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Genetic variability, correlation and path analysis studies in forage sorghum (*Sorghum bicolor* (L.) Moench) genotypes

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Abstract
The field experiment consists of 12 treatments evaluated at Pulses Research station, S. K. Nagar, S.D.A.U, Dantiwada to study genetic variability, correlation and path analysis for yield and yield attributing traits. The experiment was conducted by using randomized block design with 3 replications during *kharif* 2019. The analysis of variance showed high significant differences among genotypes for mostly characters, indicating the presence of sufficient variability. Moderate estimates of GCV and PCV was observed for plant height, green fodder yield and dry fodder yield. While, moderate GCV and high PCV observed for leaf: stem ratio. High heritability coupled with high genetic advance expressed as per cent of mean observed for green fodder yield and dry fodder yield, indicating the preponderance of additive gene action governing the inheritance nature of these characters and selection for these traits would be advantageous for genetic improvement. Plant height, leaf width and green fodder yield exerted positive and significant correlation along with positive direct effect on dry fodder yield. Hence, it would be rewarding to give due importance on the selection of these characters for rapid improvement in dry fodder yield of these crop.

Keywords: *kharif* sorghum, genetic variability, correlation and path analysis

Introduction
The word forage indicates the utilization of plant and its green succulent part directly to the feeding of domesticated animals. While, fodders are the crops that are harvested and used as hay, silage, straw, compressed, pelleted feeds *etc.*, for feeding of livestock during rough periods when there is scarcity or less availability of green forage. Sorghum (*Sorghum bicolor* L. Moench) is one of the important dual-purpose crop in worldwide both as food and fodder. It is often cross-pollinated crop comprising 2n=20 chromosome number. It's belonged to well-known grass family Poaceae. In India, it is commonly known as "Jowar". There are some species, which is used for making fodder and ethanol fuel production (Aml *et al*. 2012) [2]. Generally, it is most preferred forage crop due to its fast-growing potential, high yielding ability, superior palatability, better digestibility, high tolerance ability for variation in soil, moisture and other atmospheric conditions, good regeneration capacity and other utilizations like hay, silage, straw etc. This is important widely grown *kharif* season crop used to fulfilled the requirement of green as well as dry fodder for feeding of animals. It is very good drought tolerant, making it an outstanding choice for arid and dry areas. With the effects of rapidly urbanization, industrialization and other factors, there is low or mere scope for increasement of cultivated area. So, there are critical need arise to increase forage crop yield to meet the requirement of fodder, which is done through development and evaluation of high yielding and improved varieties of forage crops. A systemic breeding program relies on knowledge of the type and degree of population variability resulting from genetic and non-genetic causes. The study of the level of genetic variability present in the existing genotype has become crucial, since genetic variability is necessary for the beginning of an efficient and effective breeding strategy. The study of genetic advance with heritability estimates could further clarify the nature of characters which can be improved through selection. As yield is complex character and controlled by quantitative genes (Polygene) and environmental factors also exerted significantly greater impact on plant. So, deciding based solely on yield performance could be confusing and lead to a biased outcome. Therefore, there is must need is developed for better understanding of inter-relation (Positive or negative) of various

characters and also with fodder yield which leads to better genetic improvement. Correlation analysis gives details about degree and direction of association among the various characters, which is important in breeding Programme. For better understanding, correlation coefficient splits into direct and indirect contributions (effects) of various traits (independent variable) towards dependent variable, which is done through path coefficient analysis described by Dewey and Lu (1959) [4]. Therefore, the present experiment was conducted with aim to analyze and determine the characters with desirable interrelationship with dry fodder yield by utilization of various parameters like genetic variability, correlation and path coefficient in sorghum treatments.

Material and methods

The experimental material consists of 12 treatments evaluated in Randomized Block Design with three replications at Pulses Research station, S. K. Nagar, Sardarkrushinagar Dantiwada Agricultural University, Dantiwada during *kharif* – 2019. The experimental material was evaluated for ten characters *viz.*, days to 50 % flowering, plant height, no of leaves per plant, leaf length, leaf width, stem thickness, leaf: stem ratio, brix percentage, green fodder yield and dry fodder yield. Data on various quantitative and qualitative traits were collected by regular field visit. At the appropriate crop growth stage, observations were taken on five randomly selected plants from each genotype in each replication, with the exception of days to 50 % flowering. Average was worked out and final mean data were used for statistical analysis. Average was worked out and final mean data were used for statistical analysis. Analysis of variance calculated using formula suggested by Panse and Sukhatme (1978) [3]. Genetic variability parameters such as Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), Heritability and Genetic advance as *percent* of mean were worked out as per Burton (1952) [7], Allard (1960) [8] and Johnson *et al*. (1955) [9]. Table 2 displayed the categorization of genetic estimates *viz*., Sivasubramanian and Madhavamenon (1973) [16] categorized GCV and PCV, Robinson H. F. *et al*. (1949) [15] categorized heritability and GAM was categorized by Johnson *et al.* (1955) [9]. Correlation co-efficient calculated at genotypic (r_g) and phenotypic (r_p) level with the help of methods suggested by Al-Jibouri*etal*. 1958 [17]. Path coefficient analysis was worked out by following Dewey and Lu (1959) [4].

Results and Discussion

The analysis of variance revealed significant differences among the treatments for all the characters studied, which indicates that there is sufficient amount of variability present and there is ample scope for the selection of variables from these population for better genetic improvement (table 1). The values of various parameters like, GCV, PCV, heritability and GAM was displayed in table 3. In the results, the values of genotypic coefficient of variation were slightly lower than phenotypic coefficient of variation showing a sufficient effect of environment over all the characters. High PCV observed for leaf: stem ratio, while moderate PCV were observed for leaf width and stem thickness, indicates there was good environment influence on the expression of these trait. Moderate GCV and PCV recorded for various characters like, plant height, green fodder yield and dry fodder yield along with moderate GCV for leaf: stem ratio, indicates moderate variability present in population, average chances for selection and there may be greater role of environment influence on the expression of variability. Low GCV and PCV were observed for traits like, days to 50% flowering, number of leaves per plant, leaf length and brix percentage, which indicate that there was less amount of variation present in population. So, simple selection not rewarding but there is must need arises for the creation of variability for genetic improvement.

Heritability estimates is used to predict the inheritance ability of genotypes to transfer characters from one generation to another. High heritability estimates were observed for various characters like, days to 50 % flowering, plant height, leaf length, green fodder yield and dry fodder yield, indicated that all these characters were governed by additive gene action and presence of least environmental influence. Genetic advance expressed as *percent* of mean was high for green fodder yield and dry fodder yield, indicating the predominance of additive gene action and straight selection could be effective for improvement of these characters. While, other characters displayed moderate to low values. High estimates of heritability coupled with high genetic advance expressed as *percent* mean was observed for green fodder yield and dry fodder yield, indicating that these characters show preponderance of additive gene action and selection would be beneficial for genetic improvement. These results were in concordance with Sen *et al*. (2019) [13] and Kumar *et al*. (2020) [14]. High heritability coupled with moderate GAM was observed for days to flowering and plant height, indicating that these characters were controlled by both additive and non-additive genes. Ranjith *et al*. (2017) [12] recorded similar results for above traits. While, leaf width, leaf: stem ratio and brix percentage, displayed moderate heritability and moderate genetic gain, indicating late selection may be effective for further genetic enhancement.

Correlation co-efficient calculated at genotypic (r_g) and phenotypic (r_p) level. The phenotypic correlation is the observable association between a pair of traits. Whereas, genotypic correlation is inherent association with dependent character and improves the genetic make-up of the genotypes through the selection of the pod yield and its contributing traits. Based on the results, correlation coefficient analysis shows that magnitude of genotypic correlation coefficients was relatively higher than the corresponding phenotypic correlation coefficient in almost all the characters studied, indicates the inherent association between various characters which revealing least influence of an environment on the expression of the traits (table). The dry fodder yield displayed significant and positive association with various characters like, plant height (r_g = 0.833, r_p = 0.668), leaf width (r_g = 0.968, r_p = 0.594) and green fodder yield (r_g = 0.997, r_p = 0.947) at both genotypic and phenotypic level, demonstrates the advantageous association between these traits. Diwakar *et al*. (2016) [11], Dev *etal*. (2019) [6] and Arvinth *et al*. (2021) [10] recorded similar results for above traits. Therefore, high plant height, wider leaf and greater green fodder yield would ultimately increase the dry fodder yield, which indicates the bright future ahead for genetic enhancement. Dry fodder yield positive and significantly correlated with number of leaves per plant (r_g= 0.800) at genotypic level and leaf length (r_p= 0.487) at phenotypic level, revealed the beneficial association of above traits and increase in one character leads to improvement of other trait. While, green fodder yield was positive and significantly associated with plant height (r_g = 0.801, r_p = 0.654) and leaf width (r_g = 0.943, r_p = 0.568) at both genotypic and phenotypic level, indicates higher plant height and wider leaf leads to increase of green fodder yield.

Path coefficient analysis was worked out by following Dewey and Lu (1959) [4] to find out the magnitude and direction of direct and indirect effects of various yield contributing characters towards fodder yield. Dry fodder yield was considered as the dependent variable; while the remaining nine yield contributing characters were consider as the independent variables. The estimates of direct and indirect effects of various traits on dry fodder yield were presented in table5.There were many characters displayed positive and negative direct and indirect effect towards dry fodder yield. Plant height (1.212), leaf length (0.393), leaf width (0.314), leaf: stem ratio (1.950) and green fodder yield (0.832) exerted positive direct effect towards dry fodder yield. Similar results were obtained by Iyanar *et al.* (2010) [1] and Sumon *et al.* (2021) [5]. Therefore, these characters turned-out to be the major components of dry fodder yield and direct selection for these traits may be rewarding for yield improvement. While, days to flowering, number of leaves per plant, stem thickness and brix percentage displayed negative direct effect towards dry fodder yield. Hence, there was less need to give due importance for direct selection in further genetic improvement. As yield is complex character, affected by multiple factors. Residual effect indicates, there may be other traits which directly or indirectly affecting the yield component. In present study, the residual effect is negative (-0.083) which revealed that there may be less chance of other characters would affect the yield which were not included in study.

Table 1: Analysis of variance for different characters of Fodder Sorghum genotypes

Sr. No.	Characters	Mean sum of square		
		Replications	Genotypes	Error
	Degree of freedom (d.f)	2	11	22
1	Days to Flowering (50%)	1.028	79.263**	2.391
2	Plant height	3751.901**	2693.819**	291.210202
3	No of Leaves/Plant	0.930	1.405	0.902
4	Leaf Length (cm)	47.462*	65.831**	9.947
5	Leaf Width (cm)	0.302	1.079**	0.291
6	Stem thickness (mm)	1.208	1.989	1.351
7	Leaf: Stem ratio	0.008*	0.005*	0.001
8	BRIX (%)	0.695	1.602**	0.324
9	Green Fodder Yield (kg/ha)	2423356.97	145613396.6**	11420868.87
10	Dry Fodder Yield (kg/ha)	808339.36	15123299.92**	1242994.00

Table 2: Categorization of genetic estimates

Estimates	GCV&PCV (%)	Heritability (h^2_b) (%)	GAM (%)
Low	0 to 10	0 to 30	0 to 10
Moderate	10 to 20	30 to 60	10 to 20
High	More than 20	More than 60	More than 20

Table 5: Genotypic path coefficient in Fodder Sorghum

Char.	DF	PH	NL/P	LL	LW	ST	L:SR	Brix	GFY	Genetic correlation
DF	-1.874	0.544	-0.017	-0.069	0.104	-0.179	1.456	-0.007	0.184	0.141
PH	-0.840	1.212	-0.011	0.046	0.234	-0.105	-0.355	-0.014	0.666	0.833**
NL/P	-1.301	0.527	-0.024	0.266	0.138	0.873	-0.422	0.002	0.741	0.800**
LL	0.329	0.142	-0.017	0.393	0.269	0.047	-1.098	-0.005	0.474	0.533
LW	-0.620	0.902	-0.011	0.336	0.314	-0.197	-0.604	-0.020	0.867	0.968**
ST	-0.627	0.238	0.040	-0.034	0.116	-0.536	0.644	-0.006	0.075	-0.090
L:SR	-1.399	-0.221	0.005	-0.221	-0.097	-0.177	1.950	0.002	-0.365	-0.522
Brix	-0.351	0.434	0.001	0.046	0.164	-0.085	-0.101	-0.039	0.296	0.366
GFY	-0.415	0.971	-0.022	0.224	0.328	-0.049	-0.857	-0.014	0.832	0.997**
Residual effect: -0.083										

Table 4: Genotypic and Phenotypic correlation coefficient among ten characters in fodder sorghum

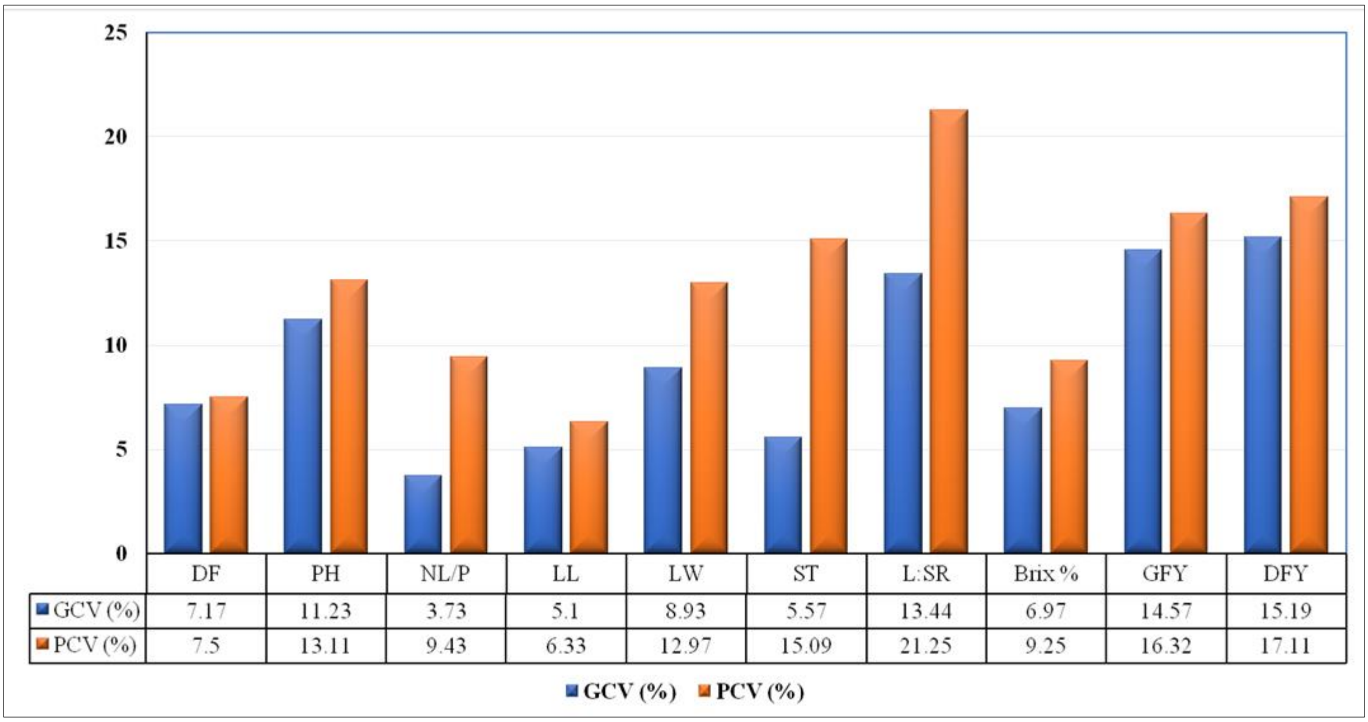
Sr. No.	Character		Days to 50% flowering	Plant height	No of Leaves/Plant	Leaf Length	Leaf Width	Stem thickness	Leaf: Stem ratio	BRIX (%)	Green Fodder Yield	Dry Fodder Yield
1	Daysto 50 %flowering	r_g	1.000	0.449	0.694*	-0.175	0.331	0.335	0.747**	0.187	0.221	0.141
		r_p	1.000	0.348*	0.258	-0.127	0.276	0.219	0.558**	0.185	0.155	0.097
2	Plant height	r_g		1.000	0.435	0.117	0.745**	0.196	-0.182	0.359	0.801**	0.833**
		r_p		1.000	0.313	-0.035	0.502**	0.121	-0.098	0.182	0.654**	0.668**
3	No of Leaves/Plant	r_g			1.000	0.678*	0.439	0.845**	-0.216	-0.052	0.892**	0.800**
		r_p			1.000	0.022	0.266	-0.084	0.138	-0.162	0.314	0.292
4	Leaf Length	r_g				1.000	0.856**	-0.087	-0.563	0.117	0.570	0.533
		r_p				1.000	0.470**	-0.025	-0.285	-0.024	0.460**	0.487**
5	Leaf Width	r_g					1.000	0.369	-0.310	0.523	0.943**	0.968**
		r_p					1.000	0.287	-0.139	0.284	0.568**	0.594**
6	Stem thickness	r_g						1.000	0.331	0.158	0.091	-0.090
		r_p						1.000	0.220	0.321	-0.029	0.040
7	Leaf: Stem ratio	r_g							1.000	-0.052	-0.440	-0.522
		r_p							1.000	0.050	-0.236	-0.255
8	BRIX (%)	r_g								1.000	0.357	0.366
		r_p								1.000	0.191	0.183
9	Green Fodder Yield	r_g									1.000	0.997**
		r_p									1.000	0.947**
10	Dry Fodder Yield	r_g										1.000
		r_p										1.000

Table 3: Range of variation, mean, variability parameters, heritability and genetic advance for ten characters in Fodder Sorghum

Sr. No	Characters	Range	Mean	σ^2_g	σ^2_p	σ^2_e	GCV (%)	PCV (%)	h^2_b (%)	GAM (%)
1	Days to Flowering (50%)	63-82	70.61	25.62	28.01	2.39	7.17	7.50	91.46	14.12
2	Plant height	188.2-323	252.00	800.86	1092.08	291.21	11.23	13.11	73.33	19.81
3	No of Leaves/Plant	8.8-13.4	10.97	0.17	1.07	0.90	3.73	9.43	15.67	3.04
4	Leaf Length (cm)	70.4-93.2	84.51	18.63	28.57	9.95	5.10	6.33	65.19	8.49
5	Leaf Width (cm)	4.1-7.3	5.74	0.26	0.55	0.29	8.93	12.97	47.43	12.67
6	Stem thickness (mm)	6.08-11.49	8.28	0.21	1.56	1.35	5.57	15.09	13.62	4.23
7	Leaf: Stem ratio	0.15-0.36	0.23	0.001	0.002	0.001	13.44	21.25	40.21	17.51
8	BRIX (%)	6.6-10.95	9.36	0.42	0.75	0.32	6.97	9.25	56.81	10.82
9	Green Fodder Yield (kg/ha)	27777.71-56855.64	45889.03	44730840	56151710	11420870	14.57	16.32	79.66	26.80
10	Dry Fodder Yield (kg/ha)	8628.819- 17494.044	14159.406	4626768.64	5869762.63	1242993.99	15.19	17.11	78.82	27.78

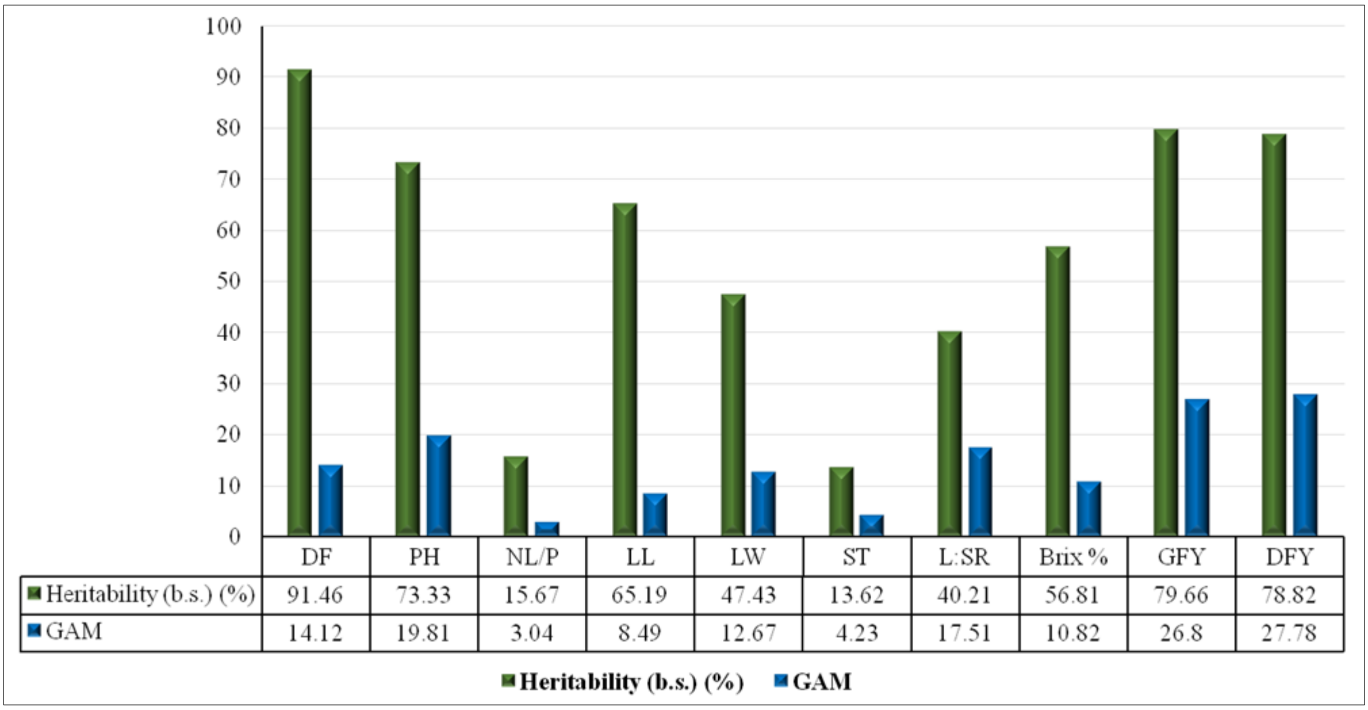
Table 6: Mean values of treatments for different characters in Fodder Sorghum

No.	Treatment	Days to flowering	Plant height (cm)	No of Leaves per Plant	Leaf Length (cm)	Leaf Width (cm)	Stem thickness (mm)	Leaf: Stem ratio	BRIX (%)	Green Fodder Yield (kg/ha)	Dry Fodder Yield (kg/ha)
1	SRF-332	81	290.7	12.73	84.02	6.10	7.23	0.262	9.67	55161	16903
2	SRF-353	72	215.3	10.80	86.83	5.97	8.69	0.234	9.15	45114	13633
3	SRF-372	78	257.0	11.20	87.01	6.31	9.15	0.287	9.62	43735	12845
4	SRF-382	72	233.7	10.67	82.07	5.16	8.94	0.284	9.10	44917	13515
5	SRF-389	72	236.3	9.87	72.35	4.71	8.47	0.277	10.17	32506	10063
6	DSF-117	65	223.7	10.80	89.15	5.85	8.21	0.199	9.83	45981	13515
7	DSF-153	68	253.3	11.07	84.80	5.91	8.62	0.267	9.22	46454	14894
8	DSF-168	67	290.7	11.20	82.57	6.08	7.91	0.186	9.33	55122	16824
9	AFS-65	67	218.3	11.13	81.85	4.61	7.21	0.225	7.30	34673	10678
10	GFS-6 (LC)	68	268.0	11.07	86.17	5.93	8.99	0.176	9.87	48266	15563
11	GAFS-12 (LC)	65	235.3	10.80	90.33	5.71	6.84	0.205	9.82	46099	14854
12	CSV-21F (NC)	74	301.7	10.27	87.03	6.49	9.16	0.221	9.35	52640	16627
General mean		70.75	252	10.97	84.52	5.74	8.28	0.235	9.37	45889	14159
Range	Minimum	65	215.3	9.87	72.35	4.61	6.84	0.176	7.30	32506	10063
	Maximum	81	301.7	12.73	90.33	6.49	9.16	0.287	10.17	55161	16903
S.E.m. ±		0.89	9.85	0.55	1.82	0.31	0.67	0.02	0.33	1951.14	643.69
C.D. at 5%		2.62	28.90	1.48	5.34	0.91	1.89	0.06	0.96	5722.50	1887.87
C.V.%		2.19	6.77	8.66	3.73	9.40	14.03	16.31	6.08	7.36	7.87



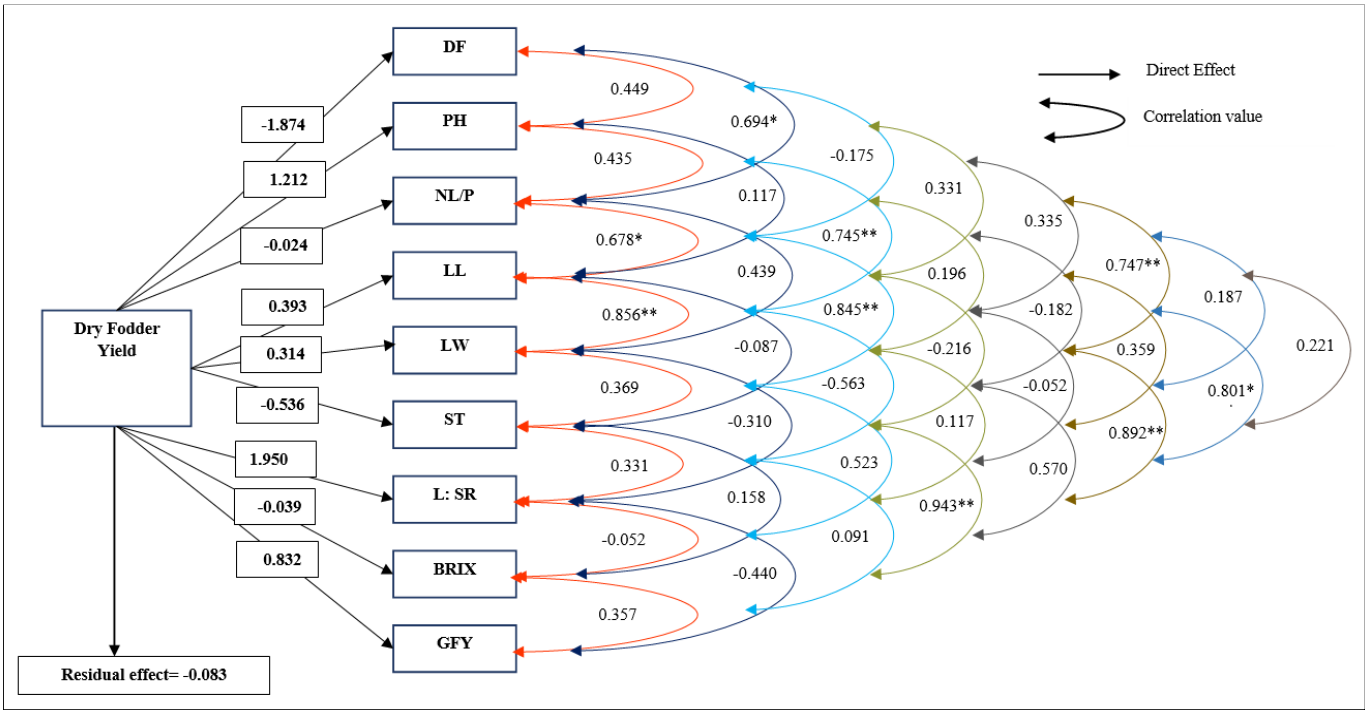
here, DF= Days to flowering, PH= Plant height, NL/P= No. of leaves per plant, LL= Leaf length, LW= Leaf width, ST= Stem thickness, L:SR= Leaf: stem ratio, GFY= Green fodder yield, DFY= Dry fodder yield.

Fig 1: Graphical comparison of Genotypic and Phenotypic coefficient of variation



here, DF= Days to flowering, PH= Plant height, NL/P= No. of leaves per plant, LL= Leaf length, LW= Leaf width, ST= Stem thickness, L:SR= Leaf: stem ratio, GFY= Green fodder yield, DFY= Dry fodder yield.

Fig 2: Graphical comparison of Heritability and Genetic Advance as *percent* of mean



Where, DF= Days to flowering, PH= Plant height, NL/P= No. of leaves per plant, LL= Leaf length, LW= Leaf width, ST= Stem thickness, L:SR= Leaf: stem ratio, GFY= Green fodder yield, DFY= Dry fodder yield.

Fig 3: Genotypic path diagram in Fodder Sorghum

Conclusion

It was necessary to select the proper treatments and beneficial traits for efficient genetic enhancement. The analysis of variance showed high significant differences among genotypes for mostly characters under study. High heritability coupled with high genetic advance expressed as *per cent* of mean observed for green fodder yield and dry fodder yield, indicating the preponderance of additive gene action governing the inheritance nature of these characters and selection for these traits would be advantageous for genetic improvement. The higher mean values of the genotypes for dry fodder yield were observed for SRF- 332 followed by DSF- 168 andCSV-21F 9NC0 (table 6) highlights the best treatments for genetic improvement and used as parents in further breeding Programme. Based on study, plant height, leaf width and green fodder yield exerted positive correlation and also displayed positive direct effect towards dry fodder yield, which indicate that there is need to give due importance to these traits for efficient genetic improvement.

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