Study on Genetic Variability for Forage Yield and Quality Traits in Forage Sorghum [*Sorghum bicolor* L. Moench]

ABSTRACT

The initial research related to germplasm screening was carried out in the experimental area of Instructional Dairy Farm, GBPUAT Pantnagar during *Kharif* season 2018. The experimental material for this experiment consisted of two hundreds and eighty diverse germplasm lines of sorghum along with six checks *viz*., SSG 59-3, Pant Chari- 5, Pant Chari- 6, CSV-21 F, CSH-22S, and CSV-24SS. The germplasm lines were evaluated in Augmented Block Design for nineteen forage yield related traits and thirteen quality traits. The statistical analysis for genetic variability was done using ANOVA, h^2, GCV, PCV, and GA. The analysis of variance revealed that the genotypes and checks were showing highly significant difference for all the traits under study indicated existence of inherent genetic differences among genotypes for different characters. Mean performance of forage yield and quality related traits exhibited a wide range of variability. GCV and PCV values were observed low for most of the characters whereas high for anthracnose, zonate leaf spot and shoot fly incidence. The value of genetic advance was observed high for leaf area, green fodder yield per plant, dry fodder yield per plant, hydrocyanic acid content, plant height, anthracnose, shoot fly incidence were relatively more than other characters. Genetic advance as percent of mean was observed low for days to maturity, dry matter percent, in-vitro dry matter disappearance, neutral detergent fiber, acid detergent fiber, cellulose content whereas high for leaf area, flag leaf width, panicle length, panicle width, 1000-grains weight, grain yield per plant, green fodder yield per plant, dry fodder yield per plant, total soluble solids, silica content, anthracnose, zonate leaf spot and shoot fly incidence. Heritability values were found high for all the traits under study. The genotypes bearing the desired values for different genetic variability parameters can be exploited in future breeding programme for the improving forage sorghum genotypes. These genotypes can be used as donor parents in crop improvement programme.

Keywords: Sorghum, ANOVA, GCV, PCV, andheritability.

1. Introduction: Sorghum is one of the most important and widely grown crops in the world having the area of 41.14 million hectare with the production of about 58.72 million tonnes globally whereas 5.00 million hectare and 4.50 million tonnes grain production in India **(USDA Foreign Agricultural Services, 2019).** Sorghum is called guinea-corn, dawa, or sorgho in West Africa, durra in the Sudan, mshelia in Ethiopia and Eritrea, mtama in East Africa, kaffir corn in South Africa, and amabele or mabele in several Southern African countries. It is called jowar, cholam, jonna, and jola in India. Five primary farmed sorghum races are Bicolor, Guinea, Kafir, Durra, and Caudatum **(Harlan and De Wet, 1972).** Food, fodder, feed, fuel, and fiber are produced from forage, grain, and sweet sorghum. Due to its drought resistance, fast growth, and outstanding palatability, the crop is grown in tropical and subtropical climates with varying rainfall, temperature, and soil. On small holdings in stress-prone and marginal semi-arid tropics, most of the crop is cultivated. It is produced in Northern Western India for kharif and summer feed. Sorghum is the best kharif fodder for nutrition, with starch (63.68%), high digestibility (50-60%), dry matter (20-35%), sugars (8-17%), crude protein (7.5-10.0%), calcium (0.53%), phosphorus (0.24%), and crude fiber (30-32%). In addition to carbs, it has more iron (Fe) and vitamin B3 than maize and rice. Sorghum is a staple food in Asia and Africa and an important feed crop in the US, Argentina, Mexico, South Africa, and Australia **(Miller and Kebede, 1984).** Any effective breeding program depends on genetic variation and the interactions among various individuals. Plant potential for increased efficiency is determined by genetic variability; consequently, their utility for breeding is determined as well, which finally might lead to increased forage production. Genetic variability helps to explain the genetic variations between several populations inside a species or between different species. Analyzing the several genetic parameters such as analysis of variance, heritability, genetic advance helps one to determine genetic variability. Higher heterotic expression in F1 and more genetic diversity in segregating populations are the outcomes of parents with higher genetic variability **(Shekhawat *et al*., 2001).** Plant breeders can choose genetically different parents for purposeful hybridization with the assistance of precise knowledge on the type and extent of genetic variability **(Arunachalam, 1981).** The degree and kind of genetic variability determines the genetic enhancement of yield, particularly in self-pollinated crops **(Joshi and Dhawan, 1966).** In sorghum breeding, hybridization and subsequent selection are two key techniques. The initial step in a plant breeding program using hybridization is the parents' decision. Genetic diversity between parents is required to produce transgressive segregants **(Joshi et al., 2004).** Higher levels of genetic variation between parents are associated with higher levels of heterosis in offspring **(Joshi and Dhawan, 1966).** In sorghum hybridization programs, one suitable tool for parental choice is genetic variability assessment. In order to maximize genetic recombination and perhaps boost output, crossing nurseries must employ parents who have been carefully selected. Given the foregoing, screening the variability of forage sorghum lines, according to yield and quality variables is necessary to determine their suitability for various breeding programs.

2. Materials and Methods: The initial research related to germplasm screening was carried out in the experimental area of Instructional Dairy Farm, Nagla, G.B. Pant University of Agriculture and Technology. Pantnagar, District U. S. Nagar, Uttarakhand during *Kharif*, 2018. The experimental material for this experiment consisted of two hundreds and eighty diverse germplasm lines of sorghum along with six checks *viz*., SSG 59-3, Pant Chari- 5, Pant Chari- 6, CSV-21 F, CSH-22S, and CSV-24SS. The germplasm lines were evaluated in Augmented Block Design during *Kharif* season of 2018. The experiment was carried out in an Augmented Block Design **(Federer, 1956, 1961, and Federer & Raghavrao, 1975)** with each block containing 35 test entries and 6 checks which were randomly allocated in 8 blocks. All genotypes were sown on 23rd July 2018 in single row of 5 meter length with a row spacing of 45 cm. All the recommended package of practices for sorghum was followed to raise a healthy crop. The observations were recorded on days to 50% flowering, days to maturity, number of leaves per plant, number of nodes, plant height (cm), leaf length (cm), leaf width (cm), leaf area (cm^2), flag leaf length (cm), flag leaf width (cm), stem girth (cm), internodal length (cm), panicle length (cm), panicle width (cm), leaf:stem ratio, 1000-grains weight (gm), grain yield per plant (gm), green fodder yield per plant (gm), dry fodder yield per plant (gm), foliar diseases zonate leaf spot and anthracnose **(Thakur *et al.*, 2010)**, shoot fly (*Atherigona soccata*) incidence (Dead hearts %), dry matter (%), brix %, HCN content (ppm) (**Hogg and Ahlagreen, 1942)** and **Gilchrist *et al*. (1967) ,** protein content (%) **(Jeckson, 1973),** in-vitro dry matter disappearance (IVDMD) % **(Erwin and Ellinston, 1959),** neutral detergent fiber **(Van Soest, 1991),** acid detergent fiber (%) and cellulose (%) **(Van Soest, 1991),** acid detergent lignin (%), cellulose (%) and silica (%) **(Van Soest, 1991). The statistical analysis was performed by Indostat Hyderabad.**

(A) Analysis of variance and means: The analysis of variance for the augmented design was done using the method given by **Federer (1956)** as described by **Federer and Ragavarao (1975) and Petersen (1985).**

(B) Estimation of variability:

$$\text{CV (\%)} = \frac{\text{Standard deviation}}{\text{Mean}} \times 100$$

Genotypic coefficient of variation (GCV %) $= \frac{\sigma_g}{\overline{X}} \times 100$

Phenotypic coefficient of variation (PCV %) $= \frac{\sigma_p}{\overline{X}} \times 100$

Environmental coefficients of variation (ECV %) $= \frac{\sigma_e}{\overline{X}} \times 100$

Where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

σ_e = Environmental standard deviation

$\overline{X}$ = Grand mean

(C)**Estimation of Heritability:** The heritability in broad sense h^2 (b) was estimated for each character as the ratio of genotypic variance to phenotypic variance by the formula:

$$\text{Heriheritability (\%)} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

(D) **Genetic Advance:** The expected genetic advance under selection for the different characters was estimated as suggested by **Allard (1960).**

$$GA = h_b^2 \times \sigma pi \times K$$

Where,

GA = expected genetic advance

h_b^2 = heritability in broad sense

σpi = phenotypic standard deviation for ith character

K = intensity of selection, the value of which is 2.06 at 5 % **(Lush, 1949)**

3. Results and Discussion:

3.1 Analysis of variance: Analysis of variance for Augmented Block Design was conducted for nineteen morphological and thirteen nutritional quality traits at different crop maturity stage for different characters Analysis of variance for different yield and quality parameters has been presented in **Tables .1**. The genotypes and checks were showing highly significant difference for all the traits viz., days to flowering, days to maturity, number of leaves, number of nodes, plant height. Leaf length, leaf width, leaf area, flag leaf length, flag leaf width, stem girth, inter-nodal length, panicle length, panicle width, leaf:stem ratio, 1000-grains weight, grain yield per plant, green fodder yield per plant, dry fodder yield per plant, dry matter percent, total soluble solids, hydrocyanic acid content, protein percent, in-vitro dry matter disappearance, neutral detergent fiber, acid detergent fiber, cellulose content, lignin content, silica content, hemicelluloses content, anthracnose, zonate leaf spot and shoot fly incidence. The blocks were also found highly significant for all the characters under study. This type of result indicated existence of inherent genetic differences among genotypes for different characters. The analysis of variance revealed significant difference among the genotypes which validated further on the basis of genetic and statistical analysis of the data. It revealed that mean squares due to genotypes were found to be significant for all the characters. The findings of present study were found similar with the findings of **Desai *et al.*, (2000), Kadam *et al.*, (2001), Kumar *et al.*, (2014), Agrawal *et al.*, (2005) , Bello *et al.*, (2007), Rani *et al.*, (2009),** and **Jadhav *et al.*, (2017)**.

3.2 Mean performance and range of variation: The mean performance of 280 genotypes and 6 checks along with their general mean and range values were calculated. General mean, range of variability and best top 10 germplasm are mentioned in **Table .2.** The range of mean performance for days to flowering ranged from 33 days in EP-124 to 88 days in GP- 2011-110-1 with a general mean of 63.57 days. The range of mean performance for days to maturity ranged from 97 days in R-77 (09R-AGR-26) to 148 days in IS 14357 with a general mean of 127.33 days.The range of mean performance for number of leaves per plant ranged from 7.30 in CSV-17 to 23.30 in IS 28313 with a general mean of 15.35. The range of mean performance for number of nodes ranged from 5.54 in CSV-17 to 21.32 in IS 28313 with a general mean of 14.13. The range of mean performance for plant height ranged from 138.22 cm in CSV-17 to 528.33 in SMC 8 with a general mean of 362.34. The range of mean performance for leaf length ranged from 56.30 cm in C-43 to 107.20 in IS 12735 with a general mean of 82.01 cm. The range of mean performance for leaf width ranged from 3.22 cm in CO (FS) 29 to 10.52 cm In RS 673 with a general mean of 7.36 cm. The range of mean performance for leaf area ranged from 150.45 cm^2 in IS 23992 to 731.43 cm^2 in SPV 1749 with a general mean of 431.22 cm^2. The range of mean performance for flag leaf length ranged from 28.15 cm in C-43 to 53.60 in IS 12735 with a general mean of 40.98 cm. The range of mean performance for flag leaf width ranged from 1.61 cm in CO (FS)-29 to 8.31 in CSV 19 with a general mean of 3.73 cm. The range of mean performance for stem girth ranged from 1.23 cm in GMS 1338 to 3.43 cm in SMC 14 with a general mean of 2.41 cm. The range of mean performance for internodal length ranged from 16.50 cm in EJN-58 to 40.23 cm in IS 6045 with a general mean of 27.52 cm. The range of mean performance for panicle length ranged from 5.23 cm in EJN-52 to 42.53 cm in SSG-223 with a general mean of 21.90 cm. The range of mean performance for panicle width ranged from 0.13 cm in PC-1002 to 30.23 cm in SSG-227 with a general mean of 10.55 cm. The range of mean performance for leaf: stem ratio ranged from 0.18 in SPV-1750 to 0.48 in RAJ 9-1 with a general mean of 0.29. The range of mean performance for 1000-grains weight ranged from 6.10 gm in CO (FS) 29 to 43.46 gm in UP Chari-1 with a general mean of 21.44 gm. The range of mean performance for grain yield per plant ranged from 24.40 gm in CO (FS) 29 to 165.20 gm in UP Chari -1 with a general mean of 85.04 gm. The range of mean performance for green fodder yield per plant ranged from 80.32 gm in EJ-27 to 835.13 gm in Pant Chari-3 with a general mean of 314.76 gm.The range of mean performance for dry fodder yield per plant ranged from 30.33 gm in EJ-27 to 491.60 gm in IS 14241 with a general mean of 113.24 gm. The range of mean performance for dry matter percent ranged from 29.33 % in IS 9162 to 41.80 % in CSH 19 with a general mean of 35.50 %. The range of mean performance for total soluble solids percent ranged from 2.13 % in SSG-243 to 16.50 % in IS 14756 with a general mean of 6.64 %. The range of mean performance for hydrocyanic acid content ranged from 34.14 ppm in CSV-14 to 118.14 ppm in EJ-27 with a general mean of 85.98 ppm. The range of mean performance for protein percent ranged from 7.12 % in CSV 19 to 15.57 % in IS 14241 with a general mean of 11.00 %. The range of mean performance for In-vitro dry matter disappearance ranged from 41.23 % in

EJ-30 to 63.25 % in IS 9162 with a general mean of 54.46 %. The range of mean performance for neutral detergent fiber ranged from 51.21 % in IS 1219 to 60.18 % in SSG-223 with a general mean of 55.17 %. The range of mean performance for acid detergent fiber ranged from 30.57 % in EJ-42 to 40.77 % in IS 18927 with a general mean of 34.97%. The range of mean performance for cellulose content ranged from 26.68 % in UPFS-36 (Pant Chari-7) to 33.22 % in SMC-14 with a general mean of 28.86 %. The range of mean performance for lignin content ranged from 4.13 % in IS 18008-2 to 8.14 % in IS 2363 with a general mean of 5.17 %. The range of mean performance for silica content ranged from 1.12 % in EJ-42 to 3.48 % in IS 18933 with a general mean of 2.05 %. The range of mean performance for hemicelluloses content ranged from 13.81 % in IS 25733 to 29.21 % in UPFS (Pant Chari-7) with a general mean of 21.31 %. The range of mean performance for anthracnose percent from 1.25% in SEVS- 2 to 79.25% in EJN-47 with a general mean of 23.40 %. The range of mean performance for zonate leaf spot percent from 1.12% in SSG- 245 to 46.25% in IS 15008-1 with a general mean of 7.84 %. The range of mean performance for Shoot fly incidence percent from 2.25% in IS 1478 to 50.75% in R-72 (09R-AGR-23) with a general mean of 20.24 %.

Any breeding programme's success is determined on the extent of genetic variability present in the breeding population. The assessment of variability in a crop is critical for identifying lines that can generate further variability, allowing for the artificial selection of desirable, diversified genotypes. Some of the most useful mutations would go unutilized if the breeder had not detected them throughout the selection process.

3.3. Estimates of genetic variability parameters: Robinson *et al.* (1994) classified heritability values as high (>60%), moderate (30-60%) and low (less than 30 %). **Deshmukh *et al.* (1986)** classified PCV and GCV values as low (0-10%), moderate (10-20%) and high (20% and above). **Falconer and Mackay (1996)** classified genetic advance as per cent of mean as low (0-10%), moderate (10-20%) and high (20% and above). The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation, genetic advance, genetic advance as percent of mean and heritability (h^2) are presented in **Table 3**. The heritability ranged from 53.32 (cellulose content) to 89.27 (green fodder yield per plant). Genetic advance ranged from 0.05 (leaf: stem ratio) to 108.11 (leaf area. Genetic advance as percent of mean ranged from 2.70 (neutral detergent fiber) to 72.28 (zonate leaf spot). Phenotypic coefficient of variation ranged from 1.55 (neutral detergent fiber) to 35.12 (zonate leaf spot). Genotypic coefficient of variation ranged from 1.31 (neutral detergent fiber) to 35.09 (zonate leaf spot).

3.3.1 Phenotypic coefficient of variation: Phenotypic coefficient of variation was observed low for days to flowering, days to maturity, number of leaves, number of nodes, plant height, Leaf length, leaf width, flag leaf length, stem girth, inter-nodal length, leaf: stem ratio, hydrocyanic acid content, protein percent, in-vitro dry matter disappearance, neutral detergent fiber, acid detergent fiber, cellulose content, lignin content, hemicelluloses content, moderate for leaf area, flag leaf width, panicle length, panicle width, 1000-grains weight, grain yield per plant, green fodder yield per plant, dry fodder yield per plant, dry matter percent, total soluble solids and silica content whereas high for anthracnose, zonate leaf spot and shoot fly incidence.

3.3.2 Genotypic coefficient of variation: Genotypic coefficient of variation was observed low for days to flowering, days to maturity, number of leaves, number of nodes, plant height, Leaf length, leaf width, flag leaf length, stem girth, inter-nodal length, leaf: stem ratio, hydrocyanic acid content, protein percent, in-vitro dry matter disappearance, neutral detergent fiber, acid detergent fiber, cellulose content, lignin content, hemicelluloses content, moderate for leaf area, flag leaf width, panicle length, panicle width, 1000-grains weight, grain yield per plant, green fodder yield per plant, dry fodder yield per plant, dry matter percent, total soluble solids and silica content whereas high for anthracnose, zonate leaf spot and shoot fly incidence.

3.3.3 Genetic Advance: The value of genetic advance was observed high for leaf area, green fodder yield per plant, dry fodder yield per plant, hydrocyanic acid content, plant height, anthracnose, shoot fly incidence were relatively more than other characters such as days to flowering, days to maturity, , Leaf length, leaf width, flag leaf length, flag leaf width, stem girth, inter-nodal length, stem girth, inter-nodal length, panicle length, panicle width, leaf:stem ratio, 1000-grains weight, dry matter percent, total soluble solids, protein percent, in-vitro dry matter disappearance, detergent fiber, acid detergent fiber, cellulose content, lignin content, silica content and zonate leaf spot.

3.3.4 Genetic advance as percent of mean: Genetic advance as percent of mean was observed low for days to maturity, dry matter percent, in-vitro dry matter disappearance, neutral detergent fiber, acid detergent fiber, cellulose content moderate for days to flowering, number of leaves, number of nodes, plant height, Leaf length, leaf width, flag leaf length, stem girth, inter-nodal length, leaf:stem ratio, hydrocyanic acid content, protein percent, lignin content, hemicelluloses content whereas high for leaf area, flag leaf width, panicle length, panicle width, 1000-grains weight, grain yield per plant, green fodder yield per plant, dry fodder yield per plant, total soluble solids, silica content, anthracnose, zonate leaf spot and shoot fly incidence.

3.3.4 Heritability (h^2) : Heritability (h^2) was observed high for days to flowering, days to maturity, number of leaves, number of nodes, plant height. Leaf length, leaf width, leaf area, flag leaf length, flag leaf width, stem girth, inter-nodal length, panicle length, panicle width, leaf: stem ratio, 1000-grains weight, grain yield per plant, green fodder yield per plant, dry fodder yield per plant, dry matter percent, total soluble solids, hydrocyanic acid content, protein percent, in-vitro dry matter disappearance, neutral detergent fiber, acid detergent fiber, lignin content, silica content, hemicelluloses content, anthracnose, zonate leaf spot and shoot fly incidence except cellulose content. Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when coupled with heritability estimates **(Johnson *et al.,* 1955).** High heritability coupled with high genetic advance was observed for leaf area, flag leaf width, panicle length, panicle width, 1000- grains weight, grain yield per plant, green fodder yield, dry fodder yield, total soluble solids, silica content, anthracnose, zonate leaf spot and shoot fly incidence. The estimates of genetic advance help in understanding the type of gene action involved in the expression of various yield and quality characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action **(Singh and Narayanan, 1999).** The findings of present study on genetic variability parameters were observed similar with the findings of **Jain and Patel (2012), Kumar (2014), Malik *et al.*, (2015), Supriya *et al*., (2015),** and **Ahlawat *et al*., (2018).**

4. Summary and Conclusion: Significant differences in the genotypes for every variable under investigation were found by the analysis of variance, and these findings were further supported by the genetic and statistical analyses of the data. It was discovered that mean squares resulting from genotypes were significant for every character. There was a noticeable variation in the average performance across several germplasm lines. For various yield and quality parameters, the range of heritability, GCV, PCV, and genetic advance as a percentage of mean was found to be from low to high. In a program to improve crops, germplasm lines with the appropriate values of variability parameters and mean performance for yield and quality traits can be used. Overall, the results of this study showed that the genotypes under investigation exhibited significant genetic variability. Therefore, in a crop improvement program, there is a chance to directly select superior germplasm for various yield-contributing and quality traits.

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6. Tables: On next pages

Table .1: Analysis of variance of augmented block design for different characters in sorghum during 2017-18 (Y_1).

Source of variation	df	DF	DM	NL	NN	PH	LL	LW	LA	FLL	FLW	SG
Block (ignoring treatments)	**7**	285.531**	247.122**	37.693**	14.555**	9865.697**	136.789**	2.883**	20954.890**	42.773**	0.540**	0.699**
Treatment (eliminating block)	**285**	124.529**	126.304**	5.719**	5.739**	3279.075**	134.666**	2.925**	22583.380**	35.081**	2.095**	0.165**
Checks	**5**	878.283**	711.733**	8.086**	6.719**	25290.720**	1134.743**	31.130**	461307.500**	410.930**	45.798**	0.462**
Checks+Var. vs. Var.	**280**	111.069**	115.850**	5.677**	5.721**	2886.010**	116.808**	2.422**	14749.020**	28.369**	1.314**	0.159**
Error	**35**	0.493	0.857	0.001	0.870	19.110	4.760	0.380	526.770	1.010	0.290	0.010
Block (Eliminating Check+Var.)	**7**	5.036**	4.286**	0.606**	0.763**	40.250**	13.329**	1.011**	63.785**	8.197**	0.508**	0.005**
Entries (ignoring blocks)	**285**	131.418**	132.268**	6.630**	6.078**	3520.402**	137.698**	2.971**	23096.496**	35.930**	2.096**	0.182**
Varieties	**279**	115.548**	114.107**	5.437**	4.684**	3030.236**	115.917**	1.959**	11343.750**	29.138**	0.561**	0.177**
Checks vs. Varieties	**1**	824.934**	2301.952**	332.046**	391.619**	31425.020**	1229.541**	144.613**	1111057**	55.863**	211.695**	0.047**

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Source of variation	df	INL	PL	PW	L:S	TGW	GYP	GFY	DFY	DM%	TSS%	HCN
Block (ignoring treatments)	**7**	65.723**	386.928**	145.742**	0.038**	202.997**	3343.889**	30061.620**	5055.674**	4.933**	155.286**	576.028**
Treatment (eliminating block)	**285**	27.914**	51.1501**	29.901**	0.005**	73.145**	932.601**	13818.020**	3990.842**	13.338**	11.565**	319.509**
Checks	**5**	255.060**	252.0419**	161.898**	0.060**	753.043**	8975.945**	16448.780**	4067.460**	168.323**	90.692**	2031.489**

Checks+Var. vs. Var.	**280**	23.858**	47.506**	27.544**	0.004**	61.003**	788.970**	13771.044**	3989.474**	10.570**	10.152**	288.938**
Error	**35**	1.760	1.220	0.680	0.001	1.520	14.070	90.640	8.350	1.900	0.340	6.590
Block (Eliminating Check+Var.)	**7**	0.666**	6.185**	2.300**	0.004**	5.244**	18.916**	64.454**	24.505**	6.935**	0.681**	16.139**
Entries (ignoring blocks)	**285**	29.512**	60.452**	33.425**	0.006**	78.002**	1014.267**	14554.790**	4114.415**	13.289**	15.362**	333.260**
Varieties	**279**	21.756**	55.913**	29.707**	0.003**	49.980**	785.272**	14158.820**	4039.960**	9.263**	9.665**	292.638**
Checks vs. Varieties	**1**	1065.631**	367.088**	428.075**	0.421**	4520.921**	25095.53**	115562**	25121.84**	361.126**	1228.173**	3175.891**

Continued…….

Source of variation	**df**	**PP**	**IVDMD**	**NDF**	**ADF**	**C**	**L**	**S**	**HC**	**A**	**ZLS**	**SFI**
Block (ignoring treatments)	**7**	11.268**	7.161**	4.744**	1.950**	1.176**	0.051**	0.048**	1.972**	3111.520**	118.026**	1323.678**
Treatment (eliminating block)	**285**	5.766**	20.550**	5.853**	5.964**	2.928**	0.858**	0.414**	14.073**	394.529**	60.697**	221.524**
Checks	**5**	22.324**	203.695**	101.158**	29.722**	4.472**	3.449**	2.550**	49.407**	11026.400**	238.661**	210.400**
Checks+Var.vs. Var.	**280**	5.471**	17.279**	4.152**	5.540**	2.900**	0.811**	0.376**	13.422**	381.460**	57.519**	221.723**
Error	**35**	0.240	9.520	1.650	1.800	1.860	0.070	0.010	0.760	0.210	0.110	1.950
Block (Eliminating Check+Var.)	**7**	0.316**	12.538**	3.223**	2.359**	2.359**	0.007**	0.009**	0.996**	0.578**	0.0782**	0.516**
Entries (ignoring blocks)	**285**	6.035**	20.418**	5.891**	5.954**	2.899**	0.859**	0.415**	14.097**	470.938**	63.576**	254.023**
Varieties	**279**	4.964**	16.682**	4.141**	5.370**	2.881**	0.815**	0.358**	12.350**	446.638**	60.664**	254.860**
Checks vs. Varieties	**1**	223.442**	146.426**	17.661**	50.072*	0.030**	0.087**	5.830**	325.175	3973.394**	0.548**	253.361**

* Significant at 5%, ** Significant at 1%.

DF= Days to 50% flowering, **DM=** Days to maturity, **NL=** Number of leaves per plant, **NN=** Number of nodes, **PH=** Plant height (cm), **LL=** Leaf length (cm), **LW=** Leaf width (cm), **LA=** Leaf area (cm^2), **FLL=** Flag leaf length (cm), **FLW=** Flag leaf width (cm), **SG=** Stem girth (cm), **INL=** Internodal length (cm), **PL=** Panicle length (cm), **PW=** Panicle width (cm), **L:S=** Leaf:stem ratio, **TGW=** 1000-grains weight (gm), **GYP=** Grain yield per plant (gm), **GFY=** Green fodder yield per plant (gm), **DFY=** Dry fodder yield per plant (gm), **DM=** Dry matter (%), **TSS=** Total soluble solids (%), **HCN=** HCN content (ppm), **PP=** Protein content (%)**, IVDMD=** Iin-vitro dry matter disappearance**, NDF=** Neutral detergent fiber**, ADF=** Acid detergent fiber (%), **C=** Cellulose (%)**, L=** Lignin (%), **S=** Silica (%), **HC=** Hemicellulose, **A=** Anthracnose (%), **ZLS=** Zonate Leaf Spot, **SFI=** Shoot Fly Index (%)

Table .2: General mean, range of variability and best top 10 germplasm.

Sl. No.	**Character**	**General Mean**	**Range**	**Best top 10 germplasm**
1.	**DF**	63.57	33.002 to 88.00	EP 124, CSV 17, IS 33096 ,EJ 30, 9533-1, PC 1001, EJ 30, R 74 (09 R-AGR-26), EJ 25, IS 22241
2.	**DM**	127.33	97.00 to 148.00	R77 (09R-AGR-26), EP 124, R 72 (09R-AGR23), R 73 (09R-AGR24), CSV 17, R 74 (09 R-AGR-26), IS 3199, 9533-1, SSG 226, IS 21622
3.	**NL**	15.35	7.30 to 23.30	IS 14357, UPFS 34, SSG 234-1, GP-2011-372, E 28, SMC 8, (SDSL 92101 x IS 3359) x Pant Chari 5, Pant Chari 3, SMC 13, IS 28313
4.	**NN**	14.13	5.54 to 21.32	UPMC 503 x (SDSL 92101 x UPFS 23),UPMC 504 x UPMC 8,IS 14357,UPFS 34, SMC 8, GP-2011-372, Pant Chari 3, SMC 13, (SDSL 92101 x IS 3359) x Pant Chari 5, IS 28313
5.	**PH**	362.34	138.22 to 528.33	(SDSL 92101 x IS 3359) x Pant Chari 5, IS 28313, IS 18844,SSG 234-1, SMC 6,SMC 13,CSV 14,UPMC 503 x (SDSL 92101 x UPFS 23),ESRK 29, SMC 8
6.	**LL**	82.01	56.30 to 107.20	CSV 14, IS 21021, GMS 1422, IS 21461, PC 121, GP-2011-471, E 159, UPFS 39, IS 14357, IS 12735
7.	**LW**	7.36	3.22 to 11.76	Pant Chari 3, UPFS 38 x UPFS 36, 1946 (08RLD01-7-2), CS 3541-1, SPV 1749, EJN 51, EJN 59, (SDSL 92101 x IS 3359) x Pant Chari 5, CSV 19, RS 673
8.	**LA**	431.22	150.45 to 741.43	UPFS 39, RS 673, CS 3541-1, UP Chari 1, EJN 51, Nizamabad, SPV 1725, IS 2363, ICSV 111, SPV 1749
9.	**FLL**	40.98	28.15 to 53.60	CSV 14, IS 21021, GMS 1422, IS 21461, PC 121, GP-2011-471, E 159, UPFS 39, IS 14357, IS 12735
10.	**FLW**	3.73	1.61 to 8.31	Pant Chari 3, UPFS 38 x UPFS 36, 1946 (08RLD01-7-2), CS 3541-1, SPV 1749, EJN 51, EJN 59, (SDSL 92101 x IS 3359) x Pant Chari 5, RS 673, CSV 19
11.	**SG**	2.41	1.23 to 3.43	RS 673, E 28, ESRK 27, EJN 68, (SDSL 92101 x IS 3359) x Pant Chari 5, SMC 6, R 72 (09R-AGR23), ESRK 16, SMC 9, SMC 14
12.	**INL**	27.52	16.50 to 40.23	SSG 611, SMC 12, IS 21977, SSG 234, EJN 43, IS 18008-2, NSSV 259, Raj 9-1, SSG 304, IS 6045
13.	**PL**	21.90	5.23 to 42.53	SMC 2, RS 29, IS 23948-1, IS 14241, SMC 3, ART 1008, SMC 8, SSG 256, SSG 227, SSG 223
14.	**PW**	10.55	0.13 to 30.23	SMC 17, ESRK 10, SMC 11, Malwan, IS 20703-1, SSG 250, SSG 223, UPFS 38 x SSG 59-3, SMC 12, SSG 227
15.	**L:S**	0.29	0.18 to 0.48	IS 7002, MP Chari, EJ 3, HC 171, SMC 2, SSG 248, SSG 234, SMC 3, HC 260, Raj 9-1
16.	**TGW**	21.44	6.10 to 43.46	R77 (09R-AGR-26), SRF 285, SMC 6, SPV 1749, ESRK 4, UTFS 48, CSV 19, SPV 1616, HC 136, UP Chari 1
17.	**DM %**	35.50	29.33 to 41.80	IS 3359, GM 1378-1, GP-2011-372, PSSV 61, SMC 14, GMS 1338, EJN 38, Pant Chari 3, RS 673, CSV 19
18.	**TSS %**	6.64	2.13 to 16.50	IS 20782, CSV 19 , IS 6045, IS 23948-1, IS 14298-1, IS 15008-1, IS 20399, IS 21461, IS 22241, IS 14756
19.	**HCN**	85.98	34.14 to 118.14	CSV 14, EJ 42, ESRK 4, IS 2363, SSV 74, Malwan, IS 1478, EG 11, SSG 227, SSG 227
20.	**PP**	11.00	7.12 to 15.57	HC 260, CS 3541-1, IS 6193, IS 6045, E 7, SSG 250, IS 3318, 1890 (08BZL01-14-1), 1946 (08RLD01-7-2), IS 14241
21.	**IVDMD**	54.46	41.23 to 63.25	ART 1008, R 73 (09R-AGR24), E 7, SPV 1749, R 255 (09R-SS 26),GMS 1338, SMC 17, EJN 46, ESRK 26, IS 9162
22.	**NDF**	55.17	51.21 to 60.18	SSG 256, EJ 3, IS 21602-1, EJN 56, UPMC 503 x (SDSL 92101 x UPFS 23), IS 12956, PC 121, IS 3345, E 25, SSG 223
23.	**ADF**	34.97	30.57 to 40.77	1890 (08BZL01-14-1), IS 18844, ICSV 111, 9533-1, UTFS 42, SSG 263,SSG 611, EJN 40, SMC 14, IS 18927
24.	**C %**	28.86	26.68 to 33.22	IS 13566, SMC 13, UTFS 42, SSG 263, SSG 611, ICSV 111, 9533-1, EJN 40, IS 18927, SMC 14
26.	**L %**	5.17	4.13 to 8.14	SPV 1725, HJ 513, IS 18844, B 437 (09B-RUS04), SSG 234, IS 1219, GP-2011-471, EJN 46, 1890 (08BZL01-14-1), IS 2363
26.	**S %**	2.05	1.12 to 3.48	IS 21461, ICSV 702, IS 3318, PC 23, SSG 222, Nizamabad, EJ 30, EP 135, EJN 54, IS 18933
27.	**HC %**	21.31	13.81 to 29.21	GD 68717-1, UPFS 35, EJ 42, IS 14298-1, IS 14241, SSG 234-1, HC 136, ESRK 16, EJN 64, UPFS 36 (Pant Chari 7)
28.	**A %**	23.40	1.25 to 79.25	SEVS 2, IS 1478, IS 5434-1, IS 29691, PSSV 61, IS 30117, ESRK 29, 1910 (08BZL01-32-4), 1946 (08RLD01-7-2), SMC 10
29.	**ZLS %**	7.84	1.12 to 46.25	SSG 245, IS 20740, SSV 74, SSG 304, NSSV 259, PSSV 61, SPV 1750, E 159, SMC 12, IS 22241
30.	**SFI %**	20.24	2.25 to 50.75	IS 1478, IS 14298-1, IS 18008-2, IS 20399, IS 20782, SSG 212, ICSV 95119-1-2, IS 3199, IS 3237-2, IS 3314
31.	**GYP**	85.04	24.40 to 165.20	JJ 1041, R77 (09R-AGR-26), SRF 285, SMC 6, SPV 1749, ESRK 4, UTFS 48, SPV 1616, HC 136, UP Chari 1
32.	**GFY**	314.76	80.32 to 835.13	UPFS 36 (Pant Chari 7), SMC 9, EJN 52, EA 11, B 437 (09B-RUS04), UPFS 38, SMC 13, EP 122, IS 13566, Pant Chari 3
33.	**DFY**	113.24	30.33 to 491.60	B 437 (09B-RUS04), CSV 19 , EJN 38, EJN 52, EP 122, UPFS 38, SMC 13, IS 13566, Pant Chari 3, IS 14241

Table .3: Genetic variability, heritability and genetic advance, genotypic and phenotypic coefficients of variation for different characters.

Variables	h^2**(%)**	**G.A.**	**G.A.M.**	**PCV (%)**	**GCV (%)**
DF	86.60	8.11	12.76	6.21	6.19
DM	84.32	8.16	6.41	3.12	3.11
NL	81.95	1.74	11.34	5.51	5.51
NN	84.82	1.60	11.34	5.98	5.51
PH	82.56	41.59	11.48	5.59	5.57
LL	86.45	8.29	10.11	5.00	4.91
LW	86.94	1.16	15.75	8.20	7.65
LA	87.66	108.11	25.07	12.31	12.17
FLL	87.14	4.25	10.38	5.11	5.04
FLW	86.40	0.98	26.33	13.75	12.78
SG	86.24	0.29	12.05	5.96	5.85
IN L	83.69	3.73	13.54	6.79	6.57
PL	87.62	5.15	23.52	11.56	11.42
PW	87.74	3.94	37.35	18.34	18.13
L:S	88.75	0.05	16.48	8.49	8.00
TGW	87.91	6.16	28.73	14.09	13.95
GYP	88.49	22.07	25.95	12.69	12.60
GFY	89.27	80.68	25.63	12.49	12.44
DFY	88.56	31.72	28.01	13.63	13.60
DM %	85.84	2.47	6.97	3.65	3.38
TSS %	84.25	2.45	36.84	18.15	17.88
HCN	85.94	12.88	14.99	7.35	7.27
PP	85.87	1.71	15.56	7.71	7.55
IVDMD	53.98	2.43	4.47	2.95	2.17
NDF (%)	71.66	1.49	2.70	1.55	1.31
ADF	69.82	1.49	4.25	2.47	2.06
C %	53.32	1.06	3.68	2.44	1.78
L %	82.21	0.65	12.53	6.33	6.08
S %	86.67	0.46	22.53	11.12	10.94
HC %	84.60	2.66	12.49	6.23	6.06
A %	84.52	14.47	61.83	30.02	30.01
ZLS %	85.63	5.67	72.28	35.12	35.09
SFI %	82.56	10.79	53.29	25.98	25.87