Genetic Variability, Correlation and Path Analysis in Forage Bajra [*Pennisetum glaucum* (L.) R. Br.]

Sumitkumar V. Parmar[1]*, Dipakkumar P. Gohil[2], Vikram K. Suvatar[1] and Tejaskumar H. Borkhatariya[1]
[1]M.Sc. Scholar (Agri.), Department of Genetics and Plant Breeding,
B. A. College of Agriculture, AAU, Anand (Gujarat), India.
[2]Research Scientist & Head, Main Forage Research Station, AAU, Anand (Gujarat), India.

(Corresponding author: Sumitkumar V. Parmar*)

ABSTRACT: An experiment comprised of fifty diverse accessions of forage [*Pennisetum glaucum* (L.) R. Br.] was conducted in randomized complete block design with three replications during *Kharif* -2020 at Main Forage Research Station, Anand Agricultural University, Anand to study the genetic variability, heritability, genetic advance, characters association and path coefficient analysis. The magnitude of phenotypic coefficient of variation was observed higher than corresponding genotypic coefficient of variation for all the characters under study. High genotypic and phenotypic coefficient of variations were observed for crude protein yield per plant, green forage yield per plant and dry matter yield per plant, which indicated the presence of sufficient amount of variability for these traits. High heritability coupled with high genetic advance for green forage yield per plant, plant height, stem thickness, leaf width and number of leaves per plant indicated good response of selection. Plant height, leaf length, leaf width, stem thickness, dry matter yield per plant, crude protein yield per plant and neutral detergent fiber content showed positive and significant correlation with green forage yield per plant and its quality at both genotypic and phonotypic levels. Path analysis indicated dry matter yield per plant, crude protein yield per plant, number of tillers per plant and stem thickness exerted a strong positive direct effect on green forage yield per plant.

Keywords: Forage bajra, Variability, Path analysis, Correlation coefficient, Fodder quality.

INTRODUCTION

Pearl millet (*Pennisetum glaucum* L.) is familiar in most parts of the country as bajra or bajri, and also known as cat tail millet, spiked millet and bulrush millet. Pearl millet is an important food and fodder crop grown in arid and semi-arid regions of Asia and Africa. Pearl millet is one of the important staple food crops of India ranking fourth in acreage next to rice, wheat and sorghum. The pearl millet is an annual, tillering diploid ($2n = 14$) crop plant that belongs to the family Poaceae and sub-family Paniceidae. It is native to West Africa. Pearl millet is an embodiment of unique features like allogamy, protogyny, male sterility, huge genetic variability, and remarkable geographic diversity.

Pearl millet is known to tolerate acid sandy soils and is able to grow on saline soils. In India, it is mainly grown in Rajasthan, Uttar Pradesh, Gujarat, Haryana and Maharashtra, which share about 91.87 per cent of total pearl millet production. Pearl millet occupies an area of 7.38 million ha with production of 9.13 million tonnes and productivity of 1237 kg/ha of grain in the country (MAFW, 2019). The heritability estimates to aid in determining the relative amount of heritable portion in variation and thus helps to the plant breeder in selecting the elite genotypes from a diverse population.

Correlation and path analysis could be used as an important tools. It brings information about appropriate cause and effects relationship between yield and some yield components (Khan *et al*., 2003). To assess the magnitude of correlations for various characters with forage yield would be an immense help in the indirect selection for the improvement of forage yield.

MATERIAL AND METHODS

The present investigation was conducted at Main Forage Research Station, A.A.U., Anand (22° 35′N, 72° 55′E, with an altitude of 45.1 m), during *Kharif*-2020. The experimental material for the present study consisted of 50 diverse genotypes of pearl millet (Table 1) and were evaluated in randomized complete block design (RBD) with three replications at Anand under irrigated conditions. Each genotype was accommodated in single row of 5.0 m length which spaced at 30 cm apart with plant-to-plant spacing of 10 cm. The recommended agronomical and plant protection practices were followed for the successful and healthy crop.

The observations were recorded on five representative random plants in each replication for 15 characters *viz*., days to 50 % flowering, plant height at 50 % flowering

(cm), tillers per plant, leaves per plant, leaf length (cm), leaf width (cm), stem thickness (cm), leaf: stem ratio, green forage yield per plant (g), dry matter content (%), dry matter yield per plant (g), crude protein content (%), crude protein yield per plant (g), neutral detergent fibre content (%) and acid detergent fibre content (%).

The analysis of variance followed as per technique suggested by Snedecor and Cochran (1967) and reviewed by Panse and Sukhatme (1978). The genotypic, phenotypic and environmental variance were calculated as per formula suggested by Johnson *et al.* (1955). Heritability (broad sense) and genetic advance were analyzed using the formula given by Allard (1960). Phenotypic (PCV) and genotypic coefficients of variation (GCV) were classified according to Burton (1952) [< 10% = low, 10–20% = moderate and > 20% = high]. Correlation coefficient were worked out as per the method given by Hazel (1943). Path coefficient analysis was done by using correlation coefficients as suggested by Dewey and Lu (1959) and was carried out by taking green forage yield per plant as dependent variable and other observed traits as independent variables.

Table 1: List of forage bajra genotypes.

Sr. No.	Name of genotypes	Source	Sr. No.	Name of genotypes	Source
1.	AFB 3	MFRS, AAU, Anand	26	ICMV 1614	ICRISAT, Hyderabad
2.	AFB 35	MFRS, AAU, Anand	27	ICMV 1616	ICRISAT, Hyderabad
3.	AFB 42	MFRS, AAU, Anand	28	ICMV 1618	ICRISAT, Hyderabad
4.	AFB 49	MFRS, AAU, Anand	29	ICMV 1619	ICRISAT, Hyderabad
5.	AFB 53	MFRS, AAU, Anand	30	ICMV 1620	ICRISAT, Hyderabad
6.	J 2290	MFRS, AAU, Anand	31	ICMV 1622	ICRISAT, Hyderabad
7.	J 2514	MFRS, AAU, Anand	32	ICMV 1709	ICRISAT, Hyderabad
8.	MJC 2	MFRS, AAU, Anand	33	ICMV 05777	ICRISAT, Hyderabad
9.	BAIF 1	MFRS, AAU, Anand	34	ICMV 1701	ICRISAT, Hyderabad
10.	Giant Bajra	MFRS, AAU, Anand	35	ICMV 1608	ICRISAT, Hyderabad
11.	ICMB 01777	MFRS, AAU, Anand	36	ICMV 1611	ICRISAT, Hyderabad
12.	JMSB 101	MFRS, AAU, Anand	37	ICMV 1707	ICRISAT, Hyderabad
13.	91 KH 16	MPMRS, JAU, Jamnagar	38	ICMV 1605	ICRISAT, Hyderabad
14.	140 KH 16	MFRS, AAU, Anand	39	ICMV 1623	ICRISAT, Hyderabad
15.	184 KH 16	MFRS, AAU, Anand	40	RAJ Bajra	RAU, Bikaner, Rajsthan
16.	202 KH 16	MFRS, AAU, Anand	41	HC 20	UASD, Dharwad
17.	318 KH 16	MFRS, AAU, Anand	42	GFB 1	MFRS, AAU, Anand
18.	323 KH 16	MFRS, AAU, Anand	43	GAFB 4	MFRS, AAU, Anand
19.	709 KH 16	MFRS, AAU, Anand	44	FBC 16	NDDB, Anand
20.	743 KH 16	MFRS, AAU, Anand	45	AVKB 19	IGFRI, Hyderabad
21.	102 AFRLT KH 16	MFRS, AAU, Anand	46	ICMB 674	RRS, AAU, Anand
22.	114 AFRLT KH 16	MFRS, AAU, Anand	47	ICMB 901	RRS, AAU, Anand
23.	ICMV 1601	ICRISAT, Hyderabad	48	AIB 29	RRS, AAU, Anand
24.	ICMV 1602	ICRISAT, Hyderabad	49	ICMR 15944	RRS, AAU, Anand
25.	ICMV 1609	ICRISAT, Hyderabad	50	GP 138	MFRS, AAU, Anand

MFRS: Main Forage Research Station, AAU: Anand Agricultural University, MPMRS: Main Pearl Millet Research Station, JAU: Junagadh Agricultural University, ICRISAT: International Crop Research Institute for the Semi Arid Tropics, RAU: Rajasthan Agricultural University, UASD: University of Agricultural Sciences Dharwad, NDDB: National Dairy Development Board, IGFRI: Indian Grassland and Fodder Research Institute, RRS: Regional Research Station

RESULTS AND DISCUSSION

The results revealed that mean squares due to genotypes were highly significant for all the characters studied except leaf: stem ratio indicating the presence of considerable genetic variation for different traits among the genotypes under study of forage bajra. Selection can be practiced for traits (Table 2) such as plant height, number of tillers per plant per plant, number leaves per plant, leaf length and leaf width, green forage yield per plant, dry matter content, dry matter yield per plant, crude protein content, crude protein yield per plant per plant, neutral detergent fiber content and acid detergent fiber content as these traits revealed higher amount of variability for different genotypes. These results are in close agreement with Thomas *et al.* (2018) and Shalini (2019).

The magnitude of the phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the characters, which indicated effect of environment on the character expression. The high estimates of genotypic and phenotypic coefficient of variations were observed for crude protein yield per plant, green forage yield per plant and dry matter yield per plant which indicated the presence of sufficient variability for these traits in the genotypes studied. High amount of GCV and PCV suggested greater scope of selection of superior genotypes for these traits.

The high heritability was recorded for the traits *viz.,* plant height, green forage yield per plant, leaf width, stem thickness and number of leaves per plant and were least influenced by environmental modification. High

heritability for green forage yield per plant was in close harmony with Shinde (2005). High heritability coupled with high genetic advance for green forage yield per plant, plant height, stem thickness, leaf width and number of leaves per plant indicates the preponderance of additive gene action and hence, better scope for improvement of these characters through simple selection. Moderate heritability coupled with high genetic advance for crude protein yield per plant, crude protein content, number of tillers per plant and dry matter yield per plant those indicates good response to selection for these traits. These finding are in accordance with Kumar *et al.* (2014) and Ram *et al.* (2014). Low heritability coupled with low genetic advance for 50% flowering and leaf: stem ratio suggested high influence of environment and consequently its selection may not be effective. Similar results of heritability (low) were reported by Ram *et al.* (2014); Mali *et al.* (2014).

In general, the estimates of genotypic correlation were higher than the corresponding phenotypic correlation coefficient. It may result from the modifying effect of environment on the association of characters at genotypic level. The association of green forage yield per plant was positive and highly significant with plant height (rg= 0.406**, rp= 0.415**), leaf length (rg= 0.471**, rp= 0.360**), leaf width (rg= 0.386**, rp= 0.325**), stem thickness (rg= 0.624**, rp= 0.467**), dry matter yield per plant (rg= 0.932**, rp= 0.854**), crude protein yield per plant (rg= 0.849**, rp= 0.767**) and neutral detergent fiber content (rg= 0.426**, rp= 0.243**) at both genotypic and phenotypic levels indicated that these characters are the primary yield determinants and selection criteria based on these traits would be beneficial for improvement of green forage yield per plant in forage bajra. Similar

results also found by Balasaheb (2012); Shinde (2015) for plant height, leaf length and dry matter yield per plant; Singh *et al.* (2014) for stem thickness; Lokhande (2015) for plant height, leaf length, leaf width and dry matter yield per plant; Thomas *et al.* (2018); Rani *et al.* (2022) for plant height and dry matter yield per plant and Shalini (2019) for dry matter yield per plant. Borkhatariya *et al.* (2022) also found that quality parameters like crude protein and fibre content had significant genotypic effects on green fodder yield in forage crops. From these association, it appears that higher green forage yield can be obtained by improving these characters through selection. Green forage yield per plant was negative and non-significant correlation with dry matter content (rg= -0.208, rp= -0.067) and crude protein content (rg= -0.001, rp= -0.044) at both genotypic and phenotypic level.

Path analysis revealed the importance of dry matter yield per plant (0.673), crude protein yield per plant (0.240) and stem thickness (0.154) by showing high and positive direct effects towards green forage yield per plant. Shinde (2015); Shalini (2019) reported similar results. Hence, selection based on these characters *viz.*, dry matter yield per plant, crude protein yield per plant, plant height, number of tillers per plant, leaf length and stem thickness can be useful for improving the green forage yield per plant of bajra. Also, number of tillers per plant (0.061) and leaf length (0.027) having positive direct effects on green forage yield per plant. The results are in accordance with those obtained by Balasaheb (2012). The residual effect was observed low (0.027) through various characters which are not considered under study, it indicating that there was no considerable effect via such traits which are not considered under investigation.

Table 2: Variability parameters for fifteen characters of forage bajra genotypes.

Sr. No.	Characters	Variance components			GCV (%)	PCV (%)	Heritability (%) (H²b)	Genetic Advance (GA)	Genetic Advance (% of Mean)
		σ^2_g	σ^2_p	σ^2_e					
1.	Days to 50 % flowering	1.98	13.86	11.88	2.38	6.29	14.31	1.10	1.86
2.	Plant height	841.07	1089.13	248.07	18.14	20.64	77.22	52.50	32.84
3.	Number of tillers per plant	0.24	0.49	0.25	17.53	24.96	49.32	0.71	25.35
4.	Number of leaves per plant	15.74	25.89	10.15	18.01	23.11	60.79	6.37	28.93
5.	Leaf length	38.85	81.46	42.61	8.49	12.29	47.69	8.87	12.07
6.	Leaf width	0.13	0.18	0.06	16.88	20.23	69.60	0.61	29.01
7.	Stem thickness	0.02	0.03	0.01	18.49	23.06	64.29	0.22	30.54
8.	Leaf : stem ratio	0.02	0.16	0.14	11.27	32.92	11.71	0.10	7.94
9.	Green forage yield per plant	1346.24	1896.70	550.45	26.89	31.92	70.98	63.68	46.67
10.	Dry matter content	3.18	9.36	6.18	9.28	15.91	34.00	2.14	11.15
11.	Dry matter yield per plant	33.70	69.96	36.26	22.22	32.02	48.17	8.30	31.77
12.	Crude protein content	1.34	2.58	1.24	13.58	18.85	51.90	1.72	20.16
13.	Crude protein yield per plant	0.37	0.67	0.30	27.50	37.09	54.99	0.93	42.01
14.	Neutral detergent fiber content	19.36	44.46	25.10	5.51	8.35	43.55	5.98	7.49
15.	Acid detergent fiber content	22.61	71.68	49.06	10.05	17.89	31.55	5.50	11.63

Table 3: Genotypic and phenotypic correlation coefficient of fifteen characters of forage bajra.

Character		PH	NTP	NLP	LL	LW	ST	LSR	GFY	DMC	DMP	CPC	CPP	NDF	ADF
DFF	r_g	-0.170	-0.154	-0.281*	-0.004	0.398**	0.072	-0.203	0.022	-0.216	-0.057	0.141	-0.016	0.332*	-0.422**
	r_p	-0.070	-0.070	-0.090	-0.051	0.098	0.028	-0.011	-0.078	-0.091	-0.118	0.069	-0.082	-0.044	-0.035
PH	r_g		0.026	0.418**	0.925**	0.092	0.255	0.348*	0.406**	0.458**	0.577**	-0.308*	0.406**	0.159	0.090
	r_p		0.014	0.296**	0.640**	0.127	0.233**	0.171*	0.415**	0.228**	0.462**	-0.185*	0.360**	0.131	0.065
NTP	r_g			0.563**	0.006	-0.267	-0.267	0.342*	0.045	0.331*	0.155	0.053	0.151	0.216	-0.103
	r_p			0.562**	-0.019	-0.218**	-0.197*	0.038	0.059	0.155	0.123	0.044	0.147	0.108	-0.082
NLP	r_g				0.211	-0.217	-0.072	0.368**	0.271	0.390**	0.461**	-0.172	0.281*	0.200	-0.120
	r_p				0.099	-0.147	-0.089	0.042	0.240**	0.181*	0.319**	-0.114	0.220**	0.113	-0.045
LL	r_g					0.237	0.251	0.082	0.471**	0.253	0.577**	-0.194	0.478**	0.271	0.269
	r_p					0.211**	0.157	0.050	0.360**	0.118	0.368**	-0.151	0.284**	0.075	0.015
LW	r_g						0.539**	-0.062	0.386**	-0.650**	0.159	0.134	0.214	0.175	0.101
	r_p						0.422**	-0.002	0.325**	-0.339**	0.131	0.061	0.144	0.100	0.005
ST	r_g							-0.345*	0.624**	0.365*	0.176	0.448**	0.053	0.030	
	r_p							-0.098	0.467**	-0.301**	0.232**	0.059	0.256**	0.074	0.054
LSR	r_g								0.180	0.690**	0.508**	-0.049	0.424**	-0.094	-0.050
	r_p								0.068	0.096	0.037	0.130	-0.003	0.043	
GFY	r_g									-0.208	0.932**	-0.001	0.849**	0.426**	0.293*
	r_p									-0.067	0.854**	-0.044	0.767**	0.243**	0.096
DMC	r_g										0.133	-0.430**	0.006	0.115	0.013
	r_p										0.427**	-0.171*	0.299**	-0.072	-0.012
DMP	r_g											-0.154	0.869**	0.473**	0.316*
	r_p											-0.132	0.833**	0.184**	0.074
CPC	r_g												0.357*	0.159	-0.405**
	r_p												0.406**	0.087	-0.262**
CPP	r_g													0.510**	0.103
	r_p													0.202*	-0.072
NDF	r_g														0.080
	r_p														0.178*

*, ** Significant at P = 0.05 level and P = 0.01 level

DFF - Days to 50 % flowering, PH - Plant height, NTP - Number of tillers per plant, NLP - Number of leaves per plant, LL - Leaf length, LW - Leaf width, ST - Stem girth, LSR - Leaf : stem ratio, GFY - Green forage yield per plant, DMC - Dry matter content (%), DMP - Dry matter yield per plant (g), CPC - Crude protein content (%), CPP - Crude protein yield per plant (g), NDF - Neutral detergent fiber content (%), ADF - Acid detergent fiber content (%)

Table 4: Path coefficient analysis showing direct and indirect effect of various characters on green forage yield per plant of forage bajra genotypes.

Characters	DFF	PH	NTP	NLP	LL	LW	ST	LSR	DMC	DMP	CPC	CPP	NDF	ADF	Genotypic correlation with green forage yield per plant
DFF	**-0.015**	0.005	-0.009	0.019	0.000	-0.028	0.011	-0.009	0.079	-0.038	0.028	-0.004	0.024	0.014	0.022
PH	0.003	**-0.030**	0.002	-0.028	0.025	-0.006	0.039	0.015	-0.168	0.388	0.061	0.098	0.012	-0.003	0.406**
NTP	0.002	-0.001	**0.061**	-0.038	0.000	0.019	-0.041	0.015	-0.122	0.105	-0.011	0.036	0.016	0.003	0.045
NLP	0.004	-0.012	0.034	**0.068**	0.006	0.015	-0.011	0.016	-0.143	0.310	0.034	0.068	0.015	0.004	0.271
LL	0.000	-0.027	0.000	-0.014	**0.027**	-0.017	0.038	0.004	-0.093	0.388	0.038	0.115	0.020	-0.009	0.471**
LW	-0.006	-0.003	-0.016	0.015	0.006	**-0.070**	0.083	-0.003	0.239	0.107	-0.027	0.051	0.013	-0.003	0.386**
ST	-0.001	-0.008	-0.016	0.005	0.007	-0.038	**0.154**	-0.015	0.216	0.245	-0.035	0.108	0.004	-0.001	0.624**
LSR	0.003	-0.010	0.021	-0.025	0.002	0.004	-0.053	**0.043**	-0.254	0.342	0.010	0.102	-0.007	0.002	0.18
DMC	0.003	-0.014	0.020	-0.026	0.007	0.046	-0.090	0.030	**-0.368**	0.090	0.085	0.001	0.008	0.000	-0.208
DMP	0.001	-0.017	0.009	-0.031	0.016	-0.011	0.056	0.022	-0.049	**0.673**	0.031	0.209	0.034	-0.011	0.932**
CPC	-0.002	0.009	0.003	0.012	-0.005	-0.009	0.027	-0.002	0.158	-0.104	**-0.198**	0.086	0.012	0.014	-0.001
CPP	0.000	-0.012	0.009	0.019	0.013	-0.015	0.069	0.018	-0.002	0.585	-0.071	**0.240**	0.037	-0.003	0.849**
NDF	-0.005	-0.005	0.013	-0.014	0.007	-0.012	0.008	-0.004	-0.042	0.318	-0.032	0.122	**0.073**	-0.003	0.426**
ADF	0.006	-0.003	-0.006	0.008	0.007	-0.007	0.005	-0.002	-0.005	0.213	0.080	0.025	0.006	**-0.034**	0.293*

*, ** Significant at P = 0.05 level and P = 0.01 level. Residual effect = 0.0270. Bold figures show direct effect.

DFF - Days to 50 % flowering, PH - Plant height, NTP - Number of tillers per plant, NLP - Number of leaves per plant, LL - Leaf length, LW - Leaf width, ST - Stem girth, LSR - Leaf : stem ratio, DMC - Dry matter content (%), DMP - Dry matter yield per plant (g), CPC - Crude protein content (%), CPP - Crude protein yield per plant (g), NDF - Neutral detergent fiber content (%), ADF - Acid detergent fiber content (%), GC – Genotypic correlation

CONCLUSION

From the present investigation, it can be concluded that due weightage should be given to plant height, leaf length, leaf width, stem thickness, number of tillers per plant, dry matter yield per plant, crude protein yield per plant and neutral detergent fibre content while imposing selection for genetic improvement of green forage yield per plant in forage bajra. On the basis of per se performance the genotypes *viz.*, Giant Bajra, GP 138, AFB 3, ICMV 1611, 743 KH 16, ICMV 1701, ICMV 1608, ICMV 1616 can be further utilized in the future

breeding programme for the development of high yielding varieties/ hybrids in forage bajra.

FUTURE SCOPE

The results of the present investigation provided information about the association between different traits in forage bajra. The combination of the various characteristics can be used for a further selection of the important genotypes of bajra to use in breeding programmes for higher fodder production. The direct or indirect selection for the traits that are significant and positively correlated with yield can help breeders to improve the fodder yield in bajra.

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