13 Dry matter yield/plant (g)

Dry matter yield/plant showed low magnitude of positive indirect effect on green fodder yield/plant. These low positive indirect effects were obtained for green fodder yield/plant/day (0.0172), dry matter yield/plant/day (0.0170), crude protein yield/plant (0.0170), stem girth (0.0168), penultimate leaf area (0.0159), crude protein yield/plant/day (0.0151), days to 50% flowering (0.0148), plant height (0.0141), no. of leaves/plant (0.0138), no. of internodes/plant (0.0121) and internodal length (0.0115). Rest of the characters like leaf stem ratio (0.0092) and brix's value (0.0091) showed negligible positive indirect effect.

4.4.2.14 Green fodder yield/plant/day (g)

Green fodder yield/plant/day had manifested moderate positive indirect effect on green fodder yield/plant. The positive indirect effects was manifested by dry matter yield/plant (0.2358) followed by dry matter yield/plant/day (0.2327), crude protein yield/plant (0.2305), penultimate leaf area (0.2231), stem girth (0.2201), plant height (0.2008), days to 50% flowering (0.1938), internodal length (0.1876), no. of leaves/plant (0.1803), no. of internode/plant (0.1539), brix value (0.1536) and leaf stem ratio (0.1174).

4.4.3 Residual effect

The residual effect for genotypic path coefficient analysis reported negligible (r = 0.0316).

4.5 Genetic divergence for fodder and allied traits

The parental diversity is of prime importance to obtain better recombinants and superior genotypes in the segregating generations (Moll *et al.,* 1962). Genetic diversity based on multiple characters as suggested by (Mahalanobis, 1928) is an important biometrical approach which segregates genotypes/varieties into different cluster in such a manner that varieties/lines within cluster are more over less divergent as compared to varieties in different cluster. Different clusters containing a set of genotypes having maximum inter cluster distance indicates that varieties in such clusters are more genetically divergent. Knowledge of genetic diversity is of paramount significance as it is well known fact that hybridization between genetically divergent parents yield superior recombinant, high heterotic values and superior segregate in subsequent generations.

4.5.1 Contribution of individual character towards genetic divergence for fodder and allied traits

The characters which showed higher contribution (%) towards the divergence should be given prime importance during selection. Relatively high variation for a trait indicated a greater contribution to fodder yield diversity. The percentage contribution towards genetic divergence by all the 15 character under study presents in Table 4.5.

The percent contribution of individual characters toward the total divergence was found highest for green fodder yield/plant (35.70%) followed by dry matter yield/plant/day (29.41%), green fodder yield/plant/day (12.47%), stem girth (5.38%), crude protein yield/plant/day (5.16%), leaf stem ratio (2.15%), no. of leaves/plant (2.15%), brix's value (1.72%), crude protein yield/plant (1.51%), internodal length (1.08%), plant height (1.10%), dry matter yield/plant (1.08%) and where as rest of the characters *viz*., penultimate leaf area (0.86%), no. of internodes/plant (0.40%) and days to 50% flowering (0.22%) showed least contribution towards divergence.

The study comprised of 31 genotypes based on 15 agro-morphological and fodder yield contributing traits following Mahalanobis D^2 statistics. On the basis of D^2 values, the 31 genotypes were grouped into 6 clusters following Tocher's method. The cluster I was poly-genotypic with 19 genotypes followed by cluster III with 6 genotypes, cluster II with 3 genotypes and remaining clusters have only 1 genotype. Cluster wise distribution of genotypes is summarized in Table 4.6.

Table 4.5. Percentage contribution of character towards divergence in fodder Sorghum

SN	Characters	Number of Times Ranked first	Percentage (%) Contribution towards divergence
1	**Days to 50% flowering**	1	0.22%
2	**Plant height (cm)**	5	1.10%
3	**Number of leaves/plant**	10	2.15%
4	**Penultimate leaf area (cm^2)**	4	0.86%
5	**Stem girth (mm)**	25	5.38%
6	**Inter nodal length (cm)**	5	1.08%
7	**No. of internodes/plant**	2	0.40%
8	**Leaf stem ratio**	10	2.15%
9	**Brix ‘s value (%)**	8	1.72%
10	**Crude protein yield/plant (g)**	7	1.51%
11	**Crude protein yield/plant/day (g)**	24	5.16%
12	**Dry matter yield/plant/day (g)**	142	29.04%
13	**Dry matter yield/plant (g)**	5	1.08%
14	**Green fodder yield/plant/day (g)**	58	12.47%
15	**Green fodder yield/plant (g)**	166	35.70%

4.5.2 Grouping of genotypes into different cluster

Table 4.6. Distribution of fodder Sorghum genotypes in different clusters

Cluster	No. of genotypes	Name of genotypes
I	19	**IS 3717, IS 25234, ICSV 25316, ICSSH 28, ICSR 93025, IS 25340, ICSR 93026, ICSR 93022, S 35, MP Chari(C), IS 25302, ICSV 25308, IS 17349, ICSV 93046, NTJ 2, SSG 59-3(C), ICS 28001, ICSR 93034, ICSV 25306**
II	3	**ICS 14002, ICSR 14006, ICSV 12006**
III	6	**IS 15957, IS 17248, CSH 22 SS, IS 25301, IS 13705, IS 13553**
IV	1	**ICSV 93046**
V	1	**ICSV 25335**
VI	1	**IS 18542**

4.5.3 Inter and intra cluster divergence D^2 for yield and allied traits of fodder Sorghum

The intra and inter cluster D^2 mean values are presented in Table 4.7. On the basis of D^2 values, 31 genotypes were grouped into 6 clusters. Intra cluster distance ranged from (0.00) to (34.85). Divergence analysis revealed that cluster III had maximum intra cluster value (34.85) followed by cluster I (16.01), cluster II (6.71) and rest of the clusters (IV, V, VI) had no intra cluster divergence.

On other hand the inter cluster distance ranged from (28.03) to (325.62), for which D^2 value was maximum between cluster II and III (325.62), while it was minimum (28.03) for cluster IV and VI.

Table 4.7. Average intra and inter cluster divergence D^2 values among 31 genotype of fodder Sorghum

Cluster number	I	II	III	IV	V	VI
I	**16.01**	51.13	169.95	41.31	30.54	65.11
II		**6.71**	325.62	125.69	72.98	173.67
III			**34.85**	70.69	142.24	73.28
IV				**0.00**	32.25	28.03
V					**0.00**	61.52
VI						**0.00**

Cluster I was poly-genotypic and placed nearest to cluster V (30.54) followed in ascending order by cluster IV (41.31), cluster II (51.13), cluster VI (65.11) and cluster III (169.95) was distantly placed.

Cluster II was poly-genotypic (tri-genotypic) and expressed closest to cluster V (72.98) proceeded by cluster IV (125.69), cluster VI (173.67) and cluster III (325.62).

Cluster III was poly-genotypic and was found the closest to cluster IV (70.69) followed by cluster VI (73.28) and cluster V (124.24).

Cluster IV was mono-genotypic and was found nearest to cluster VI (28.03) preceded by cluster V (32.25).

Cluster V was mono-genotypic and manifest to have inter cluster distance of D^2 = 61.52 with cluster VI.

Cluster VI was found to be mono-genotypic and distance from other clusters has been described in the earliest cluster.

4.5.4 Average cluster means for fodder and allied traits

The cluster mean values for 15 characters are presented in Table 4.8.

4.5.4.1 Days to 50% flowering

The cluster mean value of days to 50 percent flowering was minimum (94.11) for cluster II and maximum for cluster VI (127.00).

4.5.4.2 Plant height (cm)

The maximum cluster mean value obtained for plant height (248.78 cm) in cluster III and minimum value was recorded by cluster II (150.33 cm).

4.5.4.3 No. of leaves/plant

Number of leaves/plant recorded highest cluster mean value (17.67) for cluster V and minimum (10.44) in cluster II.

4.5.4.4 Penultimate leaf area (cm^2)

The cluster mean values of penultimate leaf area was highest for cluster III (380.22 cm^2) and lowest for cluster II (203.89 cm^2).

4.5.4.5 Stem girth (mm)

Average cluster mean value of stem girth was recorded to be maximum for cluster III (24.26 mm) and minimum for cluster II (14.54 mm).

4.5.4.6 Internodal length (cm)

The cluster mean values of internodal length showed maximum value (17.78 cm) for cluster III and minimum (11.36 cm) for cluster V.

4.5.4.7 No. of internode/plant

The average clusters mean values of no. of internode/plant was highest for cluster V (17.67) and lowest for cluster II (10.22).

4.5.4.8 Leaf stem ratio

Leaf stem ratio recorded maximum average mean value (0.46) for cluster III, V & VI, and minimum (0.36) for cluster IV.

4.5.4.9 Brix's value (%)

The cluster mean value of brix's were recorded to be maximum in cluster III (13.08 %) and minimum in cluster V (11.10 %)

4.5.4.10 Crude protein yield/plant (g)

Crude protein yield/plant recorded highest cluster mean value for cluster III (16.72 g) and lowest for cluster II (5.39 g).

4.5.4.11 Crude protein yield/plant/day (g)

The crude protein yield/plant/day recorded maximum cluster mean value for cluster III (0.16 g) and minimum value for cluster II (0.06 g).

4.5.4.12 Dry matter yield/plant/day (g)

The average cluster mean value of dry matter yield/plant/day was maximum for cluster III (1.44 g) and minimum for cluster II (0.53 g).

4.5.4.13 Dry matter yield/plant (g)

The average mean value of dry matter yield/plant was highest for cluster III (178.85 g) and lowest for cluster II (54.43 g).

4.5.4.14 Green fodder yield per plant per day (g)

The cluster mean value of green fodder yield/plant/day was found to be maximum for cluster III (6.42g) and minimum for cluster II (2.24g).

4.5.4.15 Green fodder yield/plant (g)

The cluster mean value of green fodder yield/plant recorded maximum (750.39 g) in cluster III and minimum (218.33 g) in cluster II.

Table 4.8. Cluster mean for yield and its components traits of 31 genotypes in fodder Sorghum

Cluster no.	**I**	**II**	**III**	**IV**	**V**	**VI**
Days to 50 % flowering	102.96	94.11	117.78	113.00	110.67	127.00
Plant height (cm)	212.05	150.33	248.78	216.00	198.00	236.33
No. of leaves / plant	12.95	10.44	15.00	14.67	17.67	12.33
penultimate leaf area (cm^2)	249.91	203.89	380.22	278.00	238.00	361.67
Stem girth (mm)	17.62	14.54	24.26	23.07	18.72	22.07
Internodal length (cm)	16.15	14.42	17.78	15.43	11.36	17.53
No. of internodes / plant	13.19	10.22	14.78	14.00	17.67	14.33
Leaf stem ratio	0.41	0.42	0.46	0.36	0.46	0.46
Brix's value (%)	11.29	12.20	13.08	12.87	11.10	12.43
Crude protein yield / plant (g)	9.28	5.39	16.72	12.84	8.04	11.58
Crude protein yield / Plant / day (g)	0.10	0.06	0.16	0.12	0.07	0.09
Dry matter yield / plant/ day (g)	0.87	0.53	1.44	1.14	0.84	1.00
Dry matter yield / plant (g)	93.49	54.43	178.85	131.00	106.38	129.91
Green fodder yield / plant / day (g)	3.77	2.24	6.42	4.74	4.14	5.97
Green fodder yield / Plant (g)	**383.05**	**218.33**	**750.39**	**539.33**	**464.33**	**537.33**

4.6 Principal component analysis

Principal Component Analysis is a well-known method of dimension reduction that can be used to reduce a large set of variables to a small set that still contains most of the information in the large set (Massay, 1965; Jolliffie, 1986). It is a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components. The first principal component accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible.

In the present investigation, Eigen values, % variance and cumulative Eigen values are mentioned in Table 4.9. Out of fifteen PC, only 4 principal components (PCs) exhibited more than 1.00 Eigen value and showed about 75.851% variability among the traits studied. Out of them, only three principal components were given due importance for further explanation the PC1 had the highest variability (49.609 %) followed by PC2 (11.585%), and PC3 (7.732%), for traits under study.

Scree plot explained the percentage of variance associated between Eigen values and principal components with each PC obtained by drawing a graph. First principal component recorded the highest variation 49.609% (PC1) followed by 11.585% (PC2) and 7.732% (PC3).Total variation of three PCs were recorded to be 68.925%. Semi curve line obtained after eighth PC with little variation observed in each PC indicated that maximum variation was found in PC1; therefore selection of lines for characters under PC1 may be desirable.

Table 4.9. Eigen values, % variance and cumulative Eigen values Of Sorghum genotype

Traits	Principal component	Eigen values	% of Variance	Cumulative %
Days to 50 % flowering	PC1	7.441	49.609	49.609
Plant height (cm)	PC 2	1.738	11.585	61.193
No. of leaves/Plant	PC 3	1.160	7.732	68.925
Penultimate leaf area (cm^2)	PC 4	1.039	6.927	75.851
Stem girth (mm)	PC 5	0.763	5.086	80.937
Inter nodal Length (cm)	PC 6	0.605	4.033	84.969
No. of Inter node/plant	PC 7	0.437	2.910	87.880
Leaf stem ratio	PC 8	0.429	2.862	90.742
Brix's value (%)	PC 9	0.333	2.217	92.959
Crude protein yield/plant (g)	PC 10	0.267	1.780	94.738
Crude protein yield/plant/day(g)	PC 11	0.242	1.610	96.349
Dry matter yield/plant/day (g)	PC 12	0.198	1.321	97.670
Dry matter yield/Plant (g)	PC 13	0.176	1.174	98.843
Green fodder yield/plant/day(g)	PC 14	0.122	0.813	99.656
Green fodder yield/plant (g)	PC 15	0.052	0.344	100.000

Table 4.10. Principal component of 15 yield contributing trait of advance Sorghum genotypes

Traits	No. of PCs		
	PC1	PC2	PC3
Days to 50 % flowering	**0.563**	-0.503	0.076
Plant height (cm)	**0.702**	-0.280	0.341
No. of leaves/Plant	**0.664**	-0.362	-0.372
Penultimate leaf area (cm^2)	**0.730**	-0.209	0.234
Stem girth (mm)	**0.821**	-0.087	-0.084
Inter nodal Length (cm)	0.468	0.252	**0.572**
No. of Inter node/plant	**0.605**	-0.583	-0.089
Leaf stem ratio	0.233	-0.107	**0.647**
Brix's value (%)	0.255	**0.619**	0.094
Crude protein yield/plant (g)	**0.826**	0.340	-0.084
Crude protein yield/plant/day (g)	**0.693**	0.405	-0.133
Dry matter yield/plant/day (g)	**0.856**	0.310	-0.151
Dry matter yield/Plant (g)	**0.898**	0.021	-0.072
Green fodder yield/plant/day (g)	**0.872**	0.222	-0.055
Green fodder yield/plant (g)	**0.904**	0.008	-0.137

Extraction Method: Principal Component Analysis

Rotated component matrix revealed that the first principal component (PC1) which accounted for the highest variation (49.609%) was mostly related with traits such as days to 50% flowering, plant height, no. of leaves/plant, penultimate leaf area, stem girth, no. of internodes/plant, crude protein yield/plant, crude protein yield/plant/day, dry matter yield/plant/day, green fodder yield/plant/day, dry matter yield/plant and green fodder yield/plant.

In second principal component (PC2) consisting of mainly single trait brix value %, while PC3 was consisting of mainly two traits *viz*., inter nodal length and leaf stem ratio. Details have been indicated in table 4.10 and Table 4.11.

On the basis of PCA, most of the important yield and yield attributing traits were present in PC1, PC2 and PC3. Rotated component matrix revealed that first three PCs are representing maximum variability (68.925%) hence, the traits falling to these three PCs may be given due importance in sorghum breeding.

Table 4.11. Interpretation of rotated component matrix for the traits having maximum value in each PCs

	PC1	**PC2**	**PC3**
CHARECTORS	Days to 50 % flowering	Brix's value (%)	Internodal Length(cm)
	Plant height (cm)	-	Leaf stem ratio
	No. of leaves/Plant	-	-
	Penultimate leaf area (cm^2)	-	-
	Stem girth (mm)	-	-
	No. of Inter node/plant	-	-
	Crude protein yield/plant (g)	-	-
	Crude protein yield/plant/day(g)	-	-
	Dry matter yield/plant /day (g)	-	-
	Dry matter yield/Plant (g)	-	-
	Green fodder yield/plant /day(g)	-	-
	Green fodder yield /plant (g)	-	-

In 31 Sorghum genotypes, the top principal component scores (PC score) for all the traits were estimated in these three components and presented in Table 4.12. These scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of principal component.

Table 4.12. PC scores of advanced Sorghum genotypes

S.No.	Genotypes	PC1	PC2	PC3
1	IS 3717	0.590	-0.318	-0.583
2	IS 13553	**3.123**	-0.446	0.197
3	IS 13705	**3.562**	0.282	0.083
4	IS 15957	**6.671**	0.518	0.881
5	IS 17248	**8.224**	0.560	**1.892**
6	IS 17349	-0.031	-0.623	0.178
7	IS 18542	**2.231**	-0.705	**1.499**
8	IS 25234	0.109	-1.344	-0.064
9	S25301	**3.409**	-0.604	-0.663
10	IS 25302	-1.589	-1.785	-1.452
11	IS 25340	-0.860	**1.112**	-1.315
12	ICSV 25335	-0.080	-3.003	-2.037
13	ICSSH 28	-1.351	**1.775**	-0.213
14	CSH 22 SS	**6.076**	**2.464**	0.495
15	ICSV 93046	**1.538**	0.166	-1.879
16	ICSH 14002	-5.219	**1.176**	0.076
17	ICSH 28001	0.212	0.328	0.836
18	ICSR 14006	-4.426	**1.655**	0.530
19	ICSR 93022	-1.496	**2.178**	-0.034
20	ICSR 93025	-2.278	0.783	-0.909
21	ICSR 93026	-1.852	**1.065**	0.465
22	S 35	-1.980	**1.861**	0.791
23	NTJ 2	-1.565	-0.777	**1.397**
24	ICSR 93034	-2.607	0.906	0.463
25	ICSV 93046	-1.527	-1.544	0.254
26	ICSV25306	-2.415	-0.834	**1.320**
27	ICSV25308	-1.427	-2.035	0.354
28	ICSV 25316	-0.420	-1.199	-0.601
29	ICSV12006	-5.171	-0.120	-0.664
30	SSG 59-3	**1.077**	-0.797	-0.051
31	MP Chari	-0.530	-0.695	-1.246

$Eigen\ value > 1$

High PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype. IS 17248 had the highest PC score followed by IS 15957, CSH 22 SS, IS 13705, IS25301, IS 13553, IS 18542, ICSV 93046 and SSG 59-3 in PC1 indicated that these genotypes possesses high values of traits for days to 50% flowering, plant height, no. of leaves/plant, penultimate leaf area, stem girth, no. of inter node/plant, crude protein yield/plant, crude protein yield/plant/day, dry matter yield/plant/day, dry matter yield/Plant, green fodder yield/plant/day and green fodder yield/plant. The highest PC score of CSH 22 SS followed by ICSR 93022, S 35, ICSSH 28, ICSR 14006, ICSH 14002, IS 25340 and ICSR 93026 in PC2 was mainly related with brix's value which is mainly quality traits. The highest PC score was obtained by IS 17248 followed by IS 18542, NTJ-2 and ICSV 25306 in PC3 for characters namely inter nodal length and leaf stem ratio based on top PC scores genotypes were categorized in the Table 4.13.

Table 4.13. List of selected genotypes in each principal component

	PC1	**PC2**	**PC3**
GENOTYPES	**IS 17248**	**CSH 22 SS**	**IS 17248**
	IS 15957	ICSR 93022	**IS 18542**
	CSH 22 SS	S 35	NTJ 2
	IS 13705	ICSSH 28	ICSV25306
	IS25301	ICSR 14006	-
	IS 13553	ICSH 14002	-
	IS 18542	IS 25340	-
	ICSV 93046	ICSR 93026	-
	SSG 59-3	-	-

DISCUSSION

The experimental findings of present study “Genetic Analysis of Fodder Yield and its Components in Advanced Lines of Sorghum” have been discussed on following heads in the light of available literature.

5.1 Parameters of genetic variability

5.1.1 Genetic variability

5.1.2 Genotypic and phenotypic coefficient of variation

5.1.2 Heritability (in broad sense) and Genetic advance (as % of mean)

5.2 Correlation coefficient

5.3 Path coefficient analysis

5.4 Genetic divergence analysis

5.5 Principal component analysis

5.1 Genetic variability

The ANOVA indicated that the mean sum of squares due to genotypes were highly significant for all the traits under study *viz.,* days to 50% flowering, plant height, no. of leaves/plant, penultimate leaf area, stem girth, no. of internodes/plant, inter nodal length, leaf stem ratio, brix value, crude protein yield/plant , crude protein yield/plant/day, dry matter yield/plant/day, green fodder yield/plant/day, dry matter yield/plant, green fodder yield/plant. This indicates that substantial variability has been generated and genetic base is broadened for most of the characters among different genotypes developed through crossing diverse parents. The exploitation of the present variability may lead to develop potential and suitable genotypes in future.

The analysis of variance estimates of various parameters for assessment of genetic variability *viz.,* mean, range, GCV and PCV coefficient of variation, heritability and genetic advance (as % of mean) help the breeders in bringing improvement in quantitatively inherited traits, which directly affects the fodder yield and allied traits.

5.1.1. Genotypic and phenotypic coefficient of variation

The PCV was higher in magnitude than its corresponding GCV for all the characters under study. This indicates the influence of the environment on the expression of these characters is effective.

The high magnitude of phenotypic and genotypic coefficient of variation was recorded for fodder and allied traits *i.e.,* crude yield/plant/day, green fodder yield/plant, crude protein yield/plant, dry matter yield/plant, green fodder yield/plant/day and dry matter yield/plant/day. This indicates presence of high magnitude of genetic variance. Selection based on these traits would facilitate the successful isolation of desirable traits. The moderate estimate of phenotypic and genotypic coefficient of variation were observed in penultimate leaf area, stem girth, brix's value, no of leaves/plant, plant height and no of internode/plant. And rest of the characters shows low phenotypic and genotypic coefficient of variation.

These results are close proximity with the finding for fodder and allied traits by Kumar and Sahib (2003), Gedam *et al.,* (2015) for dry matter yield/plant, plant height, no. of leaves/plant, penultimate leaf area, brix value. Bini and Sumabai (2005), Kishore and Singh (2005), Khandelwal *et al.,* (2015) for green fodder yield/plant and dry matter yield/plant, plant height, no. of leaves/plant, penultimate leaf area. Warkad *et al.,* (2008) for plant height, no. of internode/plant, no. of leaves/plant, penultimate leaf area, crude protein yield/plant and brix value. Kumar *et al.,* (2009) for plant height, stem girth, and green fodder yield/plant. Patel *et al.,* (2013) for green fodder yield/plant, green fodder yield/plant/day and plant height. Ammanullah *et al*., (2014) plant height, penultimate leaf area and green fodder yield/plant. Malik *et al.,* (2015), Singh *et al.,* (2016) for the no. of leaves/plant, penultimate leaf area, green fodder yield/plant and stem girth. Rana *et al.,* (2016) and Vendruscolo *et al.,* (2016) for no. of leaves/plant, green fodder yield/plant and stem girth and dry matter yield/plant. Patel *et al.,* (2013), Malik *et al*., (2015) for crude protein yield/plant reported similar findings.

However, contradictory results was obtained by Kumar and Sahib (2003), Warkad *et al.,* (2008), Malik *et al*., (2015) for the days to 50% flowering, leaf stem ratio and internodal length.

5.1.2 Heritability and Genetic advance

The coefficient of variation only the extent of variability existing for various characters, but does not give any information regarding heritable portion of it. Amount of high or moderate heritability accompanied with high or moderate genetic advance indicate additive gene action involved in the inheritance of concerned traits and hence selection may be effective. While, heritability permits greater effectiveness of selection by separating out the environmental influence from the total variability and to indicate accuracy with which a genotype can be identified phenotypically. Heritability estimates along with the genetic advance are normally more helpful in predicting the genetic gain under selection than heritability estimates alone. However, it is not necessary that the character showing high heritability will also exhibit high genetic advance.

If high or moderate heritability coupled with low genetic advance or vice versa indicates predominance of non additive gene action.

Heritability in broad sense (h^2) and genetic advance were calculated for each character under study. These estimates varied from character to character. The knowledge of heritability enables to assess the amount of variance due to genetic cause, which is likely to be transferred in the progeny.

The heritability estimates varied from different agro-morphological traits; however, all the characters expressed high estimates of broad sense heritability.

The characters which show high to moderate heritability are green fodder yield/plant, dry matter yield/plant, dry matter yield/plant/day, green fodder yield/plant/day, crude protein yield/plant and crude protein yield/plant/day, penultimate leaf area, stem girth, plant height, no. of internodes/plant, leaf stem ratio. The high heritability coupled with high genetic advance as percent of mean was recorded for green fodder yield/plant, dry matter yield/plant, dry matter yield/plant/day, green fodder yield/plant/day, crude protein yield/plant and crude protein yield/plant/day. Whereas high heritability coupled with moderate genetic advance was recorded for penultimate leaf area, and remaining characters shows either moderate heritability with low genetic advance or low heritability with low genetic advance.

In conformity with the findings of the present investigation, high heritability with high genetic advance have also reported by Singh *et al.,* (2004), Rana *et al.,* (2016) for green fodder yield/plant/day and crude protein yield/plant. Warkad *et al.,* (2008), Jain *et al.,* (2008), Shreenivasa *et al*., (2000) for dry matter yield/plant. Kumar and Reddy (2013) for the green fodder yield/plant and leaf stem ratio. Malik *et al.,* (2015) for green fodder yield/plant, crude protein yield/plant and crude protein yield/plant/day, penultimate leaf area, stem girth, plant height, leaf stem ratio. Gedam *et al.,* (2015) for plant height, green fodder yield/plant and dry matter yield/plant/day. Khandelwal *et al.,* (2015) reported high for green fodder yield/plant and penultimate leaf area. Rana *et al.,* (2016) for plant height, stem girth and leaf stem ratio.

This indicates preponderance of additive genetic variance for these characters and selection may be effective.

5.2 Correlation coefficient analysis

Yield is a complex quantitative character governed by number of genes and is highly influenced by environment. Hence, the selection of superior genotypes based on yield as such is not effective. For a rational approach towards improvement of yield, selection has to be made for the components of yield. Association of yield components and yield thus assumes special importance on the basis of indirect selection. Genetic correlation between different characters of plant often arises because of linkage or pleiotropy.

Analysis of correlation coefficient revealed that the degree of association between yield and its components given the mutual relationship between yield and its components gives the mutual relationship between the yield components. It helps in direct selection of associated characters for the improvement of desirable traits.

Most of the characters are associated with each other but the extent of correlation varies with different characters pairs. A positive/negative correlation between the desired characters is favorable to the breeder as it helps in selection. However, a negative correlation hinders the recovery of the recombinants in both characters. In such a situation any strong selection applied to a character also brings about change in other character.

In the present investigation, phenotypic correlation coefficient was studied considering fifteen component traits, *viz.,* days to 50% flowering, plant height, no. of leaves/plant, penultimate leaf area, stem girth, no. of internodes/plant, internodal length, leaf stem ratio, brix value, crude protein yield/plant, crude protein yield/plant/day, dry matter yield/plant/day, green fodder yield/plant/day, dry matter yield/plant and green fodder yield/plant and all traits showed significant positive correlation with green fodder yield/plant. These findings suggest that the simultaneous selection for these traits is possible for improvement of sorghum genotypes.

These findings are in agreements with the results of Board *et al*., (2007) for stem girth, dry matter yield/plant and crude protein yield that were significantly and positively correlated with green fodder yield. Warked *et al*., (2008) for days to 50% flowering and plant height was manifested positive significant correlation with dry fodder yield. Jadav *et al.,* (2009) studied positive and significant association on green fodder yield/plant with days to 50% flowering, no. of leaves/plant, crude protein yield/plant and dry matter yield/plant. Singh *et al.,* (2009) was found green fodder yield to be positive and significantly correlated with green fodder yield/day, days to 50% flowering, no. of nodes/plant and plant height. Lyanar *et al.,* (2010) for dry fodder yield/plant, plant height and no. of leaves/plant exhibited significant and positive correlation with green fodder yield/plant. Patel *et al.* (2013) reported the association for green fodder yield/plant/day, no. of leaves/plant and dry matter yield/plant, penultimate leaf area with green fodder yield. Kumar and Reddy (2013) reported the association for days to 50% flowering and internodal length. Prakash *et al.,* (2014) found that crude protein yield, plant height, stem girth and no. of leaf/plant were significantly and positively correlated with green fodder yield/plant. Singh *et al.,* (2016) reported associations with penultimate leaf area, plant height, stem girth and no. of leaf/plant. Vendruscolo *et al.,* (2016) for the days to 50% flowering, plant height, stem girth and no. of leaf/plant, dry matter yield/plant and green fodder yield/plant/day.

This indicates that any selection based on these characters will enhance performance and improvement in fodder sorghum.

5.3 Path coefficient analysis

Path coefficient analysis is the most widely used biometrical technique in crop improvement. The information obtained from this technique, also helps in making selection based on component characters of yield. It helps in understanding the cause of association between two variables. It determines the direct effect of various characters on yield and also indirect effects via other components characters and provides the selection of superior genotypes. The path coefficient analysis a statistical device developed by Wright, (1921), is carried out at genotypic and phenotypic level by taking yield/plant as the dependent variable in order to see the causal factor. The genotypic direct and indirect effects were observed slightly higher in magnitude as compared to phenotypic direct and indirect effects.

The path analysis for fodder yield and its component traits of different characters revealed that in genotypic path coefficient for dry matter yield/plant has highest positive direct effect on green fodder yield/plant followed by green fodder yield/plant/day, dry matter yield/plant/day, crude protein yield/plant, stem girth, penultimate leaf area, crude protein yield/plant/day, days to 50% flowering, plant height, no. of leaves/plant, no. of internode/plant, internodal length, brix's value and leaf stem ratio.

Positive direct effect observed in the study for the characters on fodder yield are in confirmation with the finding of Chand, (2000) for days to 50% flowering, no. of leaves/plant, leaf stem ratio and stem girth.

Kishore and Singh (2005) for no. of leaves/plant, plant height and penultimate leaf area had positive direct effect with green fodder yield.

Warkad *et al.,* (2008) for days to 50% flowering, internodal length and dry fodder yield had positive direct effect with green fodder yield, Jadav *et al.,* (2009) for dry matter yield/plant. Sankarapandian, (2010) for no. of leaves/plant, stem girth and plant height. Patel *et al.,* (2013) for the characters no. of leaves/plant and penultimate leaf area had. Singh *et al.,* (2013) days to 50% flowering, penultimate leaf area, stem girth and internodal length. Gedam *et al.,* (2015) for no. of leave/plant and dry matter yield/plant. Rana *et al.,* (2016) and Singh *et al*., (2016) for no. of leaves/plant, stem girth and leaf stem ratio.

However, the contradictory associations were reported by Board *et al.,* (2007) estimated direct negative effect on green fodder yield via plant height, leaf stem ratio, dry matter yield/plant and brix’s value.

5.4 Genetic divergence analysis

Phenotypic and genotypic diversity would be considered as a measure of genetic diversity. It is difficult for the breeder to select most suitable genetically diverse parents for successful hybridization programme unless it provides necessary information on genetic variation and genetic divergence present in the available genetic material. The success of breeding programme through hybridization is highly dependent on genetic divergence of parents involved. The more diverse the parents more are the chances of pronounced heterotic effects and increased spectrum of variability in the segregating generations. The assessment of divergence for a set of characters using multivariate analysis like distance analysis (D^2) has been attempted. The genetic distance had a definite role to play for efficient choice of parents for hybridization programme.

The present study was aimed at analyzing the genetic divergence for fodder yield and its components among the 31 genotypes and to identify the superior and divergent parental genotypes. Mahalanobis D^2 statistics is a powerful tool widely used by breeders in quantifying the degree of divergence at genotypic level.

5.4.1 Grouping of genotypes into different clusters

The study comprised of 31 sorghum genotypes which were assessed for nature and magnitude of genetic divergence based on fodder yield its component associate characters using Mahalanobis's D^2 statistics. Clustering pattern following Tocher's method, 31 genotypes were grouped into VI clusters for fodder sorghum.

Divergence analysis revealed that fodder sorghum genotypes were grouped in 6 clusters. Clusters I (19), II (3) and III (6) were polygenotypic, whereas cluster IV, V and VI were monogenotypic, confirmed the quantum of diversity present in the material. These results indicate that there exists some homology between closely situated clusters. Therefore crossing genotypes from different clusters would produce more genetic variability for exploiting in future breeding programme.

These results are in conformity with the finding of Agrawal *et al.,* (2002), Yadav *et al.,* (2003), Mohanraj *et al.,* (2006), Yadav and Pahuja (2011), Singh *et al.,* (2013), Chikuta *et al.,* (2015), Sinha and Kumaravadivel (2016) the accession were grouped under 6 clusters.

5.4.2 Intra and inter cluster divergence D^2 values

The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Chaudhary (1985). Divergence analysis revealed that cluster III had maximum intra cluster value followed by cluster I, cluster II and rest of the clusters had no intra cluster divergence, while D^2 value was maximum in between cluster II and III followed by cluster II and VI, while it was minimum for cluster IV and VI. High heterotic combinations will obtain when genotypes of these distinctly placed clusters were crossed would give high heterosis / heterotic segregants.

The results are in agreement with the finding of Agrawal *et al.,* (2002), Yadav *et al*., (2003), Bhatt and Singh (2005), Mohanraj *et al.,* (2006), Sameer *et al.,* (2010), Yadav and Pahuja (2011) Singh *et al.,* (2013), have reported maximum inter and intra distances value between clusters. These different clusters could give heterotic response and better segregants after hybridization.

5.4.3 Cluster means showing importance of grouped characters

Average cluster means for fodder yield and its components traits were the mean value of different independent traits give higher attribute in particular cluster group, days to 50% flowering was maximum for cluster VI, the maximum mean value obtained for plant height in cluster III, no. of leaves/plant recorded highest mean value in cluster V, the mean values of penultimate leaf area was highest for cluster III, average mean value of stem girth was recorded to be maximum for cluster III, the average mean values of internodal length recorded maximum value for cluster III, no. of internode/plant recorded maximum mean value for cluster V, leaf stem ratio recorded maximum average mean value for cluster III, V and VI, the average value recorded maximum of brix's value, crude protein yield/plant, crude protein yield/plant/day, dry matter yield/plant/day, dry matter yield/plant, green fodder yield/plant/day, green fodder yield/plant for the cluster III. The genotypes exhibiting high and low character means for majority of characters, suggested that these parents can used for hybridization programme to achieve novel recombinants.

These results are in agreement with the findings of present study for Bhatt and Singh (2005) reported cluster VI had maximum mean value for days to 50% flowering, penultimate leaf area, Sameer *et al.,* (2010) and Kumar *et al.,* (2010) recorded cluster IV had maximum mean value for green fodder yield/plant, green fodder yield/plant/day and dry matter yield/plant/day. Yadav and Pahuja (2011) characterized on the basis of plant height, penultimate leaf area, stem girth, number of tillers, number of leaves/plant, and three visual fodder quality parameters in cluster II, III and VI.

5.4.4 Contribution of individual characters towards genetic divergence

The characters which showed more percentage contribution towards the divergence for fodder yield and its components traits should be considered prime during selection. The percent contribution of individual characters toward the total divergence was found highest for green fodder yield/plant followed by dry matter yield/plant/day, green fodder yield/plant/day, stem girth, crude protein yield/plant/day, no. of leaves/plant, leaf stem ratio, brix's value, crude protein yield/plant, plant height, intermodal length, dry matter yield/plant, penultimate leaf area, no. of internodes/plant and days to 50% flowering.

Bhatt and Singh (2005) studied penultimate leaf area, no. of internodes/plant and no. of leaves/plant. Kumar *et al.,* (2010) reported maximum contribution toward total genetic divergence for plant height, dry fodder yield and days to 50% flowering. Sameer *et al.,* (2010), Chikuta *et al.,* (2015) for fodder yield.

5.5 Principal component analysis

A large number of variable are often measured by plant breeder, some of which may not be sufficient discriminatory power for germplasm evaluation, characterization and management. In such case, principal component analysis (PCA) may be used to reveal pattern and eliminate redumentcy in data set as morphological, agronomical and biocamical variances routinely occurs in crop species.

Owing to lack of knowledge regarding relative importance and usefulness of variables, the investigator tries to include all the possible variables and makes the data matrix perceivably large, complicated and beyond comprehension. Therefore, the investigator requires a technique for systematic reduction and summarization of data sets.

Basically a well known data reduction technique i.e. Principal component analysis initiated by Pearson (1901) and later developed by Hotelling (1933), offers solution to this complex problem by transforming the original set of variables into smaller set of linear combinations that account for most of the variability of the original data set. The objective of principal component analysis is to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson, 1972 and Morrison, 1982) and also to rank germplasms on the basis of PC scores.

In the present investigation PCA was performed for quantitative and qualitative traits of Sorghum. Out of fifteen, only four principal components (PCs) exhibited more than 1.00 Eigen value, and showed about 75.851% variability. Therefore, these four principal components were given due importance for the further explanation. The first principal component *i.e.,* PC1 accounted for maximum proportion of total variability in the set of all variables and remaining components accounted for progressively lesser and lesser amount of variation. The first principal component accounted for maximum variability *i.e.,* 49.609 followed by PC2 (11.585%), PC3 (7.732%) and PC4 (6.927%) for traits under study.

Rotated component matrix revealed that the PC1 which accounted for the highest variability 49.609 %. PC1 accounts mostly for agro-morphological related traits like days to 50% flowering, plant height, no. of leaves/plant, penultimate leaf area, stem girth, no. of internodes/plant, green fodder yield/plant, dry matter yield/plant. PC2 was contributed by quality related trait e.g. brix's value which is a major factor responsible for sweetness in sorghum and PC3 includes internodal length and leaf stem ratio. From this study it is clear that PC 1 and PC 3 were mostly related to yield traits. PC 2 was related to quality traits. Hence present study reveals that scope of developing high yielding genotypes with better brix's value. These genotypes will have good palatability for animal and result in higher milk yield.

The results are in agreement with the findings of Ahmed et al., (2011) for having yield contributing traits were present in PC1 and PC2 was dominating by morphological traits in oat. Vikas *et al.,* (2013) similar results finding for spikelets/panicle and seed yield present in PC1. While, days to 50%flowering present in PC2. Badkul *et al.,* (2013) in soybean observed that yield contributing traits were present in PC1 and PC2 were dominated by ago-morphological traits. Chikuta *et al.* (2015) reported first four PCs explained 89%of total variation. Jain and Patel (2016) showed first three PCs explaining 70.89% of total variation.

On the basis of Principle component scores high PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype. IS 17248 had the highest PC score followed by IS 15957, CSH 22 SS, IS 13705, IS25301, IS 13553, IS 18542, ICSV 93046 and SSG 59-3 in PC1 indicated that these genotypes possesses high values of traits *viz.,* days to 50% flowering, plant height, no. of leaves/plant, penultimate leaf area, stem girth, no. of internodes/plant, crude protein yield/plant, crude protein yield/plant/day, dry matter yield/plant/day, dry matter yield/plant, green fodder yield/plant/day and green fodder yield/plant. The highest PC score of CSH 22 SS, ICSR 93022, S 35, ICSSH 28, ICSR 14006, ICSH 14002, IS 25340 and ICSR 93026 in PC2 was mainly related with brix's value which is mainly quality attributing trait. The highest PC scores was obtained by IS 17248 followed by IS 18542, NTJ 2 and ICSV25306 in PC3 for characters namely, intermodal length and leaf stem ratio fodder yield contributing traits.

Similar findings for plant height, days to 50% flowering, crude protein yield/plant and green fodder yield/plant in PC1 were reported by Bhanupriya *et al.,* (2014). Sinha and Kumaravadivel (2016) for stem girth. Jain and Patel (2016) evaluated total variation which was mainly due to green fodder yield/plant, dry matter yield/plant, stem girth, days to 50% flowering, penultimate leaf area and no. of leaves/plant.

SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FURTHER WORK

6.1 Summary

The present investigation entitled “Genetic analysis of fodder yield and its components in advanced lines of sorghum (*Sorghum bicolor* L. Moench)” was carried during *Kharif* season of 2016-17 at the Seed Breeding Farm, Department of Genetics & Plant Breeding, College of Agriculture JNKVV Jabalpur (MP). The experimental materials for the present investigation consisted of 31 sorghum genotypes along with checks. These genotypes were planted in Randomized Completely Block Design (RCBD) with three replications to estimate the genetic variability, heritability, genetic advance, correlation coefficient, path analysis and principal components for fodder yield and its components.

The observations were recorded for fodder and allied traits, the randomly selected and tagged five plants of plot size 2 X 1.6 m^2 area. Data were recorded for morphological traits such as days to 50% flowering, plant height, number of leaves/plant, internodal length, penultimate leaf area, stem girth and number of interned/plant. Agronomical traits like leaf stem ratio, green fodder yield/plant, green fodder yield/plant/day, dry matter yield/plant and dry matter yield/plant/day. And qualitative traits such as crude protein yield/plant, crude protein yield/plant/day and brix’s values evaluated as per standard procedure.

Genotypic and phenotypic coefficient of variation, broad sense heritability and genetic advance as percentage of mean was calculated. Correlation coefficient, path analysis, genetic divergence and PCA were carried out taking green fodder yield as dependent variable. The summary of present investigation is as under.

The mean data estimated for fodder and associate traits were subjected to analysis of variance revealed that mean sum of squares due to genotypes were highly significant for all the characters indicating the presence of sufficient amount of genetic variability amongst the material under study.

The high magnitude of genotypic and phenotypic coefficients of variation for fodder and allied traits was recorded for the trait crude protein yield/plant/day, green fodder yield/plant, crude protein yield/plant, dry matter yield/plant, green fodder yield/plant/day and dry matter yield/plant/day. This indicates the presence of substantial genotypic variance among these traits. The moderate estimate of genotypes coefficient of variation were observed in penultimate leaf area, stem girth, brix’s value, no. of leaves/plant, plant height and no of internode/plant. And rest of the characters exhibited low magnitude of genotypic coefficient of variation.

The heritability estimates varied from different agro-morphological traits, however, all the characters expressed high estimates of broad sense heritability.

The characters which show high to moderate heritability are green fodder yield/plant, dry matter yield/plant, dry matter yield/plant/day, green fodder yield/plant/day, crude protein yield/plant and crude protein yield/plant/day, penultimate leaf area, stem girth, plant height, no. of internodes/plant and leaf stem ratio.

The high heritability coupled with high genetic advance as percent of mean was recorded for green fodder yield/plant, dry matter yield/plant, dry matter yield/plant/day, green fodder yield/plant/day, crude protein yield/plant and crude protein yield/plant/day.

Most of the characters are associated with each other but the extent of correlation varies with different characters pairs. In the present investigation, phenotypic correlation coefficient was studied considering fifteen component traits, *viz.,* days to 50% flowering, plant height, no. of leaves/plant, penultimate leaf area, stem girth, no. of internodes/plant, internodal length, leaf stem ratio, brix value, crude protein yield/plant, crude protein yield/plant/day, dry matter yield/plant/day, green fodder yield/plant/day, dry matter yield/plant, and green fodder yield/plant and all traits showed significant positive correlation with green fodder yield/plant. These findings suggested that the simultaneous selection for these traits is possible for improvement of sorghum genotypes.

The path analysis for fodder yield and its component traits of different characters revealed that in genotypic path coefficient for dry matter yield/plant has highest positive direct effect on green fodder yield/plant followed by green fodder yield/plant/day, dry matter yield/plant/day, crude protein yield/plant, stem girth, penultimate leaf area, crude protein yield/plant/day, days to 50% flowering, plant height, no. of leaves/plant, no. of internode/plant, internodal length, brix's value and leaf stem ratio.

On the basis of D^2 values, clustering pattern following Tocher's method, 31 genotypes were grouped into VI clusters for fodder sorghum. Clusters I (19), II (3) and III (6) were polygenotypic, whereas cluster IV, V and VI were monogenotypic, confirmed the quantum of diversity present in the material.

Divergence analysis revealed that cluster III had maximum intra cluster value followed by cluster I, cluster II and rest of the clusters had no intra cluster divergence, while D^2 value was maximum in between cluster II and III followed by cluster II and VI, while it was minimum for cluster IV and VI.

The percent contribution of individual characters toward the total divergence was found highest for green fodder yield/plant followed by dry matter yield/plant/day, green fodder yield/plant/day, stem girth, crude protein yield/plant/day, no. of leaves/plant, leaf stem ratio, brix's value, crude protein yield/plant, plant height, intermodal length, dry matter yield/plant, penultimate leaf area, no. of internodes/plant and days to 50% flowering.

On the basis of Principle component scores high PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype. IS 17248 had the highest PC score followed by IS 15957, CSH 22 SS, IS 13705, IS25301, IS 13553, IS 18542, ICSV 93046 and SSG 59-3 in PC1 indicated that these genotypes possesses high values of traits *viz.,* days to 50% flowering, plant height, no. of leaves/plant, penultimate leaf area, stem girth, no. of internodes/plant, crude protein yield/plant, crude protein yield/plant/day, dry matter yield/plant/day, dry matter yield/plant, green fodder yield/plant/day and green fodder yield/plant. The highest PC score of CSH

22 SS, ICSR 93022, S 35, ICSSH 28, ICSR 14006, ICSH 14002, IS 25340 and ICSR 93026 in PC2 was mainly related with brix’s value which is mainly quality attributing trait. The highest PC scores was obtained by IS 17248 followed by IS 18542, NTJ 2 and ICSV25306 in PC3 for characters namely, intermodal length and leaf stem ratio fodder yield contributing traits. In sorghum breeding programmes these genotypes and traits may be utilized to achieve better segregates in future.

6.2 Conclusions

1. Analysis of variance revealed highly significant difference for all the traits showed large variability in the existing material.

2. High genotypic and phenotypic coefficient of variation were recorded for crude protein yield/plant/day, green fodder yield/plant, crude protein yield/plant, dry matter yield/plant, green fodder yield/plant/day, stem girth, dry matter yield/plant/day, penultimate leaf area and number of leaves/plant indicated the presence of sufficient amount of variability in the existing material.

3. High heritability coupled with high genetic advance as percentage of mean were recorded for dry matter yield/plant, green fodder yield/plant, crude protein yield/plant, dry matter yield/plant/day, crude protein yield/plant/day, green fodder yield/plant/day and penultimate leaf area. It indicates contribution of additive gene effects and selection for such traits may be rewarding.

4. The green fodder yield/plant reported positive correlation with green fodder yield/plant/day, days to 50 % flowering, number of leaves/plant, dry matter yield/plant, stem girth, dry matter yield/plant/day, crude protein yield/plant. On the other hand brix’s value has shown negative correlation at phenotypic level. Hence these traits may be considered as selection indices for improvement in sorghum breeding programme.

5. From the present investigation it can be concluded that character *viz.,* days to 50 % flowering, number of leaves/plant, internodal length, leaf stem ratio,

crude protein yield/plant, dry matter yield/plant, dry matter yield/plant/day and green fodder yield/plant/day at genotypic level possessed positive direct effect on green fodder yield/plant

6. The highest inter cluster divergence was observed between the genotypes of cluster II and cluster III followed by cluster II and VI followed by cluster I and III. Crossing between the genotypes of these most divergent clusters may lead to maximum diversity in the material.
7. On the basis of mean performance and principal component analysis four principal components (PCs) showed more than 1.00 Eigen value and about 75.85% variability. The genotypes viz., IS 17248, IS 18542, CSH 22 SS, IS 15957, ICSH 14002 and IS 13705 have been identified as promising genotype as they posses’ higher value for fodder yield and quality traits.

6.3 Suggestions for Further work

1. The promising genotypes identified for yield and quality traits shall be tested over years and locations for their stability.
2. The diversity of the genotypes shall be confirmed using molecular markers.
3. Identified superior genotypes shall be involved in future breeding programme to obtained better segregates.

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Appendex-1 Means performance of different genotypes of fodder sorghum

S.N	Variety	DFF	PH	NLP	PLA	SG	INL	NIP	LS	Brix %	CPYP	CPYPD	DMYPD	DMYP	GFYPD	GFYP
1	**IS 3717**	107.67	221.33	13.33	245.00	21.39	16.63	13.67	0.40	10.05	11.12	0.11	1.07	117.44	4.63	502.33
2	**IS 13553**	118.00	241.67	14.33	374.33	23.39	17.31	14.00	0.42	11.83	13.64	0.12	1.16	150.99	5.45	649.33
3	**IS 13705**	117.33	237.00	14.00	352.00	23.90	17.34	14.00	0.43	12.20	15.18	0.15	1.32	156.66	5.48	643.00
4	**IS 15957**	120.00	263.00	15.67	398.33	24.15	18.15	15.67	0.50	13.20	18.96	0.19	1.60	198.67	6.81	820.67
5	**IS 17248**	121.33	282.67	17.00	430.67	26.50	19.43	17.00	0.54	14.93	20.08	0.22	1.58	201.34	7.07	839.67
6	**IS 17349**	106.00	242.00	14.33	265.67	18.88	17.83	13.67	0.40	10.67	10.53	0.10	0.86	94.00	3.98	392.00
7	**IS 18542**	127.00	236.33	12.33	361.67	22.07	17.53	14.33	0.46	12.43	11.58	0.09	1.00	129.91	5.97	537.33
8	**IS 25234**	119.33	221.67	13.33	265.00	21.23	16.82	13.00	0.41	9.47	9.21	0.08	0.96	116.97	4.02	480.00
9	**IS 25301**	130.00	211.00	14.33	323.33	24.99	14.73	14.00	0.45	12.83	13.38	0.10	1.22	178.62	5.85	761.33
10	**IS 25302**	114.00	207.67	14.67	231.67	18.77	14.63	14.00	0.37	10.33	7.35	0.07	0.73	83.26	3.05	354.00
11	**IS 25340**	93.67	198.33	13.33	232.67	19.45	15.26	13.00	0.38	12.77	10.40	0.12	0.99	91.32	4.15	387.00
12	**ICSV 25335**	110.67	198.00	17.67	238.00	18.72	11.36	17.67	0.46	11.10	8.04	0.07	0.84	106.38	4.14	464.33
13	**ICSSH 28**	92..67	193.33	12.00	250.00	15.30	17.07	11.67	0.39	12.50	9.70	0.11	1.02	94.58	4.33	404.00
14	**CSH 22 SS**	100.00	257.33	14.67	402.67	22.65	19.72	14.00	0.44	13.50	19.07	0.19	1.75	186.85	7.85	788.33
15	**ICSV 93046**	113.00	216.00	14.67	278.00	23.07	15.43	14.00	0.36	12.87	12.84	0.12	1.14	131.00	4.74	539.33
16	**ICSH 14002**	98.00	142.00	10.00	198.00	14.78	13.36	9.67	0.43	13.50	4.82	0.05	0.49	50.94	2.07	213.33
17	**ICSH 28001**	105.33	246.00	12.00	289.67	17.66	17.69	14.00	0.40	12.77	10.01	0.09	0.98	105.12	4.71	431.33
18	**ICSR 14006**	93.33	144.67	10.00	202.00	16.11	15.48	9.67	0.44	12.77	6.15	0.07	0.61	59.38	2.53	240.00
19	**ICSR 93022**	92.67	196.33	12.33	197.67	16.12	16.39	11.67	0.42	14.00	11.13	0.12	0.91	90.55	3.79	356.67
20	**ICSR 93025**	100.67	181.67	12.67	192.00	14.68	15.13	12.00	0.40	12.00	9.10	0.09	0.86	88.34	3.61	363.33
21	**ICSR 93026**	94.33	202.00	12.33	181.67	16.45	16.81	11.67	0.44	11.83	8.32	0.09	0.91	91.45	3.83	366.00
22	**S 35**	97.67	179.67	11.33	219.33	17.73	16.34	11.00	0.45	14.27	8.54	0.09	0.85	87.15	3.61	360.00
23	**NTJ 2**	104.67	220.00	12.33	261.67	16.71	18.34	12.33	0.44	8.83	8.58	0.08	0.77	86.16	3.15	336.33
24	**ICSR 93034**	92.33	184.67	11.67	246.00	15.66	15.30	11.67	0.45	11.90	9.00	0.10	0.72	73.45	3.29	286.67
25	**ICSV 93046**	110.33	227.33	13.00	285.00	15.69	15.91	14.33	0.40	10.60	7.17	0.07	0.72	86.38	3.04	340.00
26	**ICSV 25306**	105.00	219.33	11.33	258.33	15.63	15.86	13.33	0.45	11.27	6.31	0.06	0.64	74.62	3.14	289.67
27	**ICSV 25308**	109.00	220.33	12.67	258.67	16.73	15.40	14.67	0.44	8.60	8.02	0.08	0.73	93.02	3.35	369.00
28	**ICSV 25316**	115.00	219.00	13..33	265.00	18.78	14.95	14.67	0.40	11.67	8.44	0.08	0.89	106.63	3.81	441.67
29	**ICSV 12006**	91.00	164.33	11.33	211.67	12.71	14.42	11.33	0.38	10.32	4.21	0.05	0.50	52.99	2.11	201.67
30	**SSG 59-3**	101.67	236.67	15.33	325.00	19.53	15.15	15.67	0.46	12.13	10.05	0.14	0.96	106.26	4.22	444.00
31	**M P Chari**	94.33	211.67	14.67	278.33	18.33	15.29	14.67	0.39	9.70	10.38	0.12	0.94	89.70	3.92	377.00

Appendix-2 Meteorological information (week-wise) during Kharif 2016-17 at Jabalpur

Standard weeks	Months and dates	Temperature		Sunshine (hrs/day)	Rainfall (mm)	Relative humidity (%)		Wind velocity	No. of rainy days
		Max.	Min.			Max.	Min.		
27	Jun 27- July 03	29.5	23.1	02.6	373.3	94	81	08.6	07
28	July / 04-10	31.1	24.5	03.0	083.6	93	79	06.4	05
29	July / 11-17	30.4	24.0	03.9	063.6	91	69	07.5	03
30	July / 18-24	31.7	24.0	04.7	061.8	91	67	04.5	03
31	July / 25-31	31.0	23.3	02.9	196.4	91	77	05.0	05
32	Aug / 01-07	28.6	23.6	01.3	132.8	93	82	06.8	04
33	Aug / 08-14	27.0	23.0	00.0	182.9	93	91	07.0	07
34	Aug / 15-21	28.8	22.1	06.1	263.2	90	76	05.9	06
35	Aug / 22-28	32.2	23.7	06.1	035.2	90	70	04.3	04
36	Aug 29 - Sept 04	30.6	23	04.5	017.6	87	63	06.9	02
37	Sept / 05-11	31.7	23.6	01.9	018.0	89	65	04.5	01
38	Sept / 12-18	33.0	23.9	06.7	03.80	92	64	03.5	00
39	Sept / 19-25	29.9	23.5	04.6	052.4	94	83	04.0	03
40	Sept 26 - Oct 02	31.9	23.9	07.3	024.2	93	64	03.0	02
41	Oct / 03-09	31.5	21.3	08.0	0000	88	51	04.2	00
42	Oct / 10-16	31.5	15.4	09.3	0000	91	32	02.5	00
43	Oct / 17-23	31.7	15.6	08.8	0000	82	29	02.9	00
44	Oct / 24-30	29.7	12.3	08.7	0000	87	34	02.4	00
45	Oct 31 – Nov 06	29.7	10.6	08.1	0000	91	24	02.2	00
46	Nov / 07-13	28.3	08.1	08.1	0000	88	24	02.0	00
47	Nov / 14-20	28.8	08.4	08.3	0000	87	23	01.4	00
48	Nov / 21-27	28.8	08.7	08.7	0000	89	27	01.7	00
49	Nov 28 – Dec 04	25.1	07.9	06.2	0000	93	43	02.1	00
50	Dec / 05-11	26.1	07.3	07.8	0000	91	28	02.0	00
51	Dec / 12-18	24.7	05.5	07.4	0000	91	30	01.8	00

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3	12th Class	M.P. Board	First	2006
4	10th Class	M.P. Board	First	2003

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c. Research and Development

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For the partial fulfilment of the master’s degree programme he was allotted a research problem on **“Genetic Analysis of Fodder Yield and its Components in Advanced Lines of Sorghum”** which was successfully conducted by him and being submitted in the form of the thesis.