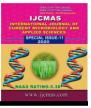


International Journal of Current Microbiology and Applied Sciences ISSN: 2319-7706 Special Issue-11 pp. 1450-1458 Journal homepage: <u>http://www.ijcmas.com</u>



Original Research Article

Character Association Studies for Grain Yield and its Attributes in Barnyard Millet

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ABSTRACT

Keywords

Barnyard millet, Variability, Heritability Barnyard millet is fast growing hardiest crop among all small millets crops. Seventeen barnyard millet genotypes developed across the country were evaluated at Agricultural Research Station, Vizianagaram during kharif, 2019 to assess genetic variability, heritability and genetic advance for seven yield and its contributing traits. Characters studied were days to 50 % flowering, plant height, days to maturity, number of productive tillers per plant, panicle length, grain yield and fodder yield per plant. The ANOVA revealed significant differences among seventeen genotypes for all the characters included under study except for plant height and panicle length which were more influenced by the environment. Crop improvement mainly depends on the availability of variability. Hence, the present study was aimed to assess the heritability, genetic advance and genetic advance as percent of mean in barnyard millet. Number of productive tillers per plant showed high PCV and moderate GCV. High heritability was observed for days to 50 % flowering followed by days to maturity. In the present study, selection for grain yield and fodder yield can be taken up via selection of days to 50% flowering and days to maturity which are highly correlated in positive direction and the later traits are expected to have preponderance of additive gene action.

Introduction

Small millets are a group of crops that are highly climate resilient and perform well even under adverse climatic conditions. Among the millet crops, barnyard millet (*Echinochloa frumentacea*) is a fast growing hardiest crop. It is also called as Sawa millet, Ooda, Oodalu, jhangora and Billion dollar grass. It is an herbaceous annual crop having chromosome number 2n=4x=36, and is a self pollinated crop. It is the second most important *kharif* small millet crop next only to finger millet (Joshi, 2013; Anuradha *et* al., 2014). It is grown as a multipurpose crop for food and fodder. Besides it also been used for the reclamation of sodicity, arsenic and cadmium affected soils (Sherif and Ali, 2007) Seeds of the crop are very nutritious. Its grain contains 11.2g/100g Proteins, 10.1g/100g fibre, 4.4g/100gminerals crude and 15.2mg/100g iron (Anonymous, 2010). The grain has low carbohydrate content and it is slowly digestible. Thus, it proved to be suitable for people suffering with diabetes mellitus (Ugare, 2008). Besides, barnyard is a fastest multipurpose crop, which yields food and forage in a short duration and at low

inputs even under adverse climatic conditions. Although barnyard millet like any other minor millet is nutritionally superior to cereals, yet its utilization is limited. Most of the varieties developed and released are selections from local germplasm of *E. frumentacea* and are susceptible to various diseases and are low yielders. The crop is mainly prone banded blight (Patro *et al.*, 2019).

In any crop improvement programme knowing about genetic variability among the population is a prerequisite. Genetic improvement through traditional breeding approaches depends mainly on the availability of diverse germplasm and the presence of variability. An insight into the nature and magnitude of genetic variability present in the gene pool is of immense value starting any systematic breeding for programme because of the presence of considerable genetic variability in the base material ensures better chances of evolving desirable plant type (Anuradha et al., 2017). Hence, an attempt was made to estimate the extent of variation for yield contributing traits in the germplasm accessions by studying PCV, GCV, Heritability and Genetic advance which may provide suitable selection indices for improvement of the crop.

Materials and Methods

Seventeen genotypes of barnyard millet were evaluated at Agriculture Research Station, Vizianagaram. Genotypes were planted in a randomized complete block design (RCBD) with three replications and a spacing of 30 × 10 cm per each entry. Every genotype was grown in 10 lines each of 3 m length. Fertilizers, DAP (87 kg/ha), MOP (42 kg/ha) and Urea (22 kg/ha) were applied basally at the time of land preparation and remaining 22 kg/ha Urea was applied three weeks after sowing. Standard management practices were followed to maintain a healthy crop. Observations were recorded on five plants for plant height (cm), number of productive tillers per plant and panicle length (cm). Days to 50% flowering, days were recorded by visualizing the entire plot. Fodder yield and grain yield were recorded on per plot basis and then converted into per hectare.

The mean of all the plants for each trait under each replication was subjected to ANOVA as per the method suggested by (Panse and Sukhathme (1967). The estimates of GCV and PCV were worked out according to the method suggested by (Burton (1952). Heritability in broad sense was calculated as per the formula given by (Lush (1940). Range of heritability was categorized as suggested by (Robinson *et al.*, (1949). Genetic advance was estimated according to the method suggested by (Johnson *et al.*, (1955). Correlations were calculated as suggested by (Johnson *et al.*, (1955).

Results and Discussions

Genetic variability in germplasm for the trait of interest is a prerequisite for the success of any breeding program. In the present study ANOVA revealed significant differences for all the traits studied except for plant height and panicle length presented in (Table 1). The extent of variability in respect of range, mean, phenotypic coefficient of variability, genotypic coefficient of variability, heritability, genetic advance and genetic advance as percent of mean presented in Table 2.

In the present study (Table 3), VMBC-333(20.59), TNEf 307 (20.50) and DHBM 93-3(20.37) had significantly out yielded the VMBC 331 (local check) for grain yield among medium duration group while among early duration group, IIMR-BM-29-17(19.66), DHBM-19-7 (19.60) and TNEf - 317(19.42) recorded significant higher grain yields compared to local check. VL-254 was the earliest with 74 days to maturity followed by BMNDL-1, BMNDL-2 and BMNDL-3 with 75 days of maturity. These genotypes can be utilized for breeding earliness in barnyard millet. VL-254 can be used for breeding non-lodging genotypes since it was observed to be the shortest (157.47) with good culm strength among all 17 genotypes studied. More number of productive tillers per plant were observed for IIMR-BM-2-17(3) and BMNDL-2(3). More panicle length is indicative of getting higher grain yield and it was recorded in TNEf 318(25.71) followed by DHBM-93-3(25.67).

The values of PCV obtained for yield and its attributing characters ranged from 5.74 for days to maturity to 24.61 for number of productive tillers per plant. The values of GCV ranged from 1.92 for plant height to 16.19 for number of productive tillers per plant. Phenotypic coefficient of variability is higher than genotypic coefficient of variability for all the characters indicating the interaction of genotypes with environment. High PCV was recorded by number of productive tillers per plant and moderate PCV was observed for fodder yield. Lower GCV was observed for all the yield attributing characters except number of productive tillers per plant which recorded moderate variability. Similar results were reported by (Renganathan and Vanniarajan, 2018).

Heritability studies ensures reliability of the selections made. Genotypic variances rather than with environmental variances determine highly heritable of traits. However, heritability informs whether the variation is genetic or non genetic while Genetic Advance as Percent Mean (GAM) enlightens the aspect of gene action. Hence heritability along with GAM studies are meaningful. High heritability and high GAM were recorded for days to 50 % flowering, days to maturity and number of productive tillers per plant indicating preponderance of additive gene action and additive gene action is very much selection responsive. Low heritability coupled with low genetic advance as percent of mean was observed for plant height and panicle length indicating that the environment play a major role in determining their phenotype and cannot be improved upon selection in the present population.

Heritability ranged from 8.40 for plant height to 92.20 for days to 50 % flowering. High heritability was recorded by days to 50 % flowering (92.20) followed by days to maturity (89.60). This is in accordance with the findings of Sood et al., (2015) and Renganathan and Vanniarajan, (2018). Genetic advance as percent of mean ranged from 1.14 for plant height to 21.95 for number of productive tillers per plant. Moderate heritability coupled with moderate genetic advance as percent of mean was observed for fodder yield and grain yield. High genetic advance as percent of mean coupled with moderate heritability was recorded by number of productive tillers per plant and high heritability coupled with high genetic advance as per cent mean was observed for days to 50% flowering and days to maturity indicating that these traits were under the influence of additive gene action and selection may be effective for this trait.

Correlation of various characters in this study helped in gaining the knowledge that grain yield was significantly associated with days to 50% flowering, days to maturity and fodder yield in positive direction. Similarly fodder yield was also in association with days to 50% flowering and days to maturity. Hence, the two quantitative traits viz., grain yield and fodder yield can be indirectly selected via days to 50% flowering and days to maturity which were supposed to be governed by additive gene action. This is in consonance with Anuradha *et al.*, (2013) in finger millet.

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reported by (Renganathan and Vanniarajan, 2018). Heritability studies ensures reliability of the selections made. Genotypic variances rather than with environmental variances determine highly heritable of traits. However, heritability informs whether the variation is genetic or non genetic while Genetic Advance as Percent Mean (GAM) enlightens the aspect of gene action. Hence heritability along with GAM studies are meaningful. High heritability and high GAM were recorded for days to 50 % flowering, days to maturity and number of productive tillers per plant indicating preponderance of additive gene action and additive gene action is very much selection responsive. Low heritability coupled with low genetic advance as percent of mean was observed for plant height and panicle length indicating that the environment play a major role in determining their phenotype and cannot be improved upon selection in the present population.

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Mean sum of squares										
S.no	Sources	Df	Days to 50 % Flowering	Days to Maturity	Plant height	Number of Productive Tillers	Panicle length	Grain Yield	Fodder Yield	
1	Treatments	16	45.532**	58.311**	142.328	0.543**	5.548	4.593**	107.161**	
2	Replication	2	3.353	1.588	703.323	0.053	14.384	0.045	0.133	
3	Error	32	1.249	2.172	111.617	0.165	3.874	1.397	21.308	

Table.1 Analysis of variance of seven characters for 17 genotypes in barnyard millet

Table.2 Estimates of genetic variability parameters of yield component attributes in barnyard millet

S.no	Characters	Mean	Max (Range)	Min (Range)	GCV	PCV	ECV	H^2	GA	GAM
1	Days to 50% flowering	47.24	52.67	42.33	8.13	8.47	2.37	92.20	8.60	21.09
2	Days to maturity	79.65	85.67	74.33	5.43	5.74	1.85	89.60	9.44	16.59
3	Plant height	166.93	179.33	157.47	1.92	6.61	6.33	8.40	1.91	1.14
4	Number of productive tillers	2.19	2.93	1.67	16.19	24.61	18.53	43.30	0.48	21.95
5	Panicle length	23.67	25.71	21.29	3.16	8.89	8.31	12.59	0.55	2.31
6	Grain yield	18.54	20.59	17.06	5.57	8.46	6.37	43.26	1.40	7.54
7	Fodder yield	55.73	65.08	48.61	9.60	12.68	8.28	57.32	8.34	14.97

S.No	Entry Name	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of productive tillers	Panicle length (cm)	Grain Yield (q/ha)	Fodder Yield (q/ha)
1	TNEf 204	50.00	82.67	179.33	2.13	24.18	17.49	54.10
2	DHBM 19-7	50.00	82.33	162.93	2.53	24.48	19.60	60.25
3	VL-254	42.67	74.33	157.47	1.67	23.33	17.65	52.31
4	BMNDL-1	42.33	74.67	160.20	2.60	22.87	17.92	49.67
5	TNEf 307	51.67	85.33	170.53	2.47	24.38	20.50	64.42
6	BMNDL-2	43.33	74.67	163.13	2.93	22.44	17.97	48.94
7	BMNDL-3	42.67	74.67	167.87	2.67	22.23	17.53	49.01
8	IIMR BM-2-17	49.00	81.67	159.67	2.93	25.61	18.12	60.05
9	IIMR BM-29- 17	49.33	82.00	164.80	2.07	22.85	19.66	61.57
10	TNEf 317	52.67	85.67	164.67	2.07	22.73	19.42	65.08
11	TNEf 318	44.00	76.33	170.47	2.13	25.71	17.55	48.94
12	VMBC-332	43.67	76.00	170.30	2.07	21.88	19.06	53.97
13	VMBC-333	50.33	83.33	167.77	1.87	24.77	20.59	62.10
14	VL-270	43.33	74.67	159.00	1.67	24.10	17.06	48.61
15	VL-207	45.00	77.00	163.07	1.67	21.29	17.53	54.63
16	DHBM 93-3	51.00	84.00	179.13	1.73	25.67	20.37	61.84
17	Local Check	52.00	84.67	177.53	2.07	23.91	17.23	51.98
	Mean	47.24	79.65	166.93	2.19	23.67	18.54	55.73
	CD (5%)	1.86	2.45	17.57	0.68	3.27	1.97	7.68
	CD (1%)	2.50	3.29	23.62	0.91	4.40	2.64	10.32
	CV (%)	2.37	1.85	6.33	18.53	8.31	6.37	8.28

Table.3 Performance of 17 barnyard millet genotypes

	Days to	Plant	No. of productive	Panicle	Grain Yield	Fodder
Characters	maturity	height (cm)	tillers	length (cm)	(q/ha)	Yield (q/ha)
Days to 50%	0.997**	0.493*	-0.067	0.422	0.589*	0.813**
flowering	0.997	0.495	-0.007	0.422	0.389	0.815
Days to maturity		0.509*	-0.057	0.428	0.618**	0.829**
Plant height (cm)			-0.167	0.282	0.193	0.139
No. of				0.016	-0.039	-0.074
productive tillers				0.010	-0.039	-0.074
Panicle length					0.242	0.269
(cm)					0.242	0.209
Grain Yield						0.849**
(q/ha)						0.049

 Table.4 Correlation of Grain yield and other charcters

Correlation of various characters in this study helped in gaining the knowledge that grain yield was significantly associated with days to 50% flowering, days to maturity and fodder yield in positive direction (Table 4). Similarly fodder yield was also in association with days to 50% flowering and days to maturity. Hence, the two quantitative traits viz., grain yield and fodder yield can be indirectly selected via days to 50% flowering and days to maturity which were supposed to be governed by additive gene action. This is in consonance with Anuradha *et al.*, (2013) in finger millet.

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