RESEARCH ARTICLE

Genetic variability and character association for fodder yield and its related traits in pearl millet over locations under rainfed conditions of Gujarat

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ABSTRACT : A set of 23 genotypes of fodder pearl millet were studied for genetic variability, heritability, genetic advance and character association of green fodder yield and its components at Jamnagar and Dhari under rainfed condition of Gujarat during *Kharif*-2014. The analysis of variance revealed highly significant differences among the genotypes for all the seven characters studied. All the genotypes showed considerable amount of variation in their mean performance with respect to the characters studied, indicates presence of sufficient variability and scope for further selection and breeding superior and desirable genotypes. The variability analysis revealed that harvest index, grain yield, dry fodder yield and green fodder yield had high magnitude of phenotypic range, genotypic co-efficient of variation, phenotypic co-efficient of variation, heritability and genetic advance expressed as percentage of mean thereby suggesting the importance of additive gene action. Hence, these characters can be improved through simple selection process. Green fodder yield had significant positive correlation with days to 50 per cent flowering, days to maturity and dry fodder yield at both genotypic and phenotypic levels indicating any increase in these traits will increase the green fodder yield.

KEY WORDS : Pearl millet, Variability, Heritability, Correlation co-efficient, Green fodder yield

INTRODUCTION

Pearl millet [*Pennisetum glaucum* (L.) R. Br.], the

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world's hardiest warm season cereal crop (Reddy *et al.,* 2012). It is an indispensable source of fodder in many regions of the world. Being a C_4 species, it has tremendous potential for biomass production, most of which is accumulated in its vegetative parts. Shashikala *et al.* (2013) mentioned that the green fodder of pearl millet is leafy, palatable and very nutritious feed stock for cattle ensuring good milk yield. Being any time forage, pearl millet, unlike sorghum, can be grazed, or cut and fed at any growth stage, as it has no HCN content. Pearl

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millet is excellent for producing silage, particularly in regions with dry spells during the rainy season. Pearl millet can produce higher silage yields with higher protein than sorghum. Pearl millet is high tolerance to high temperature and better ability to withstand drought and to grow even under low soil fertility is best suited for arid and semi arid conditions of Gujarat. It is well established fact that the progress in improvement of a crop depends on the degree of variability in the desired character in the base material. The study of relationships among quantitative characters is important for assessing the feasibility of joint selection of two or more traits and hence, for evaluating the effect of selection for secondary traits on genetic gain for the primary trait under consideration. A positive genetic correlation between two desirable traits makes the job of the plant breeder easy for improving both traits simultaneously. Therefore, the present investigation was undertaken to study the genetic variability, heritability and character association for green fodder yield and its components in fodder pearl millet genotypes during rainy season of 2014.

EXPERIMENTAL METHODS

Two seed set of 23 genotypes (IP 15535, IP 17360, IP 3525, IP 5153, IP 6113, IP 15556, IP 14537, IP 14542, IP 14522, IP 2761, ICMV 05222, ICMV 05555, ICMV 05777, IP 6202, IP 15564, IP 11431, IP 10077, ICMV 08111, IP 13150, IP 22269, IP 10429, DFMH 30 (Check) and PAC 981 (Check) of fodder pearl millet were supplied by ICRISAT, Patancheru, Hyderabad. These were evaluated at Pearl millet Research Station, Junagadh Agricultural University, Jamnagar and Grassland Research Station, Junagadh Agricultural University, Dhari, Gujarat (India) during rainy season of 2014. The design of the trail was Randomization Complete Block Design with two replications at both the locations. Each plot consisted of four rows of 4.0 m long and 60 cm apart in both locations. Middle two rows were considered for all the observations. Thus, the net plot size was 4.0 x 1.20m². The trial was planted on 24th July, 2014 and 25th July, 2014 at Jamnagar and Dhari centre, respectively. While, the trial was harvested on 31st October, 2014 and 13th November, 2014 at Jamnagar and Dhari centre, respectively. The fertilizer was applied @ 80-40-00 NPK kg per ha at both the locations. The data on different plant characters such as days to 50 per cent flowering,

days to maturity, plant height (cm), grain yield (kg/plot), dry fodder yield (kg/plot) and green fodder yield (kg/plot) were recorded. The data of green fodder yield (kg/plot), dry fodder yield (kg/plot) and grain yield (kg/plot) were converted into quintal per hectare. Mean values were subjected to standard statistical procedures namely, analysis of variance (Panse and Sukhatme, 1978), phenotypic and genotypic variances (Lush, 1940) genotypic and phenotypic co-efficient of variations (Burton, 1952) and heritability and genetic advance et al., 1955). The heritability estimates of >70 per cent was considered very high; 50-70 per cent high; 30-50 per cent moderate and <30 per cent low (Hallauer and Miranda, 1981). The genotypic correlations between green fodder yield and its related component traits and among themselves, were worked out as per the methods suggested by Al-jibouri et al. (1958).

EXPERIMENTAL RESULTS AND ANALYSIS

The analysis of variance (Table 1) revealed that the significant differences among the genotypes for all the seven characters studied, in both the locations and pooled over the locations, except grain yield and harvest index at Dhari centre. These indicated present of vast variability among the genotypes being evaluated and ample scope of improvement by selection. The range of variation and the estimate of genetic parameters which include heritability in broad sense, co-efficient of variation (PCV and GCV) and genetic advance expressed as percentage of mean for individual location and pooled over locations are presented in Table 1. The results are discussed only on pooled basis as under.

The range of phenotypic variability was found to be wide. The high phenotypic variation for green fodder yield, dry fodder yield and plant height, indicating thereby the possibility of effective selection for these traits. On the other hand, grain yield and harvest index exhibited narrow range of phenotypic variability. The remaining characters like days to 50 per cent flowering and days to maturity showed moderate magnitude of phenotypic variability. In the present study, the higher estimates of genotypic variance over environmental variance in all the characters revealed that the variation among the genotypes had a genetic basis. The estimates of phenotypic and genotypic variances were high for green fodder yield (3376.7, 2116.7), dry fodder yield (913.7,

Table 1: Analysis of variance showing mean squares and variability parameters for different traits in individual location and pooled over locations in pearl millet

Parameter		Days to 50 % flowering	Days to maturity	Plant height (cm)	Green fodder yield (q/ha)	Dry fodder yield (q/ha)	Grain yield (q/ha)	Harvest index (%)
Jamnagar (E₁)								
Mean sum	Replications (1 df)	0.20	1.78	45.75**	4560**	2143**	10.7**	36.3**
of squares	Genotypes (22 df)	133.9**	87.2**	1006**	7131**	1229**	19.12**	23.6**
	Error (22 df)	1.65	1.44	274.5	1011	381	0.88	2.89
Mean		66	92	274	272	118	7.42	6.99
Range		50-77	77-99	228-314	214-324	89-151	4.27-10.99	2.85-11.5
Phenotypic variance		67.8	44.3	640.5	4071	805	10.00	13.22
Genotypic variance		66.1	42.9	366.1	3060	424	9.12	10.33
Environment variance		1.65	1.44	274.5	1011	381	0.88	2.89
PCV %		12.55	7.25	9.25	23.49	24.05	42.62	52.03
GCV %		12.40	7.18	6.99	20.37	17.46	40.70	45.98
Heritability %		97.60	96.70	57.10	75.20	52.70	91.20	78.10
GA (% mean)		25.23	14.45	10.89	36.38	26.11	80.07	83.73
Dhari (E₂)								
Mean sum	Replications (1 df)	4.89*	266.2**	2663**	2062**	1062**	0.23	0.99
of squares	Genotypes (22 df)	92.81**	62.9**	1593**	5572**	2203**	0.54	0.87
	Error (22 df)	87.21	20.9	626	4107	1423	0.47	0.65
Mean		66	87	333	285	164	2.87	1.92
Range		54-78	74-96	300-373	223-361	126-208	2.27-3.97	1.23-3.38
Phenotypic variance		90.01	41.93	1109	4839	1813	0.51	0.76
Genotypic variance		2.80	21.03	483	732	390	0.04	0.11
Environment variance		87.21	20.90	626	4107	1423	0.47	0.65
PCV %		14.28	7.48	9.99	24.44	25.97	24.70	45.45
GCV %		2.52	5.30	6.60	9.51	12.04	6.82	17.14
Heritability %		3.10	50.20	43.60	15.10	21.50	7.60	14.20
GA (% mean)		0.92	7.73	8.97	7.62	11.50	3.88	13.31
Pooled over locations (E₁ x E₂)								
Mean sum	Replications (1 df)	0.78	68.2**	502**	3122**	1550**	3.52	12.3**
of squares	Genotypes (22 df)	84.2**	67.0**	1001**	5493**	1505**	5.23**	7.4**
	Error (22 df)	20.0	6.4	286	1260	323	0.38	0.97
Mean		66	90	304	278	141	5.15	4.46
Range		58-74	76-96	271-335	224-341	111-171	3.47-7.38	2.18-6.77
Phenotypic variance		52.1	36.7	643.7	3376.7	913.7	2.80	4.20
Genotypic variance		32.1	30.3	357.6	2116.7	591.1	2.42	3.22
Environment variance		20.0	6.4	286.1	1260.0	322.6	0.38	0.98
PCV %		10.90	6.76	8.35	20.87	21.41	32.50	46.01
GCV %		8.56	6.15	6.23	16.53	17.22	30.22	40.30
Heritability %		61.70	82.70	55.60	62.70	64.70	86.50	76.70
GA (% mean)		13.84	11.52	9.56	26.95	28.53	57.90	72.71

*and ** indicate significance of values at P=0.05 and 0.01, respectively. GCV= Genotypic co-efficient of variation;
PCV= Phenotypic co-efficient of variation;   GA (% mean)= Genetic advance as per cent of mean.

591.1) and plant height (643.7, 357.6). The phenotypic and genotypic variances were moderate for days to 50 per cent flowering (52.1, 32.1) and days to maturity (36.7, 30.3); while, they were low for the remaining characters. Similar result was reported by Borkhataria *et al*. (2005); Bhagirath *et al*. (2007) and Dapke *et al*. (2014) in pearl millet.

The relative amount of variation expressed by different traits was judged through estimates of phenotypic and genotypic co-efficient of variation. The PCV was higher than GCV for all the characters studied showing that all the traits were highly influenced by environment. However, differences between them were not of high magnitude. The characters like harvest index (46.01, 40.30%), grain yield (32.50, 30.22%), dry fodder yield (21.41, 17.22%) and green fodder yield (20.87, 16.53%) exhibited high magnitude of PCV and GCV indicating the presence of wide genetic variability for these traits and chances for improvement of these characters are fairly high. Low values of PCV and GCV were observed for days to 50 per cent flowering (10.90, 8.56%), days to maturity (6.76, 6.15%) and plant height (8.35, 6.23%). These results are in conformity with the report of Borkhataria *et al*. (2005); Bhagirath *et al*. (2007); Vidyadhar *et al.* (2007); Lakshmana *et al.* (2009) and Dapke *et al.* (2014).

The effectiveness of selection for any character depends, not only the extent of genetic variability but also

in the extent to which it will be transferred from one generation to the other generation, because, only heritable portion of variation is exploitable through selection. The estimates of heritability (broad sense) ranged from 55.60 (plant height) to 86.50 per cent (grain yield). Very high heritability estimates were recorded for grain yield (86.50%), days to maturity (82.70%) and harvest index (76.70%) suggesting the usefulness of selection based on phenotypic observations. High heritability estimate was observed for dry fodder yield (64.70%), green fodder yield (62.70%), days to 50 per cent flowering (61.70%) and plant height (55.60%). The high heritability may be due to additive gene effects hence, these traits are likely to respond to direct selection. The results achieved in the present study are in akin with Borkhataria *et al.* (2005); Bhagirath *et al.* (2007); Kumari and Nagarajan (2008) and Dapke *et al.* (2014). Genotypic co-efficient of variability along with heritability estimates provides a better picture for the amount of genetic gain expected to be obtained from phenotypic selection (Burton, 1952). It was interesting to note that high GCV was accompanied with high heritability estimates for harvest index, grain yield, dry fodder yield and green fodder yield in the present material which further revealed that selection could be more effective for the improvement of these traits.

The estimates of genetic advance did not project the actual genetic gain that has been attained in relation to the *per se* performance which obviously is not uniform

Table 2 : Genotypic (r_g) and phenotypic (r_p) corrélation co-efficients among traits in pearl millet pooled over locations

Character		Days to 50 % flowering	Days to maturity	Plant height (cm)	Green fodder yield (q/ha)	Dry fodder yield (q/ha)	Grain yield (q/ha)	Harvest index (%)
Days to 50 % flowering	r_g	1.000	0.997**	0.153	0.839**	0.852**	-0.481*	-0.660**
	r_p	1.000	0.737**	0.079	0.479*	0.488*	-0.386	-0.488*
Days to maturity	r_g		1.000	0.228	0.658**	0.723**	-0.482*	-0.625**
	r_p		1.000	0.251	0.512*	0.546**	-0.346	-0.488*
Plant height (cm)	r_g			1.000	0.071	0.153	-0.228	-0.200
	r_p			1.000	0.227	0.229	-0.032	-0.116
Green fodder yield (q/ha)	r_g				1.000	0.976**	-0.770**	-0.972**
	r_p				1.000	0.959**	-0.568**	-0.799**
Dry fodder yield (q/ha)	r_g					1.000	-0.705**	-0.930**
	r_p					1.000	-0.537**	-0.797**
Grain yield (q/ha)	r_g						1.000	0.956**
	r_p						1.000	0.866**
Harvest index (%)	r_g							1.000
	r_p							1.000

*and ** indicate significance of values at P=0.05 and 0.01, respectively

in different populations and even in the same population under different environments. Therefore, the expected genetic gain as per cent of mean was computed. Estimates of genetic advance as percentage of mean ranged from 9.56 (plant height) to 72.71 per cent (harvest index). Heritability in coupled with genetic gain was more useful than the heritability values alone in the prediction of the resultant effect for selecting the best individual genotypes (Johnson *et al.*, 1955). Genetic gain gives an indication of expected genetic progress for a particular trait under suitable selection pressure. In the present study, the characters harvest index, dry fodder yield, green fodder yield and grain yield exhibited high heritability coupled with high genetic advance expressed as percentage of mean. This indicated the predominance of additive gene action in governing the traits and their suitability of selection for further improvement among the genotypes studied. These results are in accordance with those of Bhagirath *et al.* (2007); Vidyadhar *et al.* (2007); Lakshmana *et al.* (2009) and Dapke *et al.* (2014). High heritability estimates with low to medium genetic gain was manifested for days to 50 per cent flowering, days to maturity and plant height which might be due to preponderance of non-additive gene effects. Hence, it could be suggested that improvement of these characters might be difficult through simple selection. From the study of GCV, PCV, heritability and genetic advance, it is inferred that simple selection among genotypes could bring about significant improvement in the fodder yield and its component characters as the GCV, PCV, heritability and estimated genetic advance were high.

Correlation co-efficient is a statistical measure, which denotes the degree and magnitude of association between any two casually related variables. This association is due to pleiotropic gene action or linkage or more likely both. In plant breeding correlation co-efficient analysis measures the mutual relationship between two characters and it determines character association for improvement fodder yield and other characters. Since the association pattern among yield components help to select the superior genotypes from divergent population based on more than one interrelated characters. Thus, information on the degree and magnitude of association between characters is of prime important for the breeder to initiate any selection plan. In general the genotypic correlation was generally of higher magnitude than phenotypic correlation (Table 2), indicating that inherent association between various characters studied. Green fodder yield exhibited significant positive correlation with days to 50 per cent flowering (0.839, 0.479), days to maturity (0.658, 0.512) and dry fodder yield (0.976, 0.959), while non-significant and positive correlation was observed with plant height (0.071, 0.227) at both genotypic and phenotypic levels. Negative and significant association of green fodder yield was observed with grain yield (-0.770, -0.568) and harvest index (-0.972, -0.799) at both genotypic and phenotypic levels. Interestingly, the characters which exhibited positive correlation with green fodder yield have also depicted positive association among themselves. In the present study, significant positive association was observed for dry fodder yield with days to 50 per cent flowering (0.852, 0.488) and days to maturity (0.723, 0.546); grain yield with harvest index (0.956, 0.866) and days to 50 per cent flowering with days to maturity (0.997, 0.737) at both genotypic and phenotypic levels. The similar results obtained by Bhagirath *et al.* (2007); Arulselvi *et al.* (2008); Abuali *et al.* (2012) and Dapke *et al.* (2014).

The present conclusion revealed substantial genetic variability for harvest index, grain yield, dry fodder yield and green fodder yield in the fodder pearl millet genotypes and hence, a scope for improvement through selection. The studies on correlation co-efficient indicated that the characters *viz.*, dry fodder yield, days to 50 per cent flowering, days to maturity and plant height were the predominant green fodder yield contributing characters in pearl millet.

REFERENCES

Abuali, A.I., Abdelmulla, A.A. and Idris, A.E. (2012). Character association and path analysis in pearl millet (*Pennisetum glaucum* L.). *American J. Exp. Agric.*, **2** (3): 370-381.

Al-jibouri, H.A., Miller, P.A. and Robinson, H.F. (1958). Genotypic and environmental variance and covariance in upland cotton cross of interspecific origin. *Agron. J.*, **50**: 633-637.

Arulselvi, S., Mohanasundaram and Sevi, B. (2008). Correlation and path analysis for grain yield and its components in pearl millet (*Pennisetum glaucum* L.). *Madras Agril. J.,* **95** (7-12): 311-314.

Bhagirath, Ram, Sharma, K.C. and Sastry, E.V.D. (2007). Genetic variability, correlation and path analysis in fodder yield and related traits in pearl millet (*Pennisetum glaucum* L.). *Agric. Sci. Digest*, **27**(1): 8-12.

Borkhataria, P.R., Bhatiya, V.J., Pandya, H.M. and Valu, M.G. (2005). Variability and correlation studies in pearl millet. *Natnl. J. Pl. Improv.*, **7** (1): 21.

Burton, G.W. (1952). *Quantitative inheritance in grasses. Proc. 6th Internat. Grassl &Cong.*, **1**: 277-283.

Dapke, J.S., Shah, D.S., Pawar, G.N., Dhembre, V.M. and Kumar, Mithilesh (2014).Genetic variability and character association over environment in pearl millet (*Pennisetum glaucum* L.) under dryland conditions of Gujarat. *Bioscan*, **9** (2) : 863-867.

Hallauer, A.R. and Miranda, J.B. (1981). *Quantitative genetics in maize breeding.* Lowa University Press, Ames, LOWA, USA.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Genotypic and phenotypic correlation in soybeans and their implication in selection. *Agron. J.,* **47**: 477-483.

Kumari, B.M. and Nagarajan, P. (2008).Variability and heritability analysis in pearl millet (*Pennisetum glaucum* L.). *Madras Agril. J.*, **95** (1-6): 190-192.

Lakshmana, D., Biradar, B.D. and Jolly, R.B. (2009). Variability studies in pearl millet germplasm lines (*Pennisetum glaucum* L.). *Res. On crops*, **10** (3): 687-689.

Lush, J.L. (1940). Intra-sire correlation and regression of offspring on dam as a method of estimating heritability of characters. *Proc. American Soc. Anim. Prod.,* **33**: 293-301.

Panse, W.G. and Sukhatme, P.V. (1978). *Statistical methods for agriculture workers* (3rd Rev.Ed.) ICAR, NEW DELHI, INDIA.

Reddy, A.A., Malik, D., Singh, I.P., Ardeshna, N.J., Kundu, K.K., Rao, P., Gupta, S.K., Sharma, R. and Gajanan (2012). Demand and supply for pearl millet grain and fodder by 2020 in Western India. ASI, March, 2012. 635pp.

Shashikala, T., Rai, K. N., Balaji Naik, R., Shanti, M., Chandrika, V. and Loka Reddy, K. (2013). Fodder potential of multicut pearl millet genotypes during summer season. *Internat. J. Bio-resource & Stress Mgmt.*, **4** (4) : 628-630.

Vidyadhar, B., Pooran, C., Swanalatha, Devi, I., Vijaya, S.R.M. and Ramachandraiah, D. (2007). Genetic variability and character association in pearl millet (*Pennisetum glaucum* L.) and their implications in selection. *Indian J. Agril. Res.,* **41** (2): 150-153.

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