Received: 06 Jun 2020 | Revised: 09 Nov 2020 | Accepted: 11 Nov 2020

Electronic Journal of Plant Breeding

Research Note

Descriptive statistical analysis and variability studies in germplasm collections of barnyard millet (*Echinochloa frumentacea* L.)

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Abstract
A study was conducted to evaluate the variability among fifty three genotypes of Barnyard millet in Randomized Block Design with two replications. The traits *viz.,* plant height, flag leaf width, inflorescence length, the number of racemes per panicle, length of lower raceme left, test weight, relative water content, proline content and harvest index were found to be negatively skewed indicating the predominance of additive gene action. Thus these traits could be considered for selection criteria, while selecting genotypes for crop improvement. Analysis of genetic variability revealed that peduncle length, grain yield, stem girth, the number of tillers, fodder yield, proline content and flag leaf width established relatively high GCV value and thus these characters could be exploited for successful isolation of desirable accessions for the characters concerned. High heritability coupled with high genetic advance were observed for the traits like days to 50% flowering, plant height, flag leaf length, flag leaf width, inflorescence length and panicle breadth, the number of racemes/panicle, peduncle length, length of lower raceme –right, the number of nodes, stem girth, the number of tillers, fodder yield, relative water content, proline and grain yield which implied the presence of additive gene effects, controlling these traits. Hence the selection for these traits could be effective for improvement of any desired genotype.

Keywords
Barnyard millet, Descriptive statistics, Variability

Among the millets, Barnyard millet (*Echinochloa* sp.) is one of the oldest domesticated millets in the semi-arid tropics of Asia and Africa. Barnyard millet is rich in nutrients and essential amino acids. The protein, calcium and iron content of the *Echinochloa* spp. is found to be comparable to or greater than that of major cereals. It is also cultivated at high hills under double cut production system with an increased yield (Bandyopadhyay, 2009**).** Wide distribution of the crop across the world indicates the presence of greater diversity in the crop. Diversity is in both qualitative and quantitative characters will have a direct or indirect effect on the yield of the crop. The assessment and utilization of this genetic variability is very much essential in plant breeding. Progress in plant breeding depends on identification of new sources of genetic variation for beneficial traits, in such a way that a combination of alleles produces progenies with superior performance. With this objective, the present study was conducted.

Fifty three genotypes were evaluated for the study, among which 14 were collected from Coimbatore; 10 from Madurai and 26 from Bengaluru and two National checks *viz.,* VL172 and VL29 were used along with Co (kv) 2 as local check in Randomized Block Design (RBD) with two replications. The list of genotypes used in the study is given in **Table 1.** Sowing was done with a spacing of 30 x 10cm with a row length of 3m. The data on sixteen quantitative traits and three physiological traits totally nineteen characters were recorded. Quantitative characters were taken from five uniform plants, selected from each of the replication. Observations on three

Table 1. List of genotypes used in the study

Sl. No.	Genotypes	
1	ACM 294	Madurai (10)
2	ACM 295	
3	ACM 296	
4	ACM313	
5	ACM331	
6	ACM333	
7	MA1	
8	MA10	
9	ACM 334	
10	ACM335	
11	TNEF192	Coimbatore (14)
12	TNEF193	
13	TNEF196	
14	TNEF197	
15	TNEF198	
16	TNEF199	
17	TNEF200	
18	TNEF201	
19	TNEF202	
20	TNEF203	
21	TNEF204	
22	TNEF205	
23	TNEF206	
24	TNEF207	
25	GECH1	Bengaluru (26)
26	GECH3	
27	GECH5	
28	GECH6	
29	GECH8	
30	GECH10	
31	GECH12	
32	GECH13	
33	GECH15	
34	GECH16	
35	GECH18	
36	GECH25	
37	GECH27	
38	GECH525	
39	GECH759	
40	GECH440	
41	GECH403	
42	GECH41	
43	GECH204	
44	GECH209	
45	GECH426	
46	GECH351	
47	GECH758	
48	GECH768	
49	GECH746	
50	GECH779	
51	VL 172	National Check (2)
52	VL29	
53	CO2	Local Check (1)

physiological characters were recorded on five plants selected randomly. The mean values of all the genotypes were subjected to statistical analysis using TNAUSTAT package. The analysis of variance of RBD and their significance for all the characters were worked out as suggested by Panse and Sukhatme (1964). Genetic parameters like variances, GCV, PCV, heritability and genetic advance (GA) were calculated by adapting the procedure suggested by Johnson et.*al.* (1955).

Crop improvement programme depends mainly on the degree of variability for the desired characters existing in the germplasm collection. An estimate of the extent of variability available in the germplasm would be of immense value to the breeder to efficiently design the breeding procedure for further improvement of the crop and to identify superior genotypes in the population. Studies on descriptive statistics are helpful in the estimation of simple measures of variability for preliminary evaluation.

Of all the traits studied, plant height recorded the highest mean, range, variance, standard deviation and standard error. Rinkey *et al.,* 2018 had also reported the same. This indicated the scope for selection of this trait. The traits like plant height, flag leaf width, inflorescence length, the number of racemes per panicle, length of lower raceme left, test weight, relative water content, proline content and harvest index were found to be negatively skewed (**Table 2**.) and hence in the frequency distribution curve, most of the genotypes for particular trait were distributed in the right direction which inferred that the predominance of additive gene action for these traits. The presence of additive gene action is very important for selection since it determines the fixability of traits in the further generation.

Table 2. Descriptive Statistics for 19 characters in 53 Barnyard Millet germplasm

Characters	Median	Maximum	Minimum	Range	Variance	SD	SE	Skewness
DFF	54.00	73.00	46.00	27.00	53.34	7.30	0.77	1.12
PHT (cm)	**135.90**	**175.30**	**89.40**	**85.90**	**290.08**	**17.03**	**4.89**	-0.28
FLL (cm)	22.30	33.90	14.10	19.80	14.43	3.80	0.98	0.43
FLW (cm)	2.60	3.50	0.76	2.74	0.37	0.61	0.11	-0.72
LOI	20.40	27.90	12.60	15.30	10.64	3.26	1.12	-0.27
PAB	4.00	6.60	2.10	4.50	0.67	0.82	1.12	0.69
LLR-R	2.80	3.70	2.10	1.60	0.18	0.43	0.12	0.28
LLR-L	2.40	3.00	1.40	1.60	0.16	0.40	0.32	**-0.22**
NOR	45.00	61.00	16.50	44.50	88.48	9.41	5.72	-0.34
LOP	2.10	7.50	0.50	7.00	2.43	1.56	0.20	0.89
NON	7.30	11.60	4.30	7.30	1.94	1.39	0.48	0.81
STG	2.20	4.10	0.30	3.80	1.16	1.08	0.12	**0.08**
NOT	5.50	16.50	2.50	14.00	6.86	2.62	0.75	**1.77**
PRC	**0.27**	**0.40**	**0.10**	**0.30**	**0.01**	**0.08**	**0.01**	-0.30
RWC	85.45	95.83	61.11	34.72	72.59	8.52	2.05	**-0.92**
HIN	42.85	56.82	27.61	29.20	47.71	6.91	2.97	-0.24
TWT (gm)	3.05	3.50	2.30	1.20	0.09	0.30	0.09	-0.41
FYD	23.45	54.57	9.38	45.19	106.04	10.30	1.38	0.86
GYD (gm)	12.50	36.25	4.20	32.05	56.68	7.53	1.37	1.01

The numbers bolded are the highest and lowest mean values.

The characters like days to 50% flowering, flag leaf length, panicle breadth, panicle length, length of lower raceme right, the number of nodes, stem girth , the number of tillers per plant, fodder yield and grain yield showed positive skewness, where in the frequency distribution curve, most of the genotypes were distributed in the left direction. It indicated the presence of non additive gene action which was important for exploiting hybrid vigour through heterosis breeding. Hence these traits may be improved by exploiting the diverse genotypes as parents for production of hybrids. Nirmalakumari *et al.,* (2013) also had found similar findings in little millet where in, the characters *viz*., grain yield, the number of productive tillers per plant, total number of tillers per plant, flag leaf width and flag leaf sheath length showed positive skewness indicating non- additive gene action.

In the present study, analysis of variance for randomized block design revealed significant differences among fifty three genotypes for all characters (**Table 3**). The values of phenotypic variance were greater than that of genotypic variance. The trait, the number of racemes per panicle showed a greater difference in genotypic and phenotypic variance. Very close relationship was found between GCV and PCV for most of the characters revealing the least influence of environment for their expression. Similar results had been reported by Jyoti *et al.,* 2018. Generally the PCV estimates were higher than GCV's as found by Daba (2000) showing that the apparent variation was not only due to genotypes, but also there was influence of environment. However for the majority of the traits, ECV estimates were lower than both GCV and PCV. This implied that the environment role was less for the expression of such character.

Table 3. ANOVA for 19 characters in 53 barnyard millet genotypes

Character	Mean sum of Squares		
	Replication	Treatment	Error
DFF	25.50	106.67*	0.58
PHT(cm)	158.42	576.62*	23.90
FLL(cm)	207.20	28.85*	0.96
FLW(cm)	0.81	0.74*	0.01
LOI	58.57	21.24*	1.25
PAB	2.43	1.34*	0.02
LLR-R	0.90	0.36*	0.01
LLR-L	0.001	0.32*	0.09
NOR	4.85	183.05*	32.54
LOP	0.06	4.13*	0.13
NON	10.65	3.88*	0.22
STG	0.03	2.72*	0.06
NOT	26.50	13.72*	0.55
PRC	0.000024	0.01*	0.00003
RWC	29.51	86.16*	4.20
HIN	3.191	28.97*	8.86
TWT(gm)	0.32	0.18*	0.008
FYD	599.63	211.45*	1.91
GYD(gm)	271.36	113.37*	1.88

* : Significant at 5% level

From the present investigation, high PCV and GCV were observed for the traits *viz.,* the number of tillers, grain yield/ plant, flag leaf width. Similar results had been recorded by Chidambaram and Palanisamy (1996), Nirmalakumari and Vetriventhan. (2010) and Nirubana *et al.,* 2017 for grain yield. High PCV was also recorded for traits like the number of racemes/panicle and panicle breadth, fodder yield, proline content and peduncle length. Seven traits namely, peduncle length, grain yield, stem girth, the number of tillers, fodder yield, proline content, flag leaf width established relatively high GCV value (23.71-49.63%) (**Table 4**). These results were supported by the findings of Nirubana *et al.,* 2017 and Jyoti *et al.,* 2018.

Among the nineteen traits considered in the present study, seventeen traits had higher heritability percentage greater than 60%. High heritability was followed with higher genetic advance was recorded for the traits like days to 50% flowering, plant height, flag leaf length, flag leaf width, inflorescence length and panicle breadth, the number of racemes/panicle, peduncle length, length of lower raceme –right, the number of nodes, stem girth, the number of tillers, fodder yield, relative water content, proline and grain yield which implied the predominance of additive gene effects, controlling these traits. Subramanian *et al.* (2010), Karad *et al.* (2013), Nirubana *et al.,* 2017, Jyoti *et al.,* 2018 and Vikram *et al.,* 2020 also had found similar findings where in, high heritability coupled with high genetic advance observed for grain yield, dry fodder yield and plant height which was similar to the findings of Prakash and Vanniarajan.*(*2013). Thus early simple selection could be exercised due to the presence of fixable gene effects. Grain yield is largely dependent on these traits and hence the result revealed the possibility to increase yielding capacity of the crop. The most complex and important economic trait, single plant yield exhibited high genetic advance as percentage of mean coupled with high heritability, PCV and GCV values, which indicated the availability of sufficient variation present in the genotypes under study. This observation was in agreement with the earlier reports of Nirubana *et al.,* 2017, Rinkey *et al.,* 2018 and Jyoti *et al.,* 2018.

Analysis of genetic variability revealed that peduncle length, grain yield, stem girth, the number of tillers, fodder yield, proline content and flag leaf width established

Table 4. Variability parameters for 19 characters

	PV	GV	PCV	GCV	ECV	Heritability	GA (%) of Mean
DFF	54.49	52.32	13.34	13.07	2.66	96.02	26.40
PHT	**300.26**	**276.37**	12.83	12.31	3.62	92.04	24.33
FLL	15.35	14.13	17.00	16.31	4.80	92.01	32.23
FLW	0.37	0.35	24.39	23.86	5.06	95.70	48.08
LOI	11.10	9.73	17.03	15.94	5.99	87.62	30.75
PAB	0.67	0.64	20.17	19.66	4.50	95.02	39.49
LLR-R	0.18	0.17	15.03	14.41	4.27	91.90	28.46
LLR-L	0.21	0.10	19.88	13.58	14.56	**46.67**	19.11
NOR	107.80	75.25	23.22	19.40	12.76	69.81	33.40
LOP	2.13	1.99	51.34	**49.63**	13.12	93.47	**98.85**
NON	1.97	1.64	19.04	17.39	7.75	83.41	32.72
STG	1.39	1.32	49.55	48.41	10.55	95.46	97.44
NOT	6.91	6.05	42.37	39.63	14.99	87.48	76.35
PRC	**0.006**	**0.006**	29.55	29.48	2.23	**99.52**	60.59
RWC	45.18	40.98	**10.01**	9.53	3.05	90.71	18.71
HIN	18.91	10.05	10.52	**7.67**	7.20	53.14	**11.52**
TWT	0.094	0.08	10.24	9.43	3.99	84.81	17.90
FYD	106.68	104.77	40.03	39.66	5.35	98.21	80.98
GYD	58.25	55.36	**49.96**	48.71	11.12	95.05	97.83

The numbers bolded are the highest and lowest values.

relatively high GCV value and thus these characters could be exploited for successful isolation of desirable accessions for the characters concerned. High heritability coupled with high genetic advance were observed for the traits like days to 50% flowering, plant height, flag leaf length, flag leaf width, inflorescence length and panicle breadth, the number of racemes/panicle, peduncle length, length of lower raceme –right, the number of nodes, stem girth, the number of tillers, fodder yield, relative water content, proline and grain yield which implied the presence of additive gene effects, controlling these traits. Hence, the selection for these traits could be effective for improvement of Barnyard millet.

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