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Research Article

Genetic variability and association analysis in barnyard millet (*Echinochloa frumentaceae*) under multiple environments

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Abstract
Barnyard millet is an important short duration nutricereal. A study was conducted to measure the pooled variation and association among yield and its component traits in 27 barnyard millet genotypes raised in six locations. The experiment was raised in RBD with three replications. The pooled ANOVA revealed significant difference between genotypes. High PCV and GCV were recorded for number of productive tillers, flag leaf length, flag leaf breadth, single ear head weight, fodder yield per plant, grain yield per plant. Except for days to maturity, all attributes were governed by additive gene effects, which was evident for high heritability and genetic advance values. Correlation studies exhibited significant positive relationship of grain yield with panicle length, single ear head weight, thousand grain weight and fodder yield per plant. Results of path coefficient analysis indicated that single ear head weight and days to first flowering had direct effect towards grain yield. Thus, by using single ear head weight and days to first flowering as selection indices, grain yield of barnyard millet could be augmented.

Keywords: Barnyard millet, Variability, Heritability, Genetic advance, Correlation, path analysis

INTRODUCTION

Barnyard millet (*Echinochloa frumentaceae*) is the oldest domesticated crop in the semi-arid tropics of Asia and Africa (Sood *et al*., 2020), belonging to the family of Poaceae. Among the small millets, barnyard millet is the fastest growing crop and it is cultivated in the southern and central states of India and in places with rainfall below 350 mm. It is a short duration dual-purpose crop, cultivated for food and forage under low inputs and adverse climatic conditions. Barnyard millet is a fair source of easily digestible protein and excellent source of soluble and insoluble fractions of dietary fiber, (*http://millets.res.in/millets_info.php*). The Iron (Fe) and Zinc (Zn)

contents in whole grains of barnyard millet varies from 25 ppm to 44 ppm and 36 ppm to 40 ppm respectively (Girish *et al*., 2014) . Also, it has less carbohydrate content, which is slowly digestible. This makes barnyard millet, nature's gift to mankind by rendering health benefits like reduced blood sugar level, blood pressure regulation, thyroid, cardiovascular and celiac diseases.

The evaluation of genetic diversity in germplasm and the relationships between traits is an essential step before planning any breeding programme. Quantitative and qualitative genetic improvement depends on the kind and

degree of diversity in the genetic stock; the higher the heritability of desired traits, the greater is the likelihood of improvement through selection. Hence, a study was undertaken to study the variability among 27 different genotypes, which helps in the selection and improvement of the crop to further generations. An extensive range of genetic variability existed in barnyard millet for twelve quantitative features with a focus on twenty-seven genotypes along with check MDU 1 that form the basis of the current investigation.

MATERIALS AND METHODS
A total of 27 barnyard millet genotypes *viz*., ACM BM-20-001, ACM BM-20-002, ACM BM-20-003, ACM BM-20-004, ACM BM-20-005, ACM BM-20-006, ACM BM-20-007, ACM BM-20-008, ACM BM-20-009, ACM BM-20-010, ACM BM-20-011, ACM BM-20-012, ACM BM-20-013, ACM BM-20-014, ACM BM-20-015, ACM BM-20-016, ACM BM-20-017, ACM BM-20-018, ACM BM-20-019, ACM BM-20-020 and MDU 1 (Check) obtained from Agricultural College and Research Institute, Madurai and IEC lines viz., IEC 108, IEC 109, IEC 107, IEC 350, IEC 356 and IEC 285 procured from International Crop Research Institute for Semi- Arid Tropics, Hyderabad formed the experimental material. Field experiments were performed during the year 2021 and 2022 respectively at six locations with three replications in RBD represented in **Table 1**. Each genotype was raised in a single row plot with a row length of 2 m, adopting a spacing of 20 x 15 cm. Observations were recorded on 12 quantitative characters.

RESULTS AND DISCUSSION
Crop improvement is highly determined by environment, controlled by phylogeny and by the extent and nature of the available genetic variability (Raju *et al.,* 2022). In the current study, pooled analysis of variance (**Table 1**) revealed a significant difference between 27 genotypes for all the traits and high variability was observed to allow for the selection of superior genotypes in six environments. From the pooled mean values over six environments, heritability (h^2), genetic gain (GG), genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV) were estimated (**Table 2**). High GCV was noted to be maximum for fodder

yield per plant (42.21%). It was followed by grain yield per plant (40.55%) and single ear head weight (38.82%). High PCV and GCV values for breadth of flag leaf and grain yield per plant were similar to the findings of Shet *et al*. (2009) in finger millet; Shanmuganathan (2010) and Anil kumar *et al*. (2019) in pearl millet; Vemanna *et al*. (2013) and Nirosh *et al*. (2021) in sorghum; Nandini *et al*. (2016) in little millet; Vanniarajan and Chandirakala (2020). The results on GCV and PVC of the traits, fodder yield per plant, grain yield per plant, single ear head weight and number of productive tillers were in accordance with the results of Nirubana *et al*. (2017) and Jyoti *et al*. (2018) in kodo millet. Moderate GCV was noted for days to first flowering (14.41), days to 50% flowering (13.92), plant height (15.74), panicle length (16.64) and thousand grain weight (11.47). The range of PCV for different traits in pooled environments was found to be from 13.29 to 43.53 %. PCV was the highest for fodder production per plant (43.53) and the lowest for days to maturity (9.24%). High PCV was also observed for fodder production per plant (43.53), grain yield per plant (41.88%), single ear head weight (39.23%), and quantity of productive tillers (30.99%). These results were supported by those of Nirubana *et al*. (2017) and Jyothi *et al*. (2018) in kodo millet. PCV was moderate for traits like panicle length (17.89%), flag leaf breadth (24.81%), plant height (15.86%), days to first flowering (14.49%), days to 50% flowering (14.04%), and thousand grain weight (13.29%) (**Table 2**). Less difference was observed between PCV and GCV values which indicated the lesser influence of environment for all the traits. The results were on par with Jyoti *et al.* (2018) and Vanniarajan and Chandirakala (2020).

Heritability and GAM provide an outlook for efficient selection. The heritability values of the 12 traits studied ranged from 74.85 to 98.84 %, respectively. All traits recorded maximum heritability which concur with the findings of Monika *et al.* (2021) for fodder yield. Similar findings were reported by Vanniarajan and Chandirakala (2020) and Renganathan *et al.* (2018) on barnyard millet (**Table 3**). High hertitability for grain yield per plant, plant height and flag leaf breadth were in accordance with the findings of Vetriventhan and Upadhayaya, (2018) in proso millet. According to Allard (1960), high heritability indicated the minor role of environment in trait expression.

Table 1. Agro-ecological details of the experimental environments

Code	Location	Latitude	Longitude	Altitude (m MSL)	Soil type	Temperature	Rainfall
E1	AC & RI, Madurai	9.96° N	78.21°E	166.00	Alfisol	24.6 °C – 30.4°C	950 mm
E2	Thirumangalam	9.91° N	77.98°E	164.15	Vertisol	27° C – 39 °C	857.6 mm
E3	Aruppukottai	9.30° N	78.5°E	123.00	Alfisol	21.1°C – 30.4 °C	830 mm
E4	Theni	9.96° N	77.44° E	291.97	Ultisol	21.5°C –32.3°C	883 mm
E5	DARS Chettinad	9.87° N	78.66° E	99.08	Ultisol	27°C – 36°C	920 mm
E6	AC & RI, Madurai	9.96° N	78.21°E	166.00	Alfisol	24.6 °C – 30.4°C	950 mm

Table 2. Pooled ANOVA for various quantitative traits in barnyard millet

Characters	Genotype	Environment	G * E	Pooled error
	Mean sum of squares			
Df	26	5	130	312
Days to first flowering	886.72*	64.67*	13.69*	0.62
Days to 50% flowering	1023.02*	51.87*	12.28*	0.98
Days to maturity	920.29*	99.55*	22.33*	1.23
Plant height	6422.06*	1075.05*	80.32*	5.46
Number of productive tillers	37.73*	10.94*	0.90*	0.23
Flag leaf length	585.19*	183.67*	20.10*	2.87
Flag leaf breadth	8.30*	1.52*	0.29*	0.02
Panicle length	117.56*	232.77*	13.25*	1.41
Single ear head weight	120.57*	8.65*	1.69*	0.15
Thousand grain weight	0.84*	2.33*	0.26*	0.03
Fodder yield per plant	3851.42*	1658.82*	153.99*	14.90
Grain yield per plant	1720.35*	568.22*	52.82*	6.73

* Significant at 5% level

Table 3. Magnitude of variability for twelve characters in 27 Barnyard Millet genotypes across six environments

S. No.	Characters	Vph	Vg	Coefficient of variation (%)	
				Phenotypic	Genotypic
1	Days to first flowering	53.48	52.86	14.49	14.41
2	Days to 50% flowering	60.91	59.92	14.04	13.92
3	Days to maturity	58.15	56.92	9.24	9.13
4	Plant height	382.74	377.27	15.86	15.74
5	Number of productive tillers	2.51	2.27	30.99	29.42
6	Flag leaf length	40.01	37.14	24.40	23.53
7	Flag leaf breadth	0.56	0.54	24.81	24.25
8	Panicle length	11.15	9.74	17.89	16.64
9	Single ear head weight	7.27	7.12	39.23	38.82
10	Thousand grain weight	0.14	0.11	13.29	11.47
11	Fodder yield per plant	266.68	251.78	43.53	42.21
12	Grain yield per plant	114.74	108.00	41.88	40.55

According to Vetriventhan and Nirmalakumari (2007) high heritability refers to the high level of genotypic inheritance to the next generation. The genetic advance as percent mean (GAM) ranged from 18.59% to 84.31% for 12 traits, demonstrating the effectiveness of phenotypic selection alone. Heritability is influenced by environment and hence estimates based on predicted genetic gain are more reliable (Johnson *et al*., 1955) High GAM was found for all the traits, except for days to maturity. These results were similar to the results of Nirosh *et al*. (2021) in sorghum.

High heritability along with high GAM provides a clear picture of the level of genetic enhancement attained through phenotypic selection. Here, all the traits showed high heritability and high GAM, except the trait, days to maturity which showed high heritability and moderate GAM. It showed the occurrence of additive gene action which would promote effective selection.

In concurrence with Dhanalakshmi *et al*. (2019) and Yadav *et al*. (2017) high genetic advance (**Table 2**) as a percentage of mean was observed for fodder yield per plant (84.31%), grain yield per plant (80.89%), single ear head weight (79.61%), number of productive tillers (57.55%), flag leaf breadth (48.85%), plant height (32.19%), panicle length (31.90%), days to first flowering (29.51%) and days to 50% flowering (20.53%). Days to maturity (18.59%) alone exhibited moderate GAM this was similar to the

results of Nirosh *et al.* (2021) in sorghum. For fodder yield per plant, grain yield per plant and plant height high heritability coupled with high genetic gain indicated that they were under the control of additive gene action. Hence, selection should be rewarding. These observations agreed with those of Vanniarajan and Chandirakala (2020), Prakash and Vanniarajan (2013), Sood *et al.* (2015) and Vikram *et al.* (2020).

The correlation coefficient helps to assess the mutual relationship between various plant traits and reveals the characteristics on which selection can be focused for genetic improvement of yield. Grain yield expression is influenced by a number of its component traits. Understanding the relationship between grain yield and other traits paves the way for improved selection efficiency. The positive correlation is induced by the coupling linkage phase, which controls two different traits at the genetic level.

Grain yield per plant was significantly positively correlated with most of the yield attributing traits *viz.,* panicle length, single earhead weight, thousand grain weight and fodder yield per plant **(Table 4)**. Similar findings on positive correlation between single ear head weight and thousand grain weight were reported by Vikram *et al.* (2020) and Dhanalakshmi *et al.* (2019). Also, all the yield attributing traits were significantly inter correlated among themselves. Positive correlation was found between days to first flowering, days to maturity and plant height which was identical to the results of Monika *et al.* (2021) in barnyard millet. Days to first flowering and days to maturity also had a significant positive correlation. This indicated a close relationship between the genes responsible for these traits. Hence, for augmenting yield, indirect selection upon highly correlated traits, such as

days to first flowering, days to 50% flowering, days to maturity, number of productive tillers, single ear head weight, fodder yield/ plant would be considered.

Path coefficient analysis is essential in giving a true picture on relationship between the different metric traits and it also gives the indirect contribution of different traits on grain yield per plant. High positive direct effects on grain yield were contributed by single ear head weight and days to first flowering, which indicated their influencing effect on the yield. Fodder yield per plant showed moderate positive direct effect followed by days to maturity, panicle length which exhibited low positive direct effect (**Table 6**). Selection based on these traits would help in the improvement of grain yield. Moderate direct effect and negligible negative direct effect was established on grain yield by number of productive tillers and flag leaf length. Though, many traits showed positive correlation with grain yield, the path analysis, indicated that it was due to the indirect effect of other traits. The residual effect was found as 0.05, which indicated that the above traits were reliable in contributing to yield. This indicated that 99.5% of the variation existing among the genotypes was contributed by these 12 traits.

The present study aimed at studying the extent of variation prevailing among the 27 genotypes raised at six environments. Pooled ANOVA showed that a significant difference between 27 genotypes was present for all the traits. The difference between the PCV and GCV was minimum which indicated that the less influence of the environment. High heritability and genetic advance as percent of mean of the yield contributing traits studied indicated the chance for effective selection of plants based on these 12 traits. Association analyses indicated that the

Table 4. Heritability and genetic advance as per cent of mean for 12 characters in 27 barnyard millet genotypes for combined environments

S. No	Characters	Heritability (%)	Genetic advance as per cent of mean
1	Days to first flowering	98.84	29.51
2	Days to 50% flowering	98.18	28.43
3	Days to maturity	97.48	18.59
4	Plant height	98.54	32.19
5	Number of productive tillers	90.02	57.55
6	Flag leaf length	93.01	46.75
7	Flag leaf breadth	95.65	48.85
8	Panicle length	86.15	31.90
9	Single ear head weight	98.02	79.16
10	Thousand grain weight	74.85	20.53
11	Fodder yield per plant	94.09	84.31
12	Grain yield per plant	93.86	80.89

Table 5. Genotypic correlation analysis for twelve characters in 27 barnyard millet genotypes for combined environments

Characters	DFF	DFTF	DM	PH	NPT	FLL	FLB	PL	SEW	TGW	FYD	GYP
DFF	1.000											
DFTF	0.987**	1.000										
DM	0.966**	0.954**	1.000									
PH	0.768**	0.779**	0.746**	1.000								
NPT	-0.644	-0.659	-0.616	-0.738	1.000							
FLL	0.778**	0.795**	0.762**	0.754**	-0.627	1.000						
FLB	0.774**	0.787**	0.741**	0.813**	-0.748	0.750**	1.000					
PL	0.569**	0.589**	0.560**	0.633**	-0.488	0.600**	0.628**	1.000				
SEW	0.835**	0.851**	0.804**	0.805**	-0.818	0.752**	0.837**	0.638**	1.000			
TGW	0.115	0.131	0.092	0.141	-0.078	0.194	0.149	0.128	0.131	1.000		
FYD	0.764**	0.771**	0.741**	0.706**	-0.481	0.654**	0.722**	0.616**	0.844**	0.205	1.000	
GYP	0.785**	0.793**	0.763**	0.699**	-0.502	0.668**	0.736**	0.619**	0.870**	0.178**	0.986**	1.000

*Significant at 5 per cent level; **Significant at 1 per cent level

DFF- Days to First Flowering DFTF- Days to Fifty percent Flowering DM- Days to maturity PH- Plant Height NPT- Number of Productive Tillers FLL- Flag Leaf Length FLB- flag Leaf Breadth PL- Panicle Length SEW- Single Earhead Weight TGW- Thousand Grain Weight FYD- Fodder Yield per Plant GYP- Grain Yield per Plant

Table 6. Path coefficient analysis showing direct and indirect effects of yield attributing characters on Grain Yield per Plant for pooled environments

S.No.	Characters	DFF	DFTF	DM	PH	NPT	FLL	FLB	PL	SEW	TGW	FYD	GYP
1	DFF	**0.5986**	-0.8778	0.2595	-0.0355	-0.2803	-0.0999	0.0432	0.0807	0.7669	-0.0015	0.3660	0.8200
2	DFTF	0.5950	**-0.8832**	0.2585	-0.0380	-0.2817	-0.1002	0.0474	0.0857	0.7775	-0.0010	0.3686	0.8287
3	DM	0.4675	-0.6831	**0.1712**	-0.0493	-0.2927	-0.0982	0.0482	0.1020	0.7234	0.0025	0.3309	0.7222
4	PH	-0.4687	0.6746	-0.1648	**0.0398**	0.3652	0.0956	-0.0453	-0.0860	-0.7702	0.0011	-0.2393	-0.5980
5	NPT	0.4973	-0.7342	0.1914	-0.0400	**-0.2532**	-0.1274	0.0484	0.1152	0.7205	0.0024	0.3005	0.7208
6	FLL	0.5058	-0.7333	0.1863	-0.0414	-0.3071	**-0.0948**	0.0530	0.1002	0.7674	0.0036	0.3372	0.7768
7	FLB	0.4089	-0.5847	0.1066	-0.0280	-0.2424	-0.0984	**0.0375**	0.1448	0.6562	0.0029	0.2831	0.6866
8	PL	0.5204	-0.7677	0.1940	-0.0391	-0.3250	-0.1038	0.0514	**0.1048**	0.8764	0.0007	0.3889	0.9009
9	SEW	0.5850	-0.8574	0.2652	-0.0352	-0.2691	-0.0955	0.0421	0.0706	**0.7355**	-0.0008	0.3594	0.7999
10	TGW	0.0166	-0.0830	0.0648	-0.0268	-0.0118	-0.0342	0.0303	0.0395	0.1054	**0.0156**	0.1022	0.2186
11	FYD	0.4548	-0.6862	0.1948	-0.0340	-0.2288	-0.0954	0.0446	0.1080	0.7743	0.0039	**0.4504**	0.9864

RESIDUE = 0.05

trait single ear head weight and days to first flowering had positive impact on grain yield per plant and could help in the improvement of yield along with selection based on them.

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