

**Genetic analysis for quantitative traits in forage sorghum (*Sorghum bicolor* L.
Moench)**

Thesis

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CERTIFICATE

This is to certify that the thesis entitled “**Genetic analysis for quantitative traits in forage sorghum (*Sorghum bicolor* L. Moench)**” submitted in partial fulfilment of the requirements for the degree of **Doctor of Philosophy** with major in **Genetics and Plant Breeding** and minor in **Plant Pathology** of the College of Post Graduate Studies, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, is a record of *bonafide* research carried out by **Mr. Ramraj Sen, Id. No- PG/A-3435/15**, under my supervision and no part of the thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation and source of literature have been acknowledged.

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CERTIFICATE

We, the undersigned, members of the Advisory Committee of **Mr. Ramraj Sen**,
Id. No- PG/A-3435/15, a candidate for the degree of **Doctor of Philosophy** with
major in **Genetics and Plant Breeding** and minor in **Plant Pathology** agree that the
thesis entitled “**Genetic analysis for quantitative traits in forage sorghum
(*Sorghum bicolor* L. Moench)**” may be submitted by **Mr. Ramraj Sen** in partial
fulfilment of the requirements for the degree.

(S.K. Singh)

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Member

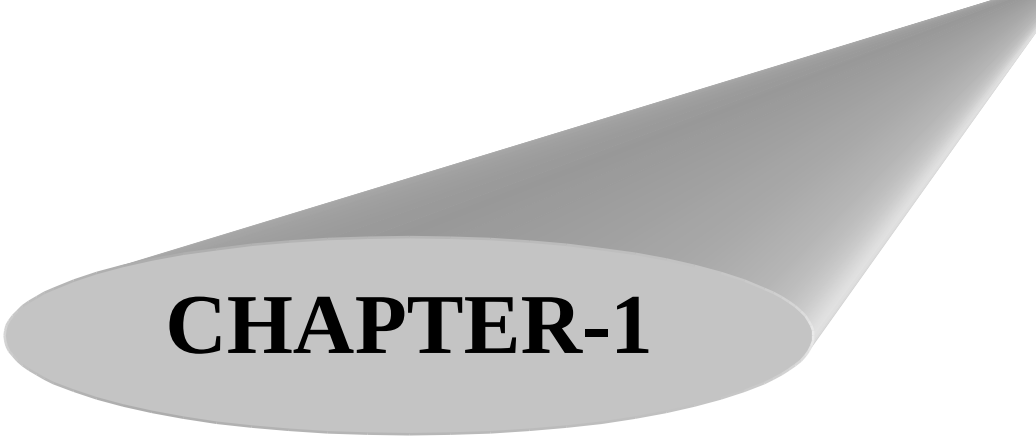
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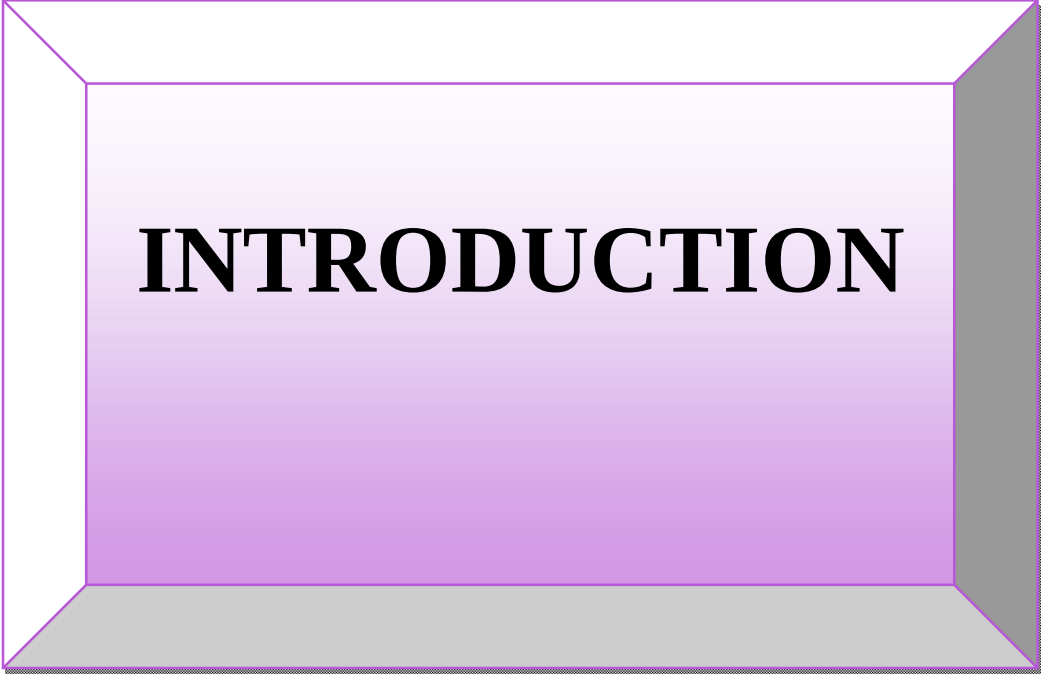
(Gopal Singh)
Member

LIST OF ABBREVIATIONS

%	-	Per cent
/	-	Per
°C	-	Degree Celsius
μ	-	Microlitre
@	-	At the rate of
a . i.	-	Active ingredient
ANOVA	-	Analysis of variance
Av	-	Average
C. D.	-	Critical Difference
cm	-	Centimeter
Con.	-	Concentration
cv.	-	Cultivar
d. f.	-	Degree of freedom
DAS	-	Days after sowing
E. S. S.	-	Error sum of square
e.g.	-	For example
<i>et al.</i>	-	And others
etc.	-	And the rest
F. cal.	-	Calculated value of 'F'
F. tab.	-	Table value of 'F'
Fig.	-	Figure
GCV	-	Genotypic coefficient of variation
GCA	-	General Combining Ability
g.	-	Gram
h.	-	Hour
ha	-	Hectare
h^2	-	Heritability
i.e.	-	That is
J.	-	Journal
kg	-	Kilogram
lbs.	-	Pounds
l.	-	Litre
Max.	-	Maximum
Min.	-	Minimum
MSS	-	Mean sum of squares
No.	-	Number
NS	-	Non-significant
PCV	-	Phenotypic coefficient of variation
Plant ⁻¹	-	Per plant
psi	-	Pounds per square inch
RBD	-	Randomized Block Design
r	-	Replication
S	-	Significant
NS	-	Non significant
S. E. (±)	-	Standard error of difference
S.S.	-	Sum of squares
Sp.	-	Species
Spp.	-	More than one species
SCA	-	Specific Combining Ability
Viz.,	-	Namely
Wt.	-	Weight



CHAPTER-1



INTRODUCTION

Sorghum being a short duration, drought and salt tolerant, well adaptive to arid regions is considered promising crop to overcome the fodder shortage in uncertain *barani* areas. It is a palatable and nutritious fodder crop for animals and there is enormous demand for green and dry fodder particularly during lean winter and summer season in the arid and semi arid region. Sorghum also called 'Global Grain' is a crop of worldwide importance due to its multipurpose use being a 4F (food, feed, fodder and fuel) crop. The tremendous increase in demand for animal products in 21st century has led to great expansion in the area allocated for fodder crops, especially under sorghum production. Although, sorghum besides use as a grain and energy crop is also widely used for the production of forage and silage for animal feed. Its leaves are broader having high palatability and provide green fodder over a longer period of time. The required quantity of quality green fodder is not available throughout the year and world food production in the next 30 years should increase by more than 75 percent to feed about 8000 million people by 2025. Due to unavailability of fodder in terms of quality as well as quantity livestock of developing countries is producing below than optimum potential. The estimated demand for milk and meat will be doubled till 2020 which directly depends upon the availability of nutritious fodder over a longer period of time (**Pahuja *et al.*, 2014**).

Sorghum is one of the gifted grass genera of the tropics. It provides food, feed, stover and fuel to millions of poor farm families and their livestock in the arid and semi arid tropical region of the world. India is notable for its huge livestock population and its economic integration with farm production, particularly under the less mechanized dry land agriculture. Sorghum is very important crop to recourse poor farmer for nutritional livelihood security and the important of sorghum because of its high fodder production potentialities and ability to use water efficiency even under drought conditions. As the diversified use of sorghum as forage is increasing owing to higher demand for fodder from dairy industry. Forage sorghum is grown in about 2.5 million ha of area in

the country. While single cut forage sorghum caters to fodder need of rainfed dry land areas and small farmers, the multi cut types are preferred for areas with irrigation and large dairy enterprises. The higher adaptability and greater biomass production potential of sorghum makes it the most popular forage crop across the country. The quality of sorghum fodder is next to maize but maize requires more moisture than sorghum hence less preferred as fodder crop (**Shinde *et al.*, 2015**).

Sorghum is an important *Kharif* seasons crop which is widely grown to meet the green as well as dry fodder requirement of the livestock. It is fast growing, adaptive to vast environmental condition and provides palatable nutritious fodder to the animals. India support 512.05 million of livestock, which includes 37.28 per cent cattle, 21.23 per cent buffalo, 12.71 per cent sheep, 26.40 per cent goat and 2.01 per cent pig. India supports nearly 20 per cent of the world's livestock being the leader in cattle (16%) and buffalo (5.5%) population. Deficiency in feed and fodder has been identified as one of the major components in achieving the desired level of livestock production. The shortage in dry fodder is 21.8 per cent compared with requirement of 560 million tones for the current livestock populations. Identification of good quality sorghum genotypes and development of location specific production technology offer an excellent opportunity to provide fodder for better nutrition to bovine population. Thus, suitable genotype and proper nutritious fodder are very important to get higher fodder yield (**Satpal *et al.*, 2015**).

Sorghum [*Sorghum bicolor* (L.) Moench] is known as poor man's crop and has the potentialities of being used solely either as food or feed or fodder. It is a member of *Poaceae* family with chromosome number $2n=20$. Its centre of origin is Ethiopia (Africa). It is an often cross pollinated crop, having average six per cent natural cross pollination. Major sorghum growing countries are USA, India, Nigeria, China, Mexico, Sudan and Argentina. Sorghum ranks first among the cereal fodder crops because of its growing ability in low fertile soil, faster growth habit, higher yield, palatability and nutritious quality. It gives almost uniform green fodder yield throughout the year. Sorghum is preferred over maize and pearl millet for forage because of its high tolerance to wide variation in soil and moisture conditions as well as better regeneration capacity.

During the last 30 years the role of sorghum as a major source of fodder has not diminished while its importance as a forage crop has increased. It is locally known as *Jowar*, an important food and fodder crop of dry land agriculture.

The important sorghum growing states in India are Maharashtra, Karnataka, Andhra Pradesh, Madhya Pradesh, Rajasthan, Tamil Nadu, Uttar Pradesh and Gujarat. The average fodder yield of sorghum in Uttar Pradesh is low because major area is covered by local and outdated varieties and selections which are not responsive to improved cultural and fertility practices. Green fodder is the cheapest source of feed for milch, beef and draft animals. Therefore, development of fodder resources of the country becomes a high priority national programme. This could be achieved through bringing more area under fodder cultivation and improving productivity of fodder crop. As there is little scope of increasing area under cultivation of fodder crops due to urbanization, industrialization and traditional inclination among farmers. Only 4.4 per cent of the total cropped area of the country is under fodder crops cultivation. Hence, only optional strategy to meet fodder requirement is to exploit crop productivity through better yielding varieties and efficient agronomic management.

Livestock is the most important component of rural economy as well as back bone of Indian agriculture characterized by mixed farming system involving crop and animal enterprises. Like green revolution, India is contemplating for white revolution, which is possible only with adequate supply of nutritious feeds and fodders. The importance of forage crop in Indian agricultural economy is obvious from the fact that of the cattle wealth. In dairy production, the cost of feed constitutes about 60-65 per cent of the total cost of milk production. To reduce the cost of milk production, continuous supply of green fodder to the animal is necessary. There is a need for continuous and steady supply of green fodder to increase milk production of animal under different intensive programmes executed for the success of white revolution. It is estimated that the 60-70 per cent of total cost in livestock production is due to feed and fodder. In India, hardly 5 per cent of the net cropped area is utilized to grow fodder. India is deficit in dry fodder by 11 per cent, green

fodder by 35 per cent and concentrates feed by 28 per cent. The common grazing lands too have been deteriorating quantitatively and qualitatively. This situation leads to poor feeding of the animal, resulting in low milk and meat yields. Due to low per capita availability of the quality products from livestock, our nation is facing the problems of malnourishment, high disease incidence and low life expectancy. Demand for animal products for human consumption is increasing day by day because of expanding human population and improvement in life style of citizens. At present as cattle population survives up to a large extent on crop residues, they are nutritionally poor hence, nutritious forage is very crucial for ensuring optimum level of milk, meat and wool production. Therefore, target could be achieved by developing the varieties or hybrids of forage crop giving high yield per unit area and better quality (**Kour and Pradhan, 2016**).

Sorghum is the fourth major cereal crop of the world in production and fifth in acreage after wheat, rice, maize and barley. Sorghum plant is unique in stature and can grow in adverse environments and is well adapted to changing climatic conditions. The crop is well adapted to the semi-arid tropics climatic regions and is one of the most efficient dry land crops to convert atmospheric carbon dioxide into sugar. Sorghum is also a major cereal fodder crop grown in arid and semi-arid areas of India throughout the year in *zaid*, *kharif* and *rabi* seasons. Sorghum is successfully grown throughout India both under irrigated and rainfed conditions for grain, ethanol and fodder production. However, fodder sorghum cultivation is limited to an estimated area of 2.60 million hectares with average green fodder productivity ranging from 35 to 70 t/ha. It meets over two-third of the total forage demand of *kharif* season in the states of western Uttar Pradesh, Haryana, Punjab, Gujarat, Rajasthan and Delhi. Sweet sorghum owing to its high fodder yielding ability coupled with sweet and juicy stalks is more often used as a fodder crop in India than for its intended use as a sugar or bio-energy crop. Sorghum varieties with higher juice brix (sugar %) can easily be ensiled for silage production. Recently, Indian Council of Agricultural Research has developed and notified several new sorghum varieties and hybrids for fodder cultivation under All-India Coordinated Sorghum Improvement Programme. However, limited information is available

on performance of these new sorghum varieties and hybrids under central Uttar Pradesh conditions for fodder cultivation purpose (**Singh and Chauhan, 2017**).

Sorghum is popular as a dual purpose crop and is next to rice and wheat in its acreage and importance in India. Sorghum grain is used as staple food by millions of people and is grown in Northern states of the country it is mainly grown as fodder during summer and *kharif* seasons as a single as well as multicut crop. The grain of sorghum forms a staple food in the diets of the rural people and used as fodder for livestock. Sorghum is cultivated during rainy and post rainy seasons. This crop is well adapted to drought-prone regions with poor soil than other cereal crops. Forage sorghum seems to be a promising option in meeting out the increasing gap between fodder requirement and availability because it bears xerophilic characteristics, wide adaptation, fast growth habit, good ratoonability, palatability and digestibility and diversified uses such as green fodder, dry roughage and silage (**Ahlawat *et al.*, 2018**).

The total area, production and productivity of jowar are 5.65 million hectare, 4.41 million tones and 780 Kg per hectare respectively in India and the total area, production and productivity are 0.16 million hectare, 0.11 million tones and 677 Kg per hectare in U.P. respectively (Agriculture statistics at a glance, 2016). The area under high yielding single cut and multicut varieties is negligible in western Uttar Pradesh. Hence, it is necessary to develop superior dual purpose varieties with a significant superiority in terms of green fodder yield and good nutritional qualities.

The breeders need various information for different selection parameters namely, genetic variability, heritability, genetic advance, correlation, path coefficient analysis, combining ability and heterosis of newly introduced genotypes. Genetic variability presents in a population is of primary importance for any successful selection programme in plant breeding. Greater the variability in crop plants provides an opportunity for selecting desirable genotypes. Heritability is an index of transmissibility of a character from the parents to its offspring and thus it is a suitable measure for assessing the magnitude of genetic portion of total variability and an aid to made improvements in crop by selection for various characters. But heritability alone does not give true

picture of genetic improvements by selection, it is essential to study the extent of heritability along with genetic advance. Correlation and path coefficient analysis are significant biometrical tools, which are in vogue for determining the rate of various yield components in different crops, leading to selection of superior genotypes. Therefore, for a rational approach to the improvement of yield, it is imperative to have information on the association between yield and its components. But correlation does not disclose the cause and effect relationship in different characters, therefore partitioned into direct and indirect effects separately by adopting the procedure of path coefficient analysis proposed by **Wright (1921)**. Forage yield is basically a function of many morphological and physiological characters; the potential of yield improvement for forage therefore, depends on the favorable alteration of one or the other of these component characters. Development of hybrids provides a good avenue for quicker exploitation of both additive and non-additive genetic variances through such alterations. Combining ability analysis as proposed by **Griffing (1956)** has widely been used in crop plants for identifying the superior parents for hybrid development. The concept of general and specific combining ability are useful for testing procedure that involves the study and comparison of the performance of homozygous inbred lines in cross combinations, as suggested by **Kemphorne (1957)**. Combining ability refers to the ability of a parent to transmit its desirable performance to its progeny in crosses. General combining ability is average performance of a genotype in cross combinations involving a set of other genotypes. Specific combining ability is an average performance of a specific cross combination expressed as deviation from the population mean. Combining ability analysis helps in selection of suitable parents for hybridization, evaluation of inbreds in terms of their genetic value and identification of superior specific cross combinations. Like green revolution, India is contemplating for white revolution which is possible only with adequate supply of nutritious feed and fodder. It is well known that the animal industry in any country revolves around sufficient quantity of good quality feed and fodder. To study the combining ability of a number of parents, Line x Tester analysis is the most appropriate procedure.

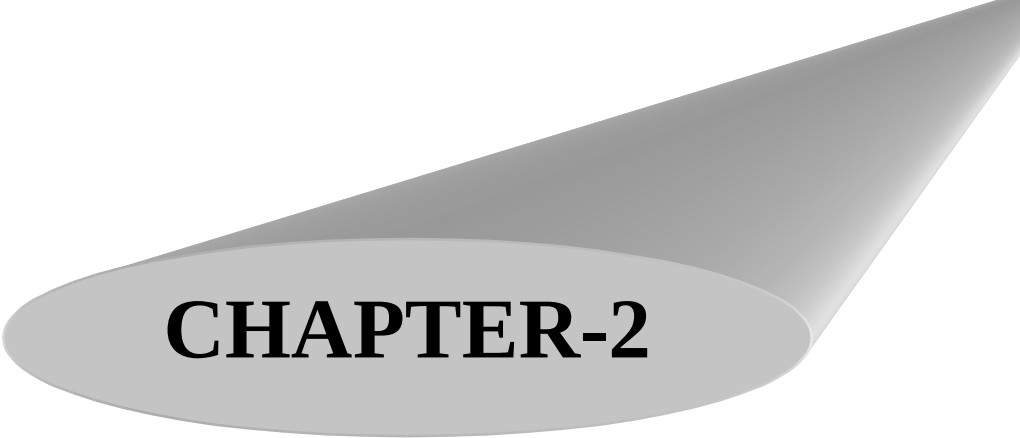
The Line x Tester analysis is one of the simplest and efficient methods of evaluating large number of inbreds/ parents for their combining ability.

Based on the information from Line x Tester analysis, development of commercially viable hybrids is possible. For improving the genetic architecture of crop through breeding efforts, utilization of heterosis is very important for maximizing the yield. The magnitude of heterosis provides information on the extent of genetic diversity of parents in developing superior F_1 s so as to exploit hybrid vigour. Although sustainable heterosis has been reported, commercial exploitation to its full potential has been possible. Hence, study of heterosis helps to exploit the vigour with present genetic variability that helps to achieve a quantum jump in yield. Grain sorghum improvement programmes was concentrated primarily on traits that influence grain yield. Little attention was given to improvement of both grain and forage attributes by breeding. Improvement of both grain and fodder traits by breeding were possible. Therefore, the present study was undertaken to assess the possibility of commercial exploitation of heterosis for grain and fodder yield along with a view of gene action in crosses involving high yielding, well adopted homozygous lines of dual purpose sorghum through estimating the heterosis over mid parent and better parent for yield and its contributing traits.

To conduct an experiment some goals have to be fixed for systematic study with an appropriate strategy in achieving the target of research. Therefore, the present investigation on “Genetic analysis for quantitative traits in forage sorghum (*Sorghum bicolor* L. Moench)” was undertaken using line $\times$ tester analysis in a set of 12 line and 4 testers of forage sorghum with the following objectives.

- To estimate variability, heritability and genetic advance.
- To estimate correlation coefficient among different characters.
- To estimate direct and indirect effect of yield components on yield through path-coefficient analysis.

- To estimate combining ability variances and effects.
- To assess the nature and magnitude of heterosis for yield and its component traits.



CHAPTER-2



REVIEW OF LITERATURE

For starting any investigation, it is very important task that breeders should have the basic knowledge about statistical and biometrical parameters related to genetic variability, heritability, genetic advance, character association, path coefficient, gene action, combining ability analysis and heterotic response in the concerned breeding material for different traits which are very useful for the selection of desirable parents, identification of superior cross combinations and formulation of suitable breeding procedure for improving the targeted traits in this crop. In the present investigation the fodder yield and quality component traits in forage sorghum was targeted. For this point of view, literatures concerning various aspects of yield and its components including quality components have been reviewed. In addition to crop related review, the basic literature regarding statistical and biometrical issues were also consulted and reviewed under following heads.

- ✓ Variability, heritability and genetic advance
- ✓ Character association and path coefficient analysis
- ✓ Combining ability analysis and gene effects
- ✓ Nature and magnitude of heterosis for yield and its components

Variability, heritability and genetic advance

Genetic variability is the most essential prerequisite for successful improvement in crop breeding. The extent of possible improvement for a particular character mainly depends upon the extent of genetic variability and its heritable proportion. Yield is a polygenic trait, where direct selection would not be a reliable approach on account of being highly influenced by environment factors. Exploitation of variability is most important and prerequisite for screening of superior genotypes.

Magnitude and nature of genetic variability determine the progress of breeding for crop improvement and play an important role for selection of best genotypes for making rapid improvement in yield and other desirable characters. Assessment of variability for the yield and its

components become absolutely essential before planning for an appropriate breeding strategy for genetic improvement. Parameters such as genotypic and phenotypic coefficient of variability are useful in detecting the amount of variability present in the germplasm.

It is a well known fact that effectiveness of selection in a crop under plant improvement programme is mainly dependent on variability present in the population and to the extent it is heritable, the greater is the genetic diversity the more will be the genetic potentiality and thereby wider is the scope for improvement of the crop. The progress due to selection in quantitative characters depends primarily on nature and magnitude of genetic variability present in the population to be improved. The genotypic variance results due to different genotypic constitution of the individuals in a population. Variability due to environmental variance, which by definition embraces all variations of non genetic origin, can have a great variety of cause and its nature depends very much on the trait and the organism studied.

Variability thus expressed in two such forms is simple and can be observed by an experimenter or breeder on plant attributes. The estimates of heritability are of much value both for breeders and geneticists for determining an index of transmissibility of a trait from parents to offspring. **Lush 1940, 1949 and Robinson *et al.* 1949** laid down information in both broad and narrow sense heritability. According to him, broad sense heritability is the ratio of total genetic variance to phenotypic variance and in narrow sense it is the ratio of additive genetic variance to phenotypic variance. Heritability and genetic advance help in determining the influence of environment on the expression of genotype and the reliability of characters. Seed yield is not a unitary character but depends on the development of various plant characters.

Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. These studies are also helpful to know about the nature and extent of variability that can be attributed to different causes, sensitive nature of the crop to environmental influences, heritability of the characters and genetic advance that can be realized in practical breeding. The progress in any

crop improvement venture depends mainly on the magnitude of genetic variability and heritability present in the source material. Since the heritability is also influenced by environment, the information on heritability alone may not help in pin-pointing characters enforcing selection. Nevertheless the heritability estimates in conjunction with the predicted genetic advance will be more reliable (**Johnson et al., 1955**). Heritability gives the information on the magnitude of inheritance of quantitative traits while genetic advance is helpful in formulation of suitable breeding procedures.

The concept of heritability is important to determine whether the phenotypic differences found among different individuals are due to difference in their genetic makeup or simply a result of environmental factor. Estimated of heritability in broad sense and genetic advance will help in knowing the nature of gene action affecting the concerned traits. Knowledge of heritability influence the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the character, to predict gain from selection and to determine the relative improvement of genetic effects.

House (1985) suggested the predictive role to indicate the reliability of phenotypic value as a guide to breeding value, as the most important function of heritability in genetic studies of quantitative character. Characters with high heritability can easily be fixed with simple selection resulting in quick progress. However, it has been accentuated that heritability alone has no practical importance without genetic advance. The limitation of estimating heritability in narrow sense, as it included both additive and epistatic gene effects, and thereby suggested the heritability estimated in the broad sense will be reliable if accompanied by a high genetic advancement. The genetic advance shown the degree of gain obtained in a character under a particular selection pressure. High heritability coupled with high genetic advance estimated offers the most suitable condition for selection.

Singh et al. (1999) revealed high genotypic and phenotypic coefficient of variation for days to 50% flowering, leaf breadth, leaf area, leaf stem ratio and fodder yield. High heritability coupled

with high genetic gain observed for plant height, stover yield, leaf area, leaf stem ratio, leaves per plant and fodder yield.

Desai *et al.* (2000) recorded significant varietal differences for all the characters except stem diameter and protein content. High genotypic and phenotypic coefficient of variation showed for dry fodder yield, green fodder yield, plant height and leaf area.

Soltani *et al.* (2001) observed high broad sense heritability and expected genetic advance for grain filling per unit area, days to maturity, number of leaves per plant and plant height.

Kadam *et al.* (2001) reported high GCV and PCV for the characters like green fodder yield, dry fodder yield, plant height, number of leaves per plant and leaf length and found significant difference for all the traits studied.

Kumar and Sahib (2003) noted high heritability coupled with high genetic advance for leaves per plant, days to 50% flowering, plant height, leaf stem ratio and dry and fodder yield per plant.

Tiwari *et al.* (2003) estimated high heritability and high genetic advance for plant height, length of leaf, length of internode, yield per plant and leaf area, indicating contribution of additive gene action in expression of these traits. Hence selection can be applied in these traits for yield improvement in sorghum.

Umakanth *et al.* (2003) reported maximum genotypic and phenotypic coefficient of variation for all the characters except crude protein and leaf length and found high heritability coupled with high genetic advance for leaves per plant, plant height, leaf area and fodder yield in sorghum.

Pattnayak *et al.* (2004) analysis of variance showed that the accessions were significant differences for all the traits. High genotypic and phenotypic coefficient of variation observed for days to 50% flowering, leaves per plant, total soluble solids, leaf breadth, stem girth and fodder yield. High heritability along with high genetic advance noted for dry fodder yield, leaf area, leaf

stem ratio, leaf length and fodder yield suggesting that there is sufficient scope for improvement if selection is based on these parameters.

Negash and Chemed (2005) conducted an experiment to study the extent of genotypic and phenotypic variability, heritability and genetic advance in sixty four sorghum germplasm using twelve quantitative morphological traits. The genotypic and phenotypic coefficients of variation were recorded maximum for plant height, leaf length, yield per plant, stem diameter and internode length and higher estimates of heritability coupled with higher genetic advance as percentage of mean for plant height, leaves per plant, leaf area and fodder yield, suggesting that additive gene actions are involved. In conclusion, significant improvement can be realized through selection for plant height, leaves per plant, leaf area and fodder yield in these attributes. **Rajguru et al.** (2005) revealed high amount of variability for number of leaves per plant, days to flowering, leaf length, leaf breadth, plant height and grain and fodder yield. High heritability was observed for all the characters except protein content and nodes per plant.

Singh et al. (2005) recorded observations on five competitive plants in each plot for six characters viz. leaf width, leaf length, leaves per plant, stem thickness, plant height and green fodder yield. Days to 50% flowering and days to milking stage were recorded on plot basis. Analysis of variance revealed significant variations among the eleven genotypes for all the characters under study.

Singh and Sirohi (2006) estimated significant variation among the eleven genotypes for all the characters. High variability was observed for green fodder yield, plant height, leaf length, days to milking stage, days to 50% flowering, stem thickness, leaves per plant and leaf width. A wide range of phenotypic and genotypic coefficients of variation was observed among all the characters. The highest phenotypic coefficient of variation (PCV) was observed for green fodder yield followed by stem thickness whereas; days to 50% flowering exhibited for lowest PCV value. The highest magnitude of GCV was observed for green fodder yield followed by stem thickness whereas lowest being for days to 50% flowering. High heritability was observed for green fodder yield, stem

thickness and plant height. The genetic advance as percent of mean was highest for green fodder yield and stem thickness. High heritability coupled with high genetic advance was observed for green fodder yield and stem thickness thereby indicating the important of additive gene effect in the inheritance of these traits and selection pressure could be profitably applied on these characters for yield improvement.

Deepalakshmi and Ganesamurthy (2007) recorded high heritability accompanied with high genetic advance as per cent of mean for days to 50% flowering, plant height, leaves per plant, leaf stem ratio and fodder yield and maximum amount of variability noted for all the characters.

Unche *et al.* (2008) noted high amount of genetic variability for most of the characters and observed higher genotypic and phenotypic coefficient of variation for yield, total biomass, days to 50% flowering, plant height, total sugar index and leaves per plant. The closer magnitude of GCV and PCV indicated that greater role were played by genotype rather than environment. High heritability coupled with high genetic advance observed for characters viz., grain and fodder yield, plant height, leaves per plant and leaf length.

Kusalkar *et al.* (2009) estimated high heritability accompanied with high genetic advance for grain yield, leaves per plant, head length, leaf width, internode length and plant height suggesting additive gene control in the inheritance of their traits and scope per selection in the improvement of these characters.

Chavan *et al.* (2010) revealed significant variance among genotypes for all the characters, which indicated presence of variability among the lines being evaluated and sample scope of improvement by selection. The high range was estimated for number of grains per panicle, plant height, grain yield per panicle, number of primary branches per panicle, harvest index, days to maturity, days to 50% flowering, test weight, panicle length and panicle width. Genotypic and phenotypic coefficient of variance observed to be high for harvest index, leaves per plant, grain and fodder yield per plant, plant height, leaf width and leaf stem ratio. High heritability was observed for grain and fodder yield, harvest index, leaf width, plant height and number of leaves per plant.

Moderate heritability estimated for days to 50 per cent flowering and panicle length and low heritability recorded for test weight and days to maturity. High heritability coupled with high genetic advance was observed for leaves per plant, plant height and grain and fodder yield. Whereas, high heritability combined with low genetic advance was recorded by panicle width, panicle length and test weight.

Vedansh *et al.* (2010) estimates of genetic parameters for fourteen characters in thirty two genotypes of forage sorghum (*Sorghum bicolor* (L.) Moench) variability were found significant for all the traits. Genotypic and phenotypic coefficient of variation was noted high for leaf stem ratio, stem, girth, total soluble solid, green fodder yield, leaf breadth and green fodder yield per day. High heritability coupled with high genetic advance observed for plant height, nodes per plant, internode length, stem girth, leaf breadth, leaves per plant, leaf stem ratio, total soluble solids and green fodder yield per day.

Kumar *et al.* (2011) reported analysis of variance highly significant difference among genotypes for all the traits. High range was observed for leaf area, green fodder yield, plant height, days to 50 % flowering, leaf length, internode length, leaves per plant, nodes per plant, total soluble solid, leaf breadth, protein content, stem girth and leaf stem ratio. Estimated of PCV was generally higher than their corresponding GCV for all the characters studies, indicating that all traits were influenced by environment. The genotypic coefficient of variability (GCV) was found maximum for leaf stem ratio followed by leaf area, green fodder yield, total soluble solid, stem girth, protein content and internode length whereas minimum being for leaf breadth, leaves per plant, and days to 50% flowering. The highest phenotypic coefficient of variation (PCV) was observed for leaf stem ratio followed by leaf area, green fodder yield, total soluble solid, protein content, stem girth, nodes per plant and internodes length whereas leaf breadth leaves per plant, plant height, leaf length and days to 50% flowering exhibited lowest value. The high heritability in broad sense was recorded for all the traits except nodes per plant and protein content. The genetic advance as percent of mean was maximum for leaf area followed by leaf stem ratio, green fodder yield, total soluble

solid and stem girth whereas, it was minimum for internode length, leaf breadth, plant height leaves per plant, leaf length, days to 50% flowering, nodes per plant and protein content. High heritability coupled with high genetic advance observed of leaf area, leaf stem ratio, green fodder yield, total soluble solids and stem girth which indicated that the substantial contribution of additive genetic variation in the expression of these traits and can be more useful in hybridization and selection for higher fodder yield.

Jain and Patel (2012) evaluated 102 land races of forage sorghum for days to 50 % flowering, plant height, number of leaves per plant, leaf length, leaf breadth and fodder yield per plant in augmented block design during 2009-10 and 2010-11 and observed highly significant differences among the accessions. High heritability accompanied with high genetic advance as per cent of mean was observed for days to 50% flowering, plant height, number of leaves per plant, leaf length and fodder yield per plant suggested that these characters are under additive gene action.

Tomar *et al.* (2012) studied the observations was recorded for seventeen quantitative traits. The phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for most of the traits which indicated influence of the environmental effect on the characters. The high heritability was observed for sixteen characters and moderate for one character *i.e.* number of leaves per plant. High heritability combined with high genetic advance as per cent of mean was observed for most of the characters, indicating that variation for these characters was due to additive gene effects and consequently the scope for improving yield through selection.

Jain and Patel (2013) studied the variability parameters and character association in single cut sorghum varieties under the arid and semi-arid condition of Gujarat. Genotypic coefficient of variation was maximum for green fodder yield followed by dry fodder yield and per day productivity. High heritability coupled with high genetic advance was observed for green fodder yield followed by dry fodder yield, leaf breadth, stem girth, leaf area and plant height.

Shivani and Sreelakshmi (2013) recorded significant differences for all the eight characters. The range of variation was found maximum for the characters viz., seed yield followed by fodder yield, panicle length, plant height and test weight, while moderate for plant height and number of leaves per plant and lowest in case of days to 50% flowering and days to maturity. In general, PCV values were marginally higher than GCV values. High heritability was observed for leaf length, test weight, number of leaves per plant, seed yield, fodder yield and plant height while

low heritability values were recorded for days to maturity and days to 50% flowering. The genetic advance was noted highest for seed yield followed by plant height, leaf length, seed yield, fodder yield, plant height, test weight and number of leaves per plant. Most of the characters recorded moderate heritability with high genetic advance indicating that the characters were stable and environment had minor impact on the expression of these traits and these characters may be considered as the most important yield contributing traits and due emphasis should be placed on these characters while breeding for higher seed and fodder yield in sorghum.

Iraddi et al. (2013) studied genetic variability, heritability and character association in large F_2 population of sweet sorghum at Directorate of Sorghum Research, Rajendranagar, Hyderabad. F_1 was generated during *kharif* 2010 and second filial generation in the following season. The mean and variance in respect of 14 quantitative characters in F_2 population indicated wide range of variability for most of the traits. However, variability range was high for the traits like days to 50% flowering, plant height, leaf area, leaves per plant, nodes per plant, stem girth, brix per cent and total soluble solids. Most of these characters except days to 50% flowering and days to maturity exhibited high heritability coupled with high genetic advance as per cent of mean indicating predominance of additive gene action in their genetic control.

Nyadanu and Dikera (2014) evaluated the sorghum varieties for yield traits using Randomized Complete Block design with four replications. The results revealed that, significant variations were recorded among the yield traits. High values for phenotypic coefficient of variation and genotypic coefficient of variation was recorded for harvest index, number of leaves, plant height, leaf width and number of grains per panicle. High heritability accompanied with high genetic advance was observed for most of the traits.

Ghorade et al. (2015) studied using thirty eight lines of sorghum. Analysis of variance indicated highly significant differences among the genotypes for all the characters. Phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the characters, the close resemblance between the corresponding estimates of PCV and GCV in almost

all the characters except panicle breadth suggested that the environment had little role in the expression of these characters. High GCV and PCV values were recorded for most of the characters. High heritability was observed for all the characters, indicating that these characters would respond positively to selection because of their broad sense heritability. The highest expected genetic advance per cent over mean was observed for the character yield per plant followed by days to 50% flowering, leaf length, leaf breadth and seed weight. In general high heritability accompanied with high expected genetic advance for the characters suggest that the genes governing these character may have additive effect. It can be mentioned here that the character yield per plant exhibited high heritability value along with high value of expected genetic advance. The phenotypic expression of this character may be governed by the genes acting additively and thereby indicating the importance of these characters for selection.

Khandelwal *et al.* (2015) an experiment at ICAR-CAZRI, Regional Research Station, Pali (Rajasthan) using 224 genotypes of sorghum to study genetic parameters and character association among yield components. Significant variation were recorded among 224 sorghum genotypes for various morphological and yield traits. The Phenotypic coefficient of variation was higher than the genotypic coefficients of variation for all the traits under investigation. High magnitude of genotypic and phenotypic coefficient of variations was observed for most of the traits. High heritability was observed for days to flowering. The association of high heritability with high genetic advance and GCV were reported in case of leaf stem ratio and leaf area. Hence short statured plants having high leaf area with plant height could be better selection criteria for further sorghum improvement programme.

Malik *et al.* (2015) estimated of twelve genetic parameters in twelve genetically diverse forage sorghum lines viz Pant chari -5, SPV-1724, HJ-513, RSSV-9, SSG-59-3, Pusa chari-23, HD-19-1, S-199, CSH-18, S-241, CSH-20 and S-437 and four tester CSV-15, HC-17,1 G-48 and Pant chari-6 were used line X tester fashion. Two varieties out of the parents viz. HC-308 and UP chari-2 were used as check. The parents and F₁s were evaluated in completely randomized block design

with three replications. Forage sorghum (*Sorghum bicolor* L. Moench) revealed significant variability for all the traits. The estimated of genotypic and phenotypic coefficient of variation were high (more than 25%) observed for leaf breadth, leaves per plant, leaf area, leaf stem ratio and green fodder yield and moderate (10-25%) was observed for leaf length, internode length, stem girth, total soluble solids and protein content and low (<10%) for days to 50% flowering. Heritability (broad sense) was high (>60%) for all traits viz. days to 50% flowering, plant height, leaf breadth, leaf length, internode length, stem girth, leaves per plant, leaf area, leaf stem ratio, total soluble solids, protein content and green fodder yield. The genetic advance as percent of mean were high (>20%) for plant height, leaf breadth, leaf length, internode length, stem girth, leaves per plant, leaf area, leaf stem ratio and green fodder yield. Based on this consideration, high heritability for plant height, leaf breadth, leaf length, internode length, stem girth, leaves per plant, leaf area, leaf stem ratio and green fodder yield coupled with high genetic advance, indicate additive genetic control in the inheritance of these traits.

Diwakar et al. (2016) conducted an experiment using 126 diverse genotypes of forage sorghum including two checks (SSG-59-3 and SMU-1) in Randomized Block Design with three replications. Observations were recorded for 24 characters. GCV and PCV observed high for stem juiciness, leaves per plant, leaf length and plant height. Heritability coupled with genetic gain had high for number of leaves per plant, leaf breadth, protein percent, leaf length and stem girth. On the basis of heritability and genetic gain, selection criteria based on number of leaves per plant, leaf length leaf breadth, stem juiciness, protein per cent may be useful for further developing good quality and high yielding forage sorghum cultivars.

Kour and Pradhan (2016) worked using 40 diverse genotypes of forage sorghum, which were grown in a RCBD with three replications and were evaluated for fifteen characters, including of green fodder yield and its components characters. Analysis of variance revealed the significant differences among the genotypes for all the character under study which indicated the presence of sufficient variability in the experimental material. Magnitude of genotypic coefficient of variation

(GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as percentage of mean were observed high for characters like leaf stem ratio, number of leaves plant, green fodder yield plant, stem girth and dry matter yield plant. Therefore, more emphasis should be laid on these component traits during selection for further improvement of green forage yield.

Singh *et al.* (2016) estimated of genetic parameters for forty genotypes of forage sorghum and showed significant variability for all the characters under study, indicated wide spectrum of variability among the genotypes. The estimates of genotypic and phenotypic coefficient of variation were high for plant height, leaves per plant, leaf area, stem girth, leaf stem ratio and green fodder yield. High heritability coupled with high genetic advance were revealed for plant height, leaf breadth, leaf length, leaves per plant, leaf area, leaf stem ratio and green fodder yield. Improvement in fodder yield can be made by selecting these yield contributed traits having high heritability coupled with high genetic advance.

Jain *et al.* (2017) studied using 144 genotypes of sorghum to study the variability parameters and genotypic and phenotypic correlations and path analysis among agronomic traits. Significant variation among all the genotypes was recorded for all the characters. Most of the characters had higher genotypic and phenotypic coefficient of variation which is indicated that character expression in this sorghum population was genetic and can be exploited in breeding programs. The genotypes also exhibited varying degrees of heritability and genetic advance. Characters such as plant height, stem girth and dry and green fodder yield responded positively to selection because of high broad sense heritability and high genetic advance.

Ranjith *et al.* (2017) evaluated that high genotypic coefficient of variation was observed for the character fodder yield per plant followed by 1000-seed weight whereas moderate for panicle breadth, plant height and grain yield per plant and low for the character 50 % flowering. High phenotypic coefficient of variation was observed for the character fodder yield per plant followed by 1000-seed weight, leaves per plant, stem diameter and panicle breadth whereas moderate for plant height and grain yield per plant and low for the character days to 50 % flowering. High

heritability in broad sense was recorded for fodder yield per plant, 1000-seed weight, leaf length, leaf area, grain yield per plant and plant height, while moderate heritability was recorded for days to 50 per cent flowering, leaf stem ratio and panicle breadth. The highest genetic advance percentage over mean was observed for the character fodder yield per plant followed by 1000-seed weight, leaf breadth, grain yield per plant, plant height and internode length while for days to 50 per cent flowering the expected genetic advance was moderate. The characters fodder yield per plant, 1000-seed weight, grain yield per plant and plant height exhibited high heritability values along with high values of expected genetic advance. The phenotypic expression of these characters may be governed by the genes acting additively and thereby indicating the importance of these characters for selection.

Singh et al. (2017) economic yield attributing characters were studied in forage sorghum for crop improvement through selecting high yielding characters. Significant variations were recorded among the genotypes for various yield traits studied. High values for phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were noted for plant height, leaf breadth, internode length and green fodder yield per plant. High heritability coupled with high genetic advance as percent of mean was revealed for plant height, leaf breadth, internode length, number of leaves per plant, leaf stem ratio, leaf area, total soluble solids and green fodder yield per plant. It was concluded that these characters could be considered as significant selection criteria for yield improvement in forage sorghum.

Rajarajan et al. (2018) observed high heritability coupled with high genetic advance as per cent of mean for most of the characters.

Kalpande et al. (2018) studied using 24 sweet grain sorghum genotypes with 2 checks of *Sorghum bicolor* (L.) Moench. These 26 genotypes were grown at Sorghum Research Station, Vasantrao Naik Marathwada Agricultural University, Parbhani during rabi 2015-16 to evaluate sweet grain sorghum land races for grain yield and per cent threshable grains at dough (milky) stage. High GCV and PCV values were recorded for the traits % threshable grains, seed yield per

plant, fodder yield, taste score, 100-seed weight, whereas, days to 50% flowering recorded low estimates of GCV and PCV. The PCV was relatively greater than GCV for all the traits. However, the magnitude of the difference was low. High degree of heritability estimates for most of the traits suggested that the characters were under genotypic control and selection could be fairly easy and improvement is possible using selection breeding for these traits. All of the characters except days to 50% flowering had high genetic advance as percent of mean were observed. High heritability accompanied with high genetic advance was observed in case of plant height, % threshable grains, seed yield per plant 100-seed weight, fodder yield and taste score. This indicated that these traits were highly heritable and selection of high performing genotypes is possible to the improvement of the characters.

Damor *et al.* (2018) investigated the magnitude of variability parameter, character association and path coefficient in different 60 genotypes of forage sorghum. The analysis of variance in this study revealed highly significant differences among all genotypes were observed for all yield and qualitative traits except leaf stem ratio and stem thickness which indicated the presence of sufficient variability in the experimental material. The values PCV were higher than GCV for all the character which indicated that the apparent variation is not only due to genotypes alone but also due to the influence of environment on the expression of these traits. High heritability accompanied with high genetic advance over mean was observed for most of the characters, which indicates that the influence of additive gene effects and provide scope for selection.

Badikar *et al.* (2018) studied genetic variability were worked out for fifteen characters in forty five genotypes of sweet sorghum. Based on mean performance the genotypes SSAVRT- 1013, SSAVRT-1026, PVR-455, ICSV-93046 and SPV-22 were found significantly superior over checks SSV-84 and RSSV-9 for all characters. Phenotypic coefficient of variation was higher than the genotypic coefficient of variation, indicating the influence environment of the expression of these traits. The character for green cane yield, total biomass, total soluble sugar, non reducing sugar, reducing sugar and juice yield showed high value of genotypic and phenotypic coefficient of variation also showed high estimates of heritability and expected genetic advance indicating presence of additive gene effect.

Correlation and path coefficient analysis

The knowledge of correlation and path analysis helps in achieving success in a breeding programme. Character association studies are also helpful while making selection in the field for increasing yield. An effective breeding programme for development of good quality and high yielding varieties requires preliminary information on the nature of association of characters with yield and among themselves. The study of correlation alone does not provide an exact picture of relative importance of direct and indirect influence of each of desired effect which sometimes leads to misinterpretation of the obtained results when more variable are included in the study and indirect association becomes more complex. The original concept of correlation was presented by **Galton (1908)** and later elaborated by **Fisher (1918)** and **Wright (1921)**. Association of economically important quantitative characters which is statistically determined by correlation coefficient has been quite helpful as basis for selection. A correlation whatever its nature phenotypic, genotypic or environmental is the ratio of appropriate covariance to the product of the two standard deviations. Essentially it is a measure of intensity of association between any two characters. Information on correlation between two characters of yield used in predicting the correlated response to directional selection as well as in the identification of some characters which may not have value in themselves but are useful indices of consideration in improvement of yield. Yield is a multiplicative product of many characters which jointly or singly influence the yield. These characters are themselves interrelated. Such inter relations of yield there by making correlation coefficient unreliable as selection indices.

Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects. In other words, it measures the direct and indirect contribution of various independent characters on a dependent character. The path diagram may be explained in term of cause and effect relationship of different variables. By path coefficient analysis, correlation coefficients can be partitioned in to two components *i.e.* direct

and indirect effects. It helps to elucidate the intrinsic nature of the observed association for complex characters like yield.

Anup and Kumar (2000) showed that green fodder yield had high positive correlations with leaf area, plant height, number of leaves per plant, number of nodes per plant and crude protein. Path analysis revealed that leaf area was the single major character which exhibited the highest positive direct effect on green fodder yield and crude protein and other independent characters had highest indirect contributions through leaf area.

Chaudhary and Arora (2001) studied genetic variability and inter relationships of 18 characters in 23 genotypes of sorghum in 4 environments. Grain yield was positively correlated with biological yield, stover yield and number of leaves per plant.

Iyanar *et al.* (2001) revealed that seed yield was significantly and positively correlated with plant height, days to 50% flowering, panicle weight and panicle length and path analysis showed that the direct contribution of panicle weight was maximum on seed yield followed by plant height, days to 50% flowering and test weight.

Yadav *et al.* (2003) conducted a study to evaluate the correlation of fodder yield and its components in 106 forage sorghum genotypes. Plant height showed significant positive correlation with leaf length, number of leaves per plant, growth rate and green fodder yield per plant while negative correlation with leaf-stem ratio, shoot fly attack. Leaf area per plant was positively correlated with number of tillers per plant, GFY and DFY. GFY and DFY were positively associated with plant height, leaf length, leaf breadth, leaves per plant, leaf area, stem girth, nodes per plant and negatively correlated with leaf stem ratio.

Kumar and Sahib (2003) recorded positive and significant association of dry stem weight per plant, leaf width, number of leaves per plant, tillers per plant and leaf stem ratio with green fodder yield. Leaf width showed negative correlation with leaf number per plant, leaf stem ratio and tillers per plant.

Awari *et al.* (2003) found that number of leaves per plant, leaf length, leaf area, total dry matter per plant, crop growth rate, ear head length, stem girth, grain weight and number of nodes per plant were positively and significantly correlated with grain and fodder yield.

Agarwal *et al.* (2003) noted that leaf length was positively and significantly correlated with both green fodder yield as well as dry matter yield. Plant height was significantly and positively correlated with dry matter yield. Total soluble solids was recorded negative with leaf length. Stem diameter was observed significant and positive with days to 50% flowering, plant height, number of leaves per plant and internode length. Number of nodes per plant was positive and significant estimated with days to 50% flowering, plant height, number of leaves per plant and total leaf area. Internodes length was positive and significant correlation observed with plant height an days to 50% flowering. Number of leaves per plant had positive and significant with plant height was found positive and significant association with days to 50% flowering.

Mallinath *et al.* (2004) revealed grain and fodder yield was significantly and positively correlated with days to 50% flowering, plant height, number of leaves, panicle weight and stem girth.

Kishore and Singh (2005) reported that days to 50% flowering showed positive and significant correlation with number of internodes per tiller. Crude protein content showed negative association with days to 50% flowering, number of leaves positive and significant with number of internodes and negative significant found with days to 50% flowering. Number of internodes was observed positive and significantly correlated with days to 50% flowering.

Negash and Chemedha (2005) observed positive and significant correlations days for 50% heading, plant height, node number per plant, panicle weight and kernel number per panicle with fodder yield.

Iyanar and Khan (2005) exhibited green fodder yield per plant positive and significant with leaf length, plant height and number of leaves. Total soluble solids recorded negative and significant correlation with green fodder yield. Plant height had positive correlation with leaf

length, number of leaves and dry fodder yield. Leaf length had highest positive association with fodder yield. Plant height exerted the highest direct effect on green fodder yield followed by leaf length, leaf breadth, number of leaves per plant and leaf stem ratio.

Chaudhary *et al.* (2005) studied stover yield exhibited positive and significant correlation with days to flowering, plant height, stem girth and green fodder yield per plot. Stem girth was positive and significant correlation with days to 50% flowering, leaf length and leaf width. Leaf width was positive and significantly correlated with days to 50% flowering and leaf length at phenotypic level. Leaf length was positive and significantly correlated with days to 50% flowering and plant height at genotypic and phenotypic levels. Number of leaves per plant was positive and significantly correlated with days to maturity. Plant height had positive and significant correlation with days to 50% flowering.

Singh *et al.* (2006) observed green fodder positive and significant with plant height followed by days to 50% flowering, days to milking stage and leaf length at genotypic and phenotypic level and path analysis revealed high direct effect plant height, leaf width, crude protein, stem thickness and days to 50% flowering on green fodder yield. Days to 50% flowering, days to milking stage, leaf length and stem thickness contributed to fodder yield mainly through indirect effect via plant height. Result indicates that selection for high plant height, days to 50% flowering, days to milking stage, leaf length and stem thickness would lead to high fodder yield.

Premalatha *et al.* (2006) revealed path analysis that the direct contribution of grain weight, number of grains per panicle, leaf area index, plant height and days to 50% flowering on yield per plant. Green fodder yield showed significantly and positively association with plant height, days to 50% flowering, grains per panicle and leaf area.

Singh and Sirohi (2007) studied using eleven genotypes of sorghum. Correlation studies indicated that fodder yield per plant exhibited stable positive association with plant height followed by days to 50% flowering, days to milking stage, leaves per plant and leaf length at genotypic and phenotypic levels. Path analysis revealed high positive and direct influence of plant height toward

green fodder yield per plant followed by leaf width and days to 50% flowering. Days to 50% flowering, days to milking stage, leaf length and stem thickness contributed to fodder yield mainly through indirect effect via plant height. Results indicated that selection for high plant height, days to 50% flowering, days to milking stage; leaf length and stem thickness would lead to high fodder yield.

Deepalakshmi and Ganesamurthy (2007) showed that high seed and fodder yield was positively and significantly correlated with days to maturity, number of leaves per plant, days to 50% flowering, plant height and ear head weight. High direct contribution of plant height followed by leaf breadth, stem girth and leaf area on green fodder yield.

Singh *et al.* (2009) observed genotypic correlation was 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 per day, days to 50% flowering, days to milking stage, leaf length, nodes per plant and plant height. This Indicates that any selection based on these characters will enhance performance and improvement in forage sorghum. Path coefficient analysis showed that green fodder yield per day, days to milking stage and days to 50% flowering were the most important characters controlling directly green fodder yield. High Indirect positive contribution of days to milking stage and green fodder yield per day mainly via days to 50% flowering, leaves per plant and plant height mainly via days to milking stage and green fodder yield per day mainly *via* leaf length. This indicates that, effectiveness of selection for high fodder yield could be enhanced by inclusion of green fodder yield per day as a selection criterion along with the days to milking stage.

Lyannar *et al.* (2010) studied genotypic correlation coefficient and path coefficient analysis were carried out using 109 genotypes of multicut fodder sorghum between fourteen fodder yields and yield related characters for each cut and subjected to pooled analysis. The result showed that all the characters except hydrocyanic acid, total soluble solids and crude protein had positive significant association with green fodder yield per plant. Among these traits dry fodder yield

exhibited high correlation coefficient with green fodder yield per plant followed by leaf length, plant height, leaf breadth and number of leaves. Plant height exerted the highest direct effect on green fodder yield followed by stem girth, leaf area and leaf stem ratio. Hence, selection for any of these traits might result in simultaneous improvement in the yield. The results of correlation and path analysis indicated that due importance should be given for plant height because of its significant correlation and high direct effect, apart from its high indirect effect through dry fodder yield.

Kumar *et al.* (2010) elucidated the association between fodder yield and its attributes in forage sorghum. Genotypic correlation was higher magnitude compared to their corresponding phenotypic correlations for most of the character combinations. Green fodder yield was found positive and significant association with leaf breadth leaves per plant and leaf area at genotypic and phenotypic level and reported the direct and positive effect of leaf length, leaf breadth, leaves per plant and leaf area on green fodder yield per plant.

Prakash *et al.* (2010) an investigation was carried out with 12 parents and their 35 hybrids (Line x Tester mating design) of sorghum to assess association of fodder yield components and their direct and indirect effects on green fodder yield per plant. Results of correlation analysis indicated that the green fodder yield per plant was found to be significantly and positively correlated with plant height, number of tillers, leaf length, leaf breadth, stem diameter, hydrocyanic acid and crude fiber. Days to 50 per cent flowering, leaf area and crude protein showed a negative association with green fodder yield per plant. Path analysis showed that plant height contributed high direct effect to green fodder yield per plant followed by leaf breadth and leaf length. Stem diameter and in *vitro* dry matter digestibility also exerted positive direct effect on green fodder yield.

Warkad *et al.* (2010) studied correlation between yield and yield contributing components and to assess the direct and indirect effects of yield components on yield. The investigation revealed that the only one character plant height showed highly significant association with yield per plant at both genotypic and phenotypic level. This indicates that strong association of this trait with yield per plant could be fruitfully exploited for enhancing the yield potential in sorghum. Among the yield components themselves, green fodder yield showed highly significant positive association with days to 50% flowering, plant height, dry fodder weight per plant and number of leaves per plant. The character number of internodes per plant exhibited very strong positive correlation with number of leaves per plant and stem girth while number of leaves showed

moderately significant positive association with stem girth. The character days to 50% flowering exhibited positive direct effect of very high magnitude on grain yield per plant followed by ear head length and 1000 seed weight, while number of leaves per plant and number of primaries per whorl. It can be concluded that the character days to 50% flowering had very high direct positive effect on grain yield per plant and had the character leaf length maximum positive indirect effect via number of internodes per plant, while most of the characters had their positive and direct effect on yield per plant via days to 50% flowering and days to maturity.

Ikanovic *et al.* (2011) studied phenotypic correlation was slightly higher than the genotypic correlation coefficient, which may be result of modifying effect environment on the association of the characters. The green fodder yield showed positive and significant correlation with plant height, number of leaves per plant, leaf area and stem girth. Path coefficient analysis exhibited direct effect plant height, days to 50% flowering, leaf breadth and leaves per plant on green fodder yield.

Jain and Patel (2012) evaluated 102 land races of forage sorghum for days to 50 % flowering, plant height, number of leaves per plant, leaf length, leaf breadth and fodder yield per plant in augmented block design. It was revealed that highly significant differences among the accessions. Fodder yield was positively and significantly correlated with number of leaves per plant, leaf length, leaf width and panicle length. The characters leaf width, number of leaves per plant, days to 50% flowering and panicle length showed positive direct effect on fodder yield. Whereas leaf length showed positive significant association with fodder yield but the direct effect of leaf length was negative with fodder yield, which may be a result of the indirect effect of this trait via other traits. Therefore these characters should be utilized in further breeding program for developing superior varieties in sorghum.

Kumar and Singh (2012) genotypic correlation was higher magnitude compared to their corresponding phenotypic correlation for most of the characters. Green fodder yield was found positive and significant association with leaf breadth, leaves per plant and leaf area at genotypic and phenotypic level. This indicates that any selection based on these characters will enhance performance and improvement in forage sorghum. Path coefficient analysis showed that leaf length,

leaf breadth, leaves per plant and leaf area were the most important characters controlling directly green fodder yield. High indirect positive contribution of leaf length, leaf breadth, leaves per plant and stem girth via leaf area and leaf stem ratio, total soluble solids and protein content via leaves per plant. This indicates that, effectiveness of selection for high fodder yield could be enhanced by inclusion of leaf length, leaf breadth leaves per plant, stem girth and leaf area as a selection criterion along with the leaf stem ratio.

Tag El-Din *et al.* (2012) an investigation was carried out with 25 restorer lines of sorghum to assess association of grain yield components and their direct and indirect effects on grain yield per panicle during 2008 and 2009. Results of correlation analysis indicated that number of kernels per head had positive and highly significant correlation with grain yield whereas, the positive and significant correlation was found between panicle length and grain yield. On the other hand there are negative and non-significant correlation between panicle width and total soluble solids. The path analysis showed that panicle length had low but positive direct effect on grain yield whereas, number of kernels per head had high positive direct effect on grain yield and positive indirect effect was through days to flowering, plant height, panicle length, panicle width and panicle internodes, whereas its indirect effect was negative through leaf area and 1000 kernel weight.

Shivani and Sreelakshmi (2013) studied the genotypic and phenotypic correlations were highly variable with each other for all the characters suggesting profound influence of environment on the expression of these characters. Days to 50 per cent flowering was positively and significantly correlated with days to maturity, plant height, number of leaves per plant and fodder yield at both genotypic and phenotypic levels. Plant height showed positive significant association with number of leaves per plant and test weight at phenotypic and genotypic levels, respectively. Positive direct effect of number of leaves per plant, test weight and fodder yield on seed yield was also observed. Hence, selection based on the above traits would be effective in increasing the yield.

Jain and Patel (2013) green fodder yield showed positive and significant correlation with dry fodder yield, green and dry fodder yield per day, number of leaves per plant, plant height, leaf

length and stem girth. It was also observed that characters that exhibited positive associations with fodder yield also showed positive associations among themselves. The characters like green and dry fodder yield per day, number of leaves per plant, plant height, leaf length and stem girth exerted positive direct effects on green fodder yield, whereas the showed indirect effect days to 50% flowering with leaf length.

Malik *et al.* (2013) studied the genotypic correlation coefficient was in general, observed to be higher than that of phenotypic correlation coefficient, indicating the existence of strong inherent association for the various characters studied however, the phenotypic expression of the correlation was influenced by the environmental factors. Green fodder yield showed significant stable positive association with leaves per plant followed by leaf area, plant height, leaf length, stem girth, protein content, total soluble solid and leaf breadth at genotypic level. Thus, it can be inferred that selection based on any one of these traits either alone or in combination, will result in identifying high yielding strains. In the present study, leaves per plant, leaf area, plant height, stem girth, leaf breadth, protein content, total soluble solid and leaf length exhibited a highly significant positive correlation, which might be due to linkage of genes determining these three traits. These results are in general agreement with leaves per plant suggests that yield could be improved substantially through selection for high degree of leaves per plant these results are in confirmation with the findings of reported positive association of green fodder yield per plant with leaves per plant suggest that yield could be improved substantially through selection for high degree of leaves per plant. These results are in confirmation with the findings of reported positive association of green fodder yield with leaves per plant as recorded in the present study. Positive association of green fodder yield with leaf area is in confirmation of the earlier workers. Positive associations of green fodder with plant height have been reported earlier by positive association of green fodder yield with leaf length is in confirmation of the earlier workers. Phenotypic and genotypic path coefficient revealed high direct contribution of leaf area, stem girth, leaf breadth, plant height and leaf stem ratio towards green fodder yield.

Patil et al. (2014) the investigation was carried out to study the correlation and path analysis in dual purpose sorghum (*Sorghum bicolor* L.) with the set of thirty seven genotypes of sorghum grown in randomized block design with four replications. The correlation analysis suggested that the magnitude of genotypic correlations was higher as compared to their corresponding phenotypic correlations indicating the inherent relationship among the characters studied. Path co-efficient analysis considering 15 characters as a causal variables showed that the number of leaves per plant had highest positive direct effect on grain yield per plant followed by panicle diameter, leaf length, protein per cent in grain and thousand grain weight. Grain yield per plant exhibited significant positive association with thousand grain weight, stem girth, leaf length, panicle length and protein per cent at both genotypic and phenotypic levels.

Raza and Naheed (2014) noted high significant and positive correlation of seed yield with number of green leaves, fodder yield, plant height, ear weight and days to flowering.

Khandelwal et al. (2015) reported that grain yield per plant was significantly and positively correlated with harvest index, 1000 seed weight, panicle length, fresh weight per plant, stem diameter and leaf area and path coefficient analysis exhibited direct effect of 1000 seed weight, harvest index, plant height, panicle length and leaf area on grain yield, hence selection of these characters may be useful criteria for further sorghum improvement programme.

Arunah et al. (2015) studied mutual association between characters of two sorghum varieties using correlation coefficient of two years experiment. The percent contribution of growth and yield components to yield was also determined with path coefficient analysis. In both years and the average over the years, a positive and highly significant correlation was observed between sorghum yield and plant height, leaf area index and total dry matter. Likewise, sorghum yield also had a positive and highly significant interaction with panicle weight and 1000- grain weight. The highest individual contribution was made by leaf area index, followed by plant height. Total dry matter, panicle length and weight also contributed positively to the final yield. The highest combined percent contribution to yield resulted from plant height via leaf area index. This was followed by

contribution from plant height via panicle weight, panicle length via leaf area index respectively. In improving sorghum yield emphasis on breeding should be on its height, leaf area index and panicle length.

Dubey *et al.* (2016) studied the characters like leaf area, leaf length, number of leaves, grain weight showed highly significant positive correlation with yield per plant. Path coefficient analysis revealed that leaf area, grain weight and number of leaves per plant, days to maturity and plant height showed high positive direct effect on yield and can be used in selection for the improvement of sorghum breeding programme.

Girish *et al.* (2016) observed that seed yield per plot showed significant positive correlation with traits *viz.*, plant height, ear head length, 100 seed weight, fodder yield and lodging percentage at both phenotypic and genotypic level. Genotypic correlation was higher magnitude than phenotypic correlation. Revealed increase in ear head length will increase the seed yield. Partitioning of yield and yield components both at phenotypic and genotypic levels into direct and indirect effects revealed that positive direct effects of ear head length, ear head diameter, days to maturity, fodder yield were relatively high and followed by less lodging percentage. Residual effects were $Pr=0.1303$ and $Gr=0.0624$ at phenotypic and genotypic levels. Indicating importance of these characters and can be strategically used to improve the seed and fodder yield of sorghum.

Rana *et al.* (2016) observed green forage yield per plant highly significant and positively correlated with stem girth, leaf length, leaf width and dry matter yield per plant at both genotypic and phenotypic level. These characters may be considered as important yield component in sorghum. Path coefficient analysis revealed high positive direct effect of dry matter yield per plant, stem girth, plant height and days to fifty per cent flowering. These traits had high magnitude of genotypic correlation with green forage yield per plant.

Singh *et al.* (2016) studied that phenotypic correlation was of higher magnitude as compare to their corresponding genotypic correlation in most of the character combination, indicating the

existence of strong influence of environmental factor for the various characters. Green fodder yield exhibited significant stable and positive correlation with leaf area, plant height, leaves per plant, leaf breadth and stem girth at genotypic and phenotypic levels. Thus, it can be inferred that selection based on any one of these characters either alone or in combination, will result in identifying high green fodder yielding strains. Path coefficient analysis of genotypic and phenotypic level exhibited high positive and direct effect of leaves per plant, stem girth, leaf length and leaf stem ratio on green fodder yield. Thus any selection based on these characters will enhance performance and improvement of fodder yield in forage sorghum.

Jain *et al.* (2017) recorded plant height, stem girth and leaf length were positively and significantly associated with green fodder and dry fodder yield per plant. Leaf breadth was positively and significantly associated with plant height, number of leaves per plant and leaf length. The path coefficient analysis indicated positive and significant correlation as well as high direct effect of dry fodder yield per plant, plant height, number of leaves per plant and stem girth on green fodder yield per plant.

Endalamaw *et al.* (2017) an experiment was carried out in Ethiopia, to determine the extent of phenotypic and genotypic relationships among 13 agronomic traits and six quality components of 28 sweet sorghum genotypes. Panicle weight and width, dry matter yield, thousand kernel weight and harvest index had significant positive correlation with grain yield and exerted favorable direct effects both at phenotypic and genotypic levels. Yield was also correlated with juice yield, sugar yield and fresh stalk yield. Therefore, these yield and quality components are suggested to receive due attention during sweet sorghum varietal selection. Moreover, days to maturity had negative correlation and imposed negative direct effect on grain yield, which may indicate the possibility to select high yielding, early maturing dual purpose varieties for dry environments. Some of the genotypes excelled as one of the two commercial sugarcane varieties used as controls for some quality traits.

Singh et al. (2017) observed green fodder yield per plant to have positive and significant correlation with plant height, number of leaves per plant, internode length, leaf area and protein content at both the levels. The result of path coefficient analysis showed that leaf area, leaf breadth, leaf length, plant height and protein content had positive direct effect on green fodder yield.

Damor et al. (2018) observed number of leaves, plant height, 50% flowering, dry matter yield per plant, crude protein yield per plant, leaf width, leaf length and number of tillers per plant had positive and high significant correlation with green forage yield per plant at genotypic and phenotypic level while, HCN content showed negative significant correlation at phenotypic level. The result of path analysis expressed that the crude protein yield per plant has the highest direct effect on green forage yield per plant followed by low and negligible direct effects of days to 50% flowering, leaf length, leaf stem ratio, stem thickness, number of tillers and number of leaves per plant.

Combining ability analysis and gene effects

The most important aspect in breeding programme is the choice of parents for hybridization. The combining ability analysis provides useful information regarding the selection of suitable parents. The concept of combining ability as a measure of gene action was given by **Sprague and Tatum, 1942** in maize. Combining ability refers to the capacity of parental genotypes to transfer superior performance to its crosses.

Combining ability can be classified into two (i) General combining ability (GCA) and (ii) Specific combining ability (SCA). General combining ability is the average performance of a line in a set of hybrid combinations and specific combining ability is regarded to those instances where certain hybrid combinations, do relatively better or worse than others on the basis of parental lines involved (**Sprague and Tatum, 1942**).

It has been realized that high yielding lines may not necessarily be able to transmit their superiority to their hybrids (**Allard, 1960**). Hence an estimate of general combining ability effect and specific combining ability effect may be more reliable test than of per se performance. The general combining ability is primarily due to additive variance and additive x additive interaction

variance, while specific combining ability is the consequence of non additive genetic variance arising due to dominance and epistatic interactions.

The relatively large general combining ability and specific combining ability variance ratio suggests the importance of additive x additive effect and low ratio indicated the presence of non additive dominance and or epistatic gene effects (**Griffing, 1956**). The identification of specific cross combination, which exhibits high degree of vigour in F_1 , can presumably be of great importance.

Hovny et al. (2000) observed high general combining ability for plant height, days to 50% flowering, leaf length, leaf breadth, total soluble solids and fodder yield and the cross ICSA88005XMR812, CSA14XICSR273, R97-1XZSV14 and R625-1X ICSR910011 had positive and highly significant for most of the traits.

Ravindrababu et al. (2001) estimated combining ability in ten sorghum lines and their 45 F_1 progenies for seedlings vigour, days to 50% flowering, plant height, dry fodder yield per plant, grain yield per plant, 1000 grain weight, brix value. The mean squares due to general combining ability and specific combining ability were highly significant for all traits. However the magnitude of gca variance showed the higher values than sca variances for all traits except brix value, indicating the preponderance of additive and additive x additive gene effects for these traits.

Kanawade et al. (2001) revealed additive gene effects in the inheritance of panicle breadth, 1000-grain weight and grain yield per plant. Plant height, days to 50% flowering, days to maturity, leaves per plant and panicle length were under the control of non-additive gene effects. In general, the parents 116A, 104A, SPV-492, RS-67, GSS-2 and CSV-14-R were found to be good general combiners.

Prabhakar (2002) exhibited positive and significant combining ability for days to flowering, days to maturity, grain yield, plant height and 1000-grain weight and observed significant and negative general combining ability effects for crude protein.

Khatod et al. (2002) studied combining ability in the F₁ crosses male and female parents of forage sorghum (*Sorghum bicolor*) using line x tester design. The crosses 104 A x AKFR 74, 104 A x AKFR 87, 29 A x AKFR 87 and 29 A x AKFR 59 were found to be the best specific combiners for yield and yield contributing characters.

Fouman et al. (2003) the crosses AICS84 x R2, AICS88005 x R1, AICS31 x RS8, A1 x R112, AICS88005 x R1, AICS31 x RS8, A2 x R112, AISC84 x R112 and AICS31 x R2 had high positive and significant specific combining ability for most of the characters. Among the parents, these parents namely, 2077A, 111A, 68740, 68786, SS032 and 68724 showed high *per se* performance and good general combiners for green fodder yield, leaf area, stem girth, leaves per plant and leaf length.

Biradar et al. (2004) combining ability analysis revealed that estimates of general combining ability variances were higher than that of specific combining ability variances for the characters, plant height, panicle length and ear head weight, indicating importance of additive gene effects in the expression of these traits. This is being supported by high degree of additive variances noticed compared to dominance variances for these traits indicating transgressive variants could be possible. However for the traits, number of primaries, grain yield per plant and 1000 grain weight and exhibited high magnitude of sca variances for days to flowering and days to maturity.

Agarwal et al. (2005) to used the parents ICSA 84, ICSA 9 and SDSL92111 good general combiners for yield and quality characters. The cross combinations namely, ICSA84 x M 20, ICSA 84 x UPMC 504, ICSA 84 x Sel. 984, ICSA 94 x SDSL92111, ICSA 95 x SDSL 92115, ICSA95 x M 19, 296 A x Pant Chari-4 and 2219 A x UPMC 504 were identified as superior crosses having high sea effects for forage yield and quality traits and role of both additive x additive and additive x dominance types of gene interactions.

Baghel et al. (2005) observed general and specific combining ability effects were found positive and significant for days to 50% flowering, grain yield, test weight, green fodder yield, total

soluble solids and leaf area and estimated the additive gene action for most of the characters and non additive gene action recorded for all the characters except protein content and days to maturity.

Umakanth and Kuriakose (2005) reported high positive and significant general combining ability effects for days to 50% flowering, plant height, leaf length, leaf breadth and test weight and observed positive and significant specific combining ability effects for plant height, panicle mass, leaves per plant, stem diameter and grain and fodder yield. The female parent was good general combiners for yield and nine hybrids were found to be best specific combiners. Additive and dominant gene action was noted for most of the characters.

Khandelwal *et al.* (2006) the female parents AKMS-14A, SU-906, SU-912, SU-923, and SUMS-1A and the male parents SU-893, S-248 and SU-678 were good general combiners for most of the traits. The sixteen hybrids were found best specific combiners for days to 50% flowering, plant height, leaf length, grain and fodder yield. All these hybrids were combination of either high x low or high x high gca parents for yield and revealed non additive gene action for all yield related traits.

Kulkarni *et al.* (2006) studied combining ability analysis for yield and yield components and observed general combining ability variance was greater than the specific combining ability variance. Among the female parents, 42A was a good general combiner for early flowering, leaves per plant, stem girth and early maturity. Line 85 A was good general combiner for plant height, panicle weight, fodder yield per plant, leaf area, grain yield per plant. Among the testers, the tester SPV 1385 and SPV 1724 were good general combiners for panicle weight, grain yield per plant and fodder yield per plant. Line SPV-1359 was a good general combiner for panicle weight, number of primaries per panicle, and early maturity and line BRJ-356 was a good general combiner for number of leaves per plant and test weight.

Chaudhary *et al.* (2006) exhibited high positive and significant specific combining effects for days to flowering, plant height, leaf length, leaf breadth, grains per panicle, grain weight and yield per plant and non additive gene action was observed for all the characters.

Mohan *et al.* (2007) estimates of variances due to specific combining ability and general combining ability and their ratio (σ^2 sca : σ^2 gca) were recorded non additive type of gene action for all the characters. Tester 3289 was found to be good general combiner for most of the traits. The crosses viz. ICS 79A x IS 3274, ICS 79A x SSG 59-3, ICS 15A x IS 3289, ICS 95A x SSG 59-3, 2219A x IS 3230, 2219A x IS 720 and ICS 95A X IS 720 exhibited higher sca effects for most of the traits and these characters can be commercially utilized. Additive gene action was observed for all the characters except days to flowering and crude protein.

Deepalakshmi *et al.* (2007) noted additive gene action for days to 50% flowering, plant height, leaves per plant, leaf length, internode length and single plant yield, suggesting that these characters are under additive gene action and gives better scope for selection. General and specific combining ability effects were observed positive and significant for plant height, internode length, nodes per plant and fodder yield per plant. Relationship between the general combining ability and *per se* performance of the parents was observed for most of the characters. Cross combinations having high *per se* performance also had high specific combining ability effect and involved one or both additive gene action of these characters.

Yadav and Pahuja (2007) studied combining ability effects in forage sorghum using line x tester analysis consisting of 10 male sterile lines and five testers and their 50 hybrids. The estimates of σ^2 sca and σ^2 gca revealed preponderance of non-additive genetic variance for all the traits. Male lines, ICS 13A, IC5 10286A, S 241 and SSG 59-3 were found to be good general combiners for most of the characters, which can further be utilized in cross combinations to get superior hybrids. The crosses AKMS 14A x IS 651 and ICS 2219A x S 241 exhibited higher sca effects for plant height, days to flowering, green and dry fodder yields and recorded non additive type of gene action for all the traits.

Rani *et al.* (2007) estimated specific combining ability (SCA) effects was dominant over general combining ability (GCA) effects for all the traits and observed negative GCA effects for

number of days to 50% flowering. Significant and positive GCA effects recorded for number of leaves per plant, leaf area, plant height. The additive gene action was noted high for all the traits.

Borole *et al.* (2008) parents 104A, SPV 1315 and SPV 727 were found to be good general combiners for most of the characters and four cross combinations were found to be best specific combiners for plant height, days to flowering, yield per plot, leaf area and leaf stem ratio. Addictive gene action was found greater than non-addictive gene action and observed additive gene action for all the characters.

Kamdi *et al.* (2009) showed that the parents and crosses differed significantly for all the characters, indicating the presence of sufficient variability in parental lines. The magnitude of variance due to SCA was greater than GCA variance for all the traits, indicating the predominance of non-additive gene action. The parents RSSV9, RSSV47, NSS05 and Kellar were fo0und to be good general combiners for majority of the characters. The hybrids RSSV9 x RSSV47, RSSV9 x Kellar, RSSV47 x Kellar, RSSV64 x NSS05 and RSSV64 x NARISS41 noted high significant and positive sca effects for most of the characters.

Patel and Patel (2010) studied combining ability for green fodder yield and quality attributes was studied using three male sterile lines, sixteen male parents and 48 hybrids in RBD with three replications in three environments created by different dates of sowing. Parents Indore 9A, PB22, ASF7, PB181 and PB45 were identified to be as good general combiners for majority of yield and yield components. The cross combinations viz., Indore 9A $\times$ PB22, 3660 A $\times$ Sholapari and 3660 A $\times$ PB45 exhibited positive and significant sca effect for most of the traits in overall environmental conditions and estimated preponderance of non-additive gene action for all the characters.

Ghazy and Sakr (2011) estimates the magnitude of GCA and SCA effects as well as the genetic parameters involved in forage yield and its component in sorghum. Three male and fourteen females parents were crossed according to line x tester mating design, and assess combining ability and nature of gene action. The results of variance over the two years revealed that highly significant

differences among tested crosses for all the traits, indicating the existence of wide variability among the genotypes. The general combining ability effects was observed positive and significant for all the characters except leaf stem ratio. Specific combining ability effects were found positive and significant for internode length, leaves per plant, plant height and leaf area. Additive gene action played the major role in the genetic expression for all traits.

Kanbar *et al.* (2011) studied the first year using eight local cultivars and crossed with two exotic sterile lines using line×tester method. In second year, the hybrids were grown along with their parents in a randomized complete block design with three replications to estimate general combining ability and specific combining ability (SCA). The results showed that some parents had significant positive general combining ability for most of the characters such as Baladi-1, Baladi-4 and Ezraa-7. The hybrids Baladi1×SPL10A, Baladi4×SPL10A and Ezraa-7×SPL-10A) recorded significant and positive specific combining ability effects for all the traits except total soluble solids and crude protein and mostly characters governed by non additive gene action.

Vinaykumar *et al.* (2011) assessed the combining ability and nature of gene action in respect of yield and its attributing traits in 72 new hybrids of sweet sorghum developed by crossing 4 male sterile lines with 18 testers in Line x Tester mating design and grown in randomized block design with two replications. The variance among the lines in respect of their general combining ability was highly significant for days to 50 per cent flowering, nodes per plant and yield, where as variance among testers was significant for most of the traits.. The variance due to line x tester interaction was significant for all the characters, indicating differential response of lines with different testers. SCA variance was relatively higher than GCA for all the traits, indicating predominance of non-additive gene action in the genetic control of these characters. Parents ICSA 38, ICSA 102, ICSV 93046, E 36-1, ICSV 700, SEREDO and GD 65008 were identified to be good general combiners for most of the characters except days to 50% flowering, juice yield and leaf area, indicating their ability in transmitting additive genes in the desirable direction to their progenies. Highly significant *sca* effects was observed in most of the hybrids for all the characters

studied and good specific combiners for different characters involved parents with high x high, high x low, low x high and low x low general combinations.

Akabari *et al.* (2012) estimated the combining ability and heterosis using 45 F₁ hybrids along with fifteen fodder sorghum genotypes (three male sterile lines and fifteen restorer lines) to know the pattern of inheritance of some morphological traits for selecting superior genotypes. The experiment was carried out according to line x tester mating design. Analysis of variance revealed significant differences among genotypes, parents, hybrids and line x tester interactions for all the traits. Variances of SCA was higher than the GCA variances for all traits which indicated predominance of non-additive gene action in the inheritance of the traits. The parents SURAT-2, SURAT-1, C-10-2, GUNDARI, AFS-30 and S-1049 were observed to be good general combiners for most of the characters. The cross combinations SURAT-1 x C-10-2, SURAT-4 x UP CHARI3 and SURAT-2 x PHULE AMRUTA were found to be the best specific combiners for most of the traits. The hybrid SURAT-1 x C-10-2 and SURAT-4 x UP CHARI2 were also found to be the best specific combiners for days to 50% flowering and tillers per plant, stem girth and total soluble solids.

Tariq *et al.* (2012) studied combining ability and heterosis for some fodder yield and its component traits among nine sorghum crosses and their six parents in a randomized complete block design with three replications under irrigated conditions. Highly significant differences for genotype, general combining ability and specific combining ability were observed for all the characters under assessment. However, general combining ability variances was lower than the specific combining ability variances for all the evaluated parameters. All the traits under study showed greater dominant variance than the additive variance having degree of dominance greater than unity. The sorghum line V-1 indicated the highest general combining ability effects in the desired directions for plant height, TSS-9 for number of tillers plant, CSV-1 and CSV-13 for stem thickness, fresh weight plant and dry weight plant. Nine crosses recorded significant and positive specific combining ability effects for most of the characters.

Goyal et al. (2013) analysis of variance showed significant variation among the populations (male parents), CMS lines (female parents), hybrids and parent versus hybrids comparison for all the characters except photosynthetic capacity. The analysis of variance for combining ability in normal environment and water stress environments showed that the mean squares due to males and females were significant for all the characters except for photosynthetic capacity and green fodder yield in case of females under stress environment, which indicated the importance of specific combining ability in the genetic expression of these characters among hybrids. The differences in gca are mainly due to additive genetic effects and higher order additive interaction. In contrast, the differences in sca are attributed to non-additive dominance and other types of epistasis. The ratios of sca and gca variances in both the environments indicated the preponderance of non additive gene action in the interaction of all the traits. The prevalence of non-additive gene action for all the characters, suggested that development of hybrids would be beneficial in forage sorghum. The lines, 2077A, AKMS-14A and NSS1007A were identified with significant and positive gca effects for green and dry fodder yield. The line, 2077A had highest gca effects for most of the characters. Line AKMS-14A observed significant and positive gca effects for all the characters except photosynthetic capacity and specific leaf weight. The line NSS1007A was observed as a good general combiner for specific leaf weight, photosynthetic capacity and proline content, whereas NSS1008A was good general combiner for green fodder yield and specific leaf weight. Three lines viz., 2077A, NSS1007A and NSS1008A also had significant gca effects for most of the characters. Lines 940031A and NSS1005A were found to be good general combiners for yield. The lines 940031A, 2077A and NSS1005A were good general combiners for physiological traits affecting water use efficiency with significant gca effects for relative water content, leaf area index and proline content in stress environment. The female NSS1007A was good general combiner for leaf area index and proline content and NSS1008A had significant gca effects for proline content also. Estimates of gca effects for the populations under environments showed that the population RSSV-9 was good general combiner male parent for green fodder yield and dry fodder yield in both the

environments. In normal environment RSSV-9 had significant gca effects for proline content, however, under water stress environment, the same population was good combiner for relative water content, photosynthetic capacity and proline content. The cross combinations viz., 94002A x RSSV-9, 940031A x SSG59-3, AKMS-14A x HC308, NSS1002A x HC308 and NSS1007A x Ramkel appeared to be the promising with high sca effects for most of the characters, therefore, these traits can be considered for further evaluation in the future breeding programmes. The preponderance of non-additive gene action was found for all the characters. The crosses, which showed very high level of sca effects, can be exploited further in future breeding programme to develop high yielding genotypes in forage sorghum.

Abdelmula *et al.* (2014) estimated the magnitude of general, specific combining ability and heterosis for forage yield and quality characters of forage sorghum. Five exotic cytoplasmic male sterile lines of forage sorghum were crossed with eleven fertile local inbred lines, as testers, to produce 55 F₁ hybrids. Both parental lines and their F₁ hybrids were evaluated for yield and quality traits at four environments. The results revealed that the predominance of additive gene effect was high for forage yield and dry yields, whereas there was predominance of non-additive gene effect for most of the quality traits. For forage fresh and dry yields, the testers exhibited higher contribution to the GCA variance than the lines. The best general combiners for forage yields were Aklamoi and Kambal among testers and Atlas and E. sumac among lines. Lines E. sumac and Blue Ribbon and testers Wad Ahmed and S.42ANK were the best general combiners for most of the characters. The hybrid E. sumac × Aklamoi observed high positive and significant SCA effects for all the character except days to 50% flowering and crude protein. Therefore, it could be concluded that the most suitable parental lines for improving forage yield could be Aklamoi and Kambal among testers and E. sumac and Atlas among lines.

Akabari and Parmar (2014) recorded genotype SURAT-2 among females and GUNDRI and C-10-2 among males exhibited highest positive and significant general combining abilities effects for all the characters except quality traits. Cross combinations namely, SURAT-1 x C-10-2,

SURAT-4 x UP CHARI1 and SURAT-2 x PHULE AMRUT exhibited the highest positive and significant specific combining ability effects for most of the characters.

Aaref *et al.* (2016) studied combining ability and heterosis for yield and its component among twenty eight sorghum hybrids were grown in the two locations. The layout was made RCBD with three replications. The highly significant differences for genotype, general and specific combining abilities were observed for all the components under assessment in the two locations. Additive and non-additive gene actions were found for days to 50% flowering, plant height, number of green leaves per plant, grain weight and preponderance of non-additive gene actions for yield per plant in the two locations. Parent P2 was the best general combiner for grain weight, while P6 was found to be good general combiner for most of the characters. Parents P8 and P9 observed good general combiners in for yield per plant. The crosses namely, P1 x P2, P1 x P3, P2 x P7, P3 x P4, P4 x P6, P4 x P8, P5 x P7, P6 x P7, P6 x P8 and P7 x P8, Sohag x Assiut and P2 x P6 which had highly significant and positive SCA effects for grain yield per plant and grain weight. It can be concluded that possibility of use the superior crosses for improving sorghum traits by breeding processes and selection in sequent generations.

Jain and Patel (2016) was used seven sorghum lines, three testers and twenty one crosses developed in line × tester fashion were evaluated for general combining ability, specific combining ability effects and magnitude of heterosis and heterobeltiosis in a randomized block design. Genetic variability among genotypes were assessed high for days to 50% flowering, days to maturity, plant height, and number of leaves per plant, leaf length, leaf width, grain yield, 100 seed weight and dry fodder yield. Combining ability analysis revealed that the estimates of SCA variance were higher than GCA variance for all the traits, indicating the preponderance of non additive gene action in the expression of these traits. The line SPV 2114 and GJ 39 considered as superior general combiner for grain yield, dry fodder yield and other yield contributing traits. The most promising crosses namely, SPV 2117 x GJ 39, SPV 2117 x SSV 74, SPV 2110 x SSV 84, CSV 15 x SSV 84, SPV

2116 x GJ 39, 2114 x GJ 39, SPV 2125 x SSV 84 and DS 2570 x SSV 74 were found to be best specific combiners for most of the characters.

Kumar and Shrotria (2016) analysis for combining ability revealed significant mean sum of squares of both general combining ability (GCA) and specific combining ability (SCA) for most of the characters, indicated presence of both additive and non-additive gene actions. The parental genotypes 32 A2, MR 750 A2 and PC 6 were found to be good general combiners for green and dry fodder yield, respectively. Cross combination viz., 32 A2 x PC 6 and MR 750 A2 x HC 26 PC 6 were found to be best specific combiners for all the characters except days to 50% flowering. These parental genotypes and their crosses could be used further in breeding programme for selection and enhancement of yield in sorghum.

Rini et al. (2016) showed that the lines B69 and PI-150-21-A were found to be good general combiners for yield and yield component. Hybrid P150-21-A x PI 150-20-A exhibited positive and significant SCA effects for all the characters except plant height.

Chikuta et al. (2017) estimated the combining ability of grain and forage sorghum genotypes to determine general combining ability, specific combining ability and heterosis for several traits as a criteria for improving dual purpose sorghum cultivars. Four grain and four forage sorghum cultivars were crossed to generate twenty three crosses following the half diallel mating design. Data were taken and analyzed on leaf area, days to flowering, leaf stem ratio, plant height, leaves per plant, seed weight, grain yield, forage yield and biomass. Results indicated that the gene action for the traits under observation was controlled by both additive and non additive genetic effects. Majority of the parental lines had significant GCA for all traits except line 20 for grain yield, lines 22 and 34 for plant height, line 35 for leaf-stem ratio, and line 22 for days to flowering. Significant and positive SCA effects observed for all the traits except leaf area and leaf stem ratio indicating the role of dominance gene action which indicates that genetic gains can be achieved by conventional breeding for these traits.

Dehinwal et al. (2017) studied twenty four hybrids (derived from mating four testers with six lines in L x T design) along with their parents and checks (SSG 59-3 and MFSH 4) at two locations with two dates

of sowing (Early and late sowing) during the *khariif* season of 2015-16. Data on five randomly taken plants from each genotype in each replication were recorded on different quantitative characters at first cut (55 days after sowing) and second cut (45 days after first cut). The ratio of σ^2 GCA/ σ^2 SCA was less than unity for all the characters indicating preponderance of non-additive gene action (dominance and epistasis). Among female parents 9A and 14A was the best combiner for green fodder yield and 14A for dry fodder yield in more than two different environments. Among male parents, HJ 513 and G 46 were found to be the best general combiner for green fodder yield and dry fodder yield. The cross combination of 465A $\times$ HJ 513 and 9A $\times$ IS 2389 exhibited high and positive SCA effects for green fodder yield as well as for dry fodder yield. This suggests the usefulness of heterosis breeding or any breeding plan which makes use of specific combining ability effects for improvement in these traits.

Singh and Singh (2017) estimated the variance among line with respect to gca was found highly significant for all the attributes and variance among testers with respect to gca was recorded highly significant for all the traits except stem girth. The variances among crosses due to interaction between lines $\times$ testers genotypes with respect to sca were expressed highly significant for all the characters except stem girth and number of leaves per plant. Average degree of dominance (δ^2_s/δ^2_g) 0.5 exhibited partial dominance for plant height, leaf length, leaf breadth, internode length, leaf area, leaf stem ratio and green fodder yield and over dominance was observed for days to 50% flowering, number of leaves per plant, stem girth, total soluble solids and protein content. GCA effects and per se performance among the parents HC260, Pusa Chari23, SPV815, PusaChari6, HC260 and HC171 were found to be as good general combiner and the F₁'s hybrids i.e. HC260 $\times$ HC308, HC260 $\times$ G48, SSG-59-3 $\times$ G48, HJ513 $\times$ HC308, HJ513 $\times$ HC171, ICSV700 $\times$ HC308, UP Chari2 $\times$ G48, UP Chari1 $\times$ Pant Chari6, Pusa Chari9 $\times$ HC171 and Rajasthan Chari1 $\times$ G48 were identified with significant and positive SCA for fodder yield which may be utilized for obtaining transgressive segment in the next generation and also could be exploited for development of hybrids.

Pal et al. (2017) studied heterosis and combining ability analysis of 10 $\times$ 10 diallel (excluding reciprocal) set of crosses in forage sorghum were done for yield and its contributing characters. All the 45 F₁

hybrids and their ten parents were grown and selfed during *Kharif* season of 2013 for producing F₂ seeds. All the 45 F₁ hybrids and 45 F₂ populations along with ten parents were sown in randomized block design with three replication at Crop Research Center of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut during the *Kharif* season of 2013. Observation were recorded on days to 50% flowering, plant height, leaf breadth, leaf length, leaves per plant, leaf area, leaf stem ratio, stem girth, total soluble solids, protein content and green fodder yield. ANOVA for combining ability revealed that the parent SSG 59-3 exhibited high general combining ability effect for all the characters except days to 50% flowering, leaf breadth, leaf stem ratio, stem girth, total soluble solids and protein content in both F₁ and F₂ generations. Promising parents viz., HC 171, UP Chari 2, Pant Chari 5 and Pant Chari 6 which were having high general combining ability effects in desirable direction for green fodder yield and yield components character like plant height, leaf breadth, leaf length and stem girth may be incorporated in crossing programme to have better genotypes for better green fodder yield. The cross combinations namely, UP Chari 2 × HC 171, Pant Chari 5 × RSSV 9, Pant Chari 5 × SSG 59-3, SSG 59-3 × Pusa Chari 23, CSV 15 × Pant Chari 6, G 48 × HC 171, CPVI 1724 × HC 171 and Pant Chari 5 × G 48, which exhibited good specific combining ability effects for green fodder yield and its contributing traits such as days to 50% flowering, leaf breadth, leaf length, leaves per plant, leaf stem ratio and stem girth in both F₁ and F₂ generations. Nine cross combinations which revealed highest value of heterosis for leaves per plant and green fodder yield viz., SSG 59-3 × CSV 15, Pant Chari 5 × CSV 15, RSSV9 × HC 171, CSV 15 × UP Chari 2, G 48 × UP Chari 2, Pant Chari 5 × HC 171, G 48 × HC 171, Pant Chari 6 × CPVI 1724 and SSG59-3 × Pusa Chari 23 over better parent as well as economic parent may be exploited for developing hybrids for better yield in forage sorghum.

Ingle et al. (2018) conducted an investigation to assess the magnitude of heterosis and combining ability of thirty F₁ hybrids of *rabi* sorghum (*Sorghum bicolor* (L.) Moench) developed by crossing three lines and ten testers in line x tester fashion with respect to phenotypic trait, grain yield and its components. The hybrids and their parents were evaluated to estimate the heterosis and combining ability governing quantitative traits. Among thirty hybrids, three potential hybrids AKRMS 30A X AKRB 431, AKRMS 30A X AKRB 335-3, AKRMS 30A X AKRB 428 were found to be good specific combiners with highest standard heterosis and *per se* performance for grain yield per plant over both checks CSH 15R and CSH 19R. AKRMS 30A was the good general

combiner with other males. The estimates of general combining ability and specific combining ability revealed the presence of both additive and non-additive genetic components for most of the traits under study.

Soujanya *et al.* (2018) an experiment was conducted to exploit heterosis in F₁ hybrids of sweet sorghum (*Sorghum bicolor* L.) and to identify parents with desirable genetic effects with respect to single cut green fodder yield and quality traits. All the 48 F₁ hybrids produced by crossing four lines and twelve testers in line x tester mating design were evaluated to assess general and specific combining ability and gene action governing the green fodder yield and quality traits. Analysis of variance revealed the presence of sufficient variation in the experimental material. The SCA variance was greater in magnitude than GCA variance for most of the characters studied, indicating the preponderance of non additive gene action for several characters. Line 185A and testers RSSV138-1, RSSV466 and RSSV404 emerged as good general combiners for single cut green fodder yield where as PMS71A, NSSV14, SSV84 were found to be good combiners for most of the characters. Based on *sca* effects, 185A x RSSV466, 185A x RSSV138-1, PMS71A x RSSV138-1 and PMS71A x RSSV404 were identified as good specific combiners for green fodder yield.

Manifestation of heterosis

The impulse of progress in crop improvement through plant breeding has been propelled by a better understanding and an appropriate exploitation of heterosis *i.e.* the gain in vigour on crossing two inbreds. This phenomenon was first reported by **Koelreuter (1763)**. However, **Shull (1914)** proposed the term heterosis as the development stimulus resulting from the union of different gametes and hybrids vigour as the manifest of heterosis. Later on **Powers (1945)** suggested that the term heterosis should be used only when hybrids is either superior or inferior to both the parents. **Gowen (1952)** further suggested that a decrease in vigour due to inbreeding and increase in vigour due to crossing (two genetically different homozygous inbred lines) are manifestation of the same

phenomenon *i.e.* heterozygosis. Therefore, heterosis is one aspect of heterozygosis and inbreeding depression is the consequence of hybridization.

Jinks and Jones (1958) stated that heterosis is complex genetically phenomenon depending upon the balance of the additive, dominance and interaction of the homozygous/ heterozygous components as well as on the distribution of genes in the parental lines. **Fonseca and Patterson (1968)** described heterosis as an improvement of heterozygote in relation to better parents and coined a new term heterobeltiosis. **Mather and Jinks (1971)** defined heterosis as the amount by which the mean of F_1 family exceeds its better parents. For the economic point of view, a third term for heterosis is generally being used as standard heterosis for comparing performance of F_1 hybrid over the check which may be a released variety/hybrid or the standard parent for the specific character.

Sorghum being an often cross pollinated crop has unique opportunity of it being exploited both for additive genetic component by developing hybrids. Besides commercial exploitation of heterosis in grain sorghum there is substantial literature available as evidences suggested scope for exploitation of heterosis in fodder sorghum too. The recent concept of multicut fodder sorghum hybrids between sorghum too. The recent concept of multicut fodder sorghum hybrids between sorghum x sudan grass is opening the new vistas in this direction where commercial exploitation of luxuriant heterosis by crossing cytoplasmic male sterile lines of sorghum with sudan grass pollinators produce highly heterotic hybrids capable of giving high fodder yield in subsequent cutting.

Shaug *et al.* (2000) recorded high positive and significant heterosis over better parent for plant height, tillers number, forage yield, total soluble solids, stem girth, dry matter percentage and dry matter yield.

Kadam *et al.* (2001) noted high positive significant heterosis over relative and better parent for green fodder yield, dry fodder yield, plant height, number of leaves per plant and leaf length.

Pandian and Doss (2001) showed high positive and significant heterosis over standard parent for plant height, leaf area, total soluble solids, yield, crude protein and leaf stem ratio.

Grewal *et al.* (2003) revealed the thirteen crosses positive and significant heterosis over better parent for fodder yield, dry fodder yield, plant height, number of tillers per plant, days to 50% flowering and total soluble sugar.

Umakant *et al.* (2003) studied on thirty two hybrids of resulting from eight line and four tester observations were recorded on five randomly selected plants for plant height, head weight, number of primaries per panicle, 100 seeds weight and grain and fodder yield per plant. Heterosis was estimated over the mid parent and better parent positive and significant for most of the character in sorghum.

Chaudhary *et al.* (2004) reported high positive and significant heterosis over mid and better parent for leaf length, leaf breadth, stem girth, leaf stem ratio, leaves per plant and fodder yield. The highest negative heterosis was recorded for crude protein and total soluble solids. The twelve crosses were recorded high heterosis over better parent for most of the traits.

Agarwal and Shrotria (2005) studied the magnitude of heterosis and inbreeding depression of fifty hybrids of forage sorghum were made line x tester mating design. Observations were recorded on quantitative and qualitative traits viz., days to 50% flowering, plant height, leaf length, leaf width, fifth leaf area, stem diameter, total soluble solids, protein content, digestibility percentage, green and dry fodder yield. Variable magnitude of three types of heterosis (better parent, mid parent and standard parent) was observed for different cross combinations for all the traits. Best crosses namely, ICSA 94 x Pant Chari-4, ICSA94 x SDSL92111, ICSA94 X SDSL92113, ICSA94X SDSL92140, ICSA94 X Selection 984, ICSA95XICSV96062 and 296A x SDSL92111 were found high positive and significant for all the characters except days to 50% flowering and digestibility percentage.

Patil and Biradar (2005) noted high significant positive heterosis over mid parent and better parent for days to 50% flowering, yield per plant, number of leaves per plant, leaf length and leaf area.

Desai *et al.* (2006) reported high magnitude of relative heterosis and heterobeltiosis were recorded for all the characters except plant height and days to 50% flowering.

Premalatha *et al.* (2006) observed nine hybrids to be superior significant over relative and better parent for most of the characters and negative for grains per panicle and plant height.

Khapre *et al.* (2007) showed high significant and positive heterobeltiosis for all the characters except panicle length, seed weight and crude protein.

Prabhakar and Raut (2010) the cross combinations viz., SL-19B × SLR-13, SL-19B × SLR-17, SL-19B × SLR-30 and SL-19B × SLR-39 observed high significant and positive heterosis over standard parent and better parent for most of the characters.

Prakash *et al.* (2010) investigated the possibility of exploiting heterosis breeding for improved fodder yield in sorghum. Seven cytoplasmic female sterile lines and five testers were crossed in a line x tester mating design. A total of thirty five F₁ hybrids along with twelve parents were evaluated for days to 50 % flowering, plant height, number of tillers, number of leaves per plant, leaf length, leaf breadth, stem diameter, green fodder yield and dry fodder yield. Among the thirty five hybrid combinations, two hybrids namely, ICSA 547 x PKB 192 and ICSA615 x PKB17 had high positive and significant heterosis over mid and better parent for all the traits except number of tillers per plant and leaf breadth.

Patel and Patel (2011) experimental material comprised of three male sterile lines used as female parents, sixteen genotypes used as male parents, one standard check variety and forty eight F₁ hybrids in a line x tester fashion and all entries were studied in randomized complete block design with three replications. The results expression of heterosis in the positive direction was in maximum number of hybrids for green fodder yield, leaf length, number of nodes per plant, dry matter yield and crude protein, while the magnitude of heterosis in the negative direction was

observed for days to flowering, leaf width, leaf stem ratio, stem thickness, dry matter content, HCN content and NDF content. The hybrid AKMS 14A x S 1049 revealed high positive and significant heterosis over better parent for most of the characters. The crosses 3660 A x PB 22, Indore 9 A x PB 22, AKMS 14A x HC 171 and AKMS 14A x PB 78 were recorded high significant and positive heterosis over standard parent for all the traits except low HCN content and NDF content, suggesting that heterosis breeding programme could be useful for developing superior genotype for green fodder yield.

Akabari *et al.* (2012) study of combining ability and heterosis using 45 F₁ hybrids along with fifteen fodder sorghum genotypes (three male sterile lines and fifteen restorer lines) to know the pattern of inheritance of some morphological traits for selecting superior genotypes and experiment was carried out according to line x tester mating design. Analysis of variance revealed significant differences among genotypes, parents, hybrids and line x tester interactions for all the traits. Hybrid SURAT1 x C-10-2 was found significant and positive heterosis over better parent for most of the characters. Cross combinations viz., SURAT1XGUNDRI, SURAT4XAFS-30, SURAT-2XSURAT-1, SURAT-C-10-2XGUNDARI and AFS-30XS-1049 were found high positive and significant for all the characters except days to 50% flowering and number of tillers per plant, therefore, these characters can be used further improving breeding programme for selection of transgressive segregants in forage sorghum.

Goyal *et al.* (2013) analysis of variance showed significant variation among the populations (male parents), CMS lines (female parents), hybrids and parent versus hybrids comparison for all the characters except for photosynthetic capacity (data not shown). The significant positive heterosis over check hybrid PSC-1 was exhibited by the hybrids for all the characters. A total of 47 hybrids, only ten hybrids viz., 94002A x RSSV-9, AKMS-14A x RSSV-9, AKMS27-A x RSSV-9, 2077A x RSSV-9, NSS1007A x RAMKEL, NSS1002A x HC308, NSS1005A x HC308, NSS1006A x RSSV-9, NSS1005A x RAMKEL and NSS1008A x RSSV-9 exhibited significant and

positive heterosis over standard and better parent for most of the characters. Therefore, these traits can be considered for further evaluation in the future breeding programmes.

Jain and Patel (2013) studied the magnitude of heterosis, heterobeltiosis and economic heterosis in thirty six crosses by crossing the nine different parents in 9 x 9 diallel fashion (excluding reciprocals) and observations were recorded on nine characters viz., days to 50 per cent flowering, days to maturity, plant height, number of leaves per plant, leaf length, leaf breadth, grain yield per plant, stover yield per plant and 100 seed weight. The crosses namely, SPV 2110 x GFS 5, GFS 5 x GJ 39 and SPV 2113 x CSV 15 showed high heterosis over mid parent and better parent for most of the traits. In addition to this, cross combination viz., CSV 15 x SSV 84, SPV 2113 x SPV 1616, SPV 2110 x GJ 39 and GJ 39 x SSV 84 showed good heterosis for stover yield and their contributing characters. Thus, these crosses in future can be exploited easily for dual purpose attributes by conventional breeding procedure.

Pandey and Shrotri (2013) estimated variable magnitude of three types of heterosis viz., relative parent, better parent and standard heterosis as exhibited by different cross combinations for all the characters indicated the presence of different degree of divergence in the parental material for all the characters. The range of heterobeltiosis, mid parent heterosis and economic heterosis varied from one character to another. Maximum number of positive significant crosses for all three types of heterosis was reported for dry fodder yield (42, 51 and 52 for heterobeltiosis, mid parent heterosis and economic heterosis, respectively), followed by leaf length, green fodder yield, number of basal tillers and leaf width. For commercial exploitation of heterosis for fodder yield, two crosses viz., ICSA-271 x UTM-523 and ICSA-271 x 700R were identified as the best cross combinations as they showed significant heterosis in desirable direction over the better parent, mid parent and standard check, for important component traits besides green and dry fodder yield (during both the years and also in pooled analysis). This indicated the presence of non additive gene action for fodder yield and its components. On the basis of pooled analysis six crosses were identified as best for green and dry fodder yield and component characters. For green fodder yield maximum better

parent heterosis was recorded in the cross ICSA- 271 x UTM-523 (56.87), followed by ICSA-276 x UPM 512 (36.63) and ICSA-467 x PC 5 (31.10). For dry fodder yield maximum positive heterobeltiosis was observed in the cross ICSA-276 x UPM-512 (118.99) followed by ICSA-467 x PC-5 (99.16) and 993100A x UPM 8 (74.24). These crosses were also superior in *per se* performance. Heterosis for end product *i.e.* fodder yield is being manifested as the cumulative effect of heterosis for component traits.

Akabari and Parmar (2014) investigated the possibility of exploiting heterosis in breeding for improved quality in forage sorghum [*Sorghum bicolor* (L.) Moench] and identify parents with desirable genetic effect. Forty five hybrids produced by crossing 3 cytoplasmic male sterile lines with 15 local males were evaluated for quality trait. Line x tester analysis was performed to study general and specific combining ability. The magnitudes of mid parent, better parent heterosis and standard heterosis were investigated. Hybrids with best heterotic and specific effects for some traits were also among the best in *per se* performance for the same traits. Crosses SURAT-1 x C-10-2 and SURAT-1 x GUNDRI exhibited significant heterosis in desirable direction for most of the characters. It was concluded that exploiting heterosis in forage sorghum to improve quality traits might be promising.

Mohammed *et al.* (2014) estimated the magnitude of heterosis and general and specific combining ability for forage yield and quality characters of forage sorghum. Five exotic cytoplasmic male sterile lines of forage sorghum were crossed with eleven fertile local inbred lines, as testers, to produce fifty five hybrids. Both parental lines and their hybrids was field evaluated for yield and quality traits at four environments. The magnitudes of mid-parent, better-parent and standard parent heterosis were estimated. The hybrid ESUMACXAKLAMOI revealed high estimates of heterosis for most of the characters.

More *et al.* (2014) used 83 genotypes (9 lines, 7 testers, 63 hybrid and 4 checks) to study the for heterosis, GCA and SCA estimation considered for the development of high yielding and grain mold tolerance cultivars by using line x tester mating system were sown in randomized block

design with two replications. Among the hybrid PMS37A x RS 29 recorded maximum yield with heterosis over the mid parent, better parent and standard check respectively. This cross found to be superior in terms of days to maturity, plant height and yield. It was followed by PMS 29 x KR 200, PMS 9A x KR 191, PMS 6A x KR 199 and PMS 28A x KR 192, indicating the predominance of non additive gene action. Group mean indicate that crosses involving PMS 37A, PMS 28A and PMS 29A as female and KR 199, C 43 and RS 29 as males exhibited higher yield. In relation to grain mold attributes the crosses involving PMS 7A, PMS 8A and PMS 9A as females and KR 199, KR 192 and IB 12 as males exhibited the higher values for almost all the attributes.

Tariq *et al.* (2014) recorded high significant and positive heterosis over mid parent for total sugar content (44.39%) in cross CVS-13 x RARI-S-10, for total cyanide content (29.22%) and crude fiber (23.04%) in cross V-1 x CVS-13, crude protein (54.01%) and crude fat (24.33%) in cross SPV-462 x YSS-9 and total ash (53.75%) in cross V-1 x SPV-462. Whereas, the cross SPV-462 x YSS-9 showed the highest and significant mid-parent heterosis in negative direction for total cyanide content (-37.46%), cross CVS-13 x RARI-S-10 for crude protein (-32.82%), the cross CVS-13 x YSS-9 for crude fat (-15.35%) and the cross V-1 x CVS-13 for nitrogen free extract.(-14.79%). The cross SPV-462 x YSS-9 indicated highest, significant and positive better parent heterosis for most of the traits while no cross showed significant heterobeltiosis for nitrogen free extract in positive direction. All the crosses showed significant and negative heterobeltiosis for total cyanide content except for the cross V-1 x CVS-13.

Kalpande *et al.* (2015) analysis of variance revealed the significant variation for all the characters and range of mean performance, heterosis over mid parent, better parent and standard check were estimated. For grain yield plant the range was 32.51-54.67 g. in parental lines and 22.24-71.39 g. in crosses while for the fodder yield plant the range was 33.63-98.53 g. in parental lines and 32.93-114.53 g. in crosses which indicated that the range for mean performance did not vary significantly for most of the characters except grain yield plant and fodder yield plant. For the important characters like grain yield plant and fodder yield plant range appeared to be widened in

crosses as compared to parents. To determine the heterotic potential of the hybrids, average heterosis (over mid parent), heterobeltiosis (over better parent) and standard heterosis (over standard check) were calculated for all the characters. Top ranking crosses with significant standard heterosis for grain yield along with the desirable and significant standard heterosis for the component traits. Out of fifty four crosses, seventeen crosses exhibited positive significant standard heterosis over the check CSH 19 R for grain yield plant and appeared best for development of high yielding sorghum hybrid. Along with grain yield, these seventeen cross combinations also showed desirable and significant standard heterosis for some the component traits also. The best cross combination was AKRMS-68-1A $\times$ AKSV-219R with the highest positive significant for grain and fodder yield per plant. The cross combination AKRMS-66-2A $\times$ Rb local3 with recorded mid parent heterosis of and heterobeltiosis for most of the characters. The best cross combination was AKRMS-80-1A $\times$ Rb-369-1 with standard heterosis, mid parent heterosis and heterobeltiosis for grain yield per plant, number of grains per panicle and fodder yield per plant. The fourth top ranking cross combination was AKRMS 80-1 A $\times$ Rb-400 with the standard heterosis of 26.89%, mid parent heterosis of 63.73% and the heterobeltiosis of 32.52% for grain yield per plant. This cross also recorded positive significant standard heterosis for fodder yield per plant. The hybrid was AKRMS 66-2 A $\times$ Rb 413-1 with the positive significant heterosis for days to maturity, number of grains per panicle and fodder yield per plant. Rest of the twelve cross combinations also showed positive and significant standard heterosis, average heterosis and heterobeltiosis for grain yield per plant. This clearly indicated that these crosses can be very well exploited using heterosis breeding for development of high yielding sorghum hybrids.

Ringo *et al.* (2015) reported female lines were highly significant for all traits except days to 50% flowering (DAF). Desired heterobeltiosis for DAF varied from -5.23 to -14% indicating of early maturing material that can escape terminal drought in rainfed cultivation system. Lowest (desired) heterobeltiosis for plant height was -53.61% with crosses ICSA15 $\times$ Tegemeo and ATX623 $\times$ KARI-MTAMA1 most promising for this trait. Grain yield showed average heterosis and heterobeltiosis of up to 81.90% and 77.18% respectively both expressed in ICSA11 $\times$ S35. The parents KARI MTAMA1, IESV91104DL, S35, BTX623,

ICSB12 and ICSB11 produced hybrids that yielded high with medium height and maturity therefore could be included to develop hybrid sorghum.

Aaref *et al.* (2016) crosses namely, P1 x P 2, P1 x P3, P2 x P7, P3 x P4, P4 x P6, P4 x P8, P5 x P7, P6 x P7, P6 x P8 and P7 x P8 showed positive and significant heterosis over mid and better parents for most of the characters. It can be concluded that possibility of use the superior crosses for improving yield sorghum traits by breeding processes and selection in sequent generations.

Kale and Desai (2016) estimated the heterosis in F₁ hybrids of sorghum with respect to yield and its components using 54 hybrids developed through line x tester mating design involving eighteen females (lines) and three males (testers). Result of analysis of variance for means revealed significant differences for all the twelve characters. The high standard heterosis was obtained for grain yield per plant and panicle weight and medium level of heterosis was found for plant height, leaves per plant, primaries per panicle, dry stover yield and harvest index and low for days to 50 per cent flowering, days to maturity, panicle length, 1000 grain weight and protein content and recorded high positive and significant heterosis over better and standard parent for most of the characters.

Kumar *et al.* (2016) observed positive and significant heterosis over mid parent as well as better parent for all the characters, indicating role of over dominance in the expression of heterosis of these traits. Contrastingly non significant mid parent heterosis was recorded in respect of brix%, sucrose and total soluble sugars. Desirably significant estimates of better parent heterosis were recorded in all the crosses for days to 50% flowering. Yield was found to be one of the most heterotic traits, as all the crosses depicted significant positive heterosis over their mid parent and better parent values. Among thirteen characters studied, majority of the characters exhibited mid parent as well as better parent heterosis in desirable direction in all four crosses indicating predominant role of non fixable inter allelic interactions and/or over dominance in the expression of heterosis in respect of these traits. Heterosis for end product *i.e.*, yield is being manifested as the cumulative effect of heterosis for component traits as hybrids exhibited positive and significant heterosis for yield as well as its component traits. The magnitude of heterosis for yield and its component traits suggested enough diversity among the parental lines. Incidentally, there has been

enough consistency among the performance of the hybrids over the crosses as degree of heterosis did not differ much between crosses and seasons with a very few exceptions which may be due to considerable disharmony between gene combinations in the parents involved and considerable genotype by environment interaction. Low and negative heterosis can be attributed to the presence of large epistatic gene effects or to incomplete dominant gene effects. Heterosis results of dominance type of gene action and heterosis is absent where the traits are governed only by additive gene action.

Rini *et al.* (2016) showed that hybrids which have high mid parent heterosis for yield were B-69 x Numbu with 72%, PI 150-21-A x Numbu with 66%, PI 150-20-A x Numbu with 63% and PI 10-90-A x Kawali with 62% higher yield compared to the average of the two parents. The hybrid PI 10-90-A x Kawali and B69 x Numbu also showed high better parent heterosis, which means that the two hybrids have yield per plant 33 % and 35% higher than the highest yielding parents. The four hybrids are good candidate for sorghum hybrid varieties with high yield potential.

Chikuta *et al.* (2017) studied four grain and four forage sorghum cultivars were crossed to generate twenty three crosses in the half diallel mating design scheme at Makerere University Agricultural Research institute, Kabanyolo in 2013. The crosses were evaluated at three locations in Uganda during two rainy seasons of 2014. Data were taken and analyzed on leaf area, leaf stem ratio, plant height, seed weight, grain yield, forage yield and biomass. Results indicated that the gene action for the traits under observation was controlled by both additive and non additive genetic effects. Most of the crosses showed high positive and significant heterosis over mid and better parents for all the characters except plant height. This study suggested that both inter and intra allelic interactions were involved in the expression of these traits.

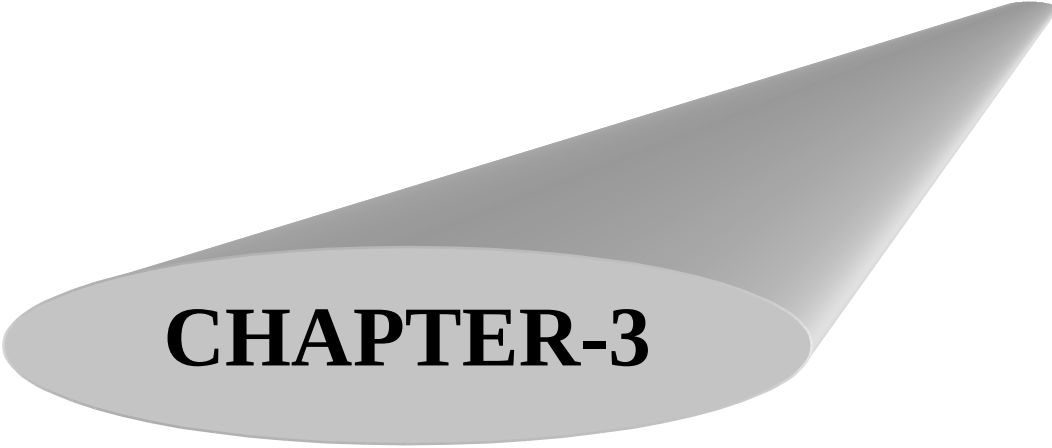
Dehinwal *et al.* (2017) a study was made in sorghum with line x taster (6 females x 4 males) to estimate the magnitude of heterosis among different cross combinations for yield and its component traits. The analysis of variance was found highly significant for all the traits, which indicated that the presence of sufficient variability among hybrids and their parents. Among male

parents, HJ 541 and G 46 and among female parents, 467A and 56A showed maximum green and dry fodder yield. Maximum heterosis for green fodder yield and some other characters as comparison with all the four environments over both the checks was showed by 9A × IS 2389 (81.1 % and 75.3 % respectively). Along with green fodder yield this hybrid is also better for dry fodder yield and leaf breadth. Hybrid 465A × HJ 513 demonstrate better heterosis for green fodder yield as well as for other traits. Hybrid 467A × G 46 showed better heterosis for green fodder yield as well as for dry fodder yield. This is also better for plant height, leaf length, leaf breadth and stem diameter.

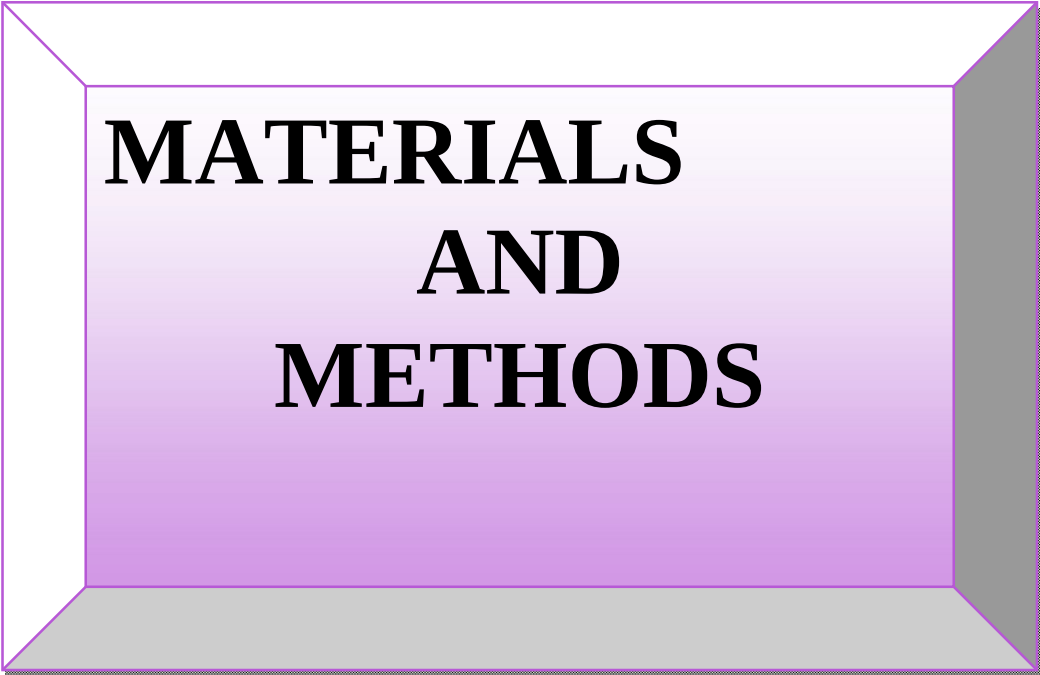
Pal et al. (2017) studied all the 45 F₁ hybrids and 45 F₂ populations along with ten parents were sown in randomized block design with three replications at crop research center of SVPUA&T, Meerut during the *Kharif* season of 2013. Observation were recorded on days to 50% flowering, plant height, leaf breadth, leaf length, leaves per plant, leaf area, leaf stem ratio, stem girth, total soluble solids, protein content and green fodder yield. Nine cross combinations which revealed highest value of heterosis for leaves per plant and green fodder yield viz., SSG 59-3 × CSV 15, Pant Chari 5 × CSV 15, RSSV9 × HC 171, CSV 15 × UP Chari 2, G 48 × UP Chari 2, Pant Chari 5 × HC 171, G 48 × HC 171, Pant Chari 6 × CPVI 1724 and SSG59-3 × Pusa Chari 23 over better parent as well as economic parent may be exploited for developing hybrids for better yield in forage sorghum.

Ingle et al. (2018) heterosis has been considered as well proven method for increasing yield and for improvement of trait in crops, thereof the exploitation of heterosis for the hybrid development programme considered as one of the greatest breakthrough in plant breeding. The present investigation was conducted to assess the magnitude of heterosis and combining ability of thirty F₁ hybrids of *rabi* sorghum (*Sorghum bicolor* (L.) Moench) developed by crossing three lines and ten testers in line x tester fashion with respect to phenotypic trait, grain yield and its components. The hybrids and their parents were evaluated to estimate the heterosis and combining ability governing quantitative traits. Among thirty hybrids, nine potential hybrids observed positive and significant heterosis over mid parent as well as better parent for most of the characters, indicating role of over dominance in the expression of heterosis of these traits.

Soujanya *et al.* (2018) all the 48 F₁ hybrids produced by crossing four lines and twelve testers in line x tester mating design were evaluated to assess general and specific combining ability and gene action governing the green fodder yield and quality traits. The estimates of heterosis over the best standard check revealed significant heterosis in desirable direction for most of the traits in these cross combinations namely 185A x RSSV466, PMS71A x SSV 74, 185A x RSSV466, PMS 71 A x RSSV404, .185 A x RSSV 466, ICS 38 A x SSV 84 and 185 A x NSSV 14.



CHAPTER-3



MATERIALS AND METHODS

The detail of the experimental materials and methods, used in the present study, are described in this chapter under the following headings:

Location of trial

The present investigation was carried out at Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut, situated at an elevation of about 219.75 meters above mean sea level 29°01' N latitude and 77°45' E longitude, representing the North Western Plain Zone. During the period when experiment was in the field, the weather condition remained suitable for the normal healthy growth of the crop.

Experimental material

The experimental material (listed below) was used to generate F₁s for the present investigation was generated by crossing 12 lines x 4 testers of forage sorghum in a line x tester fashion during *Kharif* 2016.

Sl. No.	Genotypes/Lines	Sources	Genotypes/Testers	Sources
1.	UP Chari- 4	Pantnagar	MP Chari	Jawalpur
2.	G- 48	-	HC- 171	Hisar
3.	HC- 260	Hisar	UP Chari- 3	Pantnagar
4.	UP Chari- 2	Pantnagar	HJ- 513	Hisar
5.	SSV- 84	Rahuri		
6.	Pusa Chari- 6	New Delhi		
7.	Pant Chari- 4	Pantnagar		
8.	HC- 136	Hisar		
9.	Pant Chari- 7	Pantnagar		

10.	Pant Chari- 3	Pantnagar
11.	UP Chari- 1	Pantnagar
12.	Jawahar Chari- 6	Jawalpur

Experimental Design

The experimental material of the present investigation comprising of 48 F₁s along with 16 parents (12 lines and 4 testers) were evaluated in a completely randomized block design with three replications during *Kharif* 2017. Each of 48 F₁s was planted in five meter long single row plot and the parents were planted in two rows. The rows were spaced 30 cm apart and plant to plant distance was maintained at 10 cm by proper thinning. The border rows were also planted to neutralize the border effect.

Observations Recorded

Observations on eleven yield and yield attributing characters were recorded as per procedure given below:

Days to 50% flowering: Days to 50% flowering were calculated by counting the number of days taken from sowing to when one half of the plot reached the half bloom stage.

Plant height (cm): The plant height was measured from the ground level to the top of the panicle.

Leaf breadth (cm): Breadth of fourth leaf from the base was measured at the point where it has maximum width.

Leaf length (cm): Length of the fourth leaf from the top was measured.

Leaves per plant: Total number of leaves in each plant was counted.

Leaf area (cm²): The total leaf area of the main stem was calculated by multiplying the total number of leaves with the actual leaf of the fourth leaf was estimated as length x breadth x 0.71. Here the leaf product constant.

Total leaf area (cm²) = leaf length (cm) x leaf breadth x 0.71

Stem girth (mm): The circumference of the stem at fourth internode from the base was measured with the help of vernier calipers.

Leaf stem ratio: Leaf stem ratio was calculated by taking ratio of weight of total stem and weight of total leaves of that plant.

Total soluble solids (%): It was determined with the help of a Hand Refractometer. A drop of juice squeezed by bending from fourth internode of the stem was put on the specimen chamber of the refractometer and the value on the scale having shaded portion was recorded. This value on shaded scale gives the brix reading of the total soluble solids (T.S.S.) contents of the stock juice in percentage.

Protein content (%): Microkjeldhal method as given by Jackson (1973) for protein estimation was followed. Two randomly selected plants in each plot were chopped dried at 50°C temperature and finely ground sample (0.2 g) of plant material was accurately weighed and transferred to a Microkjeldhal digestion flask and 5 ml of sulphuric acid and 4 g of digestion mixture (consisting one part of copper sulphate and five parts of potassium sulphate) were added to it. The flask was then kept on digestion rack until green colored liquor was obtained. The liquor was allowed to cool and then transferred quantitatively to 50 ml volumetric flask. To make up the volume with distilled water to 50 ml, 20 ml of this digest was taken in distillation apparatus and adequate quantity of forty percent Sodium hydroxide solution was added to the distillation flask and kept for distillation. The distillation process was continued till all the ammonia was distilled and absorbed in an excess quantity of four percent of boric acid solution was titrated with standardized 0.1 N H₂SO₄ to obtain a point purple or colorless end point. A blank was also run simultaneously in which only 20 ml distilled water has been used instead of acid digest. The percent nitrogen sample was calculated as follows:

$$\text{Protein \% in sample} = \% \text{ Nitrogen in sample} \times 6.25$$

$$\% \text{ Nitrogen in sample} = \frac{(S-B) \times 0.014 \times 100 \times N}{\text{Weight of sample (0.2 g)}}$$

Where,

S = Titrated value for sample (ml)

B = Titrated value for blank (ml)

N = Normality of H₂SO₄

W = Weight of sample in (g) = 0.2 g

The protein for all plots in each replication was obtained.

Green fodder yield (g/plant): The harvested plants were immediately weighed by spring balance to obtain green fodder yield (g/plant).

Statistical Methods

In the present investigation line x tester design was followed and the replication wise mean values of the treatments were subjected to the following statistical genetical analyses

- Analysis of variance
- Parameters of variability
- Character association
- Path coefficient analysis
- Combining ability analysis
- Manifestation of heterosis

Analysis of variance

The data for different characters were statistically analyzed as per the procedure outlined by **Panse and Sukhatme (1969)**. The analysis of variance was based on the following linear model of **Fisher (1918)**.

$$y_{ij} = \mu + g_i + r_j + e_{ij}$$

where,

i = 1, 2,----- r (replication)

j = 1, 2, -----t (treatment)

Y_{ij} = Phenotypic observation of the ith genotype in the jth replication

μ = general mean

g_i = effect of i th genotype

r_j = effect of j th replication

e_{ij} = random error associated with the i th genotype
in the j th replication

Analysis of variance

Source	df	MS	Expected MS	'F' cal
Replication	$r-1$	M_r	$\sigma^2_e + g\sigma^2_r$	M_r/M_e
Genotypes	$g-1$	M_g	$\sigma^2_e + r\sigma^2_g$	M_g/M_e
Error	$(r-1)(g-1)$	M_e	σ^2_e	

Total	$(rg-1)$			

Where,

r = number of replications

g = number of genotypes

σ^2_r = variance due to replications

σ^2_g = variance due to genotypes

σ^2_e = experimental error variance

The genotypic and phenotypic variances were calculated as below:

Genotypic variance (σ^2_g) = $M_g - M_e/r$

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

Error variance (σ^2_e) = M_e

Standard errors

$$\text{Standard error of mean SE(m)} = \sqrt{\text{Me}/r}$$

$$\text{Standard error of difference SE(d)} = \sqrt{2\text{Me}/r}$$

Where,

$$\text{Me} = \text{error mean square}$$

$$r = \text{number of replications}$$

Critical differences

For comparing the means of any two genotypes:

$$\text{CD at 5\%} = \text{SE (d)} \times t' \text{ value at 5\% level of significance at error d.f.}$$

Coefficient of variation

$$\text{CV (\%)} = \left\{ \sqrt{\text{Me}} / \text{Grand mean} \right\} \times 100$$

Estimation of parameters of variability

The following parameters were estimated by following the **Burton (1952)** and **Johnson *et al.* (1955)**.

$$\text{(I) Genotypic coefficient of variation (GCV \%)} = \left(\frac{\sigma^2_g}{\bar{x}} \right) \times 100$$

$$\text{(II) Phenotypic coefficient of variation (PCV \%)} = \left(\frac{\sigma^2_p}{\bar{x}} \right) \times 100$$

Where,

$$\sigma^2_g = \text{genotypic standard deviation}$$

$$\sigma^2_p = \text{phenotypic standard deviation}$$

$$\bar{x} = \text{grand mean}$$

$$\text{(III) Heritability in broad sense (h}^2\text{\%)} = \left\{ \sigma^2_g / (\sigma^2_g + \sigma^2_e/r) \right\} \times 100$$

$$\text{(IV) Genetic advance (GA)} = K \times \sigma^2_p \times h^2$$

Where,

$$K = \text{Selection differential at 5\% selection intensity, (K=2.06)}$$

$$\text{Genetic advance as percentage of mean (GA \%)} = (GA/\bar{x}) \times 100$$

For convenience following classifications were used for describing various parameters of variability in the text:

PCV and GCV	> 25%	High
	10-25%	Moderate
	< 10%	Low
Heritability (h^2)	> 60%	High
	30-60%	Moderate
	< 30%	Low
Genetic advance	> 20%	High
	10-20%	Moderate
	< 10%	Low

Estimation of correlation coefficients

Phenotypic coefficients of correlation were worked out following analysis of covariance involving all possible paired combinations among the characters studies.

Analysis of covariance

Source	d.f.	Mean sum of products	Expected mean sum of products
Replication	(r-1)	M_{rxy}	$\sigma^2_{exy} + \sigma^2_{rxy}$
Genotypes	(g-1)	M_{gxy}	$\sigma^2_{exy} + \sigma^2_{gxy}$
Error	(r-1)(g-1)	M_{exy}	σ^2_{exy}

The genotypic and phenotypic covariances were calculated as follows:

$$\sigma^2_{gxy} = (M_{gxy} - M_{exy})/r$$

$$\sigma^2_{pxy} = \sigma^2_{gxy} + \sigma^2_{exy}$$

$$\sigma^2_{exy} = M_{exy}$$

where,

$$r = \text{number of replications}$$

$$g = \text{number of genotypes}$$

$$\sigma^2_{gxy} = \text{genotypic covariance between traits x and y}$$

$$\sigma^2_{pxy} = \text{phenotypic covariance between traits x and y}$$

$$\sigma^2_{exy} = \text{environmental covariance between traits x and y}$$

$$M_{gxy} = \text{mean sum of squares due to genotypes from the analysis of covariance between traits x and y}$$

$$M_{exy} = \text{mean sum of squares due to error from the analysis of covariance between traits x and y}$$

The phenotypic, genotypic and environmental coefficients of correlation were computed as per the methods suggested by **Robinson *et al.* (1951)** as under:

Phenotypic coefficient of correlation (r_{pxy})

$$r_{pxy} = \sigma^2_{pxy} / (\sigma^2_{px} \times \sigma^2_{py})^{1/2}$$

where,

$$\sigma^2_{pxy} = \text{phenotypic covariance between two traits x and y}$$

$$\sigma^2_{px} = \text{phenotypic variance of trait x}$$

$$\sigma^2_{py} = \text{genotypic variance of trait y.}$$

Genotypic coefficient of correlation (r_{gxy})

$$r_{gxy} = \sigma^2_{gxy} / (\sigma^2_{gx} \times \sigma^2_{gy})^{1/2}$$

Where,

$$\sigma^2_{gxy} = \text{genotypic covariance between two traits x and y.}$$

$$\sigma^2_{gx} = \text{genotypic variance of trait x}$$

$$\sigma^2_{gy} = \text{genotypic variance of trait y}$$

Environmental coefficient of correlation (r_{exy})

$$r_{xy} = \sigma^2_{gxy} / (\sigma^2_{ex} \times \sigma^2_{ey})^{1/2}$$

Where,

$$\sigma^2_{gxy} = \text{environmental covariance between trait x and y}$$

$$\sigma^2_{ex} = \text{environmental variance of trait x}$$

$$\sigma^2_{ey} = \text{environmental variance of trait y}$$

Test of significance

The significance of phenotypic coefficient of correlation at (g-2) degree of freedom where, 'g' is the number of genotypes, and environmental coefficient of correlation at {(r-1) (g-1)-1} degree of freedom, where, 'r' and 'g' stand for number of replication and genotypes respectively, were tested at 5 per cent level of significance against the table values of correlation coefficient (**Fisher and Yates, 1938**).

Path coefficient analysis

The path coefficients were calculated by employing the method suggested by **Dewey and Lu (1959)**. This was accomplished by solving a set of equations of the form:

$$P_{y1} + P_{y2r12} + P_{y3r13} + \dots + P_{ynr1n} = r_{y1}$$

$$P_{y1r12} + P_{y2} + P_{y3r23} + \dots + P_{ynr2n} = r_{y2}$$

$$P_{y1rn1} + P_{y2rn2} + P_{y3rn3} + \dots + P_{yn} = r_{yn}$$

Where,

$P_{y1}, P_{y2}, \dots, P_{yn}$ are the direct path effects of 1, 2, ..., n variables on the dependent variable 'y'.

$r_{12}, r_{13}, \dots, r_{n(n-1)}$ are the possible coefficients of correlation between various independent variables and $r_{y1}, r_{y2}, \dots, r_{yn}$ are the coefficients of correlation of independent variables with dependent variable 'y'.

The degree of determination (P^2_{xR}) of such variable/variables on the dependent variable was calculated as follows:

$$\text{Residual effects } (P_{xR}) = (1 - R^2)^{1/2}$$

Where,

$$R^2 = \frac{\sum_{i=1}^n \sigma^2_{\text{Piyriy}}}{\sigma^2_{\text{Piyriy}}}$$

Combining Ability Analysis

Combining ability analysis was carried out following **Kempthorne, 1957** using the following model.

$$X_{ijk} = \mu + g_i + g_j + S_{ijk} + e_{ijk}$$

Where,

μ = general mean;

g_i = gca effect of j^{th} line;

g_j = gca effect of j^{th} tester;

s_{ij} = sca effect of ij^{th} combination; and

e_{ijk} = error associated with the observation x_{ijk}

i = number of lines 1, 2-----l

j = number of tester parents 1, 2-----t

k = number of replications 1, 2-----r

The analysis of variance for parents and hybrids was carried out as follows:

Source	d.f.	M.S.	Expected squares	mean
Crosses	(lt -1)			
Lines	(l-1)	M(l)	$\sigma^2_e + \sigma^2_{lxt} + t \sigma^2_l$	
Tester	(t-1)	M(t)	$\sigma^2_e + \sigma^2_{lxt} + l \sigma^2_t$	
Line x tester	((l-1) (t-1))	M(lxt)	$\sigma^2_e + \sigma^2_{lxt}$	
Error	(lt-1)	Me	σ^2_e	

Total	(rlt-1)
-------	---------

Where,

$M(l)$ = Mean sum of squares due to lines,

$M(t)$ = Mean sum of squares due to testers,

$M(lxt)$ = Mean sum of squares due to lines x testers,

Me = Mean sum of squares due to error,

σ^2_e = Environmental variance,

σ^2_{lxt} = Variance due to lines x testers,

σ^2_l = Variance due to lines ,

σ^2_t = Variance due to testers,

As the F_1 generation of crosses was evaluated in the present material, so

$$\sigma^2_{gca} = \sigma^2_t = \sigma^2_l = 1/2 \sigma^2_A$$

and $\sigma^2_{sca} = \sigma^2_{lxt} = \sigma^2_D$

Average degree of dominance was estimated as: $\sigma^2_D / \sigma^2_A)^{0.05}$

Where,

σ^2_A = Additive genetic variance

σ^2_D = Dominance genetic variance

Estimation of GCA Effects

(a) gca effect of i^{th} line

$$\hat{g}_i = \frac{X_{i..}}{t} - \frac{X_{...}}{lt}$$

(b). gca effect of j^{th} tester

$$\hat{g}_j = \frac{X_{j..}}{l} - \frac{X_{...}}{lt}$$

Estimation of SCA Effects

$$\hat{S}_{ij} = \frac{X_{ij}}{l} - \frac{X_{j..}}{t} - \frac{X_{i..}}{r} + \frac{X_{...}}{lrt}$$

Where,

$\hat{g}_i$ = general combining ability of i^{th} lines,

X_i = total of i^{th} male parent over all female and replications

$X_{..}$ = total of all hybrid combinations

$\hat{g}_j$ = general combining ability of testers,

X_j = total of j^{th} female parent over all male parents and replications

X_{ij} = (IJth) combination totals over all replications

l = number of lines

t = number of testers

r = number of replications

Standard errors for combining ability effects are as given below:

$$SE \text{ (gca for line)} = \sqrt{\frac{Me}{rt}}$$

$$SE \text{ (gca for tester)} = \sqrt{\frac{Me}{rl}}$$

$$SE \text{ (sca effect)} = \sqrt{\frac{Me}{r}}$$

$$SE \text{ (} g_i - g_j \text{) line} = \sqrt{\frac{2Me}{rt}}$$

$$SE \text{ (} g_i - g_j \text{) tester} = \sqrt{\frac{2Me}{rl}}$$

$$SE \text{ (} S_{ij} - S_{kl} \text{)} = \sqrt{\frac{2Me}{r}}$$

Estimation of Heterosis

Heterosis expressed as percentage increase or decrease of F_1 s over better parent (heterobeltiosis) and over mid parent (relative heterosis) was calculated by **Fonseca and Patterson, 1968** using following formulae:

$$\text{Heterobeltiosis} = \frac{\bar{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

$$\text{Relative heterosis} = \frac{\bar{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

Where,

$\bar{F}$ = mean of the particular F_1 individuals

$\overline{BP}$ = mean of the better parent in a cross

$\overline{MP}$ = mean of the two parents involved in a particular cross

The critical differences were calculated by using the following standard errors:

$$\text{SE of } (\bar{F} - \overline{MP}) = \sqrt{\frac{3Me}{2r}}$$

$$\text{SE of } (\bar{F}_1 - \overline{BP}) = \sqrt{\frac{2Me}{r}}$$

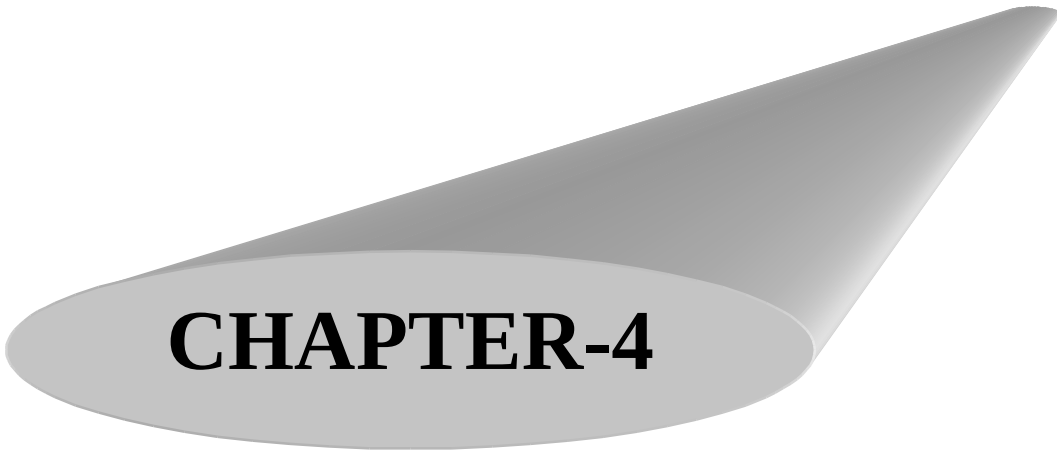
Where,

Me = error mean square

r = number of replications

Critical difference = SE x t value at error degree of freedom at 5 % and 1 % level of significance.

The standard error (i) was used for calculating CD to test the relative heterosis and (ii) was used for heterobeltiosis.



CHAPTER-4



EXPERIMENTAL RESULTS

In the present investigation 12 diverse lines and 4 testers were used as female and male, respectively. Sixteen parents and their 48 F_1 's were grown at Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut during *Kharif* 2017. Data on eleven traits namely, days to 50% flowering, plant height, number of leaves per plant, stem girth, leaf length, leaf breadth, total soluble solids, leaf area leaf stem ratio, protein content and green fodder yield per plant were recorded. The data compiled were subjected to statistical analysis to work out following parameters:

Analysis of variance

Analysis of variance for the randomized complete block design was for all the eleven attributes of 64 treatments *i.e.* 48 F_1 's, 12 lines and 4 testers presented in Table-1. The Mean square values due to treatments showed highly significant differences among the used material in the present investigation for all the traits *viz.*, days to 50% flowering, plant height, number of leaves per plant, stem girth, leaf length, leaf breadth, total soluble solids, leaf area leaf stem ratio, protein content and green fodder yield per plant, which indicated the wide spectrum of variation among the genotypes.

Estimates of variability parameters

The estimates of variability parameters like; phenotypic coefficient of variation, genotypic coefficient of variation, heritability and expected genetic advance expressed as percentage of mean for all the characters are given in Table-2.

Phenotypic coefficients of variation (PCV)

High phenotypic coefficients of variation (more than 25%) revealed for plant height (32.08), stem girth (32.27), leaf stem ratio (27.96) and green fodder yield per plant (25.38). Moderate percentage of phenotypic coefficients of variation (10-25%) was recorded for leaf area (10.12) and low (<10%) phenotypic coefficients of variation for days to 50% flowering (8.51), leaf length

Table: 1 Analysis of variance for eleven characters of parents and F₁ generation of forage sorghum

Source of variance	d.f.	Days to 50% flowering	Plant height (cm)	No. of leaves per plant	Stem girth (mm)	Leaf length (cm)	Leaf breadth (cm)	Total soluble solids (%)	Leaf area (cm ²)	Leaf stem ratio	Protein content (%)	Green fodder yield (g)
Replication	2	1.82	60.97	0.71	0.10	0.31	0.06	0.04	97.71	0.05	0.06	222.58
Treatment	63	165.17**	3878.20**	3.70**	15.85**	53.89**	1.29**	2.48**	5513.58**	0.15**	1.86**	34748.74**
Error	126	0.72	178.32	0.43	1.03	2.01	0.02	0.13	128.35	0.03	0.05	404.85

* Significant at 5% level and ** Significant at 1% level

(5.77), leaf breadth (8.33), number of leaves per plant (8.27), total soluble solids (9.74) and protein content (9.85).

Genotypic coefficient of variation (GCV)

High genotypic coefficients of variation (more than 25%) revealed for plant height (31.30), stem girth (31.16), leaf stem ratio (27.40) and green fodder yield per plant (25.03) whereas low genotypic coefficients of variation (<10%) for days to 50% flowering (8.45), leaf length (5.46), leaf breadth (8.15), number of leaves per plant (7.00), leaf area (9.77), total soluble solids (9.04) and protein content (9.46).. In general, the value of genotypic coefficient of variance was lower than the respective phenotypic coefficient of variance.

Heritability (h^2)

High heritability (>60%) was recorded for all the characters namely, days to 50% flowering (99.00), plant height (87.40), leaf length (90.00), leaf breadth (96.00), number of leaves per plant (72.00), leaf area (93.30), stem girth (83.00), leaf stem ratio (94.00), total soluble solids (86.00), protein content (92.20) and green fodder yield per plant (97.00).

Genetic advance (GA)

Expected genetic advance expressed as percentage of mean was reported high (> 20%) for plant height (21.75), leaf area (29.45), stem girth (20.92), leaf stem ratio (34.72), leaf area (29.95) and green fodder yield per plant (40.55). Moderate genetic advance as percentage of mean (10-20%) expressed for days to 50% flowering (17.30), leaf length (10.65), leaf breadth (16.44), number of leaves per plant (12.19), total soluble solids (17.26) and protein content (18.72).

Estimates of correlation coefficients

The results on correlation coefficient, computed at phenotypic and genotypic levels for all the possible paired combinations among eleven metric attributes are presented in Table-3.

At phenotypic level, green fodder yield per plant exhibited significant and positive correlation with leaf area (0.48) followed by stem girth (0.40), plant height (0.38), number of leaves per plant (0.35) and leaf length (0.34). Days to 50% flowering emerged significant and

Table: 2 Mean performance and parameters of variability for various traits studied in forage sorghum

Sl. No.	Character	GCV (%)	PCV (%)	Genetic Advance	GA as % mean	Heritability (%)
1.	Days to 50% Flowering	8.45	8.51	15.15	17.30	99.00
2.	Plant height (cm)	31.30	32.08	27.62	21.75	87.40
3.	Leaf length(cm)	5.46	5.77	8.11	10.65	90.00
4.	Leaf breadth(cm)	8.15	8.33	1.31	16.44	96.00
5.	No. of leaves per plant	7.00	8.27	1.82	12.19	72.00
6.	Leaf area (cm²)	9.77	10.12	24.32	29.45	93.30
7.	Stem girth (mm)	31.16	32.27	24.16	20.92	83.00
8.	Leaf stem ratio	27.40	27.96	30.14	34.72	94.00
9.	Total Soluble Solids (%)	9.04	9.74	1.69	17.26	86.00
10.	Protein content (%)	9.46	9.85	1.54	18.72	92.20
11.	Green fodder yield per plant (g)	25.03	25.38	26.61	40.55	97.00

positive association with leaf breadth (0.38) and leaf stem ratio (0.33) whereas, leaf length (-0.39) and number of leaves per plant (-0.39) observed significant and negative association with days to 50% flowering. Plant height revealed significant and positive correlation with leaf length (0.32), leaf breadth (0.33), leaf area (0.34), stem girth (0.25), total soluble solids (0.28), protein content (0.31) and green fodder yield per plant (0.38). Leaf length exhibited significant and positive association with leaf area (0.48) and green fodder yield per plant (0.34). Leaf breadth showed significant and positive correlation with leaf area (0.81), leaf stem ratio (0.30) and protein content (0.27) whereas, number of leaves per plant (-0.22) recorded negative significant correlation with leaf breadth. Number of leaves per plant observed significant and positive association with total soluble solids (0.32), protein content (0.21) and green fodder yield per plant (0.35) whereas, leaf stem ratio (-0.21) noted significant and negative association with number of leaves per plant. Leaf area expressed significant and positive correlation with leaf stem ratio (0.35), protein content (0.25) and green fodder yield per plant (0.48). Stem girth noted significant and positive association with protein content (0.26) and green fodder yield per plant (0.40). Leaf stem ratio recorded positive and significant correlation with protein content (0.23) and total soluble solids showed significant and positive association with protein content (0.38).

At the genotypic level, the estimates of correlation coefficients were generally similar to that observed at the phenotypic level, though, their magnitude was slightly lower than the corresponding phenotypic correlations. Here, also green fodder yield per plant showed significant and positive association with leaf area (0.49) followed by stem girth (0.39), plant height (0.36), leaf length (0.32) and number of leaves per plant (0.31).

Estimates of direct and indirect effects

The estimates of direct and indirect effects of different traits on green fodder yield per plant along with their correlation coefficients with green fodder yield per plant are given in Tables-4.

At phenotypic level, leaf area (0.86) displayed high order of direct effect on green fodder yield per plant followed by leaf length (0.89), plant height (0.68), number of leaves per plant (0.57)

Table: 3 Estimates of correlation coefficient for genotypic (G) and phenotypic (P) levels among different attributes of forage sorghum

*

Character		Days to 50% flowering	Plant height (cm)	Leaf length (cm)	Leaf breadth (cm)	No. of leaves per plant	Leaf area (cm ²)	Stem girth (cm)	Leaf stem ratio	Total Soluble Solids (%)	Protein content (%)	Green fodder yield per plant (g)
Days to 50% flowering	G P	1.00 1.00	0.17 0.20	- 0.31** - 0.39**	0.39** 0.38**	- 0.46** - 0.39**	0.16 0.15	- 0.05 - 0.05	0.31** 0.33**	- 0.15 - 0.16	0.19 0.18	0.01 0.03
Plant height (cm)	G P		1.00 1.00	0.25* 0.32*	0.26* 0.33*	- 0.04 - 0.06	0.33** 0.34**	0.27* 0.25*	0.02 0.04	0.32** 0.28**	0.36** 0.31**	0.36** 0.38**
Leaf length (cm)	G P			1.00 1.00	- 0.04 - 0.03	0.05 0.06	0.51** 0.48**	- 0.01 - 0.02	0.10 0.12	0.11 0.19	0.03 0.04	0.32** 0.34**
Leaf breadth (cm)	G P				1.00 1.00	- 0.28* - 0.22*	0.83** 0.81**	0.14 0.15	0.32** 0.30**	0.13 0.12	0.28** 0.27**	0.11 0.12
No. of leaves per plant	G P					1.00 1.00	- 0.13 - 0.15	0.08 0.09	- 0.25* - 0.21*	0.41** 0.32**	0.24* 0.21*	0.31** 0.35**
Leaf area (cm ²)	G P						1.00 1.00	0.09 0.09	0.37** 0.35**	0.18 0.19	0.25* 0.25*	0.49** 0.48**
Stem girth (cm)	G P							1.00 1.00	- 0.13 - 0.19	0.10 0.19	0.28** 0.26**	0.39** 0.40**
Leaf stem ratio	G P								1.00 1.00	0.16 0.18	0.22* 0.23*	- 0.04 - 0.04
Total Soluble Solids (%)	G P									1.00 1.00	0.30** 0.38**	0.20 0.28
Protein content (%)	G P										1.00 1.00	0.18 0.17

Significant at 5 % probability level and ** Significant at 1 % probability level

Table: 4 Estimates of direct and indirect effects for various traits studied towards green fodder yield in forage sorghum

Character		Days to 50% flowering	Plant height (cm)	Leaf length (cm)	leaf breadth (cm)	No. of leaves per plant	Leaf area (cm ²)	Stem girth (mm)	Leaf stem ratio	Total soluble solids (%)	Protein content (%)	Correlated with green fodder yield per plant
Days to 50% flowering	G	0.13	0.05	- 0.07	0.09	- 0.11	0.04	- 0.01	0.07	- 0.04	0.04	0.01 0.03
	P	0.11	0.02	- 0.03	0.04	- 0.04	0.01	- 0.01	0.03	- 0.01	0.02	
Plant height (cm)	G	0.07	0.66	0.08	0.08	- 0.01	0.10	0.08	0.01	0.10	0.11	0.36**
	P	0.04	0.68	0.04	0.05	- 0.01	0.06	0.05	0.01	0.06	0.06	0.38**
Leaf length (cm)	G	0.25	- 0.20	0.81	0.03	- 0.05	- 0.12	- 0.02	- 0.16	- 0.17	- 0.03	0.32**
	P	0.28	- 0.26	0.89	0.01	- 0.02	- 0.14	- 0.03	- 0.15	- 0.15	- 0.01	0.34**
Leaf breadth (cm)	G	0.59	- 0.39	- 0.06	0.11	0.43	0.16	- 0.22	0.48	- 0.20	0.42	0.11
	P	0.67	- 0.34	- 0.01	0.20	0.44	0.16	- 0.23	0.46	- 0.22	0.45	0.12
No. of leaves per plant	G	- 0.14	- 0.02	0.03	- 0.15	0.53	- 0.12	0.04	- 0.13	0.22	0.13	0.31**
	P	- 0.15	- 0.03	0.02	- 0.16	0.57	- 0.14	0.02	- 0.15	0.18	0.15	0.35**
Leaf area (cm ²)	G	0.09	0.12	0.16	0.04	0.13	0.85	0.18	0.09	0.14	0.18	0.49**
	P	0.12	0.15	0.18	0.06	0.16	0.86	0.21	0.16	0.16	0.19	0.48**
Stem girth (mm)	G	- 0.02	0.08	- 0.01	0.04	0.02	0.03	0.28	- 0.07	0.06	0.08	0.39**
	P	- 0.01	0.03	- 0.02	0.02	0.03	0.01	0.25	- 0.03	0.03	0.04	0.40**
Leaf stem ratio	G	0.42	- 0.01	0.51	- 0.02	0.32	0.58	- 0.02	- 0.06	0.46	- 0.01	- 0.04
	P	0.43	- 0.01	0.55	- 0.02	0.38	0.60	- 0.01	- 0.07	0.49	- 0.02	- 0.04
Total soluble solid (%)	G	0.02	- 0.03	- 0.02	- 0.01	0.04	- 0.02	- 0.02	- 0.02	- 0.09	- 0.03	0.20
	P	0.04	- 0.01	- 0.01	- 0.02	0.01	- 0.01	- 0.01	- 0.01	- 0.03	- 0.01	0.28
Protein content (%)	G	- 0.02	- 0.03	- 0.02	- 0.02	- 0.02	0.03	0.02	- 0.02	0.04	0.08	0.18
	P	- 0.03	- 0.04	- 0.01	- 0.02	- 0.02	0.02	0.04	- 0.03	0.05	0.09	0.17

Residual effect (Genotypic) = 0. 42 and (Phenotypic) = 0.46 Bold values indicate direct effect

and stem girth (0.25). However the trait which contributed indirect effects toward green fodder yield per plant was observed leaf length through days to 50% flowering; Leaf breadth via days to 50% flowering, number of leaves per plant, leaf stem ratio and protein content and leaf Stem ratio through days to 50% flowering, leaf length, number of leaves per plant, leaf area and total soluble solids.

At the genotypic level also high direct contribution of leaf area (0.85) displayed high order of direct effect on green fodder yield per plant followed by leaf length (0.81), plant height (0.66), number of leaves per plant (0.53) and stem girth (0.28). However the trait which contributed indirect effects toward green fodder yield per plant was observed leaf length through days to 50% flowering; Leaf breadth via days to 50% flowering, number of leaves per plant, leaf stem ratio and protein content and leaf Stem ratio through days to 50% flowering, leaf length, number of leaves per plant, leaf area and total soluble solids. Magnitudes of residual effects at both phenotypic and genotypic level were found to be low.

Combining ability analysis

Analysis of variance for line x tester

The analysis of variance for all the eleven attributes were carried out involving 16 parents and 48 F_1 's for testing the significance of differences among the treatments with a view to know the clear picture about variability among the parents and F_1 hybrids. The treatment variance partitioned in the variance due to parents, F_1 's and parent vs F_1 's. Variances due to parents were further partitioned into its components *i.e.* due to line, due to tester and line vs tester. The mean sum of squares for all the traits is presented in Table-5.

The 'F' test recorded that variance due to treatments were highly significant for all the characters *viz.*, days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth, leaf stem ratio, total soluble solids, protein content and green fodder yield per plant and showing significant differences for all the attributes to carry out genetic studies.

Variance due to parents observed highly significant for the traits namely, days to 50%

Table: 5 Analysis of variance for eleven characters in parents and F₁ generation of forage sorghum

Source of variations	d.f.	Days to 50% flowering	Plant height (cm)	Leaf length (cm)	Leaf breadth (cm)	No. of leaves per plant	Leaf area (cm ²)	Stem girth (mm)	Leaf stem ratio	Total soluble solids (%)	Protein content (%)	Green fodder yield per plant (g)
Replication	2	1.82	60.97	0.31	0.01	0.71	97.71	0.10	0.03	0.04	0.06	222.58
Treatment	63	165.17**	3878.20**	53.89**	1.29**	3.70**	5513.58**	15.85**	1.02**	2.48**	1.86**	34748.74**
Parents	15	165.87**	4634.37**	51.98**	0.60	3.46**	2958.92**	6.33**	1.62**	4.09**	1.99**	40493.01**
Line	11	210.34**	2745.94**	61.22**	0.41	4.20**	2647.76**	4.88**	0.02	3.53**	1.85**	30604.27**
Tester	3	57.79**	5865.25**	35.02**	1.31**	1.88**	4942.81**	8.21**	0.01	2.26**	3.14**	67307.78**
Parents (L vs T)	1	1.03**	21714.48**	1.32**	0.52	0.05	430.01**	16.69**	2.01**	15.70**	0.12	68824.89**
Parents vs crosses	1	77.59**	15507.93**	254.80**	11.44**	13.94**	65586.05**	156.22**	0.06	55.20**	17.62**	157291.58**
Crosses	47	166.81**	3389.43**	50.23**	1.30**	3.56**	5050.76**	15.90**	0.01	0.85**	1.49**	30308.17**
Error	126	0.72	178.32	2.01	0.02	0.43	128.35	1.03	0.01	0.13	0.05	404.85

*Significant at 5% probability level and ** Significant at 1% probability level

flowering, plant height, leaf length, number of leaves per plant, leaf area, stem girth, leaf stem ratio, leaf breadth, total soluble solids, protein content and green fodder yield per plant while partitioning due to line revealed highly significant for all the attributes except leaf breadth and leaf stem ratio under study. The variance due to testers exhibited highly significant for all the traits except leaf stem ratio. Variance due to line vs testers showed highly significant for all the characters except leaf breadth, number of leaves per plant and protein content. The variance due to parents vs crosses had highly significant for all the attributes except leaf stem ratio and variance due to crosses recorded highly significant for all the traits except leaf stem ratio.

Analysis of variance for combining ability

Analysis of variance for combining ability for all the eleven metric characters was done in F_1 's hybrids and the results are given in Table-6. The variance among line with respect to general combining ability (gca) was found highly significant for all the attributes *i.e.* days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth, leaf stem ratio, total soluble solids, protein content and green fodder yield per plant whereas variance among testers with respect to gca was also observed highly significant for all the traits. The variances among crosses due to interaction between lines x testers genotypes with respect to specific combining ability (sca) were also noted highly significant for all the characters except leaf stem ratio.

Estimates of components of variance and their magnitude

An estimate of components of variance *viz.*, δ^2g and δ^2s has been worked out through combining ability variance for all the attributes. The δ^2g were partitioned into δ^2g due to males and δ^2g due to females. The ratio between δ^2g pooled and δ^2s and average degree of dominance expressed as $(\sigma^2s/\sigma^2g)^{0.5}$ have been worked out. A ratio of 1:1 σ^2g/σ^2s indicates the equal importance of δ^2g and δ^2s expression of a particular trait while deviation between from 1:1 exhibited the relative importance of δ^2g or δ^2s depending on the value. The estimates of components of variance, their ratio and degree of dominance for different characters are presented in Table-6.

Table: 6 Analysis of variance for combining ability eleven characters in forage sorghum

Source of variation	d.f.	Days to 50% flowering	Plant height (cm)	Leaf length (cm)	Leaf breadth (cm)	No. of leaves per plant	Leaf area (cm ²)	Stem girth (mm)	Leaf stem ratio	Total soluble solids (%)	Protein content (%)	Green fodder yield per plant (g)
Line (GCA)	11	596.18**	4452.93**	123.72**	2.06**	9.35**	6900.52**	13.63**	0.84**	1.86**	2.21**	21932.20**
Tester (GCA)	3	70.18**	21250.27**	156.50**	5.18**	6.60**	21745.56**	64.68**	0.63**	2.60**	10.49**	305250.09**
Line x Tester (SCA)	33	32.47**	1411.21**	16.07**	0.69**	1.36**	2916.47**	12.22**	0.06	0.36**	0.43**	8105.44**
Error	94	0.76	164.72	2.39	0.92	1.44	95.05	1.20	0.02	1.12	1.05	539.35

* Significant at 5 % probability level, and ** Significant at 1 % probability level.

Estimates of genetic components, its ratio (σ^2g/σ^2s) average degree of dominance (σ^2s/σ^2g)^{0.5}

Source of variation	Days to 50% flowering	Plant height (cm)	Leaf length (cm)	leaf breadth (cm)	No. of leaves per plant	Leaf area (cm ²)	Stem girth (mm)	Leaf stem ratio	Total soluble solids (%)	Protein content (%)	Green fodder yield per plant (g)
$\sigma^2 A$	47.71	1056.11	17.51	0.80	1.63	1182.89	8.18	0.05	0.37	0.83	13598.86
$\sigma^2 D$	40.58	410.96	17.68	0.62	1.31	929.37	8.73	0.07	0.38	0.73	2566.86
σ^2g/ σ^2s	2.61	2.57	2.46	1.33	2.04	1.27	0.85	1.72	2.29	4.16	5.29
$(\sigma^2s/ \sigma^2g)^{0.5}$	1.31	1.28	1.23	0.67	0.64	0.64	0.43	0.86	1.14	2.08	2.65
δ^2g (males)	1.92	585.33	4.29	0.14	0.17	600.48	1.77	0.07	0.07	0.29	2467.92
δ^2g (females)	49.62	356.22	10.14	0.17	0.74	564.35	1.05	0.03	0.14	0.18	1793.95
δ^2g (pooled)	38.53	1526.51	16.86	0.53	1.08	2155.05	7.25	0.04	0.29	0.67	16300.67
δ^2s (females x males)	10.58	610.96	4.68	0.22	0.81	929.37	3.73	0.05	0.08	0.13	2566.86

The estimates of δ^2_g due to males were found to be higher than δ^2_g due to females for plant height, leaf area, stem girth, leaf stem ratio, protein content and green fodder yield per plant. A comparison of relative magnitude of these expressed to focus that additive gene action. However, the δ^2_g due to females showed higher than the δ^2_g due to males for days to 50% flowering, leaf length, leaf breadth number of leaves per plant and total soluble solids which indicates that the predominance role of additive gene action.

Reference to estimates of δ^2_A and δ^2_D for different characters exhibited that the relative magnitude of former was higher than δ^2_g (pooled) for the traits viz., days to 50% flowering, leaf length, leaf breadth, number of leaves per plant, stem girth, leaf stem ratio, total soluble solids and protein content, indicating that presence of dominance type gene action. The ratio between estimated variance owing to σ^2_g/σ^2_s was found more than unity for all the attributes except stem girth which indicates that the involvement of additive gene action.

Average degree of dominance $(\delta^2_s/\delta^2_g)^{0.5}$ exhibited less than unity for leaf breadth (0.67), number of leaves per plant (0.64), leaf area (0.64), stem girth (0.43) and leaf stem ratio (0.86) which indicated partial dominance. The mean degree of dominance was found greater than unity for days to 50% flowering (1.31), plant height (1.28), leaf length (1.23), total soluble solids (1.14), protein content (2.08) and green fodder yield per plant (2.65), indicating that the over dominance. Magnitude of δ^2_s was recorded higher than δ^2_g for plant height, leaf breadth, number of leaves per plant, leaf area, stem girth and green fodder yield per plant, indicated that the average degree of dominance was found to be dominance.

Estimates of general combining Ability Effects

The analysis of variance for general combining ability (gca) and specific combining ability (sca) for all the eleven characters are presented in Table-7 and the traits wise description are given below:

Days to 50% flowering

For days to 50% flowering, the good general combiners with positive values are desirable. The range of general combining ability effects of lines and testers were from -2.18 (UP Chari-2) to 12.73 (HC-260) and -0.17 (HJ-513) to 2.03 (HC-171), respectively. Among the lines, HC-260 (12.73), SSV-84 (9.53), HC-136 (8.74), Pant Chari-3 (9.08), UP Chari-1 (8.52) and Jawahar Chari-6 (10.47) exhibited significant and positive general combining ability effects and found to be as good general combiners for late flowering and lines UP Chari-4 (-2.01), UP Chari-2 (-2.18) and Pant Chari-4 (-1.96) revealed negative gca effects for early flowering. MP Chari (0.87), HC-171 (2.03) and UP Chari-3 (0.98) showed positive and significant gca effect among the testers for late flowering whereas tester HJ 513 (-0.17) for early flowering.

Plant height

In case of plant height the lines, UP Chari-4 (16.98), G-48 (21.98), HC-260 (22.38), SSV-84 (34.47), Pusa Chari-6 (10.42), Pant Chari-4 (10.28), HC-136 (11.23), Pant Chari-3 (33.82), UP Chari-1 (12.96) and Jawahar Chari-6 (22.90) noted positive and significant general combining ability effects and were emerged as good general combiners for tall type plant. UP Chari-2 (-8.27) recorded negative and significant gca effects and were expressed as good general combiner for dwarf type plant. Among the testers, MP Chari (16.00), HC-171 (34.06) and UP Chari-3 (18.83) were proved good general combiners for tall type plant and HJ-513 (-0.77) was observed good general combiner for dwarf type plant.

Leaf length

Out of twelve parental lines, only five genotypes viz., G-48 (2.20), HC-260 (5.64), UP Chari-2 (5.76), HC-136 (2.58) and Pant Chari-3 (5.54) recorded significant and positive general combining ability effects and appeared as good general combiners for maximum leaf length. Among the males HC-171 (2.88), UP Chari-3 (1.86) and HJ-513 (1.13) showed significant and positive general combining ability effects for leaf length.

Leaf breadth

Among the lines, HC-260 (0.50), SSV-84 (0.39), Pant Chari-4 (0.30), Pant Chari-3 (0.52), UP Chari-1 (0.59) and Jawahar Chari-6 (0.80) possessed significant and positive general combining ability effects and emerged as good general combiners for higher leaf breadth and male HC-171 (10.23) and UP Chari-3 (20.19) reported significant and positive general combining ability effects among testers.

Number of leaves per plant

Significant and positive general combining ability effects exhibited by UP Chari-4 (0.62), G-48 (0.63), UP Chari-2 (0.54), SSV-84 (0.66), Pusa Chari-6 (0.74), Pant Chari-4 (0.69), Pant Chari-3 (0.64) and Jawahar Chari-6 (2.39) among the females, whereas among the males, MP Chari (10.61) and HJ-513 (20.06) were found to be good general combiners for more number of leaves per plant.

Leaf area

Highest order significant and positive general combining ability effects, among the female lines *i.e.* G-48 (18.24), UP Chari-2 (37.22), SSV-84 (14.88), Pant Chari-4 (14.95), Pant Chari-7 (14.02), Pant Chari-3 (12.84), UP Chari-1 (22.42) and Jawahar Chari-6 (57.68) were observed and these lines were found to be as good general combiners for maximum leaf area. Among testers, MP Chari (30.66), HC-171 (29.52) and HJ-513 (31.05) had highly significant and positive gca effects for leaf area.

Stem girth

Estimates of general combining ability effects for stem girth exhibited among the lines only four genotypes had desirable effects viz., G-48 (1.48), UP Chari-2 (1.23), UP Chari-1 (1.80) and Jawahar Chari-6 (1.81) and were identified as good general combiners for thickness of stem. Among the males, MP Chari (1.68), HC-171 (0.42) and HJ-513 (1.52) showed significant and positive general combining ability effects in desirable direction.

Table: 7 Estimates of general combining ability effect for line and testers with respect to eleven characters of forage sorghum

Line/Tester	Days to 50% flowering		Plant height (cm)		Leaf length (cm)		Leaf breadth (cm)		No. of leaves per plant		Leaf area (cm ²)	
Line	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
UP Chari-4	75.12	-2.01	299.03	16.98**	72.60	-0.45	7.04	-0.01	14.20	0.62*	363.27	-0.53
G-48	80.33	12.84**	251.83	21.98**	71.20	2.20**	7.17	-0.23**	12.00	0.63*	362.66	18.24**
HC- 260	78.31	12.73**	316.90	22.38**	81.60	5.64**	7.40	0.50**	16.60	-0.13	429.07	1.69
UP Chari-2	87.00	-2.18	295.66	-8.27*	66.93	5.76**	7.36	-0.09	15.60	0.54**	349.76	37.22**
SSV-84	84.02	9.53**	209.26	34.47**	73.60	-1.68	7.57	0.39**	15.53	0.66**	395.83	14.88**
Pusa Chari- 6	72.66	0.55	294.63	10.42*	74.73	0.61	7.40	-0.13	14.80	0.74**	425.92	-4.22
Pant Chari -4	85.33	-1.96	296.66	10.28*	71.66	-0.28	7.44	0.30**	14.80	0.69**	378.57	14.95**
HC- 136	90.66	8.74**	293.10	11.23*	70.93	2.58**	8.08	0.19	14.26	0.02	420.67	-0.32
Pant Chari -7	82.64	1.39	294.23	3.85	75.00	0.15	7.42	-0.11	14.33	0.11	395.43	14.02**
Pant Chari -3	83.65	9.08**	249.80	33.82**	83.46	5.54**	7.11	0.52**	14.53	0.64**	421.58	12.84**
UP Chari-1	79.66	8.52**	296.76	12.96**	73.86	-1.75	8.03	0.59**	13.73	-0.48*	421.31	22.42**
Jawahar Chari-6	88.33	10.47**	298.86	22.90*	75.20	1.77	8.10	0.80**	13.26	2.39**	432.87	57.68**
Tester												
MP Chari	82.80	0.87**	336.60	16.00**	72.66	- 0.11	6.76	- 0.57	15.40	10.61**	349.06	30.66**
HC-171	83.73	2.03**	384.66	34.06**	78.20	2.88**	8.03	10.23**	14.33	-0.15	442.69	29.52**
UP Chari-3	88.13	0.98**	276.60	18.83**	74.46	1.86**	8.02	20.19**	13.46	0.39	424.35	- 7.10
HJ-513	92.33	-0.17	330.86	- 0.77	70.06	1.13**	8.18	- 0.15	14.40	20.06**	410.53	31.05**

Line/Tester	Stem girth (mm)		Leaf stem ratio		Total soluble solids (%)		Protein content (%)		Green fodder yield per plant (g)	
Line	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
UP Chari-4	17.41	-0.59	17.41	-0.02	9.53	0.23*	7.72	0.18	351.40	80.73**
G-48	19.56	1.48**	19.56	0.94**	6.98	0.60**	8.14	0.08	318.80	21.25**
HC-260	17.28	0.05	17.28	-0.03	10.35	0.86**	6.80	0.55**	528.00	- 0.47
UP Chari-2	17.72	1.23**	17.72	-0.02	9.70	0.51**	8.69	0.62**	568.80	-2.79
SSV-84	17.40	0.60	17.40	-0.04	7.94	0.32*	7.30	-0.09	515.50	47.92**
Pusa Chari-6	17.00	-0.69	17.00	0.83**	7.85	-0.27*	7.43	-0.11	362.90	11.90
Pant Chari -4	18.00	0.19	18.00	-0.01	8.26	-0.06	8.12	0.58**	468.56	-8.39
HC-136	17.79	0.39	17.79	-0.03	8.77	0.12	7.76	-0.23	528.96	6.03
Pant Chari -7	20.92	0.95	20.92	-0.03	8.70	-0.09	6.70	0.49**	625.56	72.19**
Pant Chari -3	18.53	0.02	18.53	0.74**	8.42	-0.06	7.66	0.01	377.93	26.49**
UP Chari-1	18.45	1.80**	18.45	0.84**	9.33	0.23**	9.11	0.59**	374.26	52.29**
Jawahar Chari-6	15.97	1.81**	15.97	0.07	6.73	0.29*	6.51	0.55**	532.66	0.44
Tester										
MP Chari	18.56	1.68**	0.34	0.73**	9.52	0.26**	6.52	-0.17	577.68	34.97**
HC-171	19.08	0.42*	0.29	0.91**	8.81	0.11	8.58	0.71**	583.93	47.39**
UP Chari-3	18.05	-0.27	0.38	- 0.32	10.48	- 0.09	7.36	0.58**	341.40	- 7.56
HJ-513	21.76	1.52**	0.39	-0.24	10.67	0.37**	8.64	- 0.04	697.90	55.20**

Leaf stem ratio

Significant and positive general combining ability effects was observed for the lines G-48 (0.94), Pusa Chari-6 (0.83), Pant Chari-3 (0.74) and UP Chari-1 (0.84) which appeared as best general combiners for leaf stem ratio. Testers MP Chari (0.73) and HC-171 (0.91) exhibited significant and positive general combining ability effects for this trait.

Total soluble solids

Female lines, UP Chari-4 (0.23), G-48 (0.60), HC-260 (0.86), UP Chari-2 (0.51), SSV-84 (0.32), UP Chari-1 (0.23) and Jawahar Chari 6 (0.29) were considered as good general combiners for total soluble solids. Among the tester, MP Chari (0.26) and HJ-513 (0.37) had significant positive gca effects for this character.

Protein content

Estimates of general combining ability effects for protein content revealed that among the female lines, six lines noted desirable effects. The best lines were HC-260 (0.55), UP Chari-2 (0.62), Pant Chari-4 (0.58), Pant Chari-7 (0.49), UP Chari-1 (59) and Jawahar Chari-6 (0.55) were found to be as good general combiners for high protein content. Among the testers, HC-171 (0.71) and UP Chari-3 (0.58) were considered as good general combiners for this character.

Green fodder yield per plant

Out of all the twelve female lines, only six lines *i.e.* UP Chari 4 (80.73), G-48 (21.25), SSV-84 (47.92), Pant Chari-7 (72.19), Pant Chari-3 (26.49) and UP Chari-1 (52.29) recorded significant and positive general combining ability effects and were proved to be good general combiners for high green fodder yield per plant. Among the tester MP Chari (34.97), HC-171 (47.39) and HJ-513 (55.20) were appeared as good general combiners this attributes.

Specific combining ability effects

The estimates of specific combining ability (sca) effects of 48 crosses for eleven traits and mean performance of these crosses are given in Table 8. The details of specific combining ability effects for different characters have presented as follows.

Days to 50% flowering

The specific combining ability effects ranged from -1.25 to 8.11. The cross combinations which gave positive and significant value of specific combining ability effects were considered desirable as they were late flowering. On the basis of this consideration hybrids *i.e.* UP Chari-4 x MP Chari (1.41), UP Chari-4 x HC-171 (1.44), UP Chari-4 x HJ-513 (1.89), G-48 x HC-171 (4.76), G-48 x UP Chari-3 (1.65), G-48 x HJ-513 (2.18), HC-260 x HC-171 (5.14), HC-260 x UP Chari-3 (3.39), UP Chari-2 x HC-171 (3.01), UP Chari-2 x UP Chari-3 (1.06), UP Chari-2 x HJ-513 (1.06), SSV-84 x MP Chari (1.43), SSV-84 x HC-171 (5.67), SSV-84 x HJ-513 (4.99), Pusa Chari-6 x HC-171 (1.79), Pusa Chari-6 x UP Chari-3 (3.54), Pusa Chari-6 x HJ-513 (1.39), Pant Chari-4 x HC-171 (2.36), Pant Chari-4 x UP Chari-3 (1.65), Pant Chari-4 x HJ-513 (1.04), HC-136 x HJ-513 (1.27), Pant Chari-7 x MP Chari (2.01), Pant Chari-7 x UP Chari-3 (1.50), Pant Chari-3 x MP Chari (4.99), Pant Chari-3 x HC-171 (5.09), Pant Chari-3 x UP Chari-3 (1.97), Pant Chari-3 x HJ-513 (8.11), UP Chari-1 x MP Chari (1.88), UP Chari-1 x HJ-513 (2.22), Jawahar Chari-6 x HC-171 (5.19), Jawahar Chari-6 x UP Chari-3 (2.88) and Jawahar Chari-6 x HJ-513 (1.94) were found to be as best specific combiners for late flowering whereas, crosses HC-260 x MP Chari (-1.03) and HC-136 x UP Chari-3 (-1.25) exhibited negative and significant specific combining ability effects and emerged as best specific combiners for early flowering.

Plant height

Tall and medium tall plant is a desirable character in forage sorghum, in case of plant height the cross combinations *viz.*, UP Chari-4 x HC-171 (24.10), UP Chari-4 x HJ-513 (27.18), G-48 x MP Chari (19.35), G-48 x HC-171 (18.21), G-48 x UP Chari-3 (14.09), G-48 x HJ-513 (12.95), UP Chari-2 x MP Chari (14.27), UP Chari-2 x HC-171 (39.68), UP Chari-2 x HJ-513 (15.17), SSV-84 x MP Chari (44.37), SSV-84 x HC-171 (28.69), SSV-84 x UP Chari-3 (18.66), SSV-84 x HJ-513 (54.40), Pant Chari-4 x HC-171 (26.69), HC-136 x MP Chari (20.40), HC-136 x HC-171 (26.16), Pant Chari-3 x UP Chari-3 (18.75), Pant Chari-3 x HJ-513 (34.57), UP Chari-1 x HJ-513 (17.73), Jawahar Chari-6 x HC-171 (16.11) and Jawahar Chari-6 x HJ-513 (14.53) revealed significant

positive specific combining ability effects and were appeared as best specific combiners for tall type plant height. Hybrids *i.e.* UP Chari-2 x UP Chari-3 (-10.24), Pant Chari-4 x UP Chari-3 (-14.86), Pant Chari-7 x HC-171 (-13.56), Pant Chari -7 x HJ-513 (-12.22), Pant Chari-3 x HC-171 (-10.36), UP Chari-1 x HC-171 (-13.05) and Jawahar Chari-6 x UP Chari-3 (-11.14) showed negative significant specific combining ability effects and were identified as good specific combiners for dwarf type plant height.

Leaf length

The cross combinations *viz.*, UP Chari-4 x HJ-513 (2.31), G-48 x HC-171 (2.95), G-48 x UP Chari-3 (3.13), UP Chari-2 x HC-171 (4.42), UP Chari-2 x HJ-513 (4.24), SSV-84 x UP Chari-3 (1.94), Pusa Chari-6 x HC-171 (2.78), Pusa Chari-6 x HJ-513 (2.54), Pant Chari-4 x MP Chari (2.76), HC-136 x UP Chari-3 (3.56), HC-136 x HJ-513 (2.38), Pant Chari-3 x MP Chari (3.09), Pant Chari-3 x UP Chari-3 (5.41), Pant Chari-3 x HJ-513 (1.86) and Jawahar Chari-6 x HJ-513 (6.23)noted significant and positive specific combining ability effects and were emerged best specific combiner for maximum leaf length and out of 48 F₁'s hybrids, only one cross SSV-84 x HC-171 (-2.06) recorded negative and significant specific combining ability effects which indicated that poor specific combiners for leaf length.

Leaf breadth

The specific combining ability effects of the cross combinations namely, UP Chari-4 x HC-171 (0.18), UP Chari- 4 x UP Chari-3 (0.53), UP Chari-4 x HJ-513 (0.50), G-48 x MP Chari (0.24), G-48 x HC-171 (0.21), G-48 x UP Chari-3 (0.25), HC-260 x HC-171 (1.15), HC-260 x UP Chari-3 (0.73), HC-260 x HJ-513 (0.50), UP Chari-2 x HC-171 (0.28), UP Chari-2 x HJ-513 (0.22), SSV-84 x MP Chari (0.28), SSV-84 x HC-171 (0.34), SSV-84 x UP Chari-3 (0.34), SSV-84 x HJ-513 (0.40), Pusa Chari-6 x HC-171 (0.22), Pusa Chari-6 x UP Chari-3 (0.51), Pusa Chari-6 x HJ-513 (0.17), Pant Chari -4 x MP Chari (0.28), Pant Chari-4 x UP Chari-3 (0.43), Pant Chari-4 x HJ-513 (0.35), HC-136 x HC-171 (0.68), HC-136 x HJ-513 (0.49), Pant Chari-7 x UP Chari-3 (0.42), Pant Chari-7 x HJ-513 (0.29), Pant Chari-3 x MP Chari (0.78), Pant Chari-3 x HC-171 (0.33), Pant

Chari-3 x HJ-513 (0.60), UP Chari-1 x MP Chari (0.76), UP Chari-1 x UP Chari-3 (0.43), Jawahar Chari-6 x MP Chari (0.33), Jawahar Chari-6 x UP Chari-3 (0.47) and Jawahar Chari-6 x HJ-513 (0.70) revealed significant positive and were appeared to be as best specific combiners for maximum leaf breadth. The hybrids viz., UP Chari-4 x MP Chari (-0.21), G-48 x HJ-513 (-0.20) and UP Chari-1 x HJ-513 (-0.25) observed negative and significant specific combining ability effects and were expressed as poor specific combiners for leaf breadth.

Number of leaves per plant

Significant and positive specific combining ability effects was reported by the crosses *i.e.*, UP Chari-4 x MP Chari (0.97), UP Chari-4 x HC-171 (1.12), UP Chari-4 x HJ-513 (2.11), HC-260 x UP Chari-3 (1.42), HC-260 x HJ-513 (0.91), UP Chari-2 x MP Chari (0.78), Pant Chari-3 x MP Chari (0.81), Pant Chari-3 x HC-171 (1.03), UP Chari-1 x MP Chari (1.06), Jawahar Chari-6 x MP Chari (0.89) and Jawahar Chari-6 x HJ-513 (1.64) and considered as best specific combiners for more number of leaves per plant. Out of 48 F₁'s hybrids, only three cross combinations UP Chari-2 x HJ-513 (-0.56), SSV-84 x HC-171 (-0.71) and HC-136 x HJ-513 (-0.71) showed negative and significant specific combining ability effects were found to be as poor specific combiners for this attribute.

Leaf area

Among the F₁'s hybrids, highest order significant and positive specific combining ability effects were recorded by UP Chari-4 x MP Chari (17.15), UP Chari-4 x HC- 171 (33.20), UP Chari-4 x UP Chari-3 (31.42), UP Chari-4 x HJ-513 (27.47), HC-260 x HC-171 (76.20), HC-260 x UP Chari-3 (44.31), HC-260 x HJ-513 (36.23), UP Chari-2 x HC-171 (15.12), SSV-84 x MP Chari (15.14), SSV-84 x HC-171 (17.86), SSV-84 x HJ-513 (14.40), Pusa Chari-6 x HC-171 (26.87), Pusa Chari-6 x UP Chari-3 (23.83), Pant Chari-4 x MP Chari (31.78), Pant Chari-4 x HC-171 (15.12), Pant Chari-4 x UP Chari-3 (36.87), Pant Chari-4 x HJ-513 (20.21), HC-136 x HC-171 (39.80), HC-136 x UP Chari-3 (20.02), HC-136 x HJ-513 (13.58), Pant Chari-7 x MP Chari (14.81), Pant Chari-7 x UP Chari-3 (24.25), Pant Chari-3 x MP Chari (36.52), Pant Chari-3 x HC-171

(17.29), Pant Chari-3 x UP Chari-3 (38.19), Pant Chari-3 x HJ-513 (57.43), UP Chari-1 x MP Chari (56.35), Jawahar Chari-6 x MP Chari (21.20), Jawahar Chari-6 x HC-171 (13.14), Jawahar Chari-6 x UP Chari-3 (16.86) and Jawahar Chari-6 x HJ-513 (18.81) for best specific combiners and cross combinations *i.e.* UP Chari-2 x HJ-513 (-15.39), UP Chari-1 x UP Chari-3 (-23.06) and UP Chari-1 x HJ-513 (-21.90) observed negative and significant specific combining ability effects for this character.

Stem girth

The specific combining ability effects ranged from -1.49 to 3.73 for stem girth, eighteen F_1 's hybrids *i.e.* UP Chari-4 x MP Chari (1.72), UP Chari-4 x HC-171 (3.13), UP Chari-4 x HJ-513 (1.82), G-48 x MP Chari (2.23), UP Chari-2 x MP Chari (1.58), SSV-84 x MP Chari (3.73), SSV-84 x HJ-513 (2.00), Pusa Chari-6 x MP Chari (1.86), Pusa Chari-6 x HJ-513 (3.37), Pant Chari-4 x MP Chari (1.16), Pant Chari-7 x MP Chari (2.51), Pant Chari-7 x UP Chari-3 (1.72), Pant Chari-3 x MP Chari (2.48), UP Chari-1 x HC-171 (2.13), UP Chari-1 x UP Chari-3 (1.95), UP Chari-1 x HJ-513 (3.60), Jawahar Chari-6 x MP Chari (3.02) and Jawahar Chari-6 x HJ-513 (3.47) exhibited significant and positive specific combining ability effects and were identified best specific combiners for thickness of stem. Only one cross was found to be as poor specific combiners for this trait and had negative significant specific combining ability effects.

Leaf stem ratio

Only sixteen cross combinations *viz.*, UP Chari-4 x MP Chari (0.12), UP Chari-4 x HC-171 (0.14), UP Chari-4 x UP Chari-3 (0.14), UP Chari-4 x HJ-513 (0.18), UP Chari-2 x UP Chari-3 (0.13), UP Chari-2 x HJ-513 (0.17), Pant Chari-4 x HJ-513 (0.14), Pant Chari-7 x HC-171 (0.17), Pant Chari-7 x HJ-513 (0.14), Pant Chari -3 x UP Chari-3 (0.13), Pant Chari -3 x HJ-513 (0.15), UP Chari-1 x MP Chari (0.15), UP Chari-1 x HC-171 (0.17), UP Chari-1 x HJ-513 (0.12), Jawahar Chari-6 x MP Chari (0.13), Jawahar Chari-6 x HC-171 (0.16) and Jawahar Chari-6 x HJ-513 (0.16) showed positive and significant specific combining ability effects and were considered desirable

best specific combiners for leaf stem ratio. Hybrid Jawahar Chari-6 x UP Chari-3 exhibited negative significant specific combining ability effects for this character.

Total soluble solids

As many as seven superior hybrids out of the forty eight crosses showed significant positive specific combining ability effects. These superior cross combinations namely, G-48 x MP Chari (0.55), G-48 x HJ-513 (0.94), HC-260 x MP Chari (0.50), HC-260 x HJ-513 (0.44), HC-136 x UP Chari-3 (0.73), Pant Chari-3 x HC-171 (0.55) UP Chari-1 x MP Chari (0.41) and Jawahar Chari-6 x UP Chari-3 (0.53) were considered as best specific combiners for total soluble solids. Hybrid UP Chari-4 x MP Chari (-0.25) were found to be as poor specific combiners.

Protein Content

The cross combinations *i.e.* HC-260 x MP Chari (0.43), HC-260 x HC-171 (0.37), UP Chari-2 x MP Chari (0.57), Pusa Chari-6 x HC-171 (0.57), Pant Chari-4 x HC-171 (0.56), Pant Chari-4 x UP Chari-3 (0.56), HC-136 x MP Chari (0.64), Pant Chari-7 x MP Chari (0.38), UP Chari-1 x MP Chari (0.85), UP Chari-1 x UP Chari-3 (0.58), Jawahar Chari-6 x MP Chari (0.31) and Jawahar Chari-6 x HC-171 (0.54) were appeared as best specific combiners for high protein content and the F₁'s hybrids namely, UP Chari-2 x HC-171 (-0.41) and Pant Chari-4 x MP Chari (-0.30) were expressed as poor specific combiners for low protein content.

Green fodder yield per plant

The *per se* performance of crosses varied from -21.68 (HC 136 x UP Chari-3) to 95.02 (UP Chari-4 x HJ-513). Out of the forty eight F₁'s hybrids, only twenty three cross combinations *viz.*, UP Chari-4 x HC-171 (78.60), UP Chari-4 x UP Chari-3 (26.74), UP Chari-4 x HJ-513 (95.02), G-48 x UP Chari-3 (51.03), G-48 x HJ-513 (24.24), HC-260 x UP Chari-3 (49.91), HC-260 x HJ-513 (28.25), SSV-84 x MP Chari (46.80), SSV-84 x HC-171 (50.52), SSV-84 x UP Chari-3 (77.42), Pusa Chari-6 x UP Chari-3 (30.72), Pusa Chari-6 x HJ-513 (60.33), HC-136 x HJ-513 (43.16), Pant Chari-7 x MP Chari (44.30), Pant Chari-7 x HC-171 (35.12), Pant Chari-3 x MP Chari (23.20), Pant Chari-3 x UP Chari-3 (82.34), Pant Chari-3 x HJ-513 (40.76), UP Chari-1 x MP Chari (50.38), UP

Table: 8 Estimates of specific combining ability effect with respect eleven characters in forage sorghum

Line x Tester (Crosses)	Days to 50% flowering		Plant height (cm)		Leaf length (cm)		Leaf breadth (cm)		No. of leaves per plant		Leaf area (cm ²)	
	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
UP Chari -4 x MP Chari	83.66	1.41**	310.00	-7.08	75.73	-0.73	7.36	-0.21*	15.33	0.97*	395.82	17.15*
UP Chari -4 x HC-171	86.53	1.44**	391.23	24.10**	78.60	-0.63	8.54	0.18*	16.66	1.12**	486.34	33.20**
UP Chari -4 x UP Chari-3	85.93	0.96	304.40	-9.85	75.53	1.04	8.86	0.53**	15.26	-0.04	475.14	31.42**
UP Chari -4 x HJ-513	87.66	1.89**	326.66	27.18**	75.53	2.31**	7.78	0.50**	15.53	2.11**	417.20	27.47**
G-48 x MP Chari	90.86	0.94	317.46	19.35*	74.33	-1.38	7.57	0.24**	15.13	0.08	403.03	7.76
G-48 x HC-171	88.06	4.76**	329.96	18.21*	75.53	2.95**	8.34	0.21**	14.46	0.17	447.24	-8.19
G-48 x UP Chari-3	91.46	1.65**	281.20	14.09**	76.86	3.13**	7.84	0.25**	14.33	0.28	430.86	4.85
G-48 x HJ-513	92.80	2.18**	327.83	12.95**	75.66	1.20	7.85	-0.20*	13.86	-0.12	422.54	-4.42
HC-260 x MP Chari	73.33	-1.03*	317.93	-4.55	82.66	0.12	7.00	-0.07	15.60	0.04	410.86	-4.33
HC-260 x HC-171	82.40	5.14**	381.90	9.36	83.73	-1.58	6.71	1.15**	15.26	0.47	399.16	76.20**
HC-260 x UP Chari-3	70.86	3.39**	320.83	1.18	80.66	0.09	8.56	0.73**	13.13	1.42**	490.25	44.31**
HC-260 x HJ-513	74.33	-0.72	333.26	-5.99	82.66	1.36	8.28	0.50**	15.80	0.91*	483.12	36.23**
UP Chari-2 x MP Chari	85.80	0.89	306.10	14.27**	72.53	1.39	7.46	-0.02	17.00	0.78*	384.58	8.30
UP Chari-2 x HC-171	84.80	3.01**	302.20	39.68**	78.33	4.42**	8.00	0.28**	15.06	-0.40	451.57	15.12*
UP Chari-2 x UP Chari-3	85.86	1.06*	299.23	-10.24**	67.60	-1.57	8.31	0.07	15.40	0.18	398.99	-8.04
UP Chari-2 x HJ-513	86.66	1.06*	323.76	15.17**	65.66	4.24**	8.42	0.22**	15.00	-0.56*	392.59	-15.39*
SSV-84 x MP Chari	81.13	1.43**	221.26	44.37**	75.73	0.51	8.24	0.28**	16.60	0.26	443.51	15.14*
SSV-84 x HC-171	91.13	5.67**	287.00	28.69**	75.93	-2.06*	8.42	0.34**	14.86	-0.71**	470.69	17.86**
SSV-84 x UP Chari-3	83.20	0.75	281.46	18.66*	75.20	1.94*	8.38	0.34**	16.00	0.06	447.45	-11.68
SSV-84 x HJ-513	78.26	4.99**	336.80	54.40**	73.60	-0.39	9.08	0.40**	15.46	-0.21	474.48	14.40*
Pusa Chari-6 x MP Chari	88.00	0.35	315.76	5.25	76.63	-0.89	7.56	0.12	16.06	-0.16	411.32	2.04

Pusa Chari-6 x HC-171	92.33	1.79**	360.06	-0.51	83.06	2.78**	8.46	0.22**	15.66	0.09	496.32	26.87**
Pusa Chari-6 x UP Chari-3	84.00	3.54**	301.36	-6.32	76.20	0.65	7.69	0.51**	15.53	0.11	416.20	23.83**
Pusa Chari-6 x HJ-513	89.73	1.39**	328.86	1.58	73.73	2.54**	8.32	0.17*	16.00	0.24	435.90	-5.08
Pant Chari -4 x MP Chari	84.80	-0.33	305.40	-4.98	73.86	2.76**	6.99	0.28**	16.20	-0.17	366.77	31.78**
Pant Chari -4 x HC-171	85.66	2.36**	387.13	26.69**	80.73	1.34	8.26	0.20	15.46	-0.15	473.84	15.12*
Pant Chari -4 x UP Chari-3	86.66	1.65**	292.70	-14.86**	75.86	1.21	8.46	0.43**	15.86	0.09	466.17	36.87**
Pant Chari -4 x HJ-513	86.86	1.04*	320.30	-6.85	75.60	0.21	7.64	0.35**	15.53	-0.17	410.04	20.21**
HC-136 x MP Chari	96.40	0.57	309.26	20.40**	75.33	1.01	7.60	-0.15	15.40	-0.11	396.98	-6.20
HC-136 x HC-171	98.13	-0.59	312.76	26.16**	77.26	0.17	9.23	0.68**	15.66	0.12	503.15	39.80**
HC-136 x UP Chari-3	94.46	-1.25*	295.90	9.86	68.80	3.56**	8.47	-0.04	15.00	0.29	413.91	20.02**
HC-136 x HJ-513	97.80	1.27*	301.53	-4.10	75.46	2.38**	7.98	0.49**	14.33	-0.71**	421.30	13.58*
Pant Chari -7 x MP Chari	86.46	2.01**	305.43	1.48	75.66	-1.39	7.16	-0.20	15.46	-0.12	384.67	14.81*
Pant Chari -7 x HC-171	91.06	-0.31	367.56	-13.56**	79.66	-0.16	8.23	0.08	15.26	0.24	459.03	-0.62
Pant Chari -7 x UP Chari-3	89.86	1.50**	298.30	-2.82	76.06	0.98	8.54	0.42**	14.26	-0.12	454.48	24.25**
Pant Chari -7 x HJ-513	90.00	0.83	308.50	-12.22**	76.40	0.58	7.78	0.29**	15.73	0.11	422.36	-8.82
Pant Chari -3 x MP Chari	83.00	4.99**	271.73	5.45	85.53	3.09**	6.27	0.78**	16.73	0.81*	379.82	36.52**
Pant Chari -3 x HC-171	86.00	5.09**	326.70	-10.36**	85.66	0.45	8.17	0.33**	14.13	1.03**	493.80	17.29*
Pant Chari -3 x UP Chari-3	75.93	1.97**	282.20	18.75*	75.06	5.41**	7.67	-0.14	15.13	0.21	408.91	38.19**
Pant Chari -3 x HJ-513	70.60	8.11**	248.48	34.57**	83.06	1.86*	8.36	0.60**	15.26	0.01	505.47	57.43**
UP Chari-1 x MP Chari	93.73	1.88**	307.33	4.27	76.73	1.57	8.91	0.76**	16.26	1.06**	492.27	56.35**
UP Chari-1 x HC-171	98.46	-0.04	366.16	-13.05**	76.93	-1.00	8.87	-0.08	13.93	-0.11	484.70	-11.39
UP Chari-1 x UP Chari-3	95.20	-0.30	300.63	0.40	73.60	0.41	8.48	0.43**	13.80	-0.01	443.61	-23.06**
UP Chari-1 x HJ-513	98.53	2.22**	302.10	17.73*	72.93	-0.99	8.62	-0.25*	14.40	-0.14	445.72	-21.90*
Jawahar Chari-6 x MP Chari	97.93	0.37	313.50	-9.50	78.13	-0.54	8.69	0.33**	12.40	0.89*	492.38	21.20**
Jawahar Chari-6 x HC-171	95.	5.19**	389.16	16.11*	80.66	-0.78	9.10	-0.05	12.60	0.07	518.22	13.14*
Jawahar Chari-6 x UP Chari-3	100.33	2.88**	309.03	-11.14	77.80	1.09	8.66	0.47**	12.46	0.18	485.07	16.86*
Jawahar Chari-6 x HJ-513	100.20	1.94**	344.30	14.53**	77.66	6.23**	9.28	0.70**	13.26	1.64**	511.69	18.81**

Line x Tester (Crosses)	Stem girth (mm)		Leaf stem ratio		Total soluble solids (%)		Protein content (%)		Green fodder yield per plant (g)	
	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
UP Chari 4 x MP Chari	19.87	1.72*	0.39	0.12*	10.36	-0.25**	8.48	0.08	514.66	19.68
UP Chari 4 x HC-171	20.39	3.13**	0.36	0.14**	10.53	0.07	9.35	0.07	586.00	78.60**
UP Chari 4 x UP Chari-3	15.89	3.67**	0.43	0.14**	10.24	-0.11	8.08	0.09	349.20	26.74*
UP Chari 4 x HJ-513	23.18	1.82**	0.38	0.18**	10.26	0.18	8.36	-0.05	390.20	95.02**
G-48 x MP Chari	22.45	2.23**	0.41	0.01	10.33	0.55**	8.36	0.07	581.86	7.41
G-48 x HC-171	21.54	-0.79	0.37	-0.01	9.86	0.14	9.16	-0.02	586.26	9.39
G-48 x UP Chari-3	20.48	-1.16	0.38	0.01	9.67	0.15	7.83	-0.05	340.90	51.03**
G-48 x HJ-513	23.14	-0.28	0.33	-0.01	8.21	0.94**	8.51	0.03	608.93	24.24*
HC-260 x MP Chari	18.58	-0.22	0.40	-0.01	10.74	0.50*	7.24	0.43*	583.56	-2.62
HC-260 x HC-171	21.08	0.17	0.39	0.01	11.22	0.14	8.92	0.37*	579.56	-9.04
HC-260 x UP Chari-3	20.78	0.56	0.39	0.01	10.90	-0.08	7.28	0.03	463.56	49.91**
HC-260 x HJ-513	21.49	-0.51	0.34	0.01	11.05	0.44*	7.90	0.03	578.16	28.25*
UP Chari-2 x MP Chari	21.56	1.58*	0.40	-0.02	10.60	-0.18	9.41	0.57**	582.96	0.04
UP Chari-2 x HC-171	21.07	-1.01	0.38	-0.02	10.86	0.13	9.30	-0.41*	589.96	-5.38
UP Chari-2 x UP Chari-3	21.23	-0.16	0.36	0.13*	10.64	0.01	8.47	0.05	412.76	2.37
UP Chari-2 x HJ-513	22.76	-0.41	0.43	0.17**	10.40	0.14	8.84	-0.11	606.13	2.97
SSV-84 x MP Chari	15.61	3.73**	0.40	0.02	10.22	0.16	8.34	0.11	586.83	46.80**
SSV-84 x HC-171	22.09	0.64	0.39	0.01	9.78	-0.13	8.93	-0.07	595.53	50.52**
SSV-84 x UP Chari-3	21.84	1.09	0.37	-0.01	9.76	-0.04	7.72	0.01	538.53	77.42**
SSV-84 x HJ-513	24.54	2.00**	0.33	-0.01	9.44	0.01	8.19	-0.15	673.76	1.90
Pusa Chari-6 x MP Chari	19.91	1.86*	0.41	0.01	10.27	0.16	8.33	0.11	589.60	-8.01
Pusa Chari-6 x HC-171	20.52	0.37	0.39	0.02	10.25	0.19	8.42	0.57**	588.43	-21.60**

Pusa Chari-6 x UP Chari-3	20.61	1.15	0.38	0.01	9.76	-0.09	7.87	0.17	394.36	30.72*
Pusa Chari-6 x HJ-513	17.88	3.37**	0.34	-0.01	9.11	-0.17	8.51	0.18	678.17	60.33**
Pant Chari -4 x MP Chari	20.10	1.16*	0.40	-0.03	10.22	-0.09	8.50	-0.30*	582.30	4.98
Pant Chari -4 x HC-171	20.45	-0.59	0.41	0.02	10.08	-0.08	9.12	0.56**	592.50	2.76
Pant Chari -4 x UP Chari-3	19.97	-0.37	0.39	-0.01	9.98	-0.07	8.94	0.56**	399.57	-5.22
Pant Chari -4 x HJ-513	21.93	-0.20	0.40	0.14**	9.93	0.15	9.32	0.11	595.04	-2.52
HC-136 x MP Chari	18.00	-1.13	0.41	0.01	10.10	-0.10	7.35	0.64**	591.46	-10.28
HC-136 x HC-171	21.65	0.41	0.39	-0.01	9.97	-0.18	9.18	0.11	602.96	-11.20
HC-136 x UP Chari-3	21.01	0.46	0.39	0.01	10.97	0.73**	7.58	0.01	407.53	-21.68**
HC-136 x HJ-513	22.60	0.26	0.35	0.02	9.92	0.05	8.52	0.12	665.13	43.16**
Pant Chari -7 x MP Chari	22.20	2.51**	0.41	0.02	10.39	0.11	7.34	0.38**	613.60	44.30**
Pant Chari -7 x HC-171	21.10	-0.70	0.33	0.17**	10.12	-0.01	8.80	0.10	635.20	35.12*
Pant Chari -7 x UP Chari-3	19.39	1.72*	0.41	0.03	10.05	0.03	7.30	-0.01	585.93	10.00
Pant Chari -7 x HJ-513	22.80	-0.09	0.39	0.14**	9.53	-0.12	8.14	0.10	657.00	-21.14**
Pant Chari -3 x MP Chari	16.28	2.48**	0.47	-0.02	10.50	0.18	8.30	0.08	635.40	23.20*
Pant Chari -3 x HC-171	21.58	0.72	0.46	0.01	10.01	0.55**	9.26	0.16	643.00	8.38
Pant Chari -3 x UP Chari-3	21.02	0.84	0.43	0.13*	9.96	-0.09	7.60	-0.10	357.33	82.34**
Pant Chari -3 x HJ-513	22.88	0.91	0.47	0.15**	9.74	0.06	8.38	-0.05	673.20	40.76**
UP Chari-1 x MP Chari	16.47	-0.48	0.62	0.15**	10.34	0.41**	9.66	0.85**	583.80	50.38**
UP Chari-1 x HC-171	21.18	2.13**	0.63	0.17**	9.90	-0.10	9.66	-0.02	585.26	39.43*
UP Chari-1 x UP Chari-3	20.31	1.95*	0.55	0.01	10.17	0.08	7.81	0.58**	348.20	-2.69
UP Chari-1 x HJ-513	16.55	3.60**	0.40	0.12**	9.95	0.13	8.78	-0.14	476.53	77.12**
Jawahar Chari-6 x MP Chari	13.92	3.02**	0.54	0.13*	10.45	0.17	7.36	0.31*	582.46	-3.68
Jawahar Chari-6 x HC-171	17.55	-1.49*	0.55	0.16**	10.13	0.10	9.08	0.54**	592.86	-5.70
Jawahar Chari-6 x UP Chari-3	19.38	1.03	0.46	-0.12*	9.29	0.53*	7.17	-0.08	360.33	53.29**
Jawahar Chari-6 x HJ-513	23.61	3.47**	0.38	0.16**	9.42	-0.04	7.74	-0.14	669.06	62.68**

Chari-1 x HC-171 (39.43), UP Chari-1 x HJ-513 (77.12), Jawahar Chari-6 x UP Chari-3 (53.29) and Jawahar Chari-6 x HJ-513 (62.68) noted significant and positive specific combining ability effects which proved as best specific combiners for high green fodder yield per plant and hybrids *i.e.*, Pusa Chari-6 x HC-171 (-21.60), HC-136 x UP Chari-3 (-21.68) and Pant Chari-7 x HJ-513 (-21.14) exhibited significant negative specific combining ability effects, which indicated that poor performance for green fodder yield per plant.

Estimation of nature and magnitude of heterosis

In the present investigation the extent of heterosis was expressed as hybrid vigour at phenotypic level in terms of percentage increase or decrease over betterparent (BP) and mid parent (relative heterosis) in respect of all the attributes under study and presented in Table-9. A brief account of result on this aspect is described, trait wise, as under.

Days to 50% flowering

Heterobeltiosis

Heterosis over better parent for days to 50% flowering was estimated over late flowering parent of the F₁'s hybrids. Hence crosses with positive heterosis were considered as desirable. Manifestation of heterosis was found in both positive and negative directions. The extent of heterosis over better parent ranged from -23.54 (Pant Chari 3 x HJ-513) to 19.59 (HC-260 x UP Chari-3). Nineteen cross combinations *i.e.* G-48 x MP Chari (3.59), G-48 x HC-171 (4.62), HC-260 x MP Chari (11.43), HC-260 x HC-171 (4.59), HC-260 x UP Chari-3 (19.59), HC-260 x HJ-513 (19.49), SSV-84 x HC-171 (18.84), Pusa Chari-6 x HC-171 (5.89), HC-136 x MP Chari (6.56), HC-136 x HC-171 (12.36), HC-136 x HJ-513 (4.02), Pant Chari-7 x HC-171 (3.41), Pant Chari-7 x UP Chari-3 (1.97), UP Chari-1 x MP Chari (6.82), UP Chari-1 x HC-171 (13.14), UP Chari-1 x HJ-513 (3.21), Jawahar Chari-6 x HC-171 (10.45), Jawahar Chari-6 x UP Chari-3 (3.79) and Jawahar Chari-6 x HJ-513 (3.66) showed positive significant heterosis over better parent for late flowering. Crosses namely, UP Chari-4 x MP Chari (-4.05), UP Chari-4 x UP Chari-3 (-2.50), UP Chari-4 x

HJ-513 (-5.05), UP Chari-2 x HJ-513 (-6.14), SSV-84 x UP Chari-3 (-5.60), SSV-84 x HJ-513 (-15.23), Pusa Chari-6 x UP Chari-3 (-4.69), Pant Chari-3 x UP Chari-3 (-13.84) and Pant Chari -3 x HJ-513 (-23.54) revealed negative significant heterosis over better parent for early flowering.

Relative heterosis

Relative heterosis varied from -14.91 (Pant Chari-3 x HJ-513) to 14.15 (SSV-84 x HC 171). Nineteen cross combinations possessed positive superiority over their mid parental values of hybrids i.e. G-48 x MP Chari (3.77), G-48 x HC-171 (4.04), HC-260 x MP Chari (5.86), HC-260 x HC-171 (5.15), HC-260 x UP Chari-3 (12.04), HC-260 x HJ-513 (10.08), SSV-84 x HC-171 (14.15), Pusa Chari-6 x HC-171 (8.03), HC-136 x MP Chari (7.91), HC-136 x HC-171 (9.28), HC-136 x HJ-513 (3.93), Pant Chari-7 x HC-171 (6.01), Pant Chari-7 x UP Chari-3 (2.01), UP Chari-1 x MP Chari (5.16), UP Chari-1 x HC-171 (9.90), UP Chari-1 x HJ-513 (4.93), Jawahar Chari-6 x HC-171 (10.62), Jawahar Chari-6 x UP Chari-3 (8.59) and Jawahar Chari-6 x HJ-513 (6.03) for late flowering. The crosses viz., UP Chari-4 x MP Chari (-1.57), UP Chari-4 x UP Chari-3 (-2.98), UP Chari-4 x HJ-513 (-2.34), UP Chari-2 x HJ-513 (-2.29), SSV-84 x HJ-513 (-6.97), Pusa Chari-6 x UP Chari-3 (-4.18), Pant Chari-3 x UP Chari-3 (-6.10) and Pant Chari-3 x HJ-513 (-14.91) expressed negative significant heterosis over mid parent for early flowering.

Plant height

Heterobeltiosis

The positive heterosis over better parent estimates was considered desirable for plant height. The heterosis for this attribute ranged from -34.26 (SSV-84 x MP Chari) to 24.90 (Pant Chari-3 x HJ-513). Out of forty eight crosses, only twelve F₁'s hybrids namely, UP Chari-4 x HC-171 (11.71), G-48 x MP Chari (15.68), G-48 x HC-171 (14.22), G-48 x HJ-513 (10.92), HC-260 x HC-171 (10.72), SSV-84 x UP Chari-3 (11.76), SSV-84 x HJ-513 (11.79), Pant Chari-4 x HC-171, Pant Cari-3 x MP Chari (19.27), Pant Chari-3 x HC-171 (15.07), Pant Chari-3 x HJ-513 (24.90) and Jawahar Chari-6 x HC-171 (11.17) noted significant and positive heterosis over better parent as considered for tall plant height. Crosses viz., UP Chari-2 x HC-171 (-21.44), SSV-84 x MP Chari (-

34.26), SSV-84 x HC-171 (-25.39), HC-136 x HC-171 (-18.69) and Jawahar Chari-6 x MP Chari (-11.86) recorded significant and negative heterosis over better parent and considered for dwarf plant height.

Relative heterosis

Heterosis over mid parent varied from -23.36 (SSV-84 x HC-171) to 24.71 (SSV-84 x HJ-513). The cross combinations namely, UP Chari-4 x HC-171 (14.45), G-48 x MP Chari (17.90), G-48 x HC-171 (13.68), G-48 x HJ-513(12.52), HC-260 x HC-171 (8.87), SSV-84 x UP Chari-3 (15.86), SSV-84 x HJ-513 (24.71), Pant Chari-4 x HC-171 (13.64), HC-136 x HC-171 (17.71), Pant Chari-3 x MP Chari (17.32), Pant Chari-3 x HC-171 (12.98) and Jawahar Chari-6 x HC-171 (11.87) showed significant and positive heterosis over mid parent for tall plant height and hybrids *i.e.* UP Chari-2 x HC-171 (-11.16), SSV-84 x MP Chari (-18.93), SSV-84 x HC-171 (23.36) and Pant Chari-3 x HJ-513 (-14.42) observed significant negative heterosis over mid parent for dwarf plant height.

Number of leaves per plant

Heterobeltiosis

Heterobeltiosis for the character number of leaves per plant ranged from -19.48 (Jawahar Chari-6 x MP Chari) to 32.75 (Pant Chari-3 x HC-171). Among all the 48 F₁'s, twelve crosses *viz.*, UP Chari-4 x HC-171 (16.28), UP Chari-4 x UP Chari-3 (17.51), G-48 x MP Chari (11.73), HC-260 x UP Chari-3 (20.88), UP Chari-2 x MP Chari (18.97), SSV-84 x UP Chari-3 (13.00), Pusa Chari-6 x HJ-513 (18.11), Pant Chari-4 x UP Chari-3 (17.21), Pant Chari-3 x MP Chari (18.66), Pant Chari-3 x HC-171 (32.75), Pant Chari-3 x HJ-513 (25.05) and Jawahar Chari-6 x HC-171 (12.09) were found significant positive heterosis over better parent for more number of leaves per plant. The crosses namely, UP Chari-4 x HJ-513 (-7.87), HC136 x HC-171 (-19.30) and Jawahar Chari-6 x MP Chari (-19.48) recorded negative and significant heterosis over better parent for this attribute.

Relative heterosis

The mid parent heterosis varied from -19.56 (HC-136 x HC-171) to 25.53 (Pant Chari-3 x HJ-513). Cross combinations *i.e.*, UP Chari-4 x HC-171 (16.82), UP Chari-4 x UP Chari-3 (10.36), G-48 x MP Chari (10.46), HC-260 x UP Chari-3 (12.64), UP Chari-2 x MP Chari (19.68), SSV-84 x UP Chari-3 (10.34), Pusa Chari-6 x HJ-513 (19.59), Pant Chari-4 x UP Chari-3 (12.26), Pant Chari-3 x MP Chari (11.80), Pant Chari-3 x HC-171 (22.08), Pant Chari-3 x HJ-513 (25.53) and Jawahar Chari-6 x HC-171 (12.70) had desirable positive significant heterosis over mid parent for more number of leaves per plant. F_1 's hybrids namely, UP Chari-4 x HJ-513 (-8.62), HC-136 x HC-171 (-19.56) and Jawahar Chari-6 x MP Chari (-13.49) estimated significant and negative heterosis over mid parent for this character.

Stem girth

Heterobeltiosis

The extent of heterosis over better parent for stem girth ranged from -15.91 (SSV-84 x MP Chari) to 28.48 (Jawahar Chari-6 x HJ-513). The twenty six crosses *viz.*, UP Chari-4 x MP Chari (17.04), UP Chari-4 x HC-171 (16.88), UP Chari-4 x HJ-513 (16.49), G-48 x MP Chari (14.79), G-48 x HC-171 (10.12), HC-260 x HC-171 (10.48), HC-260 x UP Chari-3 (15.10), UP Chari-2 x MP Chari (16.12), UP Chari-2 x HC-171 (10.45), UP Chari-2 x UP Chari-3 (17.61), SSV-84 x HC-171 (15.79), SSV-84 x UP Chari-3 (21.01), SSV-84 x HJ-513 (12.77), Pusa Chari-6 x HC-171 (17.58), Pusa Chari-6 x UP Chari-3 (14.18), Pant Chari-4 x UP Chari-3 (10.64), HC-136 x HC-171 (13.49), HC-136 x UP Chari-3 (16.40), Pant Chari-3 x MP Chari (12.28), Pant Chari-3 x HC-171 (13.14), Pant Chari-3 x UP Chari-3 (13.42), UP Chari-1 x HC-171 (11.01), UP Chari-1 x UP Chari-3 (10.08), UP Chari-1 x HJ-513 (23.95), Jawahar Chari-6 x MP Chari (25.03) and Jawahar Chari-6 x HJ-513 (28.48) possessed positive and significant heterosis over better parent and out of 48 F_1 's hybrids, only three cross combinations namely, UP Chari-4 x UP Chari-3 (-11.96), SSV-84 x MP Chari (-15.91) and UP Chari-1 x MP Chari (-11.29) exhibited negative significant heterosis over better parent for stem girth.

Relative heterosis

Relative heterosis values varied from -13.18 (SSV-84 x MP Chari) to 25.34 (SSV-84 x HJ-513). The Twenty six hybrids *i.e.*, UP Chari-4 x MP Chari (10.47), UP Chari-4 x HC-171 (11.76), UP Chari-4 x HJ-513 (18.33), G-48 x MP Chari (17.78), G-48 x HC-171 (11.49), HC-260 x HC-171 (15.93), HC-260 x UP Chari-3 (17.60), UP Chari-2 x MP Chari (18.83), UP Chari-2 x HC-171 (14.53), UP Chari-2 x UP Chari-3 (18.71), SSV-84 x HC-171 (21.13), SSV-84 x UP Chari-3 (23.24), SSV-84 x HJ-513 (25.34), Pusa Chari-6 x HC-171 (13.78), Pusa Chari-6 x UP Chari-3 (17.61), Pant Chari-4 x UP Chari-3 (10.78), HC-136 x HC-171 (17.45), HC-136 x UP Chari-3 (17.24), Pant Chari-3 x MP Chari (12.20), Pant Chari-3 x HC-171 (14.78), Pant Chari-3 x UP Chari-3 (14.91), UP Chari-1 x HC-171 (12.86), UP Chari-1 x UP Chari-3 (11.29), UP Chari-1 x HJ-513 (17.69), Jawahar Chari-6 x MP Chari (19.40) and Jawahar Chari-6 x HJ-513 (25.14) showed positive significant superiority over relative heterosis for this character. Three crosses namely, UP Chari-4 x UP Chari-3 (-11.96), SSV-84 x MP Chari (-13.18) and UP Chari-1 x MP Chari (-11.02) had negative and significant heterosis over mid parent for this attribute.

Leaf length

Heterobeltiosis

Heterobeltiosis for this attribute ranged from -10.06 (Pant Chari-3 x UP Chari-3) to 23.46 (Jawahar Chari-6 x UP Chari-3). Significant and positive heterosis over better parent was appeared by hybrids *viz.*, UP Chari-4 x MP Chari (4.22), G-48 x MP Chari (9.29), G-48 x UP Chari-3 (5.22), G-48 x HJ-513 (6.27), HC-260 x HJ-513 (8.31), UP Chari-2 x HC-171 (8.17), Pusa Chari-6 x HC-171 (9.22), Pant Chari -4 x HC-171 (8.24), Pant Chari-4 x HJ-513 (9.49), HC-136 x HJ-513 (8.39), Pant Chari-3 x MP Chari (9.48), Pant Chari-3 x HJ-513 (13.48), UP Chari-1 x MP Chari (13.88), Jawahar Chari-6 x MP Chari (18.90), Jawahar Chari-6 x HC-171 (13.15) and Jawahar Chari-6 x UP Chari-3 (23.46) for longer leaf length. Cross combinations *i.e.* UP Chari-2 x UP Chari-3 (-9.22), UP Chari-2 x HJ-513 (-9.28), HC-136 x UP Chari-3 (-8.61) and Pant Chari-3 x UP Chari-3 (-10.06) expressed negative significant heterosis over better parent.

Relative heterosis

Heterosis over mid parent varied from -14.94 (Pant Chari-3 x UP Chari-3) to 18.21 (Pant Chari-3 x HJ-513). The crosses namely, UP Chari-4 x MP Chari (4.27), G-48 x MP Chari (8.34), G-48 x UP Chari-3 (5.54), G-48 x HJ-513 (7.13), HC-260 x HJ-513 (9.01), UP Chari-2 x HC-171 (7.95), Pusa Chari-6 x HC-171 (8.63), Pant Chari -4 x HC-171 (7.74), Pant Chari-4 x HJ-513 (8.68), HC-136 x HJ-513 (7.04), Pant Chari-3 x MP Chari (9.56), Pant Chari-3 x HJ-513 (18.21), UP Chari-1 x MP Chari (14.73), Jawahar Chari-6 x MP Chari (15.68), Jawahar Chari-6 x HC-171 (15.17) and Jawahar Chari-6 x UP Chari-3 (13.96) emerged desirable positive and significant heterosis over mid parent and out of 48 F₁'s hybrids, only four hybrids viz., UP Chari-2 x UP Chari-3 (-8.38), UP Chari-2 x HJ-513 (-7.14), HC-136 x UP Chari-3 (-8.36) and Pant Chari-3 x UP Chari-3 (-14.94) noted negative significant heterosis over mid parent for leaf length.

Leaf breadth

Heterobeltiosis

Heterosis response over better parent for leaf breadth ranged from -16.43 (HC-260 x HC-171) to 23.57 (UP Chari-2 x UP Chari-3). Maximum positive and significant heterosis was recorded over better parent in the cross combinations *i.e.* UP Chari-4 x MP Chari (4.45), UP Chari-4 x HC-171 (16.39), UP Chari-4 x UP Chari-3 (10.38), G-48 x HC-171 (10.82), HC-260 x UP Chari-3 (16.64), UP Chari-2 x UP Chari-3 (23.57), SSV-84 x MP Chari (18.89), SSV-84 x HC-171 (14.81), SSV-84 x HJ-513 (20.91), Pant Chari-4 x UP Chari-3 (9.98), HC-136 x HC-171 (14.18), Pant Chari-7 x UP Chari-3 (16.40), UP Chari-1 x MP Chari (10.95), UP Chari-1 x HC-171 (10.86), Jawahar Chari-6 x MP Chari (17.24), Jawahar Chari-6 x HC-171 (12.36) and Jawahar Chari-6 x HJ-513 (16.36) indicated maximum heterosis in order to merit for more leaf breadth. Minimum heterosis namely, HC-260 x MP Chari (-15.49), HC-260 x HC-171 (-16.43), Pusa Chari-6 x UP Chari-3 (-4.15) and Pant Chari-3 x MP Chari (-11.81) was revealed significant negative over better parent in these hybrids.

Relative heterosis

Relative heterosis values varied from -13.04 (HC-260 x HC-171) to 20.45 (UP Chari-1 x MP Chari). Hybrids viz., UP Chari-4 x MP Chari (6.56), UP Chari-4 x HC-171 (13.35), UP Chari-4 x UP Chari-3 (17.56), G-48 x HC-171 (9.69), HC-260 x UP Chari-3 (10.93), UP Chari-2 x UP Chari-3 (18.06), SSV-84 x MP Chari (15.02), SSV-84 x HC-171 (17.90), SSV-84 x HJ-513 (15.23), Pant Chari-4 x UP Chari-3 (9.48), HC-136 x HC-171 (14.56), Pant Chari-7 x UP Chari-3 (10.53), UP Chari-1 x MP Chari (20.45), UP Chari-1 x HC-171 (10.46), Jawahar Chari-6 x MP Chari (16.90), Jawahar Chari-6 x HC-171 (12.85) and Jawahar Chari-6 x HJ-513 (13.91) showed significant and positive heterosis over the relative heterosis whereas the crosses namely, HC-260 x MP Chari (-11.22), HC-260 x HC-171 (-13.04) and Pant Chari-3 x MP Chari (-9.61) exhibited significant negative heterosis over mid parent for leaf breadth.

Total soluble solids

Heterobeltiosis

Heterobeltiosis for total soluble solids ranged from -23.05 (G-48 x HJ-513) to 34.94 (Jawahar Chari-6 x HC-171). Highly significant and positive heterosis values over better parent were recorded in seventeen F₁ hybrids viz., UP Chari-4 x MP Chari (8.74), UP Chari-4 x HC-171 (10.49), G-48 x MP Chari (28.54), G-48 x HC-171 (11.95), G-48 x UP Chari-3 (17.70), UP Chari-2 x MP Chari (19.27), UP Chari-2 x HC-171 (11.95), SSV-84 x HC-171 (11.04), Pusa Chari-6 x HC-171 (16.34), Pant Chari -4 x MP Chari (17.42), Pant Chari-4 x HC-171 (14.37), HC-136 x MP Chari (16.16), Pant Chari-3 x MP Chari (10.29), Jawahar Chari-6 x MP Chari (29.80), Jawahar Chari-6 x HC-171 (34.94), Jawahar Chari-6 x UP Chari-3 (11.29) and Jawahar Chari-6 x HJ-513 (19.74) for total soluble solids and cross combinations namely, G-48 x HJ-513 (-23.05) and Pant Chari-3 x HC-171 (-13.62) reported significant and negative heterosis over better parent for this trait.

Relative heterosis

Heterosis over the mid parental values varied from -16.98 (G-48 x HJ-513) to 30.35 (Jawahar Chari-6 x HC-171). Crosses *i.e.* UP Chari-4 x MP Chari (8.82), UP Chari-4 x HC-171 (14.83), G-48 x MP Chari (25.20), G-48 x HC-171 (24.89), G-48 x UP Chari-3 (10.76), UP Chari-2 x MP Chari (10.33), UP Chari-2 x HC-171 (17.35), SSV-84 x HC-171 (16.79), Pusa Chari-6 x HC-171 (23.04), Pant Chari -4 x MP Chari (14.99), Pant Chari-4 x HC-171 (18.03)), HC-136 x MP Chari (10.50), Pant Chari-3 x MP Chari (17.06), Jawahar Chari-6 x MP Chari (28.66), Jawahar Chari-6 x HC-171 (30.35), Jawahar Chari-6 x UP Chari-3 (18.04) and Jawahar Chari-6 x HJ-513 (18.26) exhibited significant and positive heterosis over mid parent for this character whereas the cross combinations namely, G-48 x HJ-513 (-16.98) and Pant Chari-3 x HC-171 (-16.21) showed significant negative relative heterosis for total soluble solids.

Leaf area

Heterobeltiosis

The twenty one F_1 's hybrids possessed significant positive heterosis over better parent for leaf area. The highest positive and significant heterosis over better parent was recorded in the crosses *viz.*, UP Chari-4 x HC-171 (29.86), UP Chari-4 x UP Chari-3 (11.97), G-48 x MP Chari (11.13), HC-260 x UP Chari-3 (14.26), HC-260 x HJ-513 (12.60), UP Chari-2 x MP Chari (19.95), UP Chari-2 x HC-171 (12.01), SSV-84 x MP Chari (12.05), SSV-84 x HC-171 (16.33), SSV-84 x HJ-513 (15.58), Pusa Chari-6 x HC-171 (12.12), Pant Chari-4 x HC-171 (17.04), Pant Chari-4 x UP Chari-3 (19.86), HC-136 x HC-171 (13.66), Pant Chari-7 x UP Chari-3 (17.10), Pant Chari-3 x HJ-513 (19.90), UP Chari-1 x MP Chari (16.84), Jawahar Chari-6 x MP Chari (23.75), Jawahar Chari-6 x HC-171 (19.06), Jawahar Chari-6 x UP Chari-3 (12.06) and Jawahar Chari-6 x HJ-513 (28.21) for leaf area. The crosses namely, Pant Chari-3 x HC-171 (-11.55) and UP Chari-1 x HC-171 (-14.49) emerged negative and significant heterosis over better parent for leaf area.

Relative heterosis

Cross combinations *i.e.* UP Chari-4 x HC-171 (20.69), UP Chari-4 x UP Chari-3 (20.65), G-48 x MP Chari (13.25), HC-260 x UP Chari-3 (14.89), HC-260 x HJ-513 (15.08), UP Chari-2 x MP Chari (10.06), UP Chari-2 x HC-171 (13.97), SSV-84 x MP Chari (19.08), SSV-84 x HC-171 (12.27), SSV-84 x HJ-513 (17.68), Pusa Chari-6 x HC-171 (14.28), Pant Chari-4 x HC-171 (15.39), Pant Chari-4 x UP Chari-3 (16.12), HC-136 x HC-171 (16.56), Pant Chari-7 x UP Chari-3 (10.88), Pant Chari-3 x HC-171 (21.49), Pant Chari-3 x HJ-513 (21.49), UP Chari-1 x MP Chari (27.80), Jawahar Char-6 x MP Chari (25.94), Jawahar Chari-6 x HC-171 (18.37), Jawahar Chari x UP Chari (13.17) and Jawahar Chari-6 x HJ-513 (21.34) revealed positive significant heterosis over mid parent whereas hybrids namely, Pant Chari x HC 171 (14.27) and UP Chari-1 x HC-171 (12.20) observed significant negative relative heterosis for this attribute.

Leaf stem ratio

Heterobeltiosis

The extent of heterosis over better parent for this attribute ranged from -16.30 (G-48 x HJ-513) to 47.57 (UP Chari-1 x HC-171). The crosses viz., UP Chari-4 x MP Chari (14.42), UP Chari-4 x HC-171 (21.84), UP Chari-4 x UP Chari-3 (13.91), G-48 x MP Chari (19.62), G-48 x HC-171 (22.48), HC-260 x MP Chari (14.86), HC-260 x HC-171 (21.81), UP Chari-2 x MP Chari (16.92), UP Chari-2 x HC-171 (26.09), SSV-84 x MP Chari (13.77), SSV-84 x HC-171 (31.70), Pusa Chari-6 x MP Chari (20.96), Pusa Chari-6 x HC-171 (22.89), Pant Chari-4 x HC-171 (32.55), HC-136 x HC-171 (28.52), Pant Chari-7 x UP Chari-3 (18.87), Pant Chari-3 x HC-171 (29.15), Pant Chari-3 x HJ-513 (19.46), UP Chari-1 x MP Chari (36.67), UP Chari-1 x HC-171 (47.57), UP Chari-1 x UP Chari-3 (15.31), Jawahar Chari-6 x HC-171 (39.34) and Jawahar Chari-6 x HJ-513 (23.55) showed significant and positive heterosis over better parent. Cross combinations namely, G-48 x HJ-513 (-16.30), SSV-84 x HJ-513 (-15.63) and HC-136 x MP Chari (-15.56) had significant negative heterosis over better parent for leaf stem ratio.

Relative heterosis

Heterosis values varied from -17.74 (HC-136 x MP Chari) to 43.70 (UP Chari-1 x HC-171). F_1 's hybrids *i.e.*, UP Chari-4 x MP Chari (15.53), UP Chari-4 x HC-171 (21.79), UP Chari-4 x UP Chari-3 (20.74), G-48 x MP Chari (21.37), G-48 x HC-171 (20.21), HC-260 x MP Chari (15.41), HC-260 x HC-171 (21.66), UP Chari-2 x MP Chari (24.08), UP Chari-2 x HC-171 (28.89), SSV-84 x MP Chari (14.86), SSV-84 x HC-171 (22.06), Pusa Chari-6 x MP Chari (20.17), Pusa Chari-6 x HC-171 (21.86), Pant Chari-4 x HC-171 (25.05), HC-136 x HC-171 (19.59), Pant Chari-7 x UP Chari-3 (17.01), Pant Chari-3 x HC-171 (29.77), Pant Chari-3 x HJ-513 (13.87), UP Chari-1 x MP Chari (34.38), UP Chari-1 x HC-171 (43.70), UP Chari-1 x UP Chari-3 (14.79), Jawahar Chari-6 x HC-171 (38.50) and Jawahar Chari-6 x HJ-513 (14.24) noted significant positive heterosis over mid parent for this trait whereas out of 48 crosses, only 3 crosses namely, G-48 x HJ-513 (-11.45), SSV-84 x HJ-513 (-10.76) and HC-136 x MP Chari (-17.74) recorded significant negative relative heterosis for leaf stem ratio.

Protein content

Heterobeltiosis

Out of forty eight cross combinations, only seventeen hybrids *viz.*, G-48 x HC-171 (9.76), HC-260 x MP Chari (9.37), UP Chari-2 x MP Chari (18.32), UP Chari-2 x HC-171 (9.10), SSV-84 x MP Chari (14.14), SSV-84 x HC-171 (14.12), Pusa Chari-6 x MP Chari (22.01), Pant Chari-4 x MP Chari (14.59), Pant Chari-4 x HC-171 (19.29), Pant Chari-4 x UP Chari-3 (10.09), Pant Chari-4 x HJ-513 (17.79), HC-136 x HC-171 (17.07), Pant Chari-7 x MP Chari (19.65), Pant Chari-3 x HC-171 (17.93), UP Chari-1 x MP Chari (16.07), Jawahar Chari-6 x MP Chari (12.87) and Jawahar Chari-6 x HC-171 (25.91) were found significant and positive heterosis over better parent for high protein content while two crosses G-48 x MP Chari (-12.78) and UP Chari-1 x UP Chari-3 (-14.26) expressed significant and negative heterosis over better parent for low protein content.

Relative heterosis

F₁'s hybrids *i.e.*, G-48 x HC-171 (9.57), HC-260 x MP Chari (8.60), UP Chari-2 x MP Chari (13.72), UP Chari-2 x HC-171 (9.78), SSV-84 x MP Chari (10.58), SSV-84 x HC-171 (12.46), Pusa Chari-6 x MP Chari (19.39), Pant Chari-4 x MP Chari (16.01), Pant Chari-4 x HC-171 (19.18), Pant Chari-4 x UP Chari-3 (15.54), Pant Chari-4 x HJ-513 (11.13), HC-136 x HC-171 (12.40), Pant Chari-7 x MP Chari (11.09), Pant Chari-3 x HC-171 (13.99), UP Chari-1 x MP Chari (13.61), Jawahar Chari-6 x MP Chari (12.99) and Jawahar Chari-6 x HC-171 (20.41) showed significant and positive heterosis over mid parent for high protein content. The two cross combinations G-48 x MP Chari (-14.09) and UP Chari-1 x UP Chari-3 (-15.14) estimated significant and negative heterosis over mid parent for low protein content.

Green fodder yield per plant

Heterobeltiosis

Expression of heterosis over better parent for green fodder yield per plant values ranged from -17.43 (UP Chari-2 x UP Chari-3) to 41.53 (Jawahar Chari-6 x HC-171). The maximum magnitude of heterosis and *per se* performance was observed positive and significant over better parent by the F₁'s hybrids *viz.*, UP Chari-4 x MP Chari (12.91), UP Chari-4 x HC-171 (30.35), UP Chari-4 x HJ-513 (26.09), G-48 x MP Chari (30.72), G-48 x HC-171 (30.40), G-48 x HJ-513 (20.75), HC-260 x UP Chari-3 (19.20), SSV-84 x UP Chari-3 (24.47), Pusa Chari-6 x MP Chari (32.06), Pusa Chari-6 x HJ-513 (32.83), Pant Chari-4 x HC-171 (31.47), Pant Chari-4 x HJ-513 (14.74), HC-136 x UP Chari-3 (22.96), Pant Chari-7 x UP Chari-3 (26.34), Pant Chari-3 x MP Chari (29.99), Pant Chari-3 x HC-171 (34.12), Pant Chari-3 x HJ-513 (23.54), UP Chari-1 x MP Chari (23.06), UP Chari-1 x HC-171 (20.23), Jawahar Chari-6 x HC-171 (41.53), Jawahar Chari-6 x UP Chari-3 (22.35) and Jawahar Chari-6 x HJ-513 (29.13). Out of forty eight cross combinations, only four crosses namely, UP Chari-2 x UP Chari-3 (-17.43), Pant Chari-4 x UP Chari-3 (-14.72), Pant Chari-7 x HJ-513 (-15.86) and UP Chari-1 x HJ-513 (11.72) exhibited significant and negative relative heterosis for green fodder yield per plant.

Relative heterosis

Heterosis over the mid parental values varied from -13.34 (Pant Chari-4 x UP Chari-3) to 33.70 (Pant Chari-3 x HC-171). F_1 's hybrids *i.e.* UP Chari-4 x MP Chari (10.79), UP Chari-4 x HC-171 (25.30), UP Chari-4 x HJ-513 (25.63), G-48 x MP Chari (29.81), G-48 x HC-171 (29.89), G-48 x HJ-513 (19.79), HC-260 x UP Chari-3 (16.64), SSV-84 x UP Chari-3 (25.69), Pusa Chari-6 x MP Chari (25.37), Pusa Chari-6 x HJ-513 (27.86), Pant Chari -4 x HC-171 (22.59), Pant Chari-4 x HJ-513 (10.02), HC-136 x UP Chari-3 (16.35), Pant Chari-7 x UP Chari-3 (21.19), Pant Chari-3 x MP Chari (32.98), Pant Chari-3 x HC-171 (33.70), Pant Chari-3 x HJ-513 (22.15), UP Chari-1 x MP Chari (22.65), UP Chari-1 x HC-171 (22.16), Jawahar Chari-6 x HC-171 (32.19), Jawahar Chari-6 x UP Chari-3 (17.55) and Jawahar Chari-6 x HJ-513 (28.74) expressed significant and positive heterosis over mid parent for green fodder yield per plant. The crosses *viz.*, UP Chari-2 x UP Chari-3 (-10.30), Pant Chari-4 x UP Chari-3 (-13.34), Pant Chari-7 x HJ-513 (-10.72) and UP Chari-1 x HJ-513 (-11.72) recorded significant and negative heterosis over mid parent for this attribute.

Table: 9 Estimates of heterosis over better parent and mid parent for eleven characters in forage sorghum

Hybrid	Days to 50% flowering		Plant height (cm)		No. of leaves per plant		Stem girth (mm)		Leaf length (cm)		Leaf breadth (cm)	
	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
UP Chari 4 x MP Chari	-1.57**	-4.05**	-0.46	-0.90	-3.60	-0.43	10.47*	17.04**	4.27**	4.22**	6.56**	4.45**
UP Chari 4 x HC-171	0.25	0.76	14.45**	11.71**	16.82**	16.28**	11.76**	16.88**	0.24	0.51	13.35**	16.39**
UP Chari 4 x UP Chari-3	-2.98**	-2.50**	5.76	1.79	10.36**	17.51**	-10.38*	-11.96*	0.72	1.43	17.56**	10.38**
UP Chari 4 x HJ-513	-2.34**	-5.05**	3.72	-1.27	-8.62**	-7.87**	18.33**	16.49**	1.89	1.04	-2.14	-1.97
G-48 x MP Chari	3.77**	3.59**	17.90**	15.68**	10.46**	11.73**	17.78**	14.79**	8.34**	9.29**	0.66	0.58
G-48 x HC-171	4.04**	4.62**	13.68**	14.22**	0.87	0.93	11.49**	10.12*	1.12	2.41	9.69**	10.82**
G-48 x UP Chari-3	0.37	0.94	1.43	1.66	2.57	1.44	4.90	4.70	5.54**	5.22**	-3.25	-2.24
G-48 x HJ-513	0.51	0.56	12.52**	10.92**	-5.05	-3.70	2.02	2.34	7.13**	6.27**	-2.26	-4.07
HC-260 x MP Chari	5.86**	11.43**	-2.70	-2.55	-2.50	-2.02	0.64	0.07	1.17	1.31	-11.22**	-15.49**
HC-260 x HC-171	5.15**	4.59*	8.87**	10.72**	-1.29	1.03	15.93**	10.48*	1.80	2.61	-13.04**	-16.43**
HC-260 x UP Chari-3	12.04**	19.59**	0.12	0.24	12.64**	20.88**	17.60**	15.10**	-3.37	-1.14	10.93**	16.64**
HC-260 x HJ-513	10.08**	19.49**	0.90	0.73	1.94	-4.82	1.07	1.26	9.01**	8.31**	1.28	1.22
UP Chari-2 x MP Chari	0.22	0.86	-3.17	-3.06	19.68**	18.97**	18.83**	16.12**	0.92	0.18	3.71	1.45
UP Chari-2 x HC-171	0.47	0.31	-11.16**	-21.44**	0.67	-3.42	14.53**	10.45**	7.95**	8.17**	3.94	2.41
UP Chari-2 x UP Chari-3	-0.85	-0.57	4.58	1.21	5.96	-1.28	18.71**	17.61**	-8.38**	-9.22**	18.06**	23.57**
UP Chari-2 x HJ-513	-2.29**	-6.14**	-3.35	-2.15	-0.33	-3.85	1.31	4.59	-7.14**	-9.28**	4.32	2.85
SSV-84 x MP Chari	-0.23	-0.01	-18.93**	-34.26**	7.33	6.87	-13.18**	-15.91**	2.56	2.90	15.02**	18.89**
SSV-84 x HC-171	14.15**	18.84**	-23.36**	-25.39**	-0.45	-4.29	21.13**	15.79**	-1.04	-2.90	17.90**	14.81**
SSV-84 x UP Chari-3	-1.42	-5.60**	15.86**	11.76**	10.34**	13.00**	23.24**	21.01**	1.58	0.98	0.44	4.40
SSV-84 x HJ-513	-6.97**	-15.23**	24.71**	11.79**	-3.34	-0.43	25.34**	12.77**	1.46	0.54	15.23**	20.91**
Pusa Chari-6 x MP Chari	0.53	0.92	-4.05	-6.19	2.40	4.33	1.98	2.25	0.98	0.54	1.73	2.16
Pusa Chari-6 x HC-171	8.03**	5.89**	-2.01	-2.40	7.55	5.86	13.78**	17.58**	8.63**	9.22**	4.63	4.31
Pusa Chari-6 x UP Chari-3	-4.18**	-4.69**	1.51	2.29	2.91	4.95	17.61**	14.18**	2.14	1.96	-0.26	-4.15**
Pusa Chari-6 x HJ-513	-0.04	-0.82	-0.15	-0.60	19.59**	18.11**	-4.72	-1.83	1.84	1.34	1.84	1.71
Pant Chari-4 x MP Chari	-1.16	-1.00	-3.55	-2.27	7.28	5.19	2.92	2.26	2.36	1.65	-1.55	-1.00
Pant Chari-4 x HC-171	-0.63	-1.00	13.64**	20.64**	6.18	4.50	0.30	0.20	7.74**	8.24**	1.85	2.90

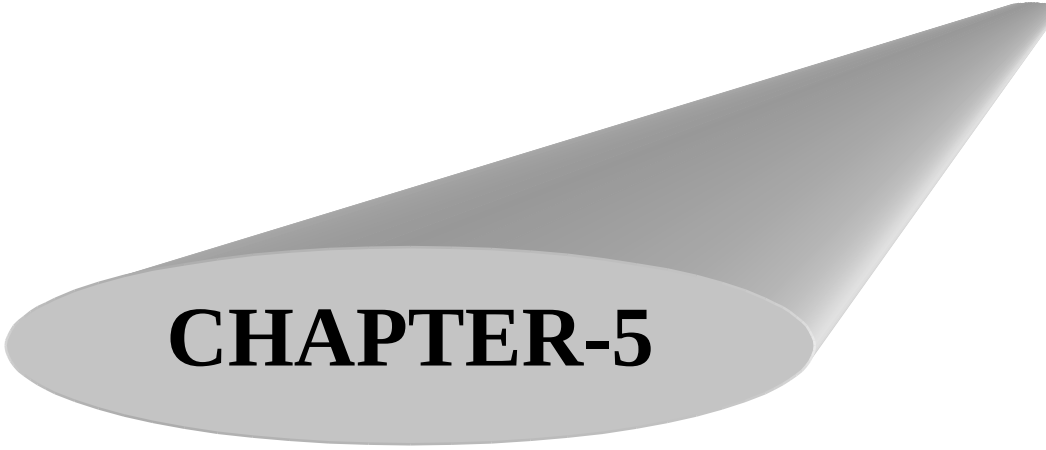
Pant Chari-4 x UP Chari-3	-0.76	-0.60	-2.12	-1.34	12.26**	17.21**	10.78**	10.64*	0.83	1.88	9.48**	9.98**
Pant Chari-4 x HJ-513	-0.87	-0.92	-2.08	-3.19	6.39	4.95	1.29	1.77	8.68**	9.49**	-2.22	-3.68
HC-136 x MP Chari	7.91**	6.56**	-1.77	-1.12	-3.82	0.50	-0.95	-3.02	0.92	0.67	2.42	2.94
HC-136 x HC-171	9.28**	12.36**	17.71**	-18.69**	-19.56**	-19.30**	17.45**	13.49**	1.62	1.19	14.56**	14.18**
HC-136 x UP Chari-3	-0.68	-0.46	3.88	0.96	1.17	5.14	17.24**	16.40**	-8.36**	-8.61**	3.17	4.78
HC-136 x HJ-513	3.93**	4.02**	-3.35	-2.87	-0.20	-0.46	4.26	3.83	7.04**	8.39**	-1.84	-2.44
Pant Chari-7 x MP Chari	0.21	0.82	-3.17	-4.26	-4.04	0.43	2.48	3.15	2.48	0.89	0.89	3.59
Pant Chari-7 x HC-171	6.01**	3.41**	3.28	4.45	3.51	2.51	0.53	0.89	1.00	1.88	3.51	2.49
Pant Chari-7 x UP Chari-3	2.01**	1.97*	4.51	1.38	-2.64	-0.47	-0.48	-0.30	1.78	1.42	10.53**	16.40**
Pant Chari-7 x HJ-513	-0.22	-0.53	-1.30	-1.76	-0.51	0.26	3.86	4.78	1.33	1.87	-0.26	-4.01
Pant Chari-3 x MP Chari	0.14	0.24	17.32**	19.27**	11.80**	18.66**	12.20**	12.28**	9.56**	9.48**	-9.61**	-11.81**
Pant Chari-3 x HC-171	0.32	0.71	12.98**	15.07**	22.08**	32.75**	14.78**	13.14**	1.98	2.64	1.92	1.74
Pant Chari-3 x UP Chari-3	-6.10**	-13.84**	1.22	2.02	2.10	4.13	14.91**	13.42**	-14.94**	-10.06**	1.37	4.40
Pant Chari-3 x HJ-513	-14.91**	-23.54**	-14.42**	24.90**	25.53**	25.05**	3.55	5.11	18.21**	13.48**	1.37	2.20
UP Chari-1 x MP Chari	5.16**	6.82*	-2.95	-1.69	-1.67	5.63	-11.02**	-11.29**	14.73**	13.88**	20.45**	10.95**
UP Chari-1 x HC-171	9.90**	13.14**	1.47	1.81	-0.71	-2.79	12.86**	11.01**	1.18	1.62	10.46**	10.86**
UP Chari-1 x UP Chari-3	0.70	0.28	1.87	1.30	1.47	0.49	11.29**	10.08**	-0.76	-1.16	0.69	0.64
UP Chari-1 x HJ-513	4.93**	3.21**	0.73	0.69	2.37	0.43	17.69**	23.95**	-1.34	-1.26	1.29	1.29
Jawahar Chari-6 x MP Chari	0.14	0.31	-1.33	-1.86	-13.49**	-19.48**	19.40**	25.03**	15.68**	18.90**	16.90**	17.24**
Jawahar Chari-6 x HC-171	10.62**	10.45**	11.87**	11.17**	12.70**	12.09**	0.15	1.00	15.17**	13.15**	12.85**	12.34**
Jawahar Chari-6 x UP Chari-3	8.59**	3.79**	1.40	3.40	-6.73	-7.43	3.91	3.35	13.96**	23.46**	3.36	2.83
Jawahar Chari-6 x HJ-513	6.03**	3.66**	2.35	4.06	-4.10	-4.87	25.14**	28.48**	0.93	0.28	13.91**	16.36**

*, ** significant at 5%, and 1% respectively.

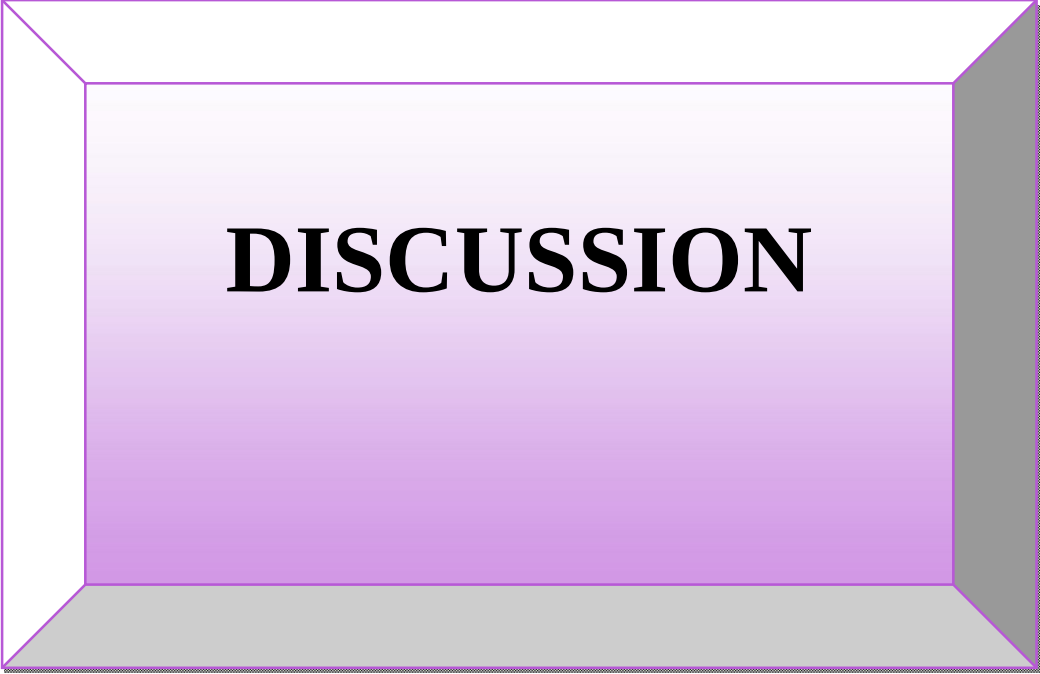
Hybrid	Total soluble solids (%)		Leaf area (cm ²)		Leaf stem ratio		Protein content (%)		Green fodder yield per plant (g)	
	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
UP Chari 4 x MP Chari	8.82**	8.74**	1.13	1.96	15.53**	14.42**	-1.05	-1.84	10.79**	12.91**
UP Chari 4 x HC-171	14.83**	10.49**	20.69**	29.86**	21.79**	21.84**	-1.76	-1.01	25.30**	30.35**
UP Chari 4 x UP Chari-3	2.33	2.29	20.65**	11.97**	20.74**	13.91**	0.16	0.66	-0.81	-0.63
UP Chari 4 x HJ-513	-1.62	-3.81	1.83	1.62	-3.17	-4.20	-2.24	-3.24	25.63**	26.09**
G-48 x MP Chari	25.20**	28.54**	13.25**	11.13**	21.37**	19.62**	-14.09**	-12.78**	29.81**	30.72**
G-48 x HC-171	24.89**	11.95**	1.07	1.03	20.21**	22.48**	9.57**	9.76**	29.89**	30.40**
G-48 x UP Chari-3	10.76**	17.70**	1.49	1.54	-0.11	-0.35	-1.08	-3.77	3.27	0.15
G-48 x HJ-513	-16.98**	-23.05**	2.30	2.93	-11.45**	-16.30**	1.43	1.54	19.79**	20.75**
HC-260 x MP Chari	3.08	3.73	-3.60	-4.24	15.41**	14.86**	8.60**	9.37**	4.56	1.02
HC-260 x HC-171	1.15	1.44	-0.42	-0.83	21.66**	21.81**	1.94	3.96	4.24	0.75
HC-260 x UP Chari-3	4.64	4.01	-14.89**	-14.26**	1.09	2.43	2.87	1.00	16.64**	19.20**
HC-260 x HJ-513	3.14	3.56	15.08**	12.60**	-0.50	-0.94	2.33	1.56	-5.68	-1.16
UP Chari-2 x MP Chari	10.33**	19.27**	10.06**	19.95**	24.08**	16.92**	13.72**	18.32**	1.70	0.92
UP Chari-2 x HC-171	17.35**	11.95**	13.97**	12.01	28.89**	26.09**	9.78**	9.10**	2.36	1.03
UP Chari-2 x UP Chari-3	1.42	1.53	3.08	3.98	-3.28	-4.35	1.59	1.49	-10.30**	-17.43**
UP Chari-2 x HJ-513	-2.06	-2.56	3.27	4.37	2.46	2.57	2.06	1.80	-4.30	-3.15
SSV-84 x MP Chari	1.02	1.35	19.08**	12.05**	14.86**	13.77**	10.58**	14.14**	2.36	1.58
SSV-84 x HC-171	16.79**	11.04**	12.27**	16.33**	22.06**	31.70**	12.46**	14.12**	1.33	1.99
SSV-84 x UP Chari-3	2.93	1.87	3.11	3.44	-1.18	-2.78	2.36	2.98	25.69**	24.47**
SSV-84 x HJ-513	1.47	1.49	17.68**	15.58**	-10.76**	-15.63**	2.72	2.24	1.05	3.46
Pusa Chari-6 x MP Chari	2.27	2.91	2.15	3.43	20.17**	20.96**	19.39**	22.01**	25.37**	32.06**
Pusa Chari-6 x HC-171	23.04**	16.34**	14.28**	12.12**	21.86**	22.89**	-1.25	-1.79	2.30	0.77
Pusa Chari-6 x UP Chari-3	1.47	0.87	-2.10	-2.28	-0.81	-1.22	-0.44	-0.92	1.99	2.67
Pusa Chari-6 x HJ-513	-1.62	-1.62	2.23	-2.34	-4.63	-3.45	-1.89	-1.54	27.86**	32.83**
Pant Chari-4 x MP Chari	14.99**	17.42**	0.81	-3.12	-3.64	1.55	16.01**	14.59*	1.31	0.80
Pant Chari-4 x HC-171	18.03**	14.37**	15.39**	17.04**	25.05**	32.55**	19.18**	19.29**	22.59**	31.47**
Pant Chari-4 x UP Chari-3	3.47	3.77	16.12**	19.86**	2.07	2.78	15.54**	10.09**	-13.34**	-14.72**

Pant Chari-4 x HJ-513	2.89	2.93	0.93	-0.12	-2.38	-2.35	11.13**	17.79**	10.02**	14.74**
HC-136 x MP Chari	10.50**	16.16**	3.15	-3.63	-17.74**	-15.56**	2.89	2.32	3.89	2.39
HC-136 x HC-171	1.42	1.16	16.56**	13.66**	19.59**	28.52*	12.40**	17.07**	4.36	3.26
HC-136 x UP Chari-3	3.99	3.71	-2.04	-2.46	-2.65	2.43	0.31	2.32	16.35**	22.96**
HC-136 x HJ-513	2.02	2.06	1.37	-0.15	-3.61	-1.92	3.90	1.39	4.43	4.70
Pant Chari-7 x MP Chari	1.05	1.17	3.34	-2.72	-2.15	2.19	11.09**	19.65**	1.99	1.91
Pant Chari-7 x HC-171	1.53	1.83	1.54	3.69	1.17	1.21	1.27	2.64	4.04	1.54
Pant Chari-7 x UP Chari-3	4.79	4.07	10.88**	17.10**	17.01**	18.87*	3.84	0.82	21.19**	26.34**
Pant Chari-7 x HJ-513	-1.62	-0.68	0.81	2.88	1.07	1.01	2.08	3.86	-10.72**	-15.86**
Pant Chari-3 x MP Chari	17.06**	10.29**	-1.43	-1.90	1.03	2.30	1.05	1.35	32.98**	29.99**
Pant Chari-3 x HC-171	-16.21**	-13.62**	-14.27**	-11.55**	29.77**	29.15**	13.99**	17.93**	33.70**	34.12**
Pant Chari-3 x UP Chari-3	3.47	2.90	-3.32	-3.64	0.23	0.47	1.24	0.78	-0.65	-3.45
Pant Chari-3 x HJ-513	2.09	2.68	21.49**	19.90**	13.87**	19.46**	2.82	3.01	22.15**	23.54**
UP Chari-1 x MP Chari	1.69	1.61	27.80**	16.84**	34.38**	36.67**	13.61**	16.07**	22.65**	23.06**
UP Chari-1 x HC-171	2.11	2.07	-12.20**	-14.49**	43.70**	47.57*	0.27	0.07	22.16**	20.23**
UP Chari-1 x UP Chari-3	2.69	2.93	4.91	4.54	14.79**	15.31*	-15.14**	-14.26**	-2.69	-2.96
UP Chari-1 x HJ-513	-0.50	-1.75	3.16**	-3.79	-1.97	-1.41	-1.13	-3.66	-11.11**	-11.72**
Jawahar Chari-6 x MP Chari	28.66**	29.80**	25.94**	23.75**	2.34	2.24	12.99**	12.87**	0.92	0.83
Jawahar Chari-6 x HC-171	30.35**	34.94**	18.37**	19.06**	38.50**	39.34**	20.41**	25.91**	32.19**	41.53**
Jawahar Chari-6 x UP Chari-3	18.04**	11.29**	13.17**	12.06**	4.57	3.16	3.41	2.54	17.55**	22.35**
Jawahar Chari-6 x HJ-513	18.26**	19.74**	21.34**	28.21**	14.24**	23.55**	2.11	0.49	28.74**	29.13**

*, ** significant at 5% and 1% respectively.



CHAPTER-5



DISCUSSION

Several selection procedures are now available for handling of breeding population in naturally self-fertilized breeding population following hybridizations but the choice of efficient and appropriate breeding procedures, depend on to a large extent the knowledge of selection of plants or progenies within segregating population and the genetic system controlling desirable traits, to be selected and then either by selfing or back crossing, favorable genes are fixed for these traits in homozygous lines. Genetics and plant breeding play an important role in any research designed for achieving food, fiber, nutrition and environmental security. Major development ushering in national and international scenario in the recent years warrant resetting the priorities and programmes related to crop improvement especially in breeding approaches. Thus, in turn, it requires a visionary approach guided by evaluation of strengths, weaknesses, opportunities and threats to research and development efforts in genetics and plant breeding.

The breeding methods and selection techniques have considerably changed in self, cross and often cross pollinated crops under the impact of biometrical genetics. Development in biometrical genetics have helped in better understanding of the genetic architecture is quantitative attributes of economic importance (**Dudley and Moll, 1969**). Yield is a complex end product of a number of components most of which are under polygenic control. All changes in yield must be accompanied by changes in one or more of the components. The concept of line x tester analysis was developed by **Kempthorne in 1957**. It is a modified form or extension of top cross scheme. In case of top cross only one tester is used, while in case of line x tester cross several tester are used.

The first step in evaluating the potential of new inbred lines or pure lines is to cross them to a common parent and compare the performance of their hybrids. The common parent is referred to as the tester and the hybrids produced are known as test crosses or top crosses. The tester is the same for all the inbred lines under evaluation. The ultimate goal of any plant breeding programme is to develop improved genotypes which are better than the existing ones in producing the economic

yield. This requires genetic amelioration through maximum utilization of allelic resources to develop ideal genotype. Synthesis of such genotypes would depend upon the sound knowledge and understanding of nature and magnitude of gene actions involved in the inheritance of agronomically important characters and selection of suitable parents and breeding methodology (**Grafius, 1959**).

The information about inheritance of important qualitative and quantitative traits, identification of superior parents and crosses on the basis of combining ability and understanding of nature and magnitude of heterosis for important characters are required for development of superior strains as varieties through effective and efficient manipulation of available genetic variability. Various designs have been exploited to assess the breeding value of parent through the analysis of variance and combining ability. The judicious selection of parents to be used in hybridization is an important step for any systematic breeding programme particularly in case of quantitative traits.

The present study entitled “Genetic analysis for quantitative traits in forage sorghum (*Sorghum bicolor* L. Moench)” was formulated to get the precise information regarding the genetic architecture of various metric traits like estimation of variability, heritability, genetic advance, correlation coefficient, path analysis, combining ability and heterosis through line x tester analysis which may help in developing suitable breeding strategy for this crop improvement.

The material of the study consisted of twelve genetically diverse lines viz., UP Chari-4, G-48, HC-260, UP Chari-2, SSV-84, Pusa Chari-6, Pant Chari-4, HC-136, Pant Chari-7, Pant Chari-3, UP Chari-1 and Jawahar Chari-6 and four testers namely, MP Chari, HC-171, UP Chari-3 and HJ-513 were used. The lines were crossed to testers in line $\times$ tester fashion. The parents and F_1 's were evaluated in a completely randomized block design with three replications during *kharif* 2017 at the Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut. The observations were on eleven characters i.e. days to 50% flowering, plant height, number of leaves per plant, stem girth, leaf length, leaf breadth, total soluble solids, leaf area, leaf stem ratio, protein content and green fodder yield per plant and were subjected to statistical and biometrical analysis. Results obtained on these parameters have been discussed here under:

Studies on nature and magnitude of variation for fodder yield and other related traits

Selection on the basis of every breeding programme operates only on variation that is of genetic nature (**Johansen, 1909**). A wide range of variability present in any crop always provides the better chances of selecting the desired types (**Vavilov, 1951**). The success of plant improvement lies in careful management of variability and techniques to be employed in each case will depend upon clear understanding of the extent and nature of variability.

According to **Fisher (1918)**, the continuous variation showed by quantitative characters with which most of the plant breeders have to deal with, includes the heritable and non heritable components. The heritable component is the consequence of genotypes and the non heritable part is mainly due to unknown environmental factors. As it is very difficult to assess the genotypes directly, it is possible only through the assessment of phenotypic expression in the existing material. Therefore, the study of phenotypic variability for various traits under investigation is of great importance.

Genetic variability, heritability and genetic advance

Existence of genetic variability in the population provides ample opportunities for selection being effective. The pool of genotypes was therefore, assessed for variability analysis. The existence of wide diversity among the constituent genotype with regard to characters under study was confirmed through various statistical parameters.

A thorough screening of the material studied (Table-1) under present investigation exhibited sufficient variability for all the eleven characters *i.e.* days to 50% flowering, plant height, number of leaves per plant, stem girth, leaf length, leaf breadth, total soluble solids, leaf area, leaf stem ratio, protein content and green fodder yield per plant which indicated that sufficient variability existed in the present set of material and further genetic analysis and study would be meaningful. High amount of genetic variability for all the attributes has also been reported earlier by **Singh *et al.* (1999)**, **Desai *et al.* (2000)**, **Soltani *et al.* (2001)**, **Kumar and Sahib (2003)**, **Umakanth *et al.* (2003)**, **Pattnayak *et al.* (2004)**, **Rajguru *et al.* (2005)**, **Singh *et al.* (2005)**, **Singh and Sirohi**

(2006), Deepalakshmi and Ganesamurthy (2007), Unche *et al.* (2008), Kusalkar *et al.* (2009), Vedansh *et al.* (2010), Kumar *et al.* (2011), Jain and Patel (2012), Jain and Patel (2013), Nyadanu and Dikera (2014), Ghorade *et al.* (2015), Khandelwal *et al.* (2015), Malik *et al.* (2015), Diwakar *et al.* (2016), Singh *et al.* (2016), Kour and Pradhan (2016), Jain *et al.* (2017), Ranjith *et al.* (2017), Singh *et al.* (2017), Rajarajan *et al.* (2018), Kalpande *et al.* (2018), Damor *et al.* (2018) and Badikar *et al.* (2018).

An insight into the magnitude of variability exists in a crop species is of utmost importance, as it provides the basis for effective selection. The total variation *i.e.* phenotypic variation present in the population arises due to combined action of genotypic and environmental effects. Phenotypic variability is the observable variation present in a character in the population, it includes both genotypic and environmental components of variation and as a result, its magnitude differs under different environmental conditions. Genotypic variation, on the other hand, is the components of variation, which is due to the genotypic difference among individuals within a population and is the main concern of plant breeders.

The genotypic and phenotypic variances are of little meaning as they do not have any clear limit or ceiling, and at the same time, the categorization of the genotypic variance as low or high is difficult, rendering them unsuitable for comparison of two populations with desired precision when expressed in absolute values. To overcome this difficulty, the genotypic and phenotypic coefficients of variation that are free from the unit of measurement, can be conveniently employed for making comparison between populations and different metric traits of population. The results data of genotypic coefficient of variation and phenotypic coefficient of variation, heritability and genetic advance for all the traits are given in Table-2.

Results from the present study in this context indicated that phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high (more than 25%) revealed for plant height, stem girth, leaf stem ratio and green fodder yield per plant whereas showed low (<10%) for days to 50% flowering, leaf length, leaf breadth, number of leaves per plant, leaf area,

total soluble solids and protein content. Further, the present findings exhibited that the estimates of phenotypic coefficient of variation were generally higher than their corresponding genotypic coefficient of variation for all the attributes. Earlier researchers **Soltani *et al.* (2001)**, **Kadam *et al.* (2001)**, **Umakanth *et al.* (2003)**, **Pattnayak *et al.* (2004)**, **Singh *et al.* (2005)**, **Singh and Sirohi (2006)**, **Unche *et al.* (2008)**, **Kusalkar *et al.* (2009)**, **Chavan *et al.* (2010)**, **Vedansh *et al.* (2010)**, **Kumar *et al.* (2011)**, **Tomar *et al.* (2012)**, **Jain and Patel (2013)**, **Shivani and Sreelakshmi (2013)**, **Iraddi *et al.* (2013)**, **Nyadanu and Dikera (2014)**, **Ghorade *et al.* (2015)**, **Malik *et al.* (2015)**, **Kour and Pradhan (2016)**, **Singh *et al.* (2016)**, **Ranjith *et al.* (2017)**, **Singh *et al.* (2017)**, **Rajarajan *et al.* (2018)**, **Kalpande *et al.* (2018)** and **Damor *et al.* (2018)** have reported similar findings. The high values of genotypic and phenotypic coefficient of variation for these traits, suggested that there was a possibility of improvement fodder yield in forage sorghum through direct selection.

A useful measure of considering the ratio of genetic variance to total variance is heritability and this concept is of major importance in the development of quantitative genetics. It may be described as a measure of relative importance of heredity and environment. Heritability indicates the effectiveness with which selection of genotypes can be done on the basis of its phenotypic performance.

The present study in this context recorded that an estimate of heritability (broad sense) was high (> 60%) for all characters viz., days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth, leaf stem ratio, total soluble solids, protein content and green fodder yield per plant. This indicates lesser effect of environment on these traits. Therefore, the selection based on these attributes might be effective in the improvement of this crop. High heritability estimates for most of the characters studied, have been reported earlier by **Kadam *et al.* (2001)**, **Umakanth *et al.* (2003)**, **Pattnayak *et al.* (2004)**, **Singh *et al.* (2005)**, **Singh and Sirohi (2006)**, **Unche *et al.* (2008)**, **Kusalkar *et al.* (2009)**, **Vedansh *et al.* (2010)**, **Kumar *et al.* (2011)**, **Tomar *et al.* (2012)**, **Jain and Patel (2013)**, **Shivani and Sreelakshmi (2013)**, **Nyadanu and Dikera**

(2014), Malik *et al.* (2015), Singh *et al.* (2016), Kour and Pradhan (2016), Ranjith *et al.* (2017), Singh *et al.* (2017), Rajarajan *et al.*(2018) and Kalpande *et al.* (2018).

For an effective selection, the knowledge alone on the estimates of heritability is not sufficient and genetic advance if studied along with heritability is more useful. In the present study, high (>20%) estimates of genetic advance expressed as per cent of mean have been observed for plant height, leaf area, stem girth, leaf stem ratio and green fodder yield per plant thereby, suggesting good response for selection based on *per se* performance. Earlier research have reported similar finding with respect to genetic advance, Desai *et al.* (2000), Kumar and Sahib (2003), Pattnayak *et al.* (2004), Singh *et al.* (2005), Singh and Sirohi (2006), Deepalakshmi and Ganesamurthy (2007), Unche *et al.* (2008), Kusalkar *et al.* (2009), Vedansh *et al.* (2010), Kumar *et al.* (2011), Jain and Patel (2013), Nyadanu and Dikera (2014), Khandelwal *et al.* (2015), Malik *et al.* (2015), Singh *et al.* (2016), Kour and Pradhan (2016), Jain *et al.* (2017), Ranjith *et al.* (2017), Singh *et al.* (2017), Rajarajan *et al.*(2018), Kalpande *et al.* (2018) and Badikar *et al.* (2018).

In the present study, broad sense heritability was computed which includes both additive and non-additive gene effects. Therefore, heritability estimates should be considered in conjugation with genetic advance. Based on this consideration, high heritability coupled with high genetic advance was estimated for plant height, leaf area, stem girth, leaf stem ratio and green fodder yield per plant which indicated that these traits are governed by additive gene action. Direct selection of these attributes will be effective for yield improvement. High heritability coupled with high genetic advance for some of these characters have also been reported earlier by Pattnayak *et al.* (2004), Singh *et al.* (2005), Singh and Sirohi (2006), Unche *et al.* (2008), Kusalkar *et al.* (2009), Vedansh *et al.* (2010), Kumar *et al.* (2011), Jain and Patel (2013), Nyadanu and Dikera (2014), Malik *et al.* (2015), Singh *et al.* (2016), Kour and Pradhan (2016), Jain *et al.* (2017), Ranjith *et al.* (2017), Singh *et al.* (2017) and Rajarajan *et al.*(2018).

Studies on correlation and its direct and indirect effects

It has been well established that yield is one of the most important economic character, which is influenced to a great extent by the interaction of several metric traits and by the fluctuating environmental conditions. The effectiveness of any breeding or selection programme depends upon the nature of associations between yield and other component attributes, as more directly and positively, a character is associated with yield, the more will be the success of the selection programme. Therefore, besides getting information on the nature and magnitude of variation, it is also imperative to have knowledge on the associations of yield with other traits and among themselves and their causation to identify attributes for defining an ideal plant type as well for increasing the efficiency of indirect selection. Estimates of phenotypic and genotypic coefficients of correlation and that of direct and indirect effects provide the base necessary for identification of attributes of an ideal plant type and indirect selection. The estimates of genotypic and phenotypic correlation coefficients for all the traits are given in Table-3 and Table-4.

Genotypic and phenotypic correlation coefficients worked out among eleven characters revealed that in general, phenotypic correlation coefficient was higher than the genotypic correlation coefficient which may be a result of modifying effect of environments on the association of the characters. In some cases the genotypic correlation coefficient was slightly higher than the phenotypic correlation coefficients indicating a strong inherent association between various traits. Similar results were obtained by **Anup and Kumar (2000)**, **Chaudhary and Arora (2001)**, **Iyanar et al. (2001)**, **Yadav et al. (2003)**, **Awari et al. (2003)**, **Agarwal et al. (2003)**, **Mallinath et al. (2004)**, **Kishore and Singh (2005)**, **Negash and Chemedda (2005)**, **Iyanar and Khan (2005)**, **Chaudhary et al. (2005)**, **Singh et al. (2006)**, **Premalatha et al. (2006)**, **Singh and Sirohi (2007)**, **Singh et al. (2009)**, **Lyanar et al. (2010)**, **Kumar et al. (2010)**, **Prakash et al. (2010)**, **Warkad et al. (2010)**, **Ikanovic et al. (2011)**, **Jain and Patel (2012)**, **Kumar and Singh (2012)**, **Tag El-Din et al. (2012)**, **Shivani and Sreelakshmi (2013)**, **Jain and Patel (2013)**, **Malik et al. (2013)**, **Patil et al. (2014)**, **Raza and Naheed (2014)**, **Khandelwal et al. (2015)**, **Arunah et al. (2015)**, **Dubey et al.**

(2016), Girish *et al.* (2016), Rana *et al.* (2016), Singh *et al.* (2016), Jain *et al.* (2017), Endalamaw *et al.* (2017), Singh *et al.* (2017) and Damor *et al.* (2018).

Green fodder yield per plant showed positive and significant correlation with plant height, leaf length, number of leaves per plant, leaf area and stem girth at genotypic and phenotypic level. The result indicated that by improving these traits green fodder yield could be enhanced in this crop. These result are in general agreement with the finding of Iyanar *et al.* (2001), Yadav *et al.* (2003), Agarwal *et al.* (2003), Mallinath *et al.* (2004), Negash and Chemedda (2005), Iyanar and Khan (2005), Singh *et al.* (2006), Singh and Sirohi (2007), Singh *et al.* (2009), Kumar *et al.* (2010), Prakash *et al.* (2010), Warkad *et al.* (2010), Ikanovic *et al.* (2011), Jain and Patel (2012), Kumar and Singh (2012), Shivani and Sreelakshmi (2013), Malik *et al.* (2013), Patil *et al.* (2014), Khandelwal *et al.* (2015), Arunah *et al.* (2015), Dubey *et al.* (2016), Girish *et al.* (2016), Rana *et al.* (2016), Singh *et al.* (2016), Jain *et al.* (2017), Endalamaw *et al.* (2017), Singh *et al.* (2017) and Damor *et al.* (2018). Thus, it can be inferred that selection based on any one of these characters either alone or in combination, will result in identifying high yielding strains.

Based on the estimates of genotypic and phenotypic correlations, the breeder would be able to decide the method of breeding, to be followed so that the useful correlation could be exploited and the undesirable ones could be modified by generating fresh variability to obtain new recombinants. According to AlJibouri *et al.* (1958), if negative association between characters is due to pleiotropic effects, it would be very difficult to obtain the desired recombinants, while if linkage is involved; special breeding programme is needed to break these linkages.

Miller and Rawlings (1967) have shown that the undesirable correlations could be broken by recurrent selection programmes, whereas Kaltsikes and Lee (1971) opined that if morphological traits are highly correlated with yield, a pedigree programme with yield per plant or plot as the selection criterion would be useful. From the present study on correlation, it was apparent that for improvement of these attributes, *i.e.* plant height, leaf length, number of leaves per plant, leaf area

and stem girth are more important and may be considered for enhance fodder yield through selection.

Though the correlation coefficients are quite helpful in determining the components of a complex trait like yield, yet, an exact picture of the relative importance of direct and indirect influence of each component character is not provided by such studies. Path coefficient analysis, **(Wright, 1921; Dewey and Lu, 1959)** under such circumstances plays an important role in partitioning of the correlation coefficient into direct and indirect effects of a set of independent variable on the dependent variable and determines the component characters on which selection can be based for improvement in yield.

Results on the phenotypic and genotypic path coefficient observed high positive direct contribution of leaf area followed by leaf length, plant height, number of leaves per plant and stem girth on green fodder yield per plant. This confirms the role of these traits in determining the green fodder yield per plant and therefore, their values in constructing the selection criterion. The direct contribution of leaf area, leaf length, plant height, number of leaves per plant and stem girth with green fodder yield per plant observed in this study is also in confirmation with the findings of **Singh et al. (2006), Singh and Sirohi (2007), Singh et al. (2009), Prakash et al. (2010), Warkad et al. (2010), Jain and Patel (2012), Kumar and Singh (2012), Shivani and Sreelakshmi (2013), Malik et al. (2013), Patil et al. (2014), Khandelwal et al. (2015), Arunah et al. (2015), Dubey et al. (2016), Girish et al. (2016), Rana et al. (2016), Singh et al. (2016), Jain et al. (2017), Endalamaw et al. (2017), Singh et al. (2017) and Damor et al. (2018).**

High indirect positive contribution of leaf length through days to 50% flowering; Leaf breadth via days to 50% flowering, number of leaves per plant, leaf stem ratio and protein content and leaf stem ratio through days to 50% flowering, leaf length, number of leaves per plant, leaf area and total soluble solids were responsible for their positive association with green fodder yield. These results are in general agreement with the findings of **Singh et al. (2006), Singh and Sirohi (2007), Singh et al. (2009), Warkad et al. (2010), Kumar and Singh (2012), Malik et al. (2013),**

Patil et al. (2014), Arunah et al. (2015), Girish et al. (2016), Rana et al. (2016), Singh et al. (2016), Jain et al. (2017), Endalamaw et al. (2017) and Singh et al. (2017). The contribution of residual effects that influenced green fodder yield was very low at both genotypic and phenotypic levels, indicating that these characters included in the present investigation were sufficient enough to account for the variability in the dependant character *i.e.* green fodder yield. From the overall study, there is an indication of improvement in yield through selection with high values for leaf area and leaf length.

Combining ability analysis

The major interest in the present study relates to its implication on the nature of gene action based on combining ability analysis in a group of highly selected material and in formulation of a suitable breeding procedure in this crop. The combining ability analysis under line x tester mating approach was done by the procedure advocated by **Kempthorne (1957)** which involves the study of covariances of full sibs and covariances of half sibs to get the estimates of general combining ability effect and specific combining ability effect variances and their effects. To understand the nature and magnitude of gene action, involved in expression of the attributes, the estimates of combining ability variances were subjected to get the estimates of components of genetic variances due to general combining ability effect and specific combining ability effect which are translated into additive genetic variance and dominance genetic variances.

In addition to other genetic parameters such as, the average degree of dominance is of more interest to the plant breeders (**Gardner, 1963**). The degree of dominance in the present investigation has been estimated as $(\sigma^2 D / \sigma^2 A)^{0.5}$. This formula is based on the assumption that genes are directionally distributed among the parents and all the increments have the same sign (**Kempthorne and Curnow 1961**). This procedure, thus, measures only the degree of dominance regardless of direction. If the dominance variance is in the plus and minus directions, these tend to cancel each other, and then F_1 may be equal to the mean of its better parents.

The success of any breeding programme depends to a great extent on the knowledge of genetic architecture of the population being handled. Reliable information about the nature and magnitude of gene action involved in the expression of quantitatively inherited traits of economic importance may be considered as the most desirable prerequisite of any crop improvement programme. The reliability of such information depends much on diversity of material under study.

The results of analysis of variance revealed that significant variability existed among the parents with regard to all the characters under investigation. Such divergences of parents lead to development of F_{1s} that differed significantly among themselves for all traits. The estimates of combining ability variances are translated in to genetic variance to understand the nature and magnitude of gene action and develop guidelines for selecting parents for hybridization. It is an established fact that additive genetic variance results mostly from additive gene action while non additive genetic variance is comprised of dominant and epistasis. The mean sum of squares for all the attributes is presented in Table-5.

The estimates of variance due to line x tester exhibited highly significant for days to 50% flowering, plant height, leaf length, leaf area, stem girth, leaf stem ratio, total soluble solids and green fodder yield per plant. Further partitioning of treatment variance into parents and crosses were revealed highly significant differences for all the characters *i.e.*, days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth, total soluble solids, protein content and green fodder yield per plant. Variance due to parent vs crosses was observed significant for all the traits except leaf stem ratio. These results are in general agreement with the findings **Hovny *et al.* (2000), Ravindrababu *et al.* (2001), Prabhakar (2002), Fouman *et al.* (2003), Biradar *et al.* (2004), Agarwal *et al.* (2005), Khandelwal *et al.* (2006), Kulkarni *et al.* (2006), Mohan *et al.* (2007), Yadav and Pahuja (2007), Borole *et al.* (2008), Kamdi *et al.* (2009), Patel and Patel (2010), Ghazy and Sakr (2011), Akabari *et al.* (2012), Goyal *et al.* (2013), Abdelmula *et al.* (2014), Aaref *et al.* (2016), Kumar and Shrotria (2016), Rini *et al.* (2016),**

Chikuta et al. (2017), Dehinwal et al. (2017), Singh and Singh (2017), Pal et al. (2017), Ingle et al. (2018) and Soujanya et al. (2018).

Analysis of variance for combining ability for all the eleven metric attributes was done in F₁'s hybrids and the results are given in Table-6. The variance among line with respect to gca was found highly significant for all the traits *i.e.* days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth, leaf stem ratio, total soluble solids, protein content and green fodder yield per plant. The variance among testers with respect to gca was recorded highly significant for all the characters while variances among crosses due to interaction between lines x testers genotypes with respect to sca were expressed highly significant for days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth, total soluble solids, protein content and green fodder yield per plant. Indicating that both additive and dominance genetic variance were involved in the determination of these attributes and the parents and their progenies differed for their combining ability effects. **Prabhakar (2002), Fouman et al. (2003), Biradar et al. (2004), Agarwal et al. (2005), Kulkarni et al. (2006), Yadav and Pahuja (2007), Borole et al. (2008), Kamdi et al. (2009), Patel and Patel (2010), Ghazy and Sakr (2011), Akabari et al. (2012), Goyal et al. (2013), Abdelmula et al. (2014), Aaref et al. (2016), Rini et al. (2016), Chikuta et al. (2017), Dehinwal et al. (2017), Singh and Singh (2017), Pal et al. (2017), Soujanya et al. (2018) and Ingle et al. (2018)** reported that same of the morphological and quality traits were determined by additive and other by non additive effects for yield.

The estimates of components of variance, their ratio and degree of dominance for different characters are presented in Table-6. The ratio δ^2g/δ^2s being more than unity for the traits *viz.*, days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, leaf stem ratio, total soluble solids, protein content and green fodder yield per plant which indicated that the involvement of additive gene action. To exploit the additive genetic variance in the improvement of such attributes, pedigree method of breeding can be used. Similar findings were

also observed by **Ravindrababu *et al.* (2001)**, **Fouman *et al.* (2003)**, **Biradar *et al.* (2004)**, **Agarwal *et al.* (2005)**, **Khandelwal *et al.* (2006)**, **Mohan *et al.* (2007)**, **Borole *et al.* (2008)**, **Kamdi *et al.* (2009)**, **Patel and Patel (2010)**, **Akabari *et al.* (2012)**, **Goyal *et al.* (2013)**, **Abdelmula *et al.* (2014)**, **Aaref *et al.* (2016)**, **Kumar and Shrotria (2016)**, **Rini *et al.* (2016)**, **Chikuta *et al.* (2017)**, **Dehinwal *et al.* (2017)**, **Singh and Singh (2017)**, **Pal *et al.* (2017)**, **Ingle *et al.* (2018)** and **Soujanya *et al.* (2018)**. Stem girth had less than unity, expressed non additive gene action and large amount of non additive gene action would necessitate for maintenance of heterozygosity in the population. Since this type of gene action is not fixable therefore, breeding method such as biparantal mating followed by recurrent selection may hasten the rate of genetic improvement for these traits. These results are somewhat in accordance with the findings of **Biradar *et al.* (2004)**, **Agarwal *et al.* (2005)**, **Mohan *et al.* (2007)**, **Kamdi *et al.* (2009)**, **Akabari *et al.* (2012)**, **Goyal *et al.* (2013)**, **Aaref *et al.* (2016)**, **Rini *et al.* (2016)**, **Chikuta *et al.* (2017)**, **Dehinwal *et al.* (2017)**, **Singh and Singh (2017)** and **Pal *et al.* (2017)**. Estimates of average degree of dominance $(\delta_s^2/\delta_g^2)^{0.5}$ exhibited partial dominance for leaf breadth, number of leaves per plant, leaf area, stem girth and leaf stem ratio, suggesting there by the preponderance of additive type of gene action with partial dominance in the expression of these characters in this crop. Over dominance was observed for days to 50% flowering, plant height, leaf length, total soluble solids, protein content and green fodder yield per plant which indicated that gene action is fixable and these attributes played an important role for population improvement in this crop. Magnitude of δ_s^2 was recorded higher than δ_g^2 for plant height, leaf breadth, number of leaves per plant, leaf area, stem girth and green fodder yield per plant, indicated that the average degree of dominance was found to be dominance. These findings are in close conformity with **Mohan *et al.* (2007)**, **Borole *et al.* (2008)**, **Kamdi *et al.* (2009)**, **Patel and Patel (2010)**, **Ghazy and Sakr (2011)**, **Akabari *et al.* (2012)**, **Goyal *et al.* (2013)**, **Abdelmula *et al.* (2014)**, **Aaref *et al.* (2016)**, **Kumar and Shrotria (2016)**, **Chikuta *et al.* (2017)**, **Singh and Singh (2017)**, **Pal *et al.* (2017)**, **Ingle *et al.* (2018)** and **Soujanya *et al.* (2018)**.

General combining ability effects

The knowledge of general combining ability effects is of paramount importance to a breeder because it helps in the selection of suitable parents. Average performance of a genotype in a series of hybrid combinations measured additive gene action. General combining ability is primarily a function of additive variance and additive x additive type epistasis. The different standard techniques advocated by **Griffing (1956)**, **Kemphorne (1957)** and **Kemphorne and Curnow (1961)** may or may not be compatible with one another with equal weightage and other or ranking yet will provide a realistic estimate of combining ability. The general combining ability effects of the parents for all the characters are given in Table-7.

In the present investigation, the parents among lines, UP Chari-4 were identified as a good general combiner for plant height, number of leaves per plant, total soluble solids and green fodder yield per plant. Parent G-48 appeared as a good general combiner for all the characters except leaf breadth and protein content. Genotype HC-260 was found to be good general combiner for days to 50% flowering, plant height, leaf length, leaf breadth, total soluble solids and protein content. Line UP Chari-2 emerged as a good general combiner for leaf length, number of leaves per plant, leaf area, stem girth, total soluble solids and protein content. Parent SSV-84 expressed as a good general combiner for days to 50% flowering, plant height, leaf breadth, number of leaves per plant, leaf area, total soluble solids and green fodder yield per plant. Genotype Pusa Chari-6 was proved to be good general combiner for plant height, number of leaves per plant and leaf stem ratio and line Pant Chari-4 was considered as desirable good general combiner for plant height, leaf breadth, number of leaves per plant, leaf area and protein content and parent HC-136 was identified as good general combiner for days to 50% flowering, plant height and leaf length. Line Pant Chari-7 appeared as good general combiner for leaf area, protein content and green fodder yield. Genotype Pant Chari-3 was found to be good general combiner for days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, leaf stem ratio and green fodder yield per plant. Parent UP Chari-1 emerged as a good general combiner for days to 50% flowering, plant height,

leaf breadth, leaf area, stem girth, leaf stem ratio, total soluble solids, protein content and green fodder yield per plant and line Jawahar Chari-6 was considered as desirable good general combiner for days to 50% flowering, plant height, leaf breadth, number of leaves per plant, leaf area, stem girth, total soluble solids and protein content. Among the testers MP Chari was appeared good general combiner for days to 50% flowering, plant height, number of leaves per plant, leaf area, stem girth, leaf stem ratio, total soluble solids and green fodder yield per plant. Male HC-171 possessed as a good general combiner for days to 50% flowering, plant height, leaf length, leaf breadth, leaf area, stem girth, leaf stem ratio, protein content and green fodder yield per plant. Tester UP Chari-3 emerged good general combiner for days to 50% flowering, plant height, leaf length, leaf breadth and protein content and tester HJ-513 proved as a good general combiner for leaf length, number of leaves per plant, leaf area, stem girth, total soluble solids and green fodder yield per plant. Similar results have been reported by **Hovny *et al.* (2000), Ravindrababu *et al.* (2001), Prabhakar (2002), Fouman *et al.* (2003), Biradar *et al.* (2004), Agarwal *et al.* (2005), Khandelwal *et al.* (2006), Mohan *et al.* (2007), Rani *et al.* (2007), Borole *et al.* (2008), Kamdi *et al.* (2009), Patel and Patel (2010), Ghazy and Sakr (2011), Akabari *et al.* (2012), Goyal *et al.* (2013), Abdelmula *et al.* (2014), Aaref *et al.* (2016), Jain and Patel (2016), Kumar and Shrotria (2016), Rini *et al.* (2016), Chikuta *et al.* (2017), Dehinwal *et al.* (2017), Singh and Singh (2017), Pal *et al.* (2017), Ingle *et al.* (2018) and Soujanya *et al.* (2018).**

On the basis of overall performance both general combining ability effects and *per se* performance among the lines G-48 was found to be as good general combiner for maximum 9 characters including green yield per plant, UP Chari-1 for 9 traits and Pant Chari-3 for 8 attributes. Among the testers HC-171 were appeared as good general combiner for maximum 9 characters and MP Chari for 8 traits. These parents may be handled in suitable breeding programme *visa-vis* selection breeding for improvement productivity of green fodder yield and per unit area in this crop.

High general combining ability effects showed for different attributes of economic importance may be useful for sorting out standing parents with favorable alleles for the different

components of yield. As stated by **Gilbert (1967)**, the additive parental effects as measured by general combining ability effects were of practical use to plant breeder, since non-allelic interactions unpredictable. As aforesaid parent have good general combining ability effects and high *per se* performance for most of the characters, a multiple crossing programme or an inter-mating population involving all possible crosses among them subjected to biparental mating may be expected to offer the maximum promise in selection of lines with higher yield.

Specific combining ability effects

The performance of a specific cross in a relation to general combining ability is a measure of non additive gene action. Specific combining ability is primarily a function of dominance variance, additive x dominance and dominance x dominance type of epistasis. Specific combining ability effect represent dominance and epistasis component of variation which are non fixable and hence, specific combining ability effect would not tangibly to the improvement in self pollinated crops except in cases where commercial exploitation of heterosis is feasible. To confirm whether the crosses selected on the basis of specific combining ability effects were the best performing ones, the superior crosses on the basis of mean performance and specific combining ability effect were selected.

In general, sca effects do not make any worthwhile contributions in the improvement of self-fertilizing crops except where there is possibility of commercial exploitation of heterosis. Breeder's interest normally, however, rests in obtaining transgressive segregants through crosses in order to produce homozygous lines in autogamous crops. **Jinks and Jones (1958)** further emphasized that superior *per se* performance of the hybrids may not indicate their ability to produce transgressive segregants due to close correspondence between heterosis and non additive gene effects. Therefore, study of specific combining ability in segregating generation would be a better preposition for heterosis breeding. The specific combining ability effects and *per se* performance of crosses is given in Table 8.

Out of the forty eight F_1 's hybrids, only four cross combinations viz., UP Chari-4 x HC-171, UP Chari-4 x HJ-513, UP Chari-1 x MP Chari and Jawahar Chari-6 x HJ-513 noted significant and positive specific combining ability effects which proved as best specific combiners for *per se* performance.

For instance the cross combinations UP Chari-4 x HC-171 showed high and desirable specific combining ability effects for days to 50% flowering, plant height, leaf breadth, number of leaves per plant, leaf area, stem girth, leaf stem ratio and green fodder yield per plant; UP Chari-4 x UP Chari-3 for leaf breadth, leaf area, stem girth, leaf stem ratio and green fodder yield per plant; UP Chari-4 x HJ-513 for days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth, leaf stem ratio and green fodder yield per plant; G-48 x UP Chari-3 for days to 50% flowering, plant height, leaf length, leaf breadth and green fodder yield per plant; G-48 x HJ-513 for days to 50% flowering, plant height, total soluble solids and green fodder yield per plant; HC-260 x UP Chari-3 for days to 50% flowering, leaf breadth, number of leaves per plant, leaf area, and green fodder yield per plant; HC-260 x HJ-513 for leaf breadth, number of leaves per plant, leaf area, total soluble solids and green fodder yield per plant; SSV-84 x MP Chari for days to 50% flowering, plant height, leaf breadth, leaf area, stem girth and green fodder yield per plant; SSV-84 x HC-171 for days to 50% flowering, plant height, leaf breadth, leaf area, and green fodder yield per plant; SSV-84 x UP Chari-3 for plant height, leaf length, leaf breadth and green fodder yield per plant; Pusa Chari-6 x UP Chari-3 for days to 50% flowering, leaf breadth, leaf area and green fodder yield per plant; Pusa Chari-6 x HJ-513 for days to 50% flowering, leaf length, leaf breadth, stem girth and green fodder yield per plant; HC-136 x HJ-513 for days to 50% flowering, leaf length, leaf breadth, leaf area and green fodder yield per plant; Pant Chari-7 x MP Chari for days to 50% flowering, leaf area, stem girth, protein content and green fodder yield per plant; Pant Chari-7 x HC-171 for leaf stem ratio and green fodder yield per plant; Pant Chari-3 x MP Chari for days to 50% flowering, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth and green fodder yield per plant; Pant Chari-3 x UP Chari-3 for days to 50% flowering,

plant height, leaf length, leaf area, leaf stem ratio and green fodder yield per plant; Pant Chari-3 x HJ-513 for days to 50% flowering, plant height, leaf length, leaf breadth, leaf area, leaf stem ratio, and green fodder yield per plant; UP Chari-1 x MP Chari for days to 50% flowering, leaf breadth, number of leaves per plant, leaf area, leaf stem ratio, total soluble solids, protein content and green fodder yield per plant; UP Chari-1 x HC-171 for stem girth, leaf stem ratio and green fodder yield per plant; UP Chari-1 x HJ-513 for days to 50% flowering, plant height, stem girth, leaf stem ratio and green fodder yield per plant; Jawahar Chari-6 x UP Chari-3 for days to 50% flowering, leaf breadth, leaf area, leaf stem ratio and green fodder yield per plant; Jawahar Chari-6 x HJ-513 for days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth, leaf stem ratio and green fodder yield per plant. These findings were supported by **Kanawade *et al.* (2001), Khatod *et al.* (2002), Fouman *et al.* (2003), Biradar *et al.* (2004), Baghel *et al.* (2005), Umakanth and Kuriakose (2005), Kulkarni *et al.* (2006), Chaudhary *et al.* (2006), Mohan *et al.* (2007), Deepalakshmi *et al.* (2007), Yadav and Pahuja (2007), Borole *et al.* (2008), Kamdi *et al.* (2009), Kanbar *et al.* (2011), Akabari *et al.* (2012), Goyal *et al.* (2013), Akabari and Parmar (2014), Aaref *et al.* (2016), Kumar and Shrotria (2016), Dehinwal *et al.* (2017), Singh and Singh (2017), Pal *et al.* (2017) and Ingle *et al.* (2018).**

On the basis of overall results and *per se* performance the F₁'s hybrids *i.e.* UP Chari-4 x HC-171, UP Chari-4 x HJ-513, UP Chari-1 x MP Chari and Jawahar Chari-6 x HJ-513 were proved to be as best specific combiners for maximum attributes including green fodder yield per plant for 8 to 9 other contributing traits, which may be utilized for obtaining transgressive segregants in the next generation.

These identified specific cross combinations should be exploited through heterosis breeding may be used in recombination programme for tapping desirable transgressive segregants in segregating generations. The inter mating between selected segregants in advanced generations would help to accumulate favorable, desirable alleles for further improvement in yield and its component traits. The crosses which exhibited high specific combining ability, involving good

combiner and moderate combiner, such a combination may throw up desirable transgressive segregates, if the additive genetic system is present in the good combiner and complementary effect is present in the crosses, act in the same direction so as to maximize the desirable plant attributes. Breeding for homozygous line by routine pedigree method could mean only partial exploitation of additive genetic variance in order to exploit different type of gene action in a population. It is suggested that a breeding procedure which may accumulate the fixable type of gene effect and at the same time maintains considerable heterozygosity for exploiting the dominance gene effect, might prove most beneficial in improving the population under study.

Manifestation of heterosis

Heterosis breeding, now days, retains the central position in crop improvement for obtaining higher production. Recently, a major breakthrough in hybrid breeding for yield has been made in self-fertilizing crops such as paddy, barley, tomato, egg plant and so on. The utilization of F_1 generation for commercial exploitation is technically feasible (**Briggle, 1963; Kihara and Tsunewaki, 1962**). Identification of specific parental combinations capable of producing the higher level of F_1 transgressive effects, presumably, however, is still a matter of considerable development. Hybridization among selected genotypes for a particular objective is the first step in any crop improvement programme. It is therefore, necessary to know the performance of these hybrid combinations in the first filial generation in respect of yield and its components. Although production of hybrids may be the best exploitation of heterosis however, such attempts have not met with success in this crop because of several associated problems such as fertility restoration, pollination and seed setting. However, such heterotic F_1 combinations, which in F_2 and subsequent generations show a considerable measure of residual heterotic effects, can be exploited to isolate transgressive segregants. Yield is the interaction of many direct and indirect component traits. The manifestation of heterosis would, therefore, be discussed in the light of the recent concept of genetic basis of yield (**Wilson, 1967**). The superiority of hybrids particularly over better parent is more useful in determining the feasibility of commercial exploitation of heterosis and also indicating the

parental combinations capable of producing the highest level of transgressive segregants. In this investigation, as the parents are highly adapted varieties, heterosis over mid parent and over better parent have high practical significance. Investigation on degree of heterosis is, however, important as it may be of value in deciding the directions of future breeding programmes.

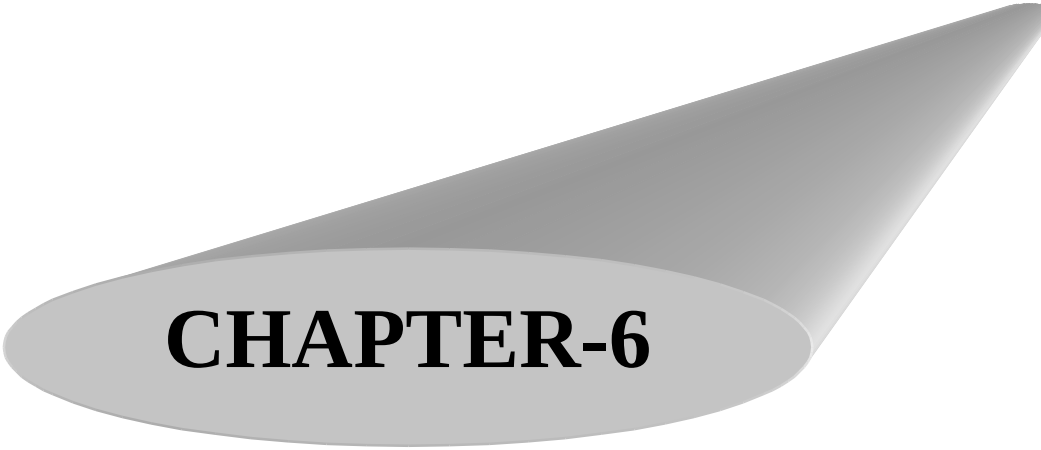
In the present investigation both heterosis (Mid parent) and heterobeltiosis (Better parent) have been worked out. Higher yield is desirable, which is reflected by positive heterosis. Yield being the most important yield component entails positive heterosis for better high yielding cultivars. The range of heterosis and number of crosses showing significant desirable heterosis over mid parent and better parent for *per se* performance has been presented in Table-9.

Maximum magnitude of heterosis and *per se* performance was exhibited highly significant and positive desirable heterosis over mid and better parent manifested in cross combinations *i.e.* UP Chari-4 x MP Chari for stem girth, leaf length, leaf breadth, total soluble solids, leaf stem ratio and green fodder yield per plant; UP Chari-4 x HC-171 for plant height, number of leaves per plant, stem girth, leaf breadth, total soluble solids, leaf area, leaf stem ratio and green fodder yield per plant; UP Chari-4 x HJ-513 for stem girth and green fodder yield per plant; G-48 x MP Chari for days to 50% flowering, plant height, number of leaves per plant, stem girth, leaf length, total soluble solids, leaf area, leaf stem ratio and green fodder yield per plant; G-48 x HC-171 for days to 50% flowering, plant height, stem girth, leaf breadth, total soluble solids, leaf stem ratio, protein content and green fodder yield per plant; G-48 x HJ-513 for plant height, leaf length and green fodder yield per plant; HC-260 x UP Chari-3 for days to 50% flowering, number of leaves per plant, stem girth, leaf breadth, leaf area and green fodder yield per plant; SSV-84 x UP Chari-3 for plant height, number of leaves per plant, stem girth and green fodder yield per plant; Pusa Chari-6 x MP Chari for leaf stem ratio, protein content and green fodder yield per plant; Pusa Chari-6 x HJ-513 for number of leaves per plant and green fodder yield per plant; Pant Chari-4 x HC-171 for plant height, leaf length, total soluble solids, leaf area, leaf stem ratio, protein content and green fodder yield per plant; Pant Chari-4 x HJ-513 for leaf length, protein content and green fodder yield per

plant; HC-136 x UP Chari-3 for stem girth and green fodder yield per plant; Pant Chari-7 x UP Chari-3 for days to 50% flowering, leaf breadth, leaf area, leaf stem ratio and green fodder yield per plant; Pant Chari-3 x MP Chari for plant height, number of leaves per plant, stem girth, leaf length, total soluble solids and green fodder yield per plant; Pant Chari-3 x HC-171 for plant height, number of leaves per plant, stem girth, leaf stem ratio, protein content and green fodder yield per plant; Pant Chari-3 x HJ-513 for plant height, number of leaves per plant, leaf length, leaf area, leaf stem ratio and green fodder yield per plant; UP Chari-1 x MP Chari for days to 50% flowering, leaf length, leaf breadth, leaf area, leaf stem ratio, protein content and green fodder yield per plant; UP Chari-1 x HC-171 for plant height, stem girth, leaf breadth, leaf stem ratio and green fodder yield per plant; Jawahar Chari-6 x HC-171 for days to 50% flowering, plant height, number of leaves per plant, leaf length, leaf breadth, total soluble solids, leaf area, leaf stem ratio, protein content and green fodder yield per plant; Jawahar Chari-6 x UP Chari-3 for days to 50% flowering, leaf length, total soluble solids, leaf area and green fodder yield per plant and Jawahar Chari-6 x HJ-513 for days to 50% flowering, stem girth, leaf breadth, total soluble solids, leaf area, leaf stem ratio and green fodder yield per plant. These results are similar in agreement with earlier reported by **Shaug *et al.* (2000), Kadam *et al.* (2001), Grewal *et al.* (2003), Chaudhary *et al.* (2004), Patil and Biradar (2005), Premalatha *et al.* (2006), Khapre *et al.* (2007), Prabhakar and Raut (2010), Patel and Patel (2011), Akabari *et al.* (2012), Goyal *et al.* (2013), Mohammed *et al.* (2014), More *et al.* (2014), Tariq *et al.* (2014), Kalpande *et al.* (2015), Ringo *et al.* (2015), Aarefet *et al.* (2016), Kale and Desai (2016), Kumar *et al.* (2016), Rini *et al.* (2016), Chikuta *et al.* (2017), Dehinwal *et al.* (2017), Pal *et al.* (2017), Ingle *et al.* (2018) and Soujanya *et al.* (2018).**

On the basis of overall results and *per se* performance the manifestation of high degree of heterosis over better parent and mid parent in certain F₁'s hybrids *i.e.* UP Chari-4 x HC-171, G-48 x MP Chari and Jawahar Chari-6 x HC-171 identified that great possibility of developing hybrid for commercial cultivation.

Considering the predominance of non additive gene action for yield and yield contributing characters manifesting high magnitude of hybrid vigour, heterosis breeding may be useful for improving yield in forage sorghum. As pointed out earlier, the possibility of exploiting hybrid vigour depends upon the extent and the cost of hybrid seed production. It is easier to produce hybrid seed of forage sorghum economically as each pollination would produce sufficient quantity of seed and therefore, the hybrid vigour can be easily be exploited for the commercial purposes in this crop.



CHAPTER-6



SUMMERY AND CONCLUSION

The present investigation entitled “Genetic analysis for quantitative traits in forage sorghum (*Sorghum bicolor* L. Moench)” was conducted to find out the genetic architecture of the breeding material through analysis variability, heritability, genetic advance, correlation coefficient, path analysis, combining ability effects and heterosis. The above parameters were worked out through line x tester analysis involving 12 lines viz., UP Chari-4, G-48, HC-260, UP Chari-2, SSV-84, Puasa Chari-6, Pant Chari-4, HC-136, Pant Chari-7, Pant Chari-3, UP Chari-1 and Jawahar Chari-6 and 4 testers namely, MP Chari, HC-171, UP Chari-3 and HJ-513. All the 48 F₁’s hybrids with parents were sown in a complete randomized block design with three replications at Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut (U.P.) during *kharif* 2017. The data were recorded for eleven quantitative traits *i.e.* days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth, leaf stem ratio, total soluble solids, protein content and green fodder yield per plant. The data observed from the experiment were analyzed on different aspects are summarized here as under:

- ✓ Analysis of variance recorded highly significant differences among the genotypes for all the characters *i.e.* days to 50% flowering, plant height, number of leaves per plant, stem girth, leaf length, leaf breadth, total soluble solids, leaf area, leaf stem ratio, protein content and green fodder yield per plant which indicated wide spectrum of variability among the genotypes.
- ✓ Phenotypic and genotypic coefficients of variation were high (more than 25%) showed for plant height, stem girth, leaf stem ratio and green fodder yield per plant, suggesting greater scope for selection of superior genotypes for these traits.
- ✓ High heritability coupled with high genetic advance expressed as per cent of mean were noted for plant height, leaf area, stem girth, leaf stem ratio and green fodder yield per plant which indicated that the influence of additive gene action for expression of these characters and hence direct selection based on these attributes may be useful for effective improvement in forage sorghum.

- ✓ Green fodder yield per plant observed positive and significant correlation with plant height, leaf length, number of leaves per plant, leaf area and stem girth at genotypic and phenotypic level which indicates that by improving these characters, improvement in fodder yield could be achieved under selection.
- ✓ Leaf area displayed high order of direct effect on green fodder yield per plant followed by leaf length, plant height, number of leaves per plant and stem girth at both phenotypic and genotypic levels. High indirect positive contribution of Leaf length through days to 50% flowering; Leaf breadth via days to 50% flowering, number of leaves per plant, leaf stem ratio and protein content and leaf stem ratio through days to 50% flowering, leaf length, number of leaves per plant, leaf area and total soluble solids, indicating that fodder yield improvement could be achieved by selection based on these attributes.
- ✓ Analysis of variance among line with respect to gca was observed highly significant for all the characters. The variance among testers with respect to gca was recorded highly significant for all the traits while variances among crosses due to interaction between lines x testers genotypes with respect to sca were expressed also highly significant for all the attributes except leaf stem ratio which indicated that both additive and dominance genetic variance were involved in the determination of these characters and the parents and their progenies differed for their combining ability effects.
- ✓ The ratio δ^2_g/δ^2_s being more than unity for the traits viz., days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, leaf stem ratio, total soluble solids, protein content and green fodder yield per plant which indicates the involvement of additive gene action. Average degree of dominance $(\delta^2_s/\delta^2_g)^{0.5}$ exhibited partial dominance for leaf breadth, number of leaves per plant, leaf area, stem girth and leaf stem ratio, suggesting there by the preponderance of additive type of gene action with partial dominance in the expression of these characters in forage sorghum. Over dominance was recorded for days to 50% flowering, plant height, leaf length, total soluble solids, protein content and green fodder yield per plant which

indicated that gene action is fixable and these attributes played an important role for population improvement in this crop. Magnitude of δ_s^2 was higher than δ_g^2 for plant height, leaf breadth, number of leaves per plant, leaf area, stem girth and green fodder yield per plant, indicating the role of dominance gene action and interaction in the expression of these traits.

- ✓ On the basis of overall performance both general combining ability effects and *per se* performance among the lines G-48 was found to be as good general combiner for maximum 9 characters including green yield per plant, UP Chari-1 for 9 traits and Pant Chari-3 for 8 attributes. Among the testers HC-171 were appeared as good general combiner for maximum 9 characters and MP Chari for 8 traits. These parents may be handled in suitable breeding programme *visa-vis* selection breeding for improvement productivity of green fodder yield per unit area in forage sorghum.
- ✓ On the basis of overall results and *per se* performance the F_1 's hybrids *i.e.* UP Chari-4 x HC-171, UP Chari-4 x HJ-513, UP Chari-1 x MP Chari and Jawahar Chari-6 x HJ-513 were proved to be as best specific combiners for maximum attributes including green fodder yield per plant and 8 to 9 other contributing characters, which may be utilized for obtaining transgressive segregants in the next generation.
- ✓ The best heterotic response for yield and other yield contributing traits exhibited (more than 30%) a reasonable and significant increase over both better and mid parents. These cross combinations in order of merit were UP Chari-4 x HC-171, G-48 x MP Chari and Jawahar Chari-6 x HC-171 may be used in heterosis breeding programme for the improvement in yield.
- ✓ On the basis of computed genetic parameters simple selection or pedigree method of breeding with inter in early segregating generation has been suggested for the exploitation of additive genetic variance for the simultaneous exploitation of both additive and non-additive gene action and breeding method such as biparental mating followed by reciprocal recurrent selection/modified recurrent selection was suggested.

Ranking of desirable parents on the basis of gca effect for different characters in forage sorghum

Characters	Best general combiner based on the significant gca effect in desirable direction
Days to 50% flowering	G-48, HC-260, SSV-84, HC-136, Pant Chari-3, UP Chari-1, Jawahar Chari-6, MP Chari, HC-171 and UP Chari-3
Plant height	UP Chari-4, G-48, HC-260, SSV-84, Pusa Chari-6, Pant Chari-4, HC-136, Pant Chari-3, UP Chari-1, Jawahar Chari-6, MP Chari, HC-171 and UP Chari-3
Leaf length	G-48, HC-260, UP Chari-2, HC-136, Pant Chari-3, HC-171, HJ-513 and UP Chari-3
Leaf breadth	HC-260, UP Chari-3, Pant Chari-4, Pant Chari-3, UP Chari-1, Jawahar Chari-6, HC-171 and SSV-84
Number of leaves per plant	HJ-513, G-48, UP Chari-2, SSV-84, Pusa Chari-6, Pant Chari-4, Pant Chari-3, Jawahar Chari-6, MP Chari and UP Chari-4
Leaf area	G-48, UP Chari-2, SSV-84, Pant Chari-4, Pant Chari-7, Pant Chari-3, UP Chari-1, Jawahar Chari-6, MP Chari, HC-171 and HJ-513
Stem girth	UP Chari-2, UP Chari-1, Jawahar Chari-6, MP Chari, HC-171 and HJ-513
Leaf stem ratio	G-48, Pusa Chari-6, Pant Chari-3, UP Chari-1, MP Chari and HC-171
Total soluble solids	UP Chari-4, G-48, HC-260, UP Chari-2, SSV-84, UP Chari-1, Jawahar Chari-6, MP Chari and HJ-513
Protein content	HC-260, UP Chari-2, Pant Chari-4, Pant Chari-7, UP Chari-1, Jawahar Chari-6, HC-171 and UP Chari-3
Green fodder yield	UP Chari-4, G-48, SSV-84, Pant Chari-7, Pant Chari-3, UP Chari-1, MP Chari, HC-171 and HJ-513

Ranking of parents based on significant gca effect for different characters in forage sorghum

Parents	Best general combiner for different characters based on significant GCA effect in desirable direction
UP Chari-4	Plant height, number of leaves per plant, total soluble solids and green fodder yield per plant
G-48	Days to 50% flowering, plant height, leaf length, number of leaves per plant, leaf area, leaf stem ratio, total soluble solids, and green fodder yield per plant
HC-260	Days to 50% flowering, plant height, leaf length, leaf breadth, total soluble solids and protein content
UP Chari-2	Leaf length, number of leaves per plant, leaf area, stem girth, total soluble solids and protein content
SSV-84	Days to 50% flowering, plant height, leaf breadth, number of leaves per plant, leaf area, total soluble solids and green fodder yield per plant
Pusa Chari-6	Plant height, number of leaves per plant and leaf stem ratio
Pant Chari-4	Plant height, leaf breadth, number of leaves per plant, leaf area and protein content
HC-136	Days to 50% flowering, plant height and leaf length
Pant Chari-7	Leaf area, protein content and green fodder yield
Pant Chari-3	Days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, leaf stem ratio and green fodder yield per plant
UP Chari-1	Days to 50% flowering, plant height, leaf breadth, leaf area, stem girth, leaf stem ratio, total soluble solids, protein content and green fodder yield per plant
Jawahar Chari-6	Days to 50% flowering, plant height, leaf breadth, number of leaves per plant, leaf area, stem girth, total soluble solids and protein content
MP Chari	Days to 50% flowering, plant height, number of leaves per plant, leaf area, stem girth, leaf stem ratio, total soluble solids and green fodder yield per plant
HC-171	Days to 50% flowering, plant height, leaf length, leaf breadth, leaf area, stem girth, leaf stem ratio, protein content and green fodder yield per plant
UP Chari-3	Days to 50% flowering, plant height, leaf length, leaf breadth and protein content
HJ-513	Leaf length, number of leaves per plant, leaf area, stem girth, total soluble solids and green fodder yield per plant

Best specific crosses sowing significant SCA effect of green fodder yield per plant and their parents gca effect in forage sorghum

L x T Crosses	SCA effect (fodder yield)	GCA effect		Other characters exhibiting significant heterosis in desirable heterosis in desirable direction
		P ₁	P ₂	
UP Chari-4 x HC-171	78.60**	80.73**	47.39**	Days to 50% flowering, plant height, leaf breadth, number of leaves per plant, leaf area, stem girth, leaf stem ratio and green fodder yield per plant
UP Chari-4 x UP Chari-3	26.74**	80.73**	- 7.56	Leaf breadth, leaf area, stem girth, leaf stem ratio and green fodder yield per plant
UP Chari-4 x HJ-513	95.02**	80.73**	55.20**	Days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth, leaf stem ratio and green fodder yield per plant
G-48 x UP Chari-3	51.03**	21.25**	- 7.56	Days to 50% flowering, plant height, leaf length, leaf breadth and green fodder yield per plant
G-48 x HJ-513	24.24**	21.25**	55.20**	Days to 50% flowering, plant height, total soluble solids and green fodder yield per plant
HC-260 x UP Chari-3	49.91**	- 0.47	- 7.56	Days to 50% flowering, leaf breadth, number of leaves per plant, leaf area, and green fodder yield per plant
HC-260 x HJ-513	28.25*	- 0.47	55.20**	Leaf breadth, number of leaves per plant, leaf area, total soluble solids and green fodder yield per plant
SSV-84 x MP Chari	49.91**	47.92**	34.97**	Days to 50% flowering, plant height, leaf breadth, leaf area, stem girth and green fodder yield per plant
SSV-84 x HC-171	28.25*	47.92**	47.39**	Days to 50% flowering, plant height, leaf breadth, leaf area, and green fodder yield per plant
SSV-84 x UP Chari-3	49.91**	47.92**	- 7.56	Plant height, leaf length, leaf breadth and green fodder yield per plant
Pusa Chari-6 x UP Chari-3	30.72*	11.90	- 7.56	Days to 50% flowering, leaf breadth, leaf area and green fodder yield per plant
Pusa Chari-6 x HJ-513	60.33**	11.90	55.20**	Days to 50% flowering, leaf length, leaf breadth, stem girth and green fodder yield per plant
HC-136 x HJ-513	30.72*	6.03	55.20**	Days to 50% flowering, leaf length, leaf breadth, leaf area and green fodder yield per plant
Pant Chri-7 x MP Chari	60.33**	72.19**	34.97**	Days to 50% flowering, leaf area, stem girth, protein content and green fodder yield per plant
Pant Chari-7 x HC-171	30.72*	72.19**	47.39**	Leaf stem ratio and green fodder yield per plant
Pant Chari-3 x MP Chari	23.20*	26.49**	34.97**	Days to 50% flowering, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth and green fodder yield per plant
Pant Chari-3 x UP Chari-3	82.34**	26.49**	- 7.56	Days to 50% flowering, plant height, leaf length, leaf area, leaf stem ratio and green fodder yield per plant
Pant Chari-3 x HJ-513	40.76**	26.49**	55.20**	Days to 50% flowering, plant height, leaf length, leaf breadth, leaf area, leaf stem ratio, and green fodder yield per plant
UP Chari-1 x MP Chari	50.38**	52.29**	34.97**	Days to 50% flowering, leaf breadth, number of leaves per plant, leaf area, leaf stem ratio, total soluble solids, protein content and green fodder yield per plant
UP Chari-1 x HC-171	39.43*	52.29**	47.39**	Stem girth, leaf stem ratio and green fodder yield per plant
UP Chari-1 x HJ-513	77.12**	52.29**	55.20**	Days to 50% flowering, plant height, stem girth, leaf stem ratio and green fodder yield per plant
Jawahar Chari-6 x UP Chari-3	53.29**	0.44	- 7.56	Days to 50% flowering, leaf breadth, leaf area, leaf stem ratio and green fodder yield per plant
Jawahar Chari-6 x HJ-513	62.68**	0.44	55.20**	Days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth, leaf stem ratio and green fodder yield per plant

Ranking of crosses exhibited highly significant heterosis over better parent for green fodder yield per plant in forage sorghum

L x T Crosses	Heterosis (%)	SCA effects	GCA effects		Other characters exhibiting significant heterosis in desirable direction
			P ₁	P ₂	
UP Chari-4 x MP Chari	12.91**	19.68	80.73**	34.97**	Stem girth, leaf length, leaf breadth, total soluble solids, leaf stem ratio and green fodder yield per plant
UP Chari-4 x HC-171	30.35**	78.60**	80.73**	47.39**	Plant height, number of leaves per plant, stem girth, leaf breadth, total soluble solids, leaf area, leaf stem ratio and green fodder yield per plant
UP Chari-4 x HJ-513	26.09**	95.02**	80.73**	55.20**	Stem girth and green fodder yield per plant
G-48 x MP Chari	30.72**	7.41	21.25**	34.97**	Days to 50% flowering, plant height, number of leaves per plant, stem girth, leaf length, total soluble solids, leaf area, leaf stem ratio and green fodder yield per plant
G-48 x HC-171	30.40**	9.39	21.25**	47.39**	Days to 50% flowering, plant height, stem girth, leaf breadth, total soluble solids, leaf stem ratio, protein content and green fodder yield per plant
G-48 x HJ-513	20.75**	24.24*	21.25**	55.20**	Plant height, leaf length and green fodder yield per plant
HC-260 x UP Chari-3	19.20**	49.91**	- 0.47	- 7.56	Days to 50% flowering, number of leaves per plant, stem girth, leaf breadth, leaf area and green fodder yield per plant
SSV-84 x UP Chari-3	24.47**	77.42**	47.92**	- 7.56	Plant height, number of leaves per plant, stem girth and green fodder yield per plant
Pusa Chari-6 x MP Chari	32.06**	-8.01	11.90	34.97**	Leaf stem ratio, protein content and green fodder yield per plant
Pusa Chari-6 x HJ-513	32.83**	60.33**	11.90	55.20**	Number of leaves per plant and green fodder yield per plant
Pant Chari-4 x HC-171	31.47**	2.76	-8.39	47.39**	Plant height, leaf length, total soluble solids, leaf area, leaf stem ratio, protein content and green fodder yield per plant
Pant Chari-4 x HJ-513	14.74**	-2.52	-8.39	55.20**	Leaf length, protein content and green fodder yield per plant
HC-136 x UP Chari-3	22.96**	-21.68**	6.03	- 7.56	Stem girth and green fodder yield per plant
Pant Chari-7 x UP Chari-3	26.34**	10.00	72.19**	- 7.56	Days to 50% flowering, leaf breadth, leaf area, leaf stem ratio and green fodder yield per plant
Pant Chari-3 x MP Chari	29.99**	23.20*	26.49**	34.97**	Plant height, number of leaves per plant, stem girth, leaf length, total soluble solids and green fodder yield per plant
Pant Chari-3 x HC-171	34.12**	8.38	26.49**	47.39**	Plant height, number of leaves per plant, stem girth, leaf stem ratio, protein content and green fodder yield per plant
Pant Chari-3 x HJ-513	23.54**	40.76**	26.49**	55.20**	Plant height, number of leaves per plant, leaf length, leaf area, leaf stem ratio and green fodder yield per plant
UP Chari-1 x MP Chari	23.06**	50.38**	52.29**	34.97**	Days to 50% flowering, leaf length, leaf breadth, leaf area, leaf stem ratio, protein content and green fodder yield per plant
UP Chari-1 x HC-171	20.23**	39.43*	52.29**	47.39**	Plant height, stem girth, leaf breadth, leaf stem ratio and green fodder yield per plant
Jawahar Chari-6 x HC-171	41.53**	-5.70	0.44	47.39**	Days to 50% flowering, plant height, number of leaves per plant, leaf length, leaf breadth, total soluble solids, leaf area, leaf stem ratio, protein content and green fodder yield per plant
Jawahar Chari-6 x UP Chari-3	22.35**	53.29**	0.44	- 7.56	Days to 50% flowering, leaf length, total soluble solids, leaf area and green fodder yield per plant
Jawahar Chari-6 x HJ-513	29.13**	62.68**	0.44	55.20**	Days to 50% flowering, stem girth, leaf breadth, total soluble solids, leaf area, leaf stem ratio and green fodder yield per plant

**LITERATURE
CITED**

- Aaref, K.A.O., Ahmad, M.S.H., Hovny, M.R.A. and Youns, O.A. (2016).** Combining ability and heterosis for some agronomic characters in grain sorghum (*Sorghum bicolor* L. Moench). *Middle East Journal of Agriculture Research*,5(2): 258-271.
- Abdelmula, A.A., Ahmed, M.I., Maarouf, I.M. and Seifeldin, G. (2014).** Combining ability and heterosis for yield and quality traits in forage sorghum (*Sorghum bicolor* L. Moench). *Tropentag, September 17-19*.
- Agarwal, M. and Shrotria, P.K. (2005).** Heterosis and inbreeding depression in forage sorghum (*Sorghum bicolor* L. Moench). *Indian J. Genet.* 65(2): 12-14.
- Agarwal, M., Singh, R. and Shrotria, P.K. (2005).** Combining ability analysis for forage yield and quality characters in sorghum (*Sorghum bicolor* L. Moench). *Forage Res.*, 31(1): 8-11.
- Agarwal, M.S., Rameshwar and Shrotria, P.K. (2003).** Correlation studies in sorghum. *Pantnagar Journal of Research*,1: 10-13.
- Agriculture Statistics at a Glance (2016).** Pp: 97-99.
- Ahlawat, N.K., Arya, V.K., Kumar, P. and Singh, S.K. (2018).** Genetic divergence in forage sorghum (*Sorghum bicolor* L. Moench). *Journal of Applied and Natural Science*, 10(1): 439-444
- Akabari, V.R. and Parmar, P.H. (2014).** Heterosis response and combining ability for green fodder yield and its quality traits in forage sorghum. *Journal of Progressive Agriculture*,5(1): 9-14
- Akabari, V.R., Parmar, H.P., Niranjana, M. and Nakarnani, D.B. (2012).** Heterosis and combining ability for green fodder yield and its contributing traits in forage sorghum (*Sorghum bicolor* L. Moench). *Forage Research*, 38(3): 156-16.

- Al-Jibouri, H.A., Millar, P.A. and Robinson, H.F. 1958.** Genotypic and environmental variance and covariance in an upland cotton cross of inter specific origin. *Agronomy Journal* 50: 633-636.
- Allard, R.W. (1960).** Principles of plant breeding. *John Wiley and sons Inc.* New York, Pp. 185.
- Anup, K.G. and Kumar, V.S. (2000).** Genetic variability and character association analysis in sudan grass. *Journal of Agricultural Sciences*, 13(4):833-839.
- Arunah, U.L., Chiezay, U.F., Aliyu, L. and Ahmed, A. (2015).** Correlation and path analysis between sorghum yield to growth and yield characters. *Journal of Biology*, 5(19): 2288-2294.
- Awari, V.R., Gadakh, S.R., Shinde, M.S. and Kusalkar, D.V. (2003).** Correlation study of morpho-physiological and yield contributing characters with grain yield in sorghum. *Annals of Plant Physiology*, 17(1): 50-20.
- Biradar, B.D., Vastrad, S.M. and Sajjanar, G.M. (2004).** Identification of combiners involving newly derived male sterile and restorer lines for yield and related traits in *rabi* sorghum (*sorghum bicolor* L. Moench). *Indian J. Genet*, 63(3): 237-238.
- Borole, D.N., Chaudhary, S.B. and Shinde, M.S. (2008).** Assessment of general combining ability of *rabi* sorghum genotypes over different environments. *Advances in Plant Sciences*, 21(2): 697-699.
- Briggle, L.W. (1963).** Heterosis in wheat, a review. *Crop science*, 3: 407-412.
- Burton, G.W. (1952).** Quantitative inheritance in grasses. Proc. 6th Int. Grassland Cong., 1:227-283.
- Chaudhary, L., Shushram and Lakshyadeep (2005).** Variability and association studies for show yield in Sorghum. *Indian J. Plang Genut. Resour.*, 18(2): 209-211.
- Chaudhary, R.K. and Arora, S. (2001).** Genetic variability and character association in sorghum. *Agricultural Science, Digest*. 21(4): 219-222.
- Chaudhary, S.B., Patil, J.V., Thombare, B.B. and Kulkarni, V.M. (2006).** Selection of parents based on combining ability studies in sorghum (*Sorghum bicolor* L. Moench). *Annals of plant physiology*, 20(1): 95-97.

- Chaudhary, S.B., Pawar, S.V., Patil, S.C. and Jambhale, V.M. (2004).** Heterosis studies in *rabi* sorghum. *Advances in Plant Sciences*, 17(1): 333-335.
- Chavan, S.K., Mahajan, R.C. and Fatak, S.U. (2010).** Genetic variability studies in sorghum. *Karnataka Journal of Agriculture Science*, 23(2): 322-323.
- Chikuta, S., Odong, T., Kabi, F. and Rubaihayo, P. (2017).** Combining ability and heterosis of selected grain and forage dual purpose sorghum genotypes. *Journal of Agricultural Science*, 9(2): 9752-9760.
- Damor, H.I., Parmar, H.P., Gohil, D.P. and Patel, A.A. (2018).** Genetic variability, character association, path coefficient in forage sorghum (*Sorghum bicolor* L. Moench), *Green Farming* Vol. 9 (2): 218-223.
- Deepalakshmi, A.J. and Ganesamurthy, K. (2007).** Studies on genetic variability and character association in *kharif* sorghum (*Sorghum bicolor* L. Moench). *Indian Journal of Agricultural Research*, 41(3): 177-182.
- Dehinwal, A.K., Pahuja, S. K., Shafiqurrahman, M., Kumar, A. and Sharma, P. (2017).** Studies on combining ability for yield and its component traits in forage sorghum. *International Journal of Pure Applied Bioscience* 5 (5):493-502.
- Dehinwal, A.K., Pahuja, S.K. and Shafiqurrahman, M. (2017).** Genetic improvement through standard heterosis for fodder yield in single cut of forage sorghum (*Sorghum bicolor* L. Moench). *Biosciences biotechnology Research Asia*, 14(1): 391-400.
- Dehniwal, A.K., Pahuja, S.K., Shafiqurrahman, M. and Kumar, A.(2017).** Assessment of quality components in multicut forage sorghum in different environment. *Forage Research*, 43(2): 151-155.
- Desai, N.J., Naik, M.R., Vashi, P.S. and Kshirsagar, R.M. (2006).** Heterosis in yield and yield components in sorghum. *Journal of Maharashtra Agricultural Universities*, 31(1): 66-68.
- Desai, S.A., Shrotria, P.K. and Singh, R. (2000).** Variability and heterosis for forage yield and its components in inter-specific crosses of forage sorghum. *Journal of Agricultural Science*, 13(2): 315-320.

- Dewey, D.R. and Lu, K.H. (1959).** A correlation and path coefficient analysis componentsof crested wheat grass. *Journal of Agronomy*, 51: 515-518.
- Diwakar, A., Ranwah, B.R., Sharma, D.B. and Sinha, S.K. (2016).** Study of variability parameters in forage sorghum (*Sorghum bicolor* L. Moench). *Research of Environment Life Science*, 9(5): 528-530.
- Dubey, M.K., Pandey, P.K., Shrotria, P.K., Chauhan, P. and Pandey, G. (2016).** Assessment of variability, correlation and path analysis for yield and yield related traits in sorghum genotypes. *Green Farming*, 7(6): 1291-1295.
- Dudley, J.W. and Moll, R.H. (1967). Interpretation and use of estimates of heritability and genetic variances in plant breeding. *American Society of agronomy*, **9(3): 257-262.**
- Endalamaw, C., Adugna, A. and Mohammed, H. (2017).** Correlation and path coefficient analysis of agronomic and quality traits in a bioenergy crop, sweet sorghum (*Sorghum bicolor* L. Moench). *African Journal of Biotechnology*, 16(47): 2189-2200.
- Fisher, R.A.(1918).** The correlation between relative on the supposition of Mendelian inheritance. *Trans. Roy Soc. Edinburgh*, 52: 399-433.
- Fisher, R.A. and Yates, F. (1938).** Statistical table for biological, agricultural and medical research, 5 AUGE. *Oliver and Boyd, Edinburgh.*
- Fonseca, S. and Patterson, F. (1968).** Hybrid vigour in a seven parent diallel crosses in common winter wheat (*Triticum aestivum* L.). *Crop Sci.*, 8: 85-88.
- Fouman, A., Ghannadha, M.R. and Moghaddam, A. (2003).** Evaluation of combining ability of sorghum lines for improving hybrid cultivars. *Genetics and Plant Breeding*, 19(2): 137-154.
- Galton, F. (1908).** Correlation and their measurement chiefly from onthromomentric data in, *Proceedings of the royal society of London*, 45(274): 135-145.

- Gardner, C.O. (1963).** Estimates of genetic parameter in cross fertilizing plants and their implication in plant breeding. In: *Statistical Genetics and Plant Breeding*. NASNRC, 982: 53-94.
- Ghazy, M.M.F. and Sakr, H.O. (2011).** Line x tester analysis across years to study combining ability in forage sorghum (*Sorghum bicolor* L. Moench). *Journal of Agriculture Chemistry and Biotechnology*, 2(3): 111-123.
- Ghorade, R.B., Kalpande, V.V. and Sonone, C.V. (2015).** Variability studies for various biometrical parameters in *kharif* sorghum. *Plant Archives*, 15(1): 201-203.
- Gilbert, N. (1967).** Additive combining abilities fitted to plant breeding data. *Biometrics*, 23:45-49.
- Girish, G., Kirarf, S.B., Lokesh, R., Vikas, Kulkarni, V., Rachappa, V., Yogesh, L.N. and Talwar, A.M. (2016).** Character association and path analysis in advanced breeding lines of *ofrabi* sorghum (*Sorghum bicolor* L. Moench). *Journal of Applied and Natural Science*, 8(1): 35-39.
- Gowen, J.W. (1952).** Heterosis, Lowastate college press, ames. *Lowa*, Pp 552.
- Goyal, M., Bajaj, R.K., Gill, B.S. and Sohu, R.S. (2013).** Combining ability and heterosis studies for yield and water use efficiency in forage sorghum (*Sorghum bicolor* L. Moench) top crosses under normal and water stress environments. *Forage Research*, 39(3):124-133.
- Grafius, J.E. (1959).** Heterosis in barley. *Agronomy journal*, 51: 551-554.
- Grewal, R.P.S., Pahuja, S.K., Yadav, R. and Singh, P. (2003).** Heterosis for fodder yield and its component traits in forage sorghum. *National Journal of Plant Improvement*, 5(1): 22-25.
- Griffing, B. (1956).** Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences*, 9: 463-493.
- House, L.R. (1985).** A guide to sorghum breeding 2nd Ed. International Crops Research Institute for the semi-arid tropics, Patancheru, India., Pp.- 206.

- Hovny, M.R.A., Bakheit, B.R., Hassaballa, E.A. and Amir, A.A. (2000).** Line x tester analysis for combining ability in grain sorghum (*Sorghum bicolor* L. Moench). *Assiut Journal of Agricultural Sciences*, 31(2): 147-161.
- Ikanovic, J., Glamoclija, D.J., Maletic, R., Popovic, V., Sokolovic, D., Spasic, M. and Rakic, S. (2011).** Path analysis of the productive traits in sorghum species. *Genetika*, 43(2): 253 -262.
- Ingle, K.P., Gahukar, S.J., Khelurkar, V.C., Ghorade, R.B., Kalpande, V.V., Jadhav, P.V. and Moharil, M.P.(2018).** Heterosis and combining ability for grain yield trait in rabi sorghum (*Sorghum bicolor* L. Moench) using line x tester mating design. *International Journal of Current Microbiology and Applied Sciences*, 6: 1925-1934.
- Iraddi, V., Raddy, T.D., Umakanth, A.V., Rani, C., Raddy, V.V. and Bhawe, M.H.V. (2013).** Genetic variability, heritability and character association studies in sweet sorghum (*Sorghum bicolor* L. Moench). *Journal of research ANGRAU*, 41(1):30-38.
- Iyanar, K. and Fazlullah, Khan, A.K.(2005).** Studies on character association and path analysis in forage sorghum for multicut habit. *Crop Research*, 29(1): 129-133.
- Iyanar, K., Gopalan, A. and Ramasamy, P. (2001).** Correlation and path analysis in sorghum. *Annals of Agricultural Research*, 22(4): 495-497.
- Jain, S.K. and Patel, P.R. (2012).** Genetic variability in land races of forage sorghum (*Sorghum bicolor* L. Moench) collected from different geographical origin of India. *International Journal of Agricultural Science*, 4(2): 182-185.
- Jain, S.K. and Patel, P.R. (2013).** Heterosis studies for yield and its attributing traits in sorghum (*Sorghum bicolor* L. Moench). *Forage Research*, 39(3): 114-117.
- Jain, S.K. and Patel, P.R. (2013).** Variability correlation and path analysis studies in sorghum (*Sorghum bicolor* L. Moench). *Forage Research*, 39(1):27-30.
- Jain, S.K. and Patel, P.R. (2016).** An assessment of combining ability and heterosis for yield and yield attributes in sorghum (*Sorghum bicolor* L. Moench). *Green Farming*, 7(4): 791-794.

- Jain, S.K., Elangovan, M. and Patel, N.V. (2017).** Correlation and path coefficient analysis for agronomical traits in forage sorghum (*Sorghum bicolor* L. Moench). *Indian Journal.Plant Genet.Resou*, 23(1):15-18.
- Jinks, J.L. and Jones, R.M. (1958).** Estimation of the components of heterosis. *Genetics*, 43: 223-234.
- Johansen, W.L. (1909).** Elemente der ExaktenErblichkeitslehre, Fisher Verlag, Jena.
- Johnson, H.W., Robinson, H.F. and Camstock, F. (1955).** Genotypic and phenotypic correlation in soybean and their implications in selection. *Agron. J.*, 47: 477-483.
- Kadam, D.E., Patil, F.B., Bhor, J.J. and Harer, P.N. (2001).** Line x tester analysis in sweet sorghum hybrids. *Journal of Maharastra Agriculture Universities*, 25(3): 318-319.
- Kale, B.H. and Desai, R.T. (2016).** Heterosis studies over different environments in sorghum (*Sorghum bicolor* L. Moench). *Advance research journal of crop improvement*, 7(1): 155-160.
- Kalpande, H.V., More, A.W., Aundhekar, R.L. and Dhutmal, R.R. (2018).** Genetic variability, heritability and genetic advance in sweet grain (*Hurda*) sorghum (*Sorghum bicolor* L. Moench). *International Journal of Current Microbiology and Applied Sciences*, 6: 400-405.
- Kalpande, V.V., Ghorade, R.B., Nair, B., Kahate, N.S. and Gunjal, S.M. (2015).** Heterosis studies for grain yield and yield component in post rainy sorghum. *Plant Archives*, 15(1): 177-180.
- Kamdi, S.R., Manjare, M.R. and Sushir, K.V. (2009).** Combining ability analysis of forage yield and component characters in sorghum (*Sorghum bicolor* L. Moench). *Crop Improvement*, 36(1): 38-40.
- Kanawade, D.G., Deshmukh, R.B., Kute, N.S., Patil, J.V. and Dhonde, S.R. (2001).** Combining ability studies in sorghum. *Indian Journal of Agricultural Research*, 35(1): 56-59.

- Kanbar, O.Z., Kanbar, A. and Shehab, S. (2011).** Combining ability and heterosis for some yield traits in sorghum (*Sorghum bicolor* (L.) Moench) using line x tester design. *Journal of Plant Production, Mansoura University*, 2(8): 1009-1016.
- Kalsikes, P.J. and Lee, J. 1971.** Quantitative inheritance in durum wheat. *Canadian Journal of genetics and cytology* 13:210-218.
- Kempthorne, O. (1957).** An introduction to genetics statistics. *John Wiley and Sons*. New York; Pp-458.
- Kempthorne, O. and Cushow, R.N. (1961).** Partial diallel cross. *Biometrics*, 17: 229-50.
- Khandelwal, V., Sharma, V. and Shrikant (2006).** Gene action for grain yield and its attributes over environment in sorghum (*Sorghum bicolor* L. Moench). *Annals of Agricultural Research*, 27(1): 16-20.
- Khandelwal, V., Shukla, M., Jodha, B.S., Nathawat, V.S. and Dashora, S.K. (2015).** Genetic Parameters and character association in sorghum (*Sorghum bicolor* L. Moench). *Indian Journal of Science and Technology*, 8(22): 974- 988.
- Khapre, P.R., Pole, S.P. and Borgaonkar, S. B. (2007).** Heterosis studies in *rabi* sorghum. *International Journal of Plant Sciences*, 2(2): 187-191.
- Khatod, J.P., Jilani, S.K., Bhople, P.P., Thawari, S.B. and Shivankar, R.S. (2002).** Combining ability studies in forage sorghum (*Sorghum bicolor* L.) through line x tester analysis. *Journal of Soils and Crops*, 12(2): 220-224.
- Kihara and Tsunewaki, K. (1962).** Pistillody of triticum durum induced by an *Aegilops* cytoplasm. *Ann. Rep. (1961) Nat. Inst. Genet. Japan*, 12: 50.
- Kishore, N. and Singh, L.N. (2005).** Variability and association studies under irrigated and rainfed situations in the submontane in forage sorghum. *Crop Res.*, 29(2): 252-258.
- Koelreuter, D.J.G. (1763).** Varlaufigenachricht von cinigen das geschlecht der pflauzonbefeffernden versuechen and beobachtangen, *Genetics*, Pp:- 266, Leizing.

- Kour, S. and Pradhan, U.K. (2016).** Genetic variability, heritability and expected genetic advance for yield and yield components in forage sorghum (*Sorghum bicolor* L. Moench). *RASHI* 1(2): 71-76.
- Kulkarni, Salimath, P.M. and Patil, M.S. (2006).** Combining ability analysis in *rabi* sorghum (*Sorghum bicolor* L. Moench). *Crop Research*, 32(3): 455-458.
- Kumar, M. H. and Sahib, K. H. (2003).** Genetic studies and correlations of biomass related characters in forage sorghum. *Journal of Research ANGRAU*, 31(3): 35-39.
- Kumar, N. and Singh, S.K. (2012).** Character association and path analysis in forage sorghum. *Progressive Agriculture*, 12(1):148-153.
- Kumar, N., Singh, S.K., Kerkhi, S.A., Singh B., Tanvir, H. and Lal, M. (2011).** Genetic variability, heritability and genetic advance for forage yield and quality traits in sorghum. *Progressive Agriculture*, 11(2): 479-481.
- Kumar, N., Singh, S.K., Singh, B. and Kerkhi, S.A. (2010).** Correlation and path analysis in forage sorghum. National Congress on Emerging Trends in Agricultural Research, 11-12 September at P.D.F.S.R. Meerut.
- Kumar, P. and Shrotria, P.K. (2016).** Combining ability & heterosis studies for yield & component traits in forage sorghum (*Sorghum bicolor* L. Moench). *Green Farming*, 7(1): 1-7.
- Kumar, S., Rao, S., Reddy, B.V.S., Ravindrababu, V. and Raddy, K.H.P. (2016).** Heterosis and inbreeding depression in tropical sweet sorghum (*sorghum bicolor* L. Moench). *Crop Research*, 51:1 <http://dx.doi.org/10.4172/2454-1761.1000104>.
- Kusalkar, D.V., Kachole, U.G., Nirmal, S.V. and Chaudhary, S.B. (2009).** Genetic variability analysis in *rabi* sorghum germplasm. *International Journal of Agricultural Science*, 5(1): 87-89.
- Lush, J.L. (1940).** Intra-Sira correlation and regression of offspring on dams as a method of estimating heritability of characters. *Proc. Ames. Soc. Animal Production*, 37: 293-301.

- Lush, J.L. (1949).** Heritability of quantitative characters in plants. *Proc. 8th Int. Con. Genet. Heredity* (Suppl. vol.): 356-375.
- Lyanar, K., Vijayakumar, G. and Khan, A.K.F. (2010).** Correlation and path analysis in multicut fodder sorghum. *Electronic Journal of Plant Breeding*, 1(4):1006-1009.
- Malik, A., Singh, S.K., Chand, P., Singh, B. and Singh, D.K. (2015).** Genetic variability, heritability and genetic advance studies on forage sorghum. *Progressive Agriculture*, 15(1): 92-94.
- Malik, A., Singh, S.K., Chand, P., Singh, B. and Singh, D.K. (2013).** Correlation and path analysis in forage sorghum. *Progressive Agriculture*, 13(1): 234-238.
- Mallinath, V., Biradar, B.D. and Chittapur, B.M. (2004).** Variability and correlation studies in pop sorghum. *Karnataka Journal of Agricultural Sciences*, 17(3): 463-467.
- Mather, K. and Jinks, J. L. (1971).** Biometrical Genetics. *Chapman and Hall*, London.
- Miller, P.A. and Rawlings, J.O. 1967a.** Selection for increased lint yield and correlated response in upland cotton. *Crop science* 7:637-640.
- Mohammed, I.A., Awadalla, A.A., Maarouf, I.M. and Seif, E.M.G. (2014).** Heterosis and combining abilities for yield and quality traits in forage sorghum (*Sorghum bicolor* L. Moench). *U. of K. Graduate College and Scientific Research..The 5th Annual Conference Agricultural and Veterinary Research, Khartoum, Sudan, Conference Proceedings*, 1(57).
- Mohan, M., Pahuja, S.K., Yadav, R. and Avtar (2007).** Combining ability studies for fodder yield and components in forage sorghum involving male sterile lines and testers. *Forage Res.*, 33(1): 17-21.
- More, A., Kalpande, H.V., Aundhekar, R.L., Chavan, S.K., Patil, V.S. and Jangampalli, S.S. (2014).** Heterosis and line x tester analysis of combining ability in *kharif* sorghum with special reference to grain mold (*Sorghum bicolor* L. Moench) *3rd International*

Conference on Agriculture & Horticulture October 27-29, Hyderabad International Convention Centre, India.

- Negash, G. and Chemed, D. (2005).** Interrelationships among quantitative traits in sorghum (*Sorghum bicolor* L. Moench) landraces from western Ethiopia. *Crop-Research Hisar*, 30(3): 432-438.
- Nyadanu, D. and Dikera, E. (2014).** Exploring variation, relationships and heritability of traits among selected accessions of sorghum (*Sorghum bicolor* L. Moench) in the upper east region of Ghana. *Journal of Plant Breeding and Genetics*, 2(3): 101-107.
- Pahuja, S.K., Arya, S., Kumari, P. and Panchta, R. (2014).** Evaluation of forage sorghum hybrids (*Sorghum bicolor* L. Moench). *Forage research*, 40(3): 159-162.
- Pal, K. Singh, S.K. Kumar, B. and Singh, C. (2017).** Studies on combining ability and heterosis in forage sorghum (*Sorghum bicolor* L. Moench). *Biochem. Cell. Arch.* Vol. 17 (1): 79-96.
- Pal, K., Singh, S.K., Kumar, B. and Singh, C. (2017).** Studies on heterosis and inbreeding depression in forage sorghum. *Biochem. Cell. Arch.* 17 (1): 117-128.
- Panday, S. and Shrotria, P.K. (2013).** Heterosis and inbreeding depression in forage sorghum (*Sorghum bicolor* L. Moench). *Forage Research*, 38(1): 35-39.
- Pandian, R.S. and Doss, D.K. (2001).** Heterosis of certain traits in single and three-way cross (hybrids of fodder sorghum). *Karnataka Journal of Agricultural-Sciences*, 14(3): 788-792.
- Panse, V.G. and Sukhatme, P.V. (1967).** Statistical methods for agricultural workers. *Indian Council of Agricultural Research*, New Delhi.
- Patel, K.V. and Patel, A.D. (2010).** Combining ability analysis for green fodder yield and quality attributes in sorghum (*Sorghum bicolor* L. Moench). *Crop Improvement*, 1(2): 187-193.
- Patel, K.V. and Patel, A.D. (2011).** Extent of heterosis for green fodder yield and its components traits in sorghum (*Sorghum bicolor* L. Moench). *International Journal of Plant Science*, 6(2): 348-351.

- Patil, C.N., Rathod, A.H., Vaghela, P.O., Yadav, S.R., Patade, S.S. and Shinde, A.S. (2014).** Study of correlation and path analysis in dual purpose sorghum (*Sorghum bicolor* L. Moench). *International Journal of Agricultural Sciences*, 10(2): 608-611.
- Patil, P.R. and Biradar, B.D. (2005).** Heterosis studies for productivity traits in *rabi* sorghum (*Sorghum bicolor* L. Moench). *Indian Journal of Genetics and Plant Breeding*, 65(3): 213-214.
- Pattnayak, V.K., Mahto, J.L. and Haider, Z.A. (2004).** Heritability studies in finger millet (*Eleusine coracana*). *Journal of Research*, 16(1): 127-129.
- Powers, L. (1945).** Relative yield of inbred lines and F₁ hybrids of tomato. *Bot.Gazette*.106:247-268.
- Prabhakar (2002).** Combining ability studies in *rabi* sorghum (*Sorghum bicolor* L. Moench). *Annals of Agricultural Research*, 23(3): 500-502.
- Prabhakar and Raut, M.S. (2010).** Exploitation of heterosis using diverse parental lines in *rabi* sorghum. *Journal of Plant Breeding*, 1(4): 680-684.
- Prakash, R., Ganesamurthy, K., Nirmalakumar, A. and Nagarajan, P. (2010).** Correlation and path analysis in sorghum (*Sorghum bicolor* L. Moench). *Electronic Journal of Plant Breeding*, 1(3): 315-318.
- Prakash, R., Ganesamurthy, K., Nirmalakumari, A. and Nagarajan, P. (2010).** Heterosis for fodder yield in sorghum (*Sorghum bicolor* L. Moench). *Electronic Journal of Plant Breeding*, 1(3): 319-327.
- Premalatha, N., Kumaravadivel, N. and Veerabadhiran, P. (2006).** Correlation and path analysis for yield and yield traits in sorghum (*Sorghum bicolor* L. Moench) through line x tester analysis. *Research on Crops*, 7(1): 187-190.
- Premalatha, N., Kumaravadivel, N. and Veerabadhiran, P. (2006).** Heterosis and combining ability for grain yield and its components in sorghum (*Sorghum bicolor* L. Moench). *Indian Journal of Genetics and Plant Breeding*, 66(2): 123-126.

- Rajarajan, K., Ganesamurthy, K. and Yuvaraja, A. (2018).** Genetic variability and diversity for shoot/root parameters under early drought stress condition in sorghum (*Sorghum bicolor* L. Moench) genotypes. *Forage Research*, 43(4): 266-269.
- Rajguru, A.B., Kashid, N.V., Kamble, M.S., Rasal, P.N. and Gosavi, A.B. (2005).** Gene action and heritability studies in *rabi* sorghum (*Sorghum bicolor* L. Moench). *Journal of Maharashtra Agricultural Universities*, 30(3): 367-368.
- Rana, D. S., Singh, B., Gupta, K., Dhaka, A. K. and Arya, S. (2012).** Response of multicut forage sorghum genotypes to different fertility levels. *Forage Research*, 37(4): 251-254
- Rana, H.R., Prajapati, K.N., Suthar, K.J. and Kher, H.R. (2016).** Study of variability correlation and path analysis in forage sorghum (*Sorghum bicolor* L. Moench). *The Bioscan*, 1(1): 259-263.
- Rani, K.J., Rana, B.S., Swarnalata, K., Rao, S.S. and Ganesh, M. (2007).** Genetic analysis of certain morpho-physiological characters in *rabi* sorghum. *Indian Journal of Genetics and Plant Breeding*, 67(3): 281-283.
- Ranjith, P., Ghorade, R.B., Kalpande, V.V. and Dange A.M. (2017).** Genetic variability, heritability and genetic advance for grain yield and yield components in sorghum. *International Journal of Farm Sciences*, 7(1): 90-93.
- Ravindrababu, Y., Pathak, A.R. and Tank, C.J. (2001).** Studies on combining ability for yield and yield attributes in sorghum (*Sorghum bicolor* L. Moench). *Crop Res.*, 22(2): 274-277.
- Raza, I. and Naheed, S. (2014).** Relationship among biometrical characters of sorghum hybrid. *Science Technology and Development*, 33(4): 175-177.
- Ringo, J., Onkware, A., Mgonja, M., Deshpande, S., Rathore, A., Mneney, E. and Gudu, S. (2015).** Heterosis for yield and its components in sorghum (*Sorghum bicolor* L. Moench) hybrids in dry lands and sub-humid environments of East Africa. *Australia Journal of Crop Science*, 9(1): 9-13.
- Rini, E.P., Trikoesoemaningtyas, Wirnas, D., Sopandial, D. and Tesso, T.T. (2016).** Heterosis of sorghum hybrid developed from local and introduced lines. *International Journal of Agronomy and Agricultural Research*, 8(3): 1-9.

- Robinson, H.F., Comstock, R.E. and Harvey, P.H. (1949).** Estimates of heritability and the degree of dominance in corn. *Agron. J.*,41: 353-359.
- Robinson, H.F., Comstock, R.E. and Harvey, P.H. (1951).** Genotypic and phenotypic correlation in corn and their implication in selection. *Agron. J.*,43: 262-67.
- Satpal, Duhan, B.S., Joshi, U.N., Godara, A.S., Arya, S. and Neelam (2015).** Response of yield quality and economics of single cut forage sorghum genotypes to different nitrogen and phosphorus levels. *Forage research*, 41(3): 170-175.
- Shaug, S.P., Lin, J.B. and Chen, Y.Y. (2000).** Selection of F₁ hybrid in forage sorghum. *Journal of Taiwan Live Stock research*, 33(2): 154-164.
- Shinde, M.S., Awari, V.R., Patil, V.R., Chavan, U.D., Dalvi, U.S. and Gadakh, S.R. (2015).** CSV30F: New high yielding single cut forage sorghum variety for *Kharif* season. *Forage research*, 41(3):194-198.
- Shivani, D. and Sreelakshmi Ch. (2013).** Genetic analysis of yield and agro-morphological traits in cms based hybrids of *rabi* sorghum. *Forage Research*, 38(4): 234-238.
- Shull, G.H. (1914).** Duplicate genes for capsule form in bursa, *Bursa Nastosis Zetscher Induktiv Abstamm U. Vererbuglehna*, 12: 97-149.
- Singh, A. and Singh, S.K. (2017).** Studies on combining ability in forage sorghum for yield and quality parameters. *Journal of Plant Development Science* Vol. 9 (8): 785-792.
- Singh, A. Singh, S.K. Chand, P. Kerkhi, S.A. Kumar, M. and Singh, R.V. (2017).** Variability, character association and path analysis studies in forage sorghum, *Journal of Plant Development Science* Vol. 9 (7): 691-694.
- Singh, D. and Chauhan, A. (2017).** Fodder yield, quality and nutrients uptake potential of different types of sorghum (*Sorghum bicolor*) varieties in Central Gujarat. *Forage Research*, 43(2): 121-128.
- Singh, K., Choudhary, L. and Choudhary, B.R. (1999).** Component analysis for grain yield in sorghum, *Indian.J. Pl. Genet. Resource*, 12(1): 86-90.

- Singh, S.K. and Sirohi, A. (2006).** Genetic variability, heritability and genetic advance in forage sorghum. *Ann. Pl. Soil. Res.*, 8(2): 166-168.
- Singh, S.K. and Sirohi, A. (2007).** Correlation and path coefficient studies in sorghum *environmental and ecology*, 5(3):514-516.
- Singh, S.K., Singh, A. and Kumar, R. (2016).** Genetic variability, character association and path analysis in forage sorghum. *Progressive Agriculture*, 16(2):214-218.
- Singh, S.K., Sirohi, A., Singh, A., Kumar, V. and Kumar, U. (2009).** Studies on correlation and path analysis in forage sorghum (*Sorghum bicolor* L. Moench). *Progressive Agriculture an International Journal*, 9 (1): 85-91.
- Singh, S.K., Sirohi, A., Singh, D. and Singh, A. (2005).** Evaluation of Sorghum varieties for green fodder. *J. Farming System Research & Development*, 11(2): 254-255.
- Singh, S.K., Sirohi, A., Singh, D., Singh, A. and Singh, S.P. (2006).** Evaluation of different varieties of sorghum for green fodder yield potential. In Souvenir Second National Symposium "Recent Trends in Hi-Tech Agriculture 04-05 November at S.V.P.U.A. & T, Meerut, Pp- 56.
- Soltani, A., Rezal, A.M. and Pour, M.R.K. (2001).** Genetic variability of some physiological and agronomic traits in grain sorghum. *Journal of Science and Technology of Agriculture and Natural Resources*, 5(1): 127-137.
- Soujanya, T., Shashikala, T. and Umakanth, A. V. (2018).** Heterosis and combining ability studies in sweet sorghum (*Sorghum bicolor* L. Moench) hybrids for green fodder yield and quality traits. *Forage Research*, 43(4): 255-260.
- Sprague, G.F. and Tatum, D.A. (1942c).** General and specific combining ability in single crosses of corn. *J. Amer Soc. Agron*, 34: 923-932.

- Tag-el-din, A.A., Hassein, E.M. and Ali, E.A. (2012).** Path coefficient and correlation assessment of yield and yield associated traits in sorghum (*Sorghum bicolor* L. Moench) genotypes. *American Eurasian Journal of Agriculture & Environment Science*, 12(6): 815-819.
- Tariq, A.S., Akram, Z., Shabbir, G., Khan, K.S. and Iqbal, M.S. (2012).** Heterosis and combining ability for quantitative traits in fodder Sorghum (*Sorghum bicolor* L. Moench). *Electronic Journal of Plant Breeding*, 3(2):775-781.
- Tariq, A.S., Akram, Z., Shabbir, G., Khan, K.S., Mahmood, T. and Iqbal, M.S. (2014).** Heterosis and combining ability evaluation for quality traits in forage sorghum (*Sorghum bicolor* L. Moench). *SABRAO Journal of Breeding and Genetics*, 46(2): 174-182.
- Tiwari, D.K., Gupta, R.S. and Mishra, R. (2003).** Study of heritability and genetic advance in grain sorghum (*Sorghum bicolor* L. Moench). *Plant Archives*, 3(2): 181-182.
- Tomar, S.S., Sivakumar, S. and Ganesamurthy, K. (2012).** Genetic variability and heritability studies for different quantitative traits in sweet sorghum (*Sorghum bicolor* L. Moench) genotypes. *Electronic journal of plant breeding*, 3(2): 806-810.
- Umakanth, A.V. and Kuriakose, S.V. (2005).** Assessment of sorghum landraces for combining ability. *Agricultural Science Digest*, 25(4): 272-274.
- Umakanth, A.V., Madhusudhana, R., Latha, K.M., Swaranalatha, K. and Rana, B.S. (2003).** Heterosis studies for yield and its components in *rabi* sorghum (*Sorghum bicolor* L. Moench). *Indian Journal of Genetics and Plant Breeding*, 63: 159-160.
- Umakanth, A.V., Madhusudhana, R., Latha, K.M., Swarnlata, K. and Rana, B.S. (2003).** Genetic divergence in land race collections of *rabi* sorghum (*Sorghum bicolor* L. Moench). *Indian Journal of Genetics and Plant Breeding*, 63(3): 257-258.
- Unche, P.B., Misal, M.B., Borgaonkar, S.B., Godhawale, G.V., Chavan, B.D. and Sawant, D.R. (2008).** Genetic variability studies in sweet sorghum (*Sorghum bicolor* L. Moench). *International Journal of Plant Sciences*, 3(1): 16-18.

- Vavilov, N.I. (1951).** The origin variation, immunity & breeding of cultivated plants (Translated from Russian By K. C. Chester), New York, *The Ronald of Press Co.*
- Vedansh, Singh, S.K., Kerkhi, S.A., Singh, A., Kumar, M. and Kumar, V. (2010).** Variability, heritability and genetic advance for forage yield and quality traits in forage sorghum (*Sorghum bicolor* L. Moench). *Progressive Agriculture*, 10(2): 400-401.
- Vinaykumar, R., Jagadeesh, B.N., Talekar, S., Sandeep, R.G. and Rao, M.R.G.(2011).** Combining ability of parents and hybrids for juice yield and its attributing traits in sweet sorghum (*Sorghum bicolor* L. Moench). *Electronic journal of plant breeding*, 2(1): 41-46.
- Wadikar, P.B., Ubale, D.L., Magar, M.R. and Thorat, G.S. (2018).** Genetic variability studies in sweet sorghum (*Sorghum bicolor* L. Moench). *International Journal of Current Microbiology and Applied Sciences*, 6: 920-923.
- Warkad, Y.N., Tidkei, R.T., Maske, N.M., Kharde, A.V. and Potdukhe, N.R. (2010).** Character association and path analysis in sorghum (*Sorghum bicolor* L. Moench). *Internation Journal of Agricultural Sciences*, 6(1): 100-104.
- Wilson, L.A. (1967).** The use of rooted leaves and grafted plants for the study of carbohydrate metabolism in sweet potato. In Tai E. A. et al., eds., *Proc. Int. Symp. Trop. Root Crops*, Section II, 46-57.
- Wright, S. (1921).** Correlation and causation. *J. Agric. Res.*, 20: 557-585.
- Yadav, R. and Pahuja, S. K. (2007).** Combining ability for fodder yield and its components in forage sorghum. *Forage research*, 32(4): 220-223.
- Yadav, R., Pahuja, S.K., Grewal, R.P.S. and Yadav, R. (2003).** Evaluation of phenotypic variability in forage sorghum genotypes. *Forage Research*, 29(3):123-128.



APPENDICES

Appendix - I
Mean performance of 48 F₁'s and sixteen parents of line x testers (12 x 4) in forage sorghum for eleven characters

Crosses / Variety	Days to 50% Flowering	Plant Height (cm)	Leaf Length (cm)	Leaf Breadth (cm)	No. of Leaves Per Plant	Leaf Area (cm²)	Stem Girth (mm)	Leaf Stem Ratio	Total Soluble Solids (%)	Protein Content (%)	Green Fodder Yield per plant (g)
UP Chari-4 x MP Chari	83.66	310.00	75.73	7.36	15.33	395.82	19.87	0.39	10.36	8.48	514.66
UP Chari-4 x HC-171	86.53	391.23	78.60	8.54	16.66	486.34	20.39	0.36	10.53	9.35	586.00
UP Chari-4 x UP Chari-3	85.93	304.40	75.53	8.86	15.26	475.14	15.89	0.43	10.24	8.08	349.20
UP Chari-4 x HJ-513	87.66	326.66	75.53	7.78	15.53	417.20	23.18	0.38	10.26	8.36	390.20
G-48 x MP Chari	90.86	317.46	74.33	7.57	15.13	403.03	22.45	0.41	10.33	8.36	581.86
G-48 x HC-171	88.06	329.96	75.53	8.34	14.46	447.24	21.54	0.37	9.86	9.16	586.26
G-48 x UP Chari-3	91.46	281.20	76.86	7.84	14.33	430.86	20.48	0.38	9.67	7.83	340.90
G-48 x HJ-513	92.80	327.83	75.66	7.85	13.86	422.54	23.14	0.33	8.21	8.51	608.93
HC-260 x MP Chari	73.33	317.93	82.66	7.00	15.60	410.86	18.58	0.40	10.74	7.24	583.56
HC-260 x HC-171	82.40	381.90	83.73	6.71	15.26	399.16	21.08	0.39	11.22	8.92	579.56
HC-260 x UP Chari-3	70.86	320.83	80.66	8.56	13.13	490.25	20.78	0.39	10.90	7.28	463.56
HC-260 x HJ-513	74.33	333.26	82.66	8.28	15.80	483.12	21.49	0.34	11.05	7.90	578.16
UP Chari-2 x MP Chari	85.80	306.10	72.53	7.46	17.00	384.58	21.56	0.40	10.60	9.41	582.96
UP Chari-2 x HC-171	84.80	302.20	78.33	8.00	15.06	451.57	21.07	0.38	10.86	9.30	589.96
UP Chari-2 x UP Chari-3	85.86	299.23	67.60	8.31	15.40	398.99	21.23	0.36	10.64	8.47	412.76
UP Chari-2 x HJ-513	86.66	323.76	65.66	8.42	15.00	392.59	22.76	0.43	10.40	8.84	606.13
SSV-84 x MP Chari	81.13	221.26	75.73	8.24	16.60	443.51	15.61	0.40	10.22	8.34	586.83
SSV-84 x HC-171	91.13	287.00	75.93	8.42	14.86	470.69	22.09	0.39	9.78	8.93	595.53
SSV-84 x UP Chari-3	83.20	281.46	75.20	8.38	16.00	447.45	21.84	0.37	9.76	7.72	538.53
SSV-84 x HJ-513	78.26	336.80	73.60	9.08	15.46	474.48	24.54	0.33	9.44	8.19	673.76
Pusa Chari-6 x MP Chari	88.00	315.76	76.63	7.56	16.06	411.32	19.91	0.41	10.27	8.33	589.60
Pusa Chari-6 x HC-171	92.33	360.06	83.06	8.46	15.66	496.32	20.52	0.39	10.25	8.42	588.43
Pusa Chari-6 x UP Chari-3	84.00	301.36	76.20	7.69	15.53	416.20	20.61	0.38	9.76	7.87	394.36

Pusa Chari-6 x HJ-513	89.73	328.86	73.73	8.32	16.00	435.90	17.88	0.34	9.11	8.51	678.17
Pant Chari-4 x MP Chari	84.80	305.40	73.86	6.99	16.20	366.77	20.10	0.40	10.22	8.50	582.30
Pant Chari-4 x HC-171	85.66	387.13	80.73	8.26	15.46	473.84	20.45	0.41	10.08	9.12	592.50
Pant Chari-4 x UP Chari-3	86.66	292.70	75.86	8.46	15.86	466.17	19.97	0.39	9.98	8.94	399.57
Pant Chari-4 x HJ-513	86.86	320.30	75.60	7.64	15.53	410.04	21.93	0.40	9.93	9.32	595.04
HC-136 x MP Chari	96.40	309.26	75.33	7.60	15.40	396.98	18.00	0.41	10.10	7.35	591.46
HC-136 x HC-171	98.13	312.76	77.26	9.23	15.66	503.15	21.65	0.39	9.97	9.18	602.96
HC-136 x UP Chari-3	94.46	295.90	68.80	8.47	15.00	413.91	21.01	0.39	10.97	7.58	407.53
HC-136 x HJ-513	97.80	301.53	75.46	7.98	14.33	421.30	22.60	0.35	9.92	8.52	665.13
Pant Chari-7 x MP Chari	86.46	305.43	75.66	7.16	15.46	384.67	22.20	0.41	10.39	7.34	613.60
Pant Chari-7 x HC-171	91.06	367.56	79.66	8.23	15.26	459.03	21.10	0.33	10.12	8.80	635.20
Pant Chari-7 x UP Chari-3	89.86	298.30	76.06	8.54	14.26	454.48	19.39	0.41	10.05	7.30	585.93
Pant Chari-7 x HJ-513	90.00	308.50	76.40	7.78	15.73	422.36	22.80	0.39	9.53	8.14	657.00
Pant Chari-3 x MP Chari	83.00	271.73	85.53	6.27	16.73	379.82	16.28	0.47	10.50	8.30	635.40
Pant Chari-3 x HC-171	86.00	326.70	85.66	8.17	14.13	493.80	21.58	0.46	10.01	9.26	643.00
Pant Chari-3 x UP Chari-3	75.93	282.20	75.06	7.67	15.13	408.91	21.02	0.43	9.96	7.60	357.33
Pant Chari-3 x HJ-513	70.60	248.48	83.06	8.36	15.26	505.47	22.88	0.47	9.74	8.38	673.20
UP Chari-1 x MP Chari	93.73	307.33	76.73	8.91	16.26	492.27	16.47	0.62	10.34	9.66	583.80
UP Chari-1 x HC-171	98.46	366.16	76.93	8.87	13.93	484.70	21.18	0.63	9.90	9.66	585.26
UP Chari-1 x UP Chari-3	95.20	300.63	73.60	8.48	13.80	443.61	20.31	0.55	10.17	7.81	348.20
UP Chari-1 x HJ-513	98.53	302.10	72.93	8.62	14.40	445.72	16.55	0.40	9.95	8.78	476.53
Jawahar Chari-6 x MP Chari	97.93	313.50	78.13	8.69	12.40	492.38	13.92	0.54	10.45	7.36	582.46
Jawahar Chari-6 x HC-171	95.	389.16	80.66	9.10	12.60	518.22	17.55	0.55	10.13	9.08	592.86
Jawahar Chari-6 x UP Chari-3	100.33	309.03	77.80	8.66	12.46	485.07	19.38	0.46	9.29	7.17	360.33
Jawahar Chari-6 x HJ-513	100.20	344.30	77.66	9.28	13.26	511.69	23.61	0.38	9.42	7.74	669.06

Female											
UP Chari-4	87.20	299.03	72.60	7.04	14.20	363.27	17.41	0.34	9.53	7.72	351.40
G-48	92.33	251.83	71.20	7.17	12.00	362.66	19.56	0.33	6.98	8.14	318.80
HC-260	73.00	316.90	81.60	7.40	16.60	429.07	17.28	0.35	10.35	6.80	528.00
UP Chari-2	85.06	295.66	66.93	7.36	15.60	349.76	17.72	0.30	9.70	8.69	568.80
SSV-84	75.93	209.26	73.60	7.57	15.53	395.83	17.40	0.35	7.94	7.30	515.50
Pusa Chari-6	87.20	294.63	74.73	7.40	14.80	425.92	17.00	0.32	7.85	7.43	362.90
Pant Chari-4	86.53	296.66	71.66	7.44	14.80	378.57	18.00	0.36	8.26	8.12	468.56
HC-136	95.86	293.10	70.93	8.08	14.26	420.67	17.79	0.36	8.77	7.76	528.96
Pant Chari-7	88.06	294.23	75.00	7.42	14.33	395.43	20.92	0.33	8.70	6.70	625.56
Pant Chari-3	73.60	249.80	83.46	7.11	14.53	421.58	18.53	0.43	8.42	7.66	377.93
UP Chari-1	95.46	296.76	73.86	8.03	13.73	421.31	18.45	0.59	9.33	9.11	374.26
Jawahar Chari-6	96.66	298.86	75.20	8.10	13.26	432.87	15.97	0.50	6.73	6.51	532.66
Male											
MP Chari	82.80	336.60	72.66	6.76	15.40	349.06	18.56	0.34	9.52	6.52	577.68
HC-171	83.73	384.66	78.20	8.03	14.33	442.69	19.08	0.29	8.81	8.58	583.93
UP Chari-3	88.13	276.60	74.46	8.02	13.46	424.35	18.05	0.38	10.48	7.36	341.40
HJ-513	92.33	330.86	70.06	8.18	14.40	410.53	21.76	0.39	10.67	8.64	697.90
Mean	87.59	310.91	76.13	7.99	14.92	433.48	19.90	0.40	9.80	8.21	534.21
Range lowest	70.60	209.26	65.66	6.27	12.00	349.06	13.92	0.29	6.73	6.51	318.80
Range highest	100.33	391.23	85.66	9.28	17.00	518.22	24.54	0.63	11.22	9.66	697.90
S.E.	0.48	7.70	0.81	0.07	0.38	6.54	0.58	0.01	0.20	0.13	11.61
C.V.	0.96	4.29	1.86	1.71	4.41	2.61	5.10	4.46	3.64	2.74	3.76
C.D. 5%	1.37	21.57	2.29	0.22	1.06	18.30	1.64	0.02	0.57	0.36	32.51
C.D. 1%	1.81	28.51	3.02	0.29	1.40	24.19	2.16	0.03	0.76	0.48	42.96

Weekly Meteorological Data (Kharif 2016) 23rd June to October- 2016

S.No.	Weeks	T.max (⁰ C)	T.min (⁰ C)	RH- Imax(%)	RH- IImin(%)	Rainfall (mm)
1	week.23	38.0	23.4	83.9	54.9	0.0
2	week.24	36.8	22.6	82.4	53.2	38.1
3	week.25	37.6.1	25.3	89.8	65.4	2.2
4	week.26	37.0	25.9	87.0	61.8	3.1
5	week.27	33.0	23.7	93.9	78.5	60.2
6	week 28	35.2	25.5	88.6	71.7	5.2
7	week 29	32.8	25.3	96.0	78.8	177.9
8	week 30	33.1	24.8	97.1	77.0	30.7
9	week 31	32.8	24.0	95.8	80.0	14.1
10	week 32	33.6	26.4	96.7	78.7	93.7
11	week 33	32.5	25.7	96.2	82.6	40.1
12	week 34	34.6	26.0	94.3	72.8	0.0
13	week 35	36.0	25.5	93.6	80.9	76.1
14	week 36	33.7	24.7	94.4	71.6	0.0
15	week 37	34.6	24.3	95.7	65.5	2.0
16	week 38	35.0	24.7	95.7	66.4	21.2
17	week 39	34.6	23.4	94.1	63.6	0.0
18	week 40	34.5	24.3	97.0	62.6	1.2
19	week 41	27.0	21.2	96.1	52.9	0.0
20	week 42	33.1	16.3	93.3	37.3	0.0
21	week 43	32.3	16.0	95.8	42.6	0.0
22	week 44	30.6	14.1	95.6	46.1	0.0
23	week 45	28.7	10.0	92.5	50.1	0.0
24	week 46	28.6	10.7	96.5	45.5	0.0

Weekly Meteorological Data (Kharif 2017) 23rd June to October- 2017

S.No.	Weeks	T.max (⁰ C)	T.min (⁰ C)	RH- Imax(%)	RH- Imin(%)	Rainfall (mm)
1	week.23	35.7	23.7	65.5	38.2	4.0
2	week.24	37.1	23.0	58.2	33.4	1.0
3	week.25	37.0	24.0	68.8	45.5	10.0
4	week.26	32.8	25.1	88.0	75.4	61.0
5	week.27	33.8	24.2	84.0	60.5	17.0
6	week 28	31.5	24.8	86.4	65.2	2.0
7	week 29	33.2	25.2	86.2	71.4	55.0
8	week 30	32.8	24.8	94.4	73.0	20.0
9	week 31	31.8	25.1	96.5	79.9	47.0
10	week 32	32.1	25.0	92.4	71.1	30.7
11	week 33	31.1	25.0	87.1	73.6	38.0
12	week 34	32.5	25.1	91.2	73.8	27.0
13	week 35	29.5	23.4	94.4	73.7	208.0
14	week 36	32.1	21.8	95.8	71.9	19.0
15	week 37	33.8	22.4	90.4	68.3	0.0
16	week 38	30.8	21.3	92.7	72.3	57.0
17	week 39	33.4	21.0	98.7	58.9	0.0
18	week 40	33.3	19.5	97.7	52.4	0.0
19	week 41	32.5	18.2	97.4	48.7	0.0
20	week 42	32.7	14.4	95.5	44.8	0.0
21	week 43	30.6	13.3	96.8	53.3	0.0
22	week 44	28.2	9.7	93.8	55.0	0.0
23	week 45	26.0	10.7	96.8	69.0	0.0
24	week 46	27.7	13.1	94.8	52.7	0.0

ABSTRACT

Name : Ramraj Sen

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Major : Genetics and Plant Breeding

Minor : Plant Pathology

Advisor : Dr. Shiv Kumar Singh

Thesis Title : “Genetic analysis for quantitative traits in forage sorghum (*Sorghum bicolor* L. Moench)”

Degree awarding by University: SVPUA&T, Meerut

The present investigation entitled “Genetic analysis for quantitative traits in forage sorghum (*Sorghum bicolor* L. Moench)” was undertaken to collect information on genetic parameters for green fodder yield and its components from a sixteen parents (12 lines and 4 testers) line x tester mating design in forage sorghum at Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut (U.P.) during *khari* 2017 with 64 treatments. The experimental material was comprised of sixteen diverse parents viz. 12 lines and four testers and their 48 F₁s excluding reciprocals of a line x tester cross. All genotypes were evaluated in a complete randomized block design with three replications. The data were recorded on eleven characters viz., days to 50% flowering, plant height, leaf length, leaf breadth, number of leaves per plant, leaf area, stem girth, leaf stem ratio, total soluble solids, protein content and green fodder yield per plant. The data recorded were subjected to various statistical analyses. Analysis of variance observed highly significant differences among the parents and F₁s for all the characters. The parents vs hybrids showed highly significant differences for all the traits. The F test indicated that the variance due to treatments were highly significant for all the traits, justifying the presence of adequate variability with regard to important characters under study. Both additive and non additive components of genetic variation appeared important in the expression of almost all the characters. For exploitation of both the additive and non additive component of variation, material may be handled through pedigree method and modified recurrent selection or biparental mating for obtaining superior segregants and genotypes. Green fodder yield per plant showed positive and significant correlation with plant height, leaf length, number of leaves per plant, leaf area and stem girth at genotypic and phenotypic level. Hence by improved that these traits, yield could be improved. Highly positive and significant direct contribution of leaf area, leaf length, plant height, number of leaves per plant and stem girth with green fodder yield per plant and high indirect positive contribution of leaf length through days to 50% flowering; Leaf breadth via days to 50% flowering, number of leaves per plant, leaf stem ratio and protein content and leaf stem ratio through days to 50% flowering, leaf length, number of leaves per plant, leaf area and total soluble solids were responsible for their positive association with green fodder yield. Promising lines viz., G-48, UP Chari-1 and Pant Chari-3 and testers viz., HC-171 and MP Chari which were having high general combining ability effects in desirable direction for green fodder yield and yield components characters may be incorporated in crossing programme to have better genotypes for better yield. The cross combinations viz., UP Chari-4 x HC-171, UP Chari-4 x HJ-513, UP Chari-1 x MP Chari and Jawahar Chari-6 x HJ-513 were found to be best specific combiners for green fodder yield and its contributing traits. These cross combinations may be exploited for development of hybrid in forage sorghum or may be incorporated in multiple cross breeding programme to have better transgressive segregants with broad genetic base for the selection in forage sorghum improvement programme. Out of 48 F₁'s only three cross combinations which showed highest value of heterosis for green fodder yield namely UP Chari-4 x HC-171, G-48 x MP Chari and Jawahar Chari-6 x HC-171 over better parent may be exploited for developing hybrids with better yield in sorghum. High heritability coupled with high genetic advance were observed for plant height, leaf area, stem girth, leaf stem ratio and green fodder yield per plant, which indicated that these attributes might also be taken directly in to consideration for improvement in sorghum through selection breeding.

Dr. S. K. Singh
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CURRICULUM-VITAE



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Academics

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High School	U.P. BOARD.	2004
Intermediate	U.P. BOARD	2006
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AREA OF INTEREST

Research and development in the field of Genetics and Plant Breeding and Teaching.

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A Study of “Path Analysis in Some Development Characters in Indian Colaza (*Brassica juncea* (L.) Czern and Coss) ”

PUBLICATIONS: Research Papers:

Ramraj Sen, Bhuri Singh & S.P. Singh (2013). Relationship among Yield Components and Selection Criteria for Yield Improvement in Indian Colaza (*Brassica juncea* (L) Czern & Coss). *The Journal of Plant Science Research*. Volume 29 [2] ISSN 0970-2539.

DECLARATION

Hereby, I assure that the information furnished above is true. If I get an opportunity to work in your concern, I assure that I shall discharge my duties to the fullest satisfaction of my Employer and to the best of my ability.

Place: Meerut, India

Date : 20-07-2018

Your's Faithful
(Ramraj Sen)