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ASSESSMENT OF VARIABILITY AT MORPHOLOGICAL LEVELS IN INDIAN BARNYARD MILLET (*ECHINOCHLOAFRUMENTACEA L.*)

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ABSTRACT

Indian Barnyard millet [*Echinochloafrumentacea* (L.)] is hexaploid crop with chromosome number $2n = x = 54$ and the second-most significant minor millet crops after finger millet among the millets, barnyard millet (*Echinochloa* sp.) is one of the oldest domesticated millets in the semiarid tropics of Asia and Africa. The protein, calcium and iron content of the *Echinochloa* spp. is found to be comparable to or greater than that of major cereals. This crop can grow in poor soil conditions with less water, fertilizer and pesticides and can withstand high temperatures, making it the perfect choice as climate-smart cereal. Keeping in view above facts, thirty Indian barnyard millet genotypes were evaluated to study, variability analysis in a Randomized Block Design (RBD) with three replications and observations were recorded for thirteen characters. The analysis of variance revealed that the differences among the genotypes were significant for all the thirteen characters under study. It suggesting that the experimental materials include a significant amount of genetic variation. The values of phenotypic coefficient of variation (PCV) were observed slightly higher than genotypic coefficient of variation (GCV) for all thirteen characters indicating minor influence of environmental factors. The high value for GCV and PCV was reported in iron, panicle weight, zinc, productive tillers per plant and for fodder yield. The results indicated that there would be wide scope for improvement by applying selection on these characters in desirable directions. Moderate GCV to high PCV and difference between these two values are found high in grain yield per plant suggesting environmental influence is there and direct selection for this trait will be not effective, while moderate values of PCV and GCV found for fingers per panicle, 1000 grain weight and protein which indicated the presence of extensive inherent variation for this trait and its further improvement is possible by applying judicious selection to the individual traits. Days to 50% flowering, days to maturity and plant height have low value of GCV and PCV indicating that selection of this traits would be ineffective due to the less variation present among genotypes. Higher heritability coupled with high genetic advance over per cent of mean was reported for characters like, productive tillers per plant, panicle weight, iron and 1000 grain weight. This role of additive gene action was confirmed and for these traits' improvement could be brought about by direct phenotypic selection over the genotypes.

Key words: GCV, PCV, Genetic Advance, Additive gene action and Barnyard millet

Introduction

A family of small-seeded grasses known as millets is widely cultivated as a cereal crop or grain for human and animal nourishment all over the world. One of the most potential under-utilized, nutritious cereal crops for feeding the underprivileged and those with diabetes is millets. According to Gowda *et al.*, (2006), small millet crops have been cultivated for more than 5000 years and are planted in many states due to their special ability to adapt

to poor, degraded soil conditions and their resistance to abiotic stress. They are group of annual grasses mainly found in the arid and semi-arid regions of the world and belongs to the grass family poaceae with small edible seeds, which do not shatter readily at maturity (Thurston, 1989) and include seven genera; Pennisetum, Panicum, Setaria, Paspalum and Echinochloa, all in the tribe Paniceae, genus Eleusine in the tribe Chlorideae and genus Eragrostis in the tribe Festuceae.

Millets are photo-insensitive and resilient to climate change. Millets are less water consuming and are capable of growing under drought conditions as well as non-irrigated conditions even in very low rainfall regimes. Millets have low carbon and water footprint (rice plants need at least 3 times more water to grow in comparison to millets). Millets strengthen food security since they are less likely to fail than other cereal crops.

According to Food and Agriculture Organization Statistics (2021), 84.17 million metric tones of millet were produced worldwide in 2019-20 from an area of 70.75 million hectares, with 20.50% of the production being from India. India leads the world in the production of pearl millet (60%) and sorghum (27%), finger millet (11%) and small millets (2%), such as little millet, kodo millet, and barnyard millet, with an annual production of about 12.46 million metric tones from an area of 8.87 million hectares. India's most famous state for growing small millets is Karnataka, which is followed by Madhya Pradesh, Uttarakhand, Tamil Nadu and Chhattisgarh. Karnataka (13%), Madhya Pradesh (8%), Haryana (7%), Gujarat (7%), Tamil Nadu (4%), Andhra Pradesh (2%), Rajasthan (27%), Maharashtra (15%), Uttar Pradesh (14%) and Karnataka (13%).

A category of crops known as small millets are incredibly climate robust and thrive even in unfavorable climatic circumstances. The hardest and fastest-growing millet crop is barnyard millet (*Echinochloafrumentacea* L.). The names Sawa millet, Ooda, Oodalu, Jhangora and Billion Dollar Grass are also used to refer to it. After finger millet, it is the second-most significant kharif small millet crop (Josh, V. 2013 and Anuradha *et al.*, 2020). As a dual-purpose crop, it is raised for both food and fodder. Additionally, it has been utilized to restore soils that have been contaminated by sodicity, arsenic, and cadmium (Sherif and Ali, 2007)

Indian barnyard millet [*Echinochloafrumentacea* L.] is hexaploid ($2n=6x=54$) (Hillu *et al.*, 1994). The crop is a tall, sturdy annual that can reach heights of 220 cm. Its life cycle can be completed in 60 to 100 days (depending on admittance and growth environment) and has the quickest growth rate of all small millets (Padulosi *et al.*, 2009). In the summer, barnyardmillet may reach a height of 2000 m above mean sea level thanks to its wide range of adaptability (Gupta *et al.*, 2009a). Flowering time, inflorescence morphology, morphological characteristics, spikelet pigmentation, plant type and other plant attributes are all varied (Obara, 1938). The ideal temperature range for *E. frumentacea* growth is 27-33°C and 15-22°C during day and night, respectively (Muldoon *et al.*, 1982).

Barnyard millet is a potent source of highly digestible protein as well as a superb source of dietary fiber. The grain contains iron (11.27 mg -11.50 mg per 100 g), phospholipids (3.20-9.84 mg), phosphorus (2.80 mg), calcium (20.31 mg - 32.78 mg), total minerals (2.02 %), total carbohydrates (68.76 %) and food dietary fiber (9 mg - 15 mg per 100 g). This millet has anti-nutritional ingredients including tannins (102.96 mg per 100 g) and phytic acid (96.00 mg per 100 g) and its protein digestibility is 40 %.

Any breeding program's genetic improvement for yield and yield qualities is greatly dependent on and impacted by the gene pool's genetic diversity. Although barnyard millet has the potential to be a food and fodder crop, its genetic resources have not yet undergone substantial research, and the crop is still not being fully utilized. In order to efficiently exploit genetic resources and create improved cultivars of barnyard millet, it is therefore necessary to investigate the degree of genetic variation and choose superior genotypes with desirable traits. Most of the conventional breeding programs are based over a valuation and characterization through morphological traits. Therefore, keeping in view above facts the present investigation was carried out on thirty barnyard millet genotypes to study the genetic variability, heritability and genetic advance for various characters.

Material and Methods

The current investigation was carried out at Hill Millet Research Station, NAU, Waghai, The Dangs. The experimental material for present investigation consisted 26 genotypes along with four checks of Indian barnyard millet were evaluated in Randomized Block Design (RBD) with three replications. Five randomly selected competitive plants selected randomly from each five rows plot in each replication excluding border except for days to 50 % flowering and days to maturity, where it was recorded on population basis. The data recorded for thirteen different characters *viz.*, days to 50% Flowering, days to maturity, plant height (cm), panicle length (cm), productive tillers per plant, fingers per panicle, panicle weight (g), grain yield per plant (g), straw yield per plant (g), 1000 grain weight (g), protein content (%) and iron content (mg/100g) and zinc content (mg/100g).

The data recorded for the different characters were subjected to analysis for calculation of different parameters of the genetic variability by standard statistical procedures. The statistics for various traits were brought to light in order to examine the variability that is commonly associated with the Randomized Block Design, as per the formula suggested by Panse and Sukhatme in (1978).

Table 1: Analysis of variance of experimental design for yield and yield contributing characters in barnyard millet.

Source of variation	df	DFE	DM	PH	PTPP	FPP	PL	PW	FY	FE	ZN	PC	TW	SYPP
Replication	2	5.91	15.01	103.51	0.14	33.2	5.48	0.06	5.73	5.94	0.03	0.89	0	0.35
Genotypes	29	70.36 **	92.78 **	281.22 **	2.26 **	58.60 **	11.42 **	43.02 **	26.30 **	114.17 **	4.44 **	2.71 **	0.58 **	3.33 **
Error	58	2.22	5.63	128.22	0.19	14.78	1.91	0.58	5.04	2.03	0.1	0.29	0.03	1.17
S.Em		0.86	1.37	6.54	0.25	2.22	0.8	0.44	1.3	0.82	0.19	0.31	0.1	0.63
CD @ 5%		2.41	3.83	18.28	0.7	6.2	2.23	1.23	3.62	2.3	0.52	0.87	0.28	1.75
CD @ 1%		3.18	5.06	24.14	0.93	8.19	2.94	1.62	4.78	3.04	0.69	1.15	0.38	2.31
CV %		2.45	2.51	7.5	14	10.98	7.49	7.85	17.81	9.65	8.79	6.1	5.9	16.17
** significant at 5 % level and * significant at 1 % level														
DFE = Days to 50% flowering; DM = Days to maturity; PH = Plant height (cm); PTPP = Productive tillers per plant; FPP = Fingers per panicle; PL = Panicle length (cm); PWT = Panicle weight (g); FY = Fodder yield (g); FE = Iron (mg/100g); ZN = Zinc content ((mg/100g); PC = Protein (%); TW = 1000 grain weight (g)GYPP = Grain yield per plant (g)														

The genotypic coefficient of variation, which measures the magnitude of genetic variation present in a particular character was estimated as per the formula suggested by Burton (1952) and heritability in broad sense has been estimated as per the formula given by Allard (1960). Expected genetic advance could be calculated by using the methodology suggested by Allard (1960) at 5 per cent selection intensity using constant 'k' as 2.06, while genetic advance as per cent of mean was worked out as suggested by Johanson *et al.*, (1955).

Analysis of variance

The analysis of variance was performed to confirm the significant genetic variation among different germplasm accessions. All 30 genotypes varied significantly in all the traits measured by an analysis of variance. The variation due to replication was not found to be significant for all the traits under study (Table 1).

Similar results for most of characters were also reported by Arya *et al.*, (2018), Chavan *et al.*, (2018), Koujalagi *et al.*, (2018), Dhanalakshmi *et al.*, (2019), Anuradha *et al.*, (2020), Prabhu *et al.*, (2020) Vikram *et al.*, (2020), Vanniarajan *et al.*, (2020) and Nehru *et al.*, (2021).

Variability studies

The progress in breeding for grain yield and yield contributing traits of any crop is phylogenetically controlled, environmentally influenced and determined by the magnitude and nature of their genetic variability. Recent studies have revealed about the importance of high variability in the germplasm which provides a scope for its improvement. Estimation of genetic parameters in the context of trait characterization is an essential component of future targeted trait-based crop improvement. The measurement and evaluation of variability are essential in drawing essential steps in

Table 2: Measures of variability parameters of thirteen characters in Indian barnyard millet.

Characters	Range of variation		Mean	Geno- typic vari- ance	Pheno- typic vari- ance	Environ- mental vari- ance	GCV (%)	PCV (%)	Heritability in broad sense (h^2_{bs}) (%)	Genetic Advance (% Mean)
	Min.	Max.								
Days to 50 % flowering	52.00	71.00	60.82	22.71	24.93	2.22	7.84	8.21	91.09	15.41
Days to maturity	83.67	103.33	94.39	29.05	34.68	5.63	5.71	6.24	83.76	10.77
Plant height (cm)	125.6	170.4	151.01	51	179.22	128.22	4.73	8.87	28.46	5.20
Productive tillers per plant	1.60	5.70	3.12	0.69	0.88	0.19	26.62	30.07	78.34	48.53
Finger per panicle	26.27	44.2	35.02	14.61	29.38	14.78	10.91	15.48	49.71	15.85
Panicle length (cm)	15.17	22.07	18.44	3.17	5.08	1.91	9.66	12.22	62.44	15.72
Panicle weight(g)	5.60	24.53	9.70	14.15	14.73	0.58	38.77	39.56	96.07	78.28
Fodder yield (g)	6.56	19.95	12.60	7.09	12.12	5.04	21.13	27.64	58.46	33.29
Iron (mg/100g)	6.23	30.31	14.78	37.38	39.41	2.03	41.37	42.48	94.84	83
Zinc (mg/100g)	1.48	6.54	3.67	1.44	1.55	0.10	32.71	33.87	93.26	65.07
Protein (%)	3.00	10.93	8.85	0.81	1.10	0.29	10.14	11.83	73.41	17.89
1000 seed weight (g)	2.22	3.84	2.99	0.18	0.22	0.03	14.38	15.54	85.58	27.40
Grain yield per plant (g)	3.29	8.40	6.70	0.72	1.89	1.17	12.65	20.53	37.99	16.06

drawing meaningful conclusion from a given set of phenotypic observations. The result of variability parameters studied are presented in Table 2.

The high value estimate for phenotypic coefficient of and genotypic coefficient of was reported in Iron, panicle weight, zinc and productive tillers per plant and for fodder yield. While grain yield found high genotypic coefficient of variation, the results indicated that there would be wide scope for improvement by applying selection on these characters in desirable directions. High value of GCV and PCV reported by Chavan *et al.*, (2018) for iron content, for productive tillers per plant Vanniarajan *et al.*, (2020) and Nehru *et al.*, (2021) and for fodder yield per plant by Vanniarajan *et al.*, (2020).

Moderate genotypic coefficient variation to high phenotypic coefficient of variation and difference between this two values are found high in grain yield per plant suggesting environmental influence is there and direct selection for this trait will be not effective Moderate value of phenotypic coefficient of variation and genotypic coefficient of variation found for fingers per panicle, 1000 grain weight and protein which indicated the presence of extensive inherent variation for this trait and its further improvement is possible by applying judicious selection to the individual traits. Similar finding were obtained by Arya *et al.*, (2018) for fingers per panicle, for 1000 grain weight Arya *et al.*, (2018), Koujalagi *et al.*, (2018) and Nehru *et al.*, (2021).

Low value of genotypic coefficient of variation and phenotypic coefficient of variation for days to 50% flowering, days to maturity and plant height indicating that selection of these traits would be ineffective due to the less variation present among genotypes for these traits. These results are in accordance with Arya *et al.*, (2018), Dhanalakshmi *et al.*, (2019), Anuradha *et al.*, (2020) and Vikram *et al.*, (2020) for days to 50 per cent flowering, Arya *et al.*, (2018), Dhanalakshmi *et al.*, (2019), Anuradha *et al.*, (2020) while low PCV and moderate GCV reported by Nehru *et al.*, (2021) for days to maturity and Anuradha *et al.*, (2020), Arya *et al.*, (2018), Koujalagi *et al.*, (2018), Vikram *et al.*, (2020) for plant height.

High heritability was reported in characters like, panicle weight (96.07%), iron (94.84%), zinc (93.26%), days to 50% flowering (91.09%), 1000 grain weight (85.58 %), days to maturity (83.76%), productive tillers per plant (78.34 %), protein (73.41%), panicle length (62.44%). The similar results were reported by Prabhu *et al.*, (2020) for days to 50% flowering, days to maturity, productive tiller and 1000 grain weight, Nehru *et al.*,

(2021) for days to 50% flowering, panicle length, productive tillers per plant, 1000 grain weight, panicle weight, zinc and protein, Vanniarajan *et al.*, (2020) for days to 50% flowering, productive tiller, Vikram *et al.*, (2020) for days to 50% flowering, productive tillers per plant and panicle weight.

Medium broad sense heritability estimates were reported in characters like, fodder yield, (58.46%), fingers per panicle (49.71%) and grain yield (37.99%). This result was in accordance with findings of Arya *et al.*, (2018) for fingers per panicle and grain yield, Anuradha *et al.*, (2020) for fodder yield and grain yield. Low Broad sense heritability was reported for only one character plant height (28.46%). The same finding was reported by Koujalagi *et al.*, (2019) and Anuradha *et al.*, (2020).

The high value estimates of genetic advance expressed as per cent of mean (Table 2) were reported in characters like iron (83.00%), panicle weight (78.28%), zinc (65.07%), productive tillers per plant (48.53%), fodder yield (33.29%), 1000 grain weight (27.40%). The same kind of result was reported by Koujalagi *et al.*, (2018) for productive tiller and 1000 grain weight, Vanniarajan *et al.*, (2020) for productive tiller and fodder yield, Vikram *et al.*, (2020) for productive tiller and panicle weight, Nehru *et al.*, (2021) for panicle weight, 1000 grain weight, zinc. Medium value for genetic advance over per cent of mean was reported in characters like protein (17.89%), grain yield (16.06%), fingers per panicle (15.85%), panicle length (15.72%), days to 50% flowering (15.41%) and days to maturity (10.77%). This result was in accordance with the finding of Arya *et al.*, (2018) for fingers per panicle and grain yield, Anuradha *et al.*, (2020) for days to maturity panicle length and grain yield, Vikram *et al.*, (2020) only for days to 50% flowering. Low value for genetic advance over percent mean was observed for one character only which was plant height. (5.20%). This result was found similar with the finding of Koujalagi *et al.*, (2018) and Anuradha *et al.*, (2020).

Higher broad sense heritability coupled with high genetic advance over percent mean was reported for characters like, productive tillers per plant, panicle weight, iron and 1000 grain weight. It suggesting that role of additive gene action was confirmed and for this traits improvement could be brought about by direct phenotypic selection over the genotypes. The findings are closely similar with Koujalagi *et al.*, (2018) for productive tiller and 1000 grain weight, Vanniarajan *et al.*, (2020) for Productive tillers, Vikram *et al.*, (2020) for productive tiller and panicle weight, Nehru *et al.*, (2021) for panicle weight.

High broad sense heritability with medium genetic advance over per cent mean was reported in characters like, days to maturity, days to 50% flowering, panicle length and zinc. It suggesting that the effect of non-additive gene action and there is a limited scope of improvement through direct phenotypic selection for these Characters. the similar finding was reported by Anuradha *et al.*, (2020) for days to maturity and Vikram *et al.*, (2020) for days to maturity.

Medium broad sense heritability with medium genetic advance over percent mean was reported for characters like fingers per panicle, fodder yield and grain yield. This finding was closely similar to the finding of Arya *et al.*, (2018) for fingers per panicle, fodder yield, grain yield, Anuradha *et al.*, (2020) for fodder yield only.

Low broad sense heritability with low genetic advance over per cent mean was reported in only one character which was plant height. Low heritability coupled with low genetic advance as percent of mean was observed for plant height indicating that the environment plays a major role in determining their phenotype and cannot be improved upon selection in the present population. The similar finding was reported by Koujalagi *et al.*, (2018) and Anuradha *et al.*, (2020).

Conclusion

The analysis of variance revealed that the differences among the genotypes were significant for all the characters under study. The genotypes were thus suitable for genetical studies, as their contribution to the genotypic sum of squares was significant for most of the characters. The high value estimate for phenotypic coefficient of and genotypic coefficient of was reported in Iron, panicle weight, zinc and productive tillers per plant and for fodder yield. While grain yield found high genotypic coefficient of variation The results indicated that there would be wide scope for improvement by applying selection on these characters in desirable directions. Moderate genotypic coefficient variation to high phenotypic coefficient of variation and difference between these two values are found high in grain yield per plant suggesting environmental influence is there and direct selection for this trait will be not effective. High heritability found for Characters like days to 50% flowering, days to maturity, productive tillers per plant, panicle length, panicle weight, iron, zinc, 1000 grain weight and protein. High value of heritability suggesting that these characters are less influence by the environmental variations and largely governed by additive genes, so improvement for these traits could be made by simple phenotypic selection.

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