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Study of genetic variability, heritability and genetic advance for yield and its component traits in pearl millet [*Pennisetum glaucum* (L.) R. Br.]

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Abstract
The present experiment was carried out to study genetic variability, heritability and genetic advance among the twenty six germplasms of pearl millet (2n=2x=14) for different fifteen characters. The analysis of variance revealed that mean sum of square of genotypes were significant for all the fifteen characters which indicated adequate genetic variability among the genotypes. High magnitude of GCV and PCV for traits like panicle weight, grain yield per plant, dry fodder yield per plant and iron content suggesting the presence of wide range of genetic variability in the germplasm for these traits. High heritability along with high genetic advance percent of mean were observed for number of effective tiller per plant, panicle length, panicle girth, panicle weight, grain yield per plant, dry fodder yield per plant, test weight, harvest index, protein content, iron content and zinc content that indicates the selection for these traits would be more effective.

Keywords: Genetic advance, heritability, pearl millet, variability

Introduction
Pearl millet is world's sixth and India's third important cereal food crop after rice and wheat. It is commonly known as cattail millet or bulrush millet in English (Adam, 1996) [1] and in India it commonly known as 'bajra'. Pearl millet grain is highly nutritive, staple food and primary source of calories for millions of people. It is annual tillering, cross pollinated, diploid crop (2n=2x=14) belongs to family Poaceae, sub family Panicoideae, tribe *paniceae* and genus *Pennisetum* is believed to be originated to Western Africa. It is highly cross-pollinated crop with genome size of 1.79 GB (Varshney *et al*., 2017) [19]. In India it occupies an area of 6.93 million hectares with production of 8.61 million tonnes with productivity of 1243 Kg/ha (Anonymous, 2020) [2]. Cultivated pearl millet displays tremendous phenotypic variability for traits such as flowering time, panicle length, grain and stover characteristics, tolerance to drought, pest and diseases as well as nutritional values. The genetic variability present in the population is the prerequisite for the success of any crop improvement programme.

Material and Methods
The materials used in the experiment contain twenty-six genotypes of pearl millet were obtained from Center for Crop Improvement, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar (Table No. 1) and evaluated during *kharif* 2020 at Agronomy Instructional Farm, Chimanbhai Patel College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar in a Randomized Block Design with three replications. Observations were recorded on five randomly selected plants for fifteen characters *viz*., days to flowering, days to maturity, plant height (cm), number of effective tiller per plant, panicle length (cm), panicle girth (mm), panicle weight (g), grain yield per plant (g), panicle harvest index (%), dry fodder yield per plant (g), test weight (g), protein content (%), iron content (ppm) and zinc content (ppm). Standard agronomic practices were followed through out the experiment. The data were subjected to statistical analysis using R studio software and genetic parameters such as phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) as per Burton (1952) [6], heritability in broad sense (h2b) and expected genetic advance as percent of mean worked out as per Johnson *et al*. (1955) [11] and Hanson (1963) [10].

Results and Discussion

The analysis of variance depicting mean sum of squares for fifteen quantitative as well as qualitative traits are given in Table No. 2. The analysis of variance revealed that mean sum of square of genotypes were significant for all the fifteen characters which indicated adequate genetic variability among the genotypes. The estimates of Range, GCV, PCV, h2bs, GAM are given in Table No. 3. The GCV % and PCV % were the highest for iron content, dry fodder yield per plant, grain yield per plant, panicle weight and number of effective tiller per plant, it was suggesting the presence of high amount of variability in the population and therefore more chances for simple selection based on the phenotypes of these traits. It has also been reported by earlier workers Subi and Idris (2013) [17] and Kumar *et al*. (2014) [13]

Analysis of variance (ANOVA) may not reveal the variability and this could be accessed through standardizing the phenotypic and genotypic variances by obtaining coefficient of variability. Further, it is essential to separate out the environmental influence from the total variability. This indicates the accuracy with which a genotype can be identified by its phenotypic performance. The estimates of heritability alone fail to indicate the response to selection. Therefore, the heritability estimates appeared to be more meaningful when accompanied by estimates of genetic advance.

The values of phenotypic coefficient of variation (PCV) were found higher than the genotypic coefficient of variation (GCV) for all the traits studied indicating the higher influence of environment on the expression of these characters, thus selection for such characters occasionally might be misleading. Higher estimates of PCV than GCV reported by Manga (2013) [14] and Basavraj *et al*. (2017) [5]. However close affinity between GCV and PCV for the traits viz., days to flowering, days to maturity, panicle length, panicle girth, panicle weight, test weight, protein content and harvest index suggesting the environmental influence was narrow for the expression of these traits.

Table 1: Experimental materials to be used.

Sr. No.	Genotype	Sr. No.	Genotype
1	15035 R	14	18587 R
2	15298 R	15	18805 R
3	15611 R	16	ICMB 04999
4	15636 R	17	1152-53 B
5	15738 R	18	2802 B
6	15990 R	19	2820 B
7	16110 R	20	2889 B
8	16127 R	21	2901 B
9	16228 R	22	5902 B
10	16834 R	23	6120 B
11	17179 R	24	7148 B
12	17369 R	25	ICMB 82333
13	18488 R	26	ICMB 97111

Note: All the genotypes were obtained from Centre for Crop Improvement, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat.

Table 2: Analysis of variance (ANOVA) for different characters of pearl millet genotypes.

Sr. No	Characters	Mean sum of square		
		Replication	Treatments	Error
	Degree of freedom	2	25	77
1	Days to flowering	0.62	80.59**	1.14
2	Days to maturity	1.70	79.83**	1.89
3	Plant height (cm)	16.05	229.21**	44.36
4	Number of effective tiller per plant	0.04	0.39**	0.03
5	Panicle length (cm)	1.50	23.05**	0.67
6	Panicle girth (mm)	0.91	28.01**	0.82
7	Panicle weight (g)	14.56	551.19**	22.44
8	Grain yield per plant (g)	7.56	522.98**	12.87
9	Panicle harvest index (%)	77.29	141.40**	28.23
10	Dry fodder yield per plant (g)	12.58	786.74**	8.84
11	Test weight (g)	0.17	4.49**	0.07
12	Harvest index (%)	4.58	405.77**	6.62
13	Protein content (%)	0.003	3.05**	0.008
14	Iron content (%)	15.82	2812.12**	19.67
15	Zinc content (%)	2.66	64.27**	2.99

*,** significant at 5% and 1% level of significance, respectively

High magnitude of GCV and PCV for traits like panicle weight, grain yield per plant, dry fodder yield per plant and iron content suggesting the presence of wide range of genetic variability in the germplasm for these traits. Moderate values for GCV and PCV were recorded for the traits viz., number of effective tiller per plant, panicle length, panicle girth, test weight, protein content and harvest index indicating moderate level of genetic variability is present among these traits.

Moderate to high coefficient of variation in terms of both genotypic and phenotypic values showed by number of effective tiller per plant, panicle length, panicle girth, panicle weight, grain yield per plant, dry fodder yield per plant, test weight, harvest index, protein content and iron content, thus selection may be more effective for these traits because the response to selection is directly proportional to the variability present in the experimental unit.

Low magnitude of GCV and PCV were observed for traits like days to flowering, days to maturity, plant height and panicle harvest index which indicates the clear variation among the lines was not only due to their genotypes but also involvement of environment and selection might not be effective for this character. These results is in conformity with the findings of Kumar *et al*. (2016) [12], Pallavi *et al*. (2020) [16] and Chauhan *et al*. (2020) [7] displaying the influence of environment on the expression of different quantitative characters.

Heritability indicates the ratio of genotypic variance to the total variance. It is a good index of the transmission of characters from parents to their offspring. Heritability was observed highest for the traits iron content (97.93%), protein content (96.19%), days to flowering (95.84%), test weight (95.38%), days to maturity (93.21%), grain yield per plant (92.96%), panicle length (91.75%), panicle girth (91.64%), panicle weight (88.70%), harvest index (87.57%), zinc content (87.21%), dry fodder yield per plant (85.62%) and number of effective tiller per plant (75.16%) suggested that heritability may be due to higher contribution of genotypic component in these characters. While, plant height (58.14%) and panicle harvest index (56.12%) had moderate heritability, indicating that these characters were less influenced by environment and direct selection for these components would be effective for further improvement in grain yield in pearl millet.

High estimates of genetic advance expressed as percent of mean found for iron content (75.22%) followed by grain yield per plant (63.22%), dry fodder yield per plant (57.24%), panicle weight (50.94%), harvest index (33.97%), test weight (30.34%), number of effective tiller per plant (29.83%), protein content (28.83%), panicle girth (27.49%) and panicle length (24.22%). Whereas, moderate values of genetic advance as percent of mean were observed for zinc content (18.53%), days to flowering (17.16%) and days to maturity (11.14%) which indicated the predominance of additive gene action and straight selection would be effective for improvement of these characters.

Relative comparison of heritability along with genetic advance percent of mean over the characters indicated that characters *viz*., number of effective tiller per plant, panicle length, panicle girth, panicle weight, grain yield per plant, dry fodder yield per plant, test weight, protein content, harvest index, iron content and zinc content had high heritability coupled with high genetic advance percent of mean. Which indicated the dominance of additive gene action and therefore, selection would be rewarded for improvement of these characters.

High heritability associated with moderate genetic advance as percent of mean for the characters *viz*., days to flowering, days to maturity and panicle harvest index. Which indicate involvement of additive or fixable gene effects in the expression of characters so simple selection may be practiced for improving these characters. Similar results were recorded by Chauhan *et al.* (2020) [7] for number of effective tiller per plant and test weight, Vagadiya *et al.* (2013) [18] for panicle length, grain yield, panicle weight and protein content, Govindraj *et al.* (2020) [9] for panicle girth, Nehra *et al*. (2017) [15] for dry fodder yield per plant, Dapke *et al.* (2014) [8] for harvest index, Anuradha *et al.* (2020) [3] for iron content, Asungre *et al.* (2022) [4] for zinc content, indicated the prevalence of additive gene action in their inheritance and suggested that the phenotypic selection for these traits will be effective.

Table 3: Variability parameters for yield and its component traits in pearl millet genotypes.

Sr. No.	Characters	Range	GCV (%)	PCV (%)	h2 b (%)	GAM (%)
1	Days to flowering	47.67-71.67	8.50	8.69	95.84	17.16
2	Days to maturity	79.33-100.00	5.60	5.80	93.21	11.14
3	Plant height (cm)	117.60-152.90	5.97	7.83	58.14	9.38
4	Number of effective tiller per plant	1.40-2.70	16.70	19.27	75.16	29.83
5	Panicle length (cm)	16.47-27.40	12.27	12.81	91.75	24.22
6	Panicle girth (mm)	16.99-28.56	13.94	14.56	91.64	27.49
7	Panicle weight (g)	27.65-76.99	26.24	27.88	88.70	50.94
8	Grain yield per plant (g)	19.14-67.51	31.83	33.01	92.96	63.22
9	Panicle harvest index (%)	66.62-91.08	7.62	10.18	56.12	11.77
10	Dry fodder yield per plant (g)	21.47-68.80	30.03	32.45	85.62	57.24
11	Test weight (g)	5.20-10.77	15.08	15.44	95.38	30.34
12	Harvest index (%)	29.42-69.97	17.62	18.83	87.57	33.97
13	Protein content (%)	5.38-9.32	14.05	14.11	96.19	28.83
14	Iron content (%)	41.27-151.73	36.90	37.29	97.93	75.22
15	Zinc content (%)	37.32-55.38	9.63	10.31	87.21	18.53

GCV (%) and PCV (%) are genotypic and phenotypic coefficient of variance, respectively. h2(b) (%) and GAM are broad sense heritability and genetic advance expressed as percent of mean, respectively.

Conclusion

In the present study high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for iron content followed by, dry fodder yield per plant, grain yield per plant and panicle weight suggesting the presence of wide range of genetic variability in the germplasm for these traits. High heritability coupled with high genetic advance as percent of mean was observed for number of effective tiller per plant, panicle length, panicle girth, panicle weight, grain yield per plant, dry fodder yield

per plant, test weight, protein content, harvest index, iron content and zinc content indicating the presence of additive genes and less environmental influence on the characters. Hence, simple phenotypic selection from the existing germplasm is suggested for further improvement. High GCV, PCV, heritability and genetic advance as a percent of mean reveals very important selection criteria for crop improvement.

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