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Genetic variability studies in little millet (*Panicum sumatrense* L.)

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Abstract
Genetic variablity was assessed in little millet (*Panicum sumatrense* L.) germplasms with 34 genotypes of little millet collected from zonal agricultural research station (ZARS) and local areas of Igatpuri tahsil, which were evaluated in RBD at ZARS, Igatpuri during *kharif* 2024. A treatment sum of squares were significant for all the characters studied indicated considerable amount of variability to be present. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters studied indicating the role of environment in expression of characters. In the present study the characters such as days to maturity, plant height (cm), grain yield per plot (kg), number of productive tillers per plant, panicle length (cm), peduncle length (cm), flag leaf length(cm), fodder yield per plot (kg), Thousand seed weight (g), crude fibre (%), iron (mg/100g) and calcium (mg/100g) showed high estimates of heritability (b.s.) which indicates high transmission of characters from parents to their offspring which will be helpful for selection in future hybridization programme
The characters *viz.*, grain yield per plot (kg), number of productive tillers per plant, flag leaf length (cm), fodder yield per plot (kg), peduncle length (cm), crude fibre (%) and Thousand seed weight (g) recorded high estimates of heritability (b.s.) accompanied by high genetic advance as percent of mean suggesting that these character could be significantly governed by additive gene action and selection of these traits could be more effective for desirable genetic improvement through simple selection.

Keywords: Genetic advance as% of mean, Genotypes, GCV, heritability, Little millet, PCV

Introduction
Little millet (*Penicum sumatrence*) belong to family Poaceae (*gramineae*), having diploid chromosome number (2n = 36), it is locally known as Kutki, Samai (Hemalatha *et al.* 2014). It is self pollinated crop. The common name of the crops is *kutki, sawa, samai, samalu* (Padulosi *et al.*, 2009) [13].
It is a significant small millet species, indigenous to the Indian subcontinent and originally domesticated in the Eastern Ghats around 4000 years ago (Ganapathy, 2017) [5]. In a tribal region of the Indian Kolli hills, despite a limited sampling area, diversity among locally produced landraces of little millet was found to be substantial for all morphological characteristics measured both within and across landraces. (Arunachalam *et al.* 2005) [4]. During 2022-23, millets were grown across 12.45 million hectares in India, yielding 15.53 million metric tons, with an average productivity of about 1,247 kg per hectare (Agriculture Statistics at a Glance, 2022) [1].
Little millet is rich in vitamin B, minerals like potassium, phosphorus, iron, zinc and magnesium. Therefore, it can address nutritional sensitive agriculture, which aims at nutritional enhancement to combat the present scenario of micronutrient malnutrition, (Arunachalam *et al.* 2005) [4]. Nutritionally, it contains 60-75 g of carbohydrates, 4-8 g of crude fiber, 7-10 g of protein, 12-30 mg of calcium, and 7-13 mg of iron per 100 g making it more among cereals (Himanshu *et al.* 2018) [8]. Lipids are relatively minor constituents in cereal grains. However, they contribute significantly to diet as a source of invisible fat and essential fatty acid. Knowledge of genetic variability in respect of yield structure in any species is valuable in plant breeding programme. It helps in choice of the best yield attributes either for selection or hybridization. This may be achieved by estimating the genetic parameters *viz.* GCV, PCV heritability and genotypic advanced for grain yield and its component characters.

Material and methods

The experiment was conducted at Zonal Agriculture Research Station, Igatpuri during *Kharif* season of 2024. The 33 little millet genotypes were evaluated with one check variety for the present studies. The seed material of these germplasms was obtained from the Zonal Agricultural Research Station (ZARS), Igatpuri and evaluated in Randomized block design with two replications. The net plot size was 3.0 m x 2.4 m. The spacing was 22.5 cm x 10.0 cm. The following data were collected for each replication for 13 characters *viz;* Days to 50% flowering, days to maturity, plant height (cm), number of tillers per plant, panicle length (cm), peduncle length (cm), Thousand seed weight (g), grain yield (kg/plot), fodder yield (kg/plot), Calcium content (mg/100 g), Crude fiber content (%) and Iron content (mg/100 g).

Analysis of variance for the Randomized Block Design were done as per the method suggested by Panse and Sukhatme (1967) [14]. The genotypic and phenotypic covariances were then calculated as per the formulae given by Johnson *et al.* (1955) [4]. Heritability estimates in broad sense (h2) were computed by the formula suggested by Lush (1940) [11]. From heritability estimates the genetic advance was estimated by the formula given by Johnson *et al.* (1955) [4]. In order to estimate the relative utility of genetic advance among characters, genetic advance as percent for mean is usually calculated. The range of genetic advance as percent of mean was classified as per suggestion by Johnson *et al.* (1955) [4].

Results and discussion

Analysis of variance exposed significant differences among the genotypes for all the quantitative characters as presented in Table 1. The mean of square due to genotype showed highly significant difference for all the traits *viz*., days to 50 per cent flowering, days to maturity, plant height, panicle length, peduncle length, flag leaf length, number of productive tillers per plant, Thousand seed weight, fodder yield per plot, crude fiber content, iron content, calcium content and grain yield per plot indicating that adequate variability was found in the genotype studied for these characters because of diverse genotypes. These results were confined by Nandini *et al.* (2018) [12], Gopikrishnan *et al.* (2022) [7] and Sarak *et al.* (2023) [15].

The parameters range, GCV and PCV, heritability in broad sense and genetic advance as per cent of mean have been presented in Table 2. Fodder yield per plot (32.34%) showed high estimates of GCV accomplished by grain yield per plot (31.28%). While Thousand seed weight (18.54%), peduncle length (18.26%), flag leaf length (16.95%), number of productive tillers per plant (13.03%), panicle length (11.83%), plant height (11.00%) and crude fiber (10.77%) exhibited medium GCV. However, iron (8.94%), calcium (6.16%), days to maturity (2.81%) and days to 50 per cent flowering (2.03%) exhibited low GCV.

Fodder yield per plot (33.78%) showed high estimates of PCV accomplished by grain yield per plot (32.93%) and peduncle length (21.13%). The medium PCV were recorded in Thousand seed weight (19.15%), flag leaf length (18.88%), number of productive tillers per plant (16.17%), panicle length (14.68%), plant height (12.56%) and crude fiber (11.20%). However, iron (9.22%), calcium (7.19%), days to 50 per cent flowering (2.96%) and days to maturity (3.29%) exhibited low PCV.

In present investigation, fodder yield per plot (kg) and grain yield per plot (kg) exhibited high GCV and PCV effects indicating the presence of large variation among the genotypes for these characters. However, medium estimates of genotypic (GCV) and phenotypic coefficients of variations (PCV) were shown by Thousand seed weight (g), number of productive tillers per plant, and crude fiber (%). While, days to 50% flowering, days to maturity, iron (mg/100 g), and calcium (mg/100 g) estimates low GCV and PCV effects.

Compatible outcomes were reported by Anuradha *et al.* (2017) [3] for fodder yield per plot, grain yield per plot in little millet and Geetha *et al.* (2018) [6] reported similar finding for the character grain yield in little millet.

This study depicted high heritability for all character except days 50 percent flowering indicating that these traits are governed predominantly by additive gene action and have less environmental influence in their expression and direct phenotypic selection can be followed for these characters in breeding programme for development of high yielding genotypes. It is supported by similar finding of Kavya *et al.* (2017) [10] for thousand grain weight, grain yield plant^{-1} and fodder yield plant^{-1} and Anteneh *et al.* (2019) [2] for grain yield in finger millet.

Table 1: Analysis of variance (ANOVA) for thirteen characters in little millet

Sr. No.	Character	Mean Sum of Square		
		Replication (1)	Genotypes (33)	Error (33)
1.	Days to 50 per cent flowering	0.06	12.95**	4.66
2.	Days to maturity	0.94	29.54**	4.67
3.	Plant height (cm)	1.19	440.17**	57.82
4.	Panicle length (cm)	2.88	25.13**	5.34
5.	Peduncle length (cm)	0.014	9.72**	1.40
6.	Flag leaf length (cm)	0.13	35.43**	3.79
7.	Number of productive tillers per plant	0.05	0.78**	0.16
8.	Thousand seed weight (g)	0.00021	0.16**	0.005
9.	Fodder yield per plot (kg)	0.001	0.14**	0.006
10.	Crude fiber%	0.00079	0.97**	0.03
11.	Iron (mg/100g)	0.05	1.38**	0.043
12.	Calcium (mg/100g)	0.21	2.27**	0.35
13.	Grain yield per plot (kg)	0.000001	0.008**	0.0004

** indicate significant at 1 per cent level, respectively

Note: Figures in the parenthesis indicates the degrees of freedom

Table 2: Parameters of genetic variability for yield and yield contributing characters in little millet genotypes

Sr. No.	Name of the characters	General mean	GCV%	PCV%	ECV%	Heritability [h^2 (b.s.)]%	G.A.	G.A. as% of means
1.	Days to 50% flowering	100.09	2.03	2.96	2.15	47.05	2.87	2.87
2.	Days to maturity	125.62	2.81	3.29	1.72	72.71	6.19	4.93
3.	Plant height (cm)	125.66	11.00	12.56	6.05	76.78	24.96	19.86
4.	Panicle length (cm)	26.59	11.83	14.68	8.69	64.97	5.22	19.64
5.	Peduncle length (cm)	11.16	18.26	21.13	10.63	74.68	3.62	32.51
6.	Flag leaf length (cm)	23.45	16.95	18.88	8.30	80.63	7.35	31.36
7.	No. of productive tillers/ plant	4.26	13.03	16.17	9.57	64.94	0.92	21.63
8.	Thousand seed weight (g)	1.49	18.54	19.15	4.81	93.69	0.55	36.97
9.	Fodder yield/plot (kg)	0.80	32.34	33.78	9.75	91.66	0.51	63.79
10.	Crude Fiber%	6.35	10.77	11.20	3.07	92.48	1.35	21.34
11.	Iron (mg/100g)	9.15	8.94	9.22	2.26	93.95	1.63	17.85
12.	Calcium (mg/100g)	15.89	6.16	7.19	3.72	73.29	1.72	10.68
13.	Grain yield/plot (kg)	0.20	31.28	32.93	10.28	90.25	0.12	61.23

Conclusion

The genotypic and phenotypic coefficient of variation (GCV and PCV) were categorized as high, medium, or low. Among the traits, fodder yield per plot and grain yield per plot recorded the highest GCV and PCV values, reflecting a broad range of variation. Traits like Thousand seed weight, number of productive tillers, and crude fiber exhibited moderate levels of both. In contrast, traits such as days to 50% flowering, days to maturity, iron, and calcium showed low estimates for both, indicating relatively limited genetic variability in these characteristics.

In the present study grain yield per plot, number of productive tillers per plant, fodder yield per plot, peduncle length, Thousand seed weight, crude fiber and flag leaf length recorded high estimates of heritability (b.s.) accompanied by high genetic advance as per cent of mean suggesting that these characters could be significantly governed by additive gene action and selection of these traits could be more effective for desirable genetic improvement through simple selection. While, the character days to maturity showed high heritability coupled with low genetic advance, therefore selection of such character is not rewarding because of presence of non- additive gene action and heterosis breeding may be useful.

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