

Genetic Variability and Association Studies of Yield and its Components in Little Millet (*Panicum sumatrense* L.)

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ABSTRACT

In this study, 28 little millet genotypes were evaluated at the Regional Agricultural Research Station, Nandyal, in Andhra Pradesh, India during *Kharif*, 2022. The results revealed significant genetic variability for the studied traits with moderate to high ranges of phenotypic and genotypic coefficients of variation and low environmental coefficient of variation, indicating the potential for genetic improvement of little millet genotypes. Almost all traits exhibited high heritability and genetic advance, with the exception of plant height, which had a moderate heritability and low genetic advance as a percentage of the mean. It indicates the preponderance of additive gene action in the controlling all the traits except plant height, allowing for advancement through effective selection. Correlation analysis identified significant relationships between traits. The number of productive tillers per plant, 1000-grain weight and fodder yield has positive correlations with grain yield, suggesting that these traits may be utilised as selection criteria to improve the productivity and performance of little millet.

Keywords: *Little millet, Genetic variability, Heritability, Genetic advance and Trait association*

Little millet (*Panicum sumatrense* L.) is a small-grain cereal crop of the family Poaceae, sub-family Panicoideae and the tribe Paniceae (Rachie, 1975). It is predominantly grown in countries with limited agricultural resources, such as arid and semi-arid regions of Asia and Africa. Little millet is valued for its resilience to adverse environmental conditions, short growing cycle and high nutrient content. In comparison to other cereals, it is more nutritious since it includes more carbohydrate (60-75 g), crude fibre (4-8 g), protein (7-10 g), calcium (12-30 mg), and iron (7-13 mg) per 100 g (Himanshu *et al.*, 2018). However, to maximize its potential as a sustainable food source and enhance its productivity, it is essential to understand the genetic variability within little millet accessions and the underlying factors influencing its performance.

In order to enhance the productivity and performance of little millet, it is crucial to understand the nature and extent of genetic variability for the adoption of efficient breeding techniques and development of improved varieties. Understanding the variability, heritability, together with genetic advancements, might assist in anticipating prospective benefits under selection. The correlation study for

several traits could aid us in enhancing the process of direct and indirect trait selection and ensures better chances of evolving desirable plant type. The correlation study for several traits could aid us in enhancing the process of direct and indirect trait selection and ensures better chances of evolving desirable plant type. Therefore, an attempt was made to quantify the level of variation for yield attributing traits in the set of selected genotypes by investigating phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as a percentage of the mean. A detailed analysis of the correlations between different traits and their impact on yield, which may provide suitable selection indices for crop improvement.

MATERIAL AND METHODS

In this experiment 24 little millet genotypes along with four checks (CLMV 1, BL 6, OLM 203 and DHLM 36-3) were evaluated in three replications in a randomised complete block design (RCBD) at the Regional Agricultural Research Station, Nandyal, Andhra Pradesh during *Kharif*, 2022. Each genotype seeded in 10 rows of 3 m length spaced 22.5 cm apart with 10 cm between hills. To achieve good crop

growth, standard cultural and agronomic practises were adopted. Five competitive plants per genotype were selected randomly for recording observations on different characters *viz.*, plant height (cm), number of productive tillers per plant, while observations on days to 50% flowering, days to maturity, fodder yield (kg/ha) and grain yield (kg/ha) were recorded on plot basis. For 1000-grain weight, a sample of 1000 grains were counted randomly from the threshed seed and the weight was recorded in grams. Statistical analysis was performed on mean of five plants. The analysis of variance (ANOVA) method was used, as described by Singh and Chowdary (1985). The variability parameters, genotypic and phenotypic coefficients of variation (GCV and PCV), were calculated using Burton's method (1952). To calculate estimates of broad sense heritability, the method proposed by Lush (1940) was used. The expected genetic advance was calculated using the method proposed by Johnson *et al.*, (1955). PCV and GCV and genetic advance and genetic advance as a percentage of the mean were divided into three categories: low (0-10%), moderate (10.1-20%), and high (>20%). Heritability was divided into three categories: low (0-30%), moderate (30.1-60%), and high (>60%) (Robinson *et al.*, 1949). Statistical analysis was done by using WINDOSTAT program.

RESULTS AND DISCUSSION

Analysis of variance exposed significant differences among the genotypes for all the quantitative traits in the experimental material. Likewise, significant differences for genotypes were also reported by Anuradha *et al.* (2017) and Sarak *et al.* (2023). The total variability in each of the seven traits could be divided into three components *viz.*, phenotypic, genotypic and environmental variation. Out of these, the genotypic variation, serves to distinguish between the heritable and non-heritable share of variation with regard to the studied traits. The mean, range of variation and the estimate of genetic parameters such as heritability in broad sense, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and genetic advance as per cent of mean are presented in Table. 1. The mean values of all the traits in the current analysis showed significant variances. The range for the trait grain yield was 758 to 1996 kg/ha, days to 50% flowering from 46 to 87,

days to maturity from 76 to 117, plant height from 99.93 to 143.27 cm, the number of productive tillers per plant was 3 to 7, 1000 - grain weight from 1.53 to 2.57 g and fodder yield ranged from 3148 to 9679 kg/ha. The experimental material had broad range of variability and favourable mean performance for most of the traits studied (Fig 1). These genotypes might be exploited as potential lines for simultaneous improvement of grain yield and other yield attributing traits.

The result showed that magnitude of phenotypic variance was larger than genotypic variance, indicating the influence of the environment in their expression. High estimates of GCV and PCV were observed for grain yield (25.73, 31.71), fodder yield (25.68, 31.08), number of productive tillers per plant (21.49, 27.31) and day to 50% flowering (23.69, 24.63). Genotypes possessed a high level of inherent variability, making them more useful for selection. Therefore, practicing easy selection can be done for further improvement these traits. Similar kind of findings were also reported by Nancy Mano Sneha *et al.* (2023), Matere *et al.* (2022), Muni Khyathi *et al.* (2022) and Madhavilatha *et al.*, (2020).

Days to flowering exhibited a significant level of genetic variability, as evidenced by the genotypic coefficient of variation of 23.69% and a high heritability of 92.50%. The relatively moderate coefficient of variation (CV) and high phenotypic coefficient of variation suggest a moderate to high level of variability among the tested genotypes. Notably, the substantial genetic advance as a percentage of the mean of 46.93% highlights the potential for early flowering selection. Days to maturity displayed a relatively lower level of genetic variation, as indicated by the GCV of 16.12%. However, the high heritability of 93.50 signifies the strong influence of genetic factors on this trait. The CV and PCV values, although lower compared to other traits, still indicate major variability in days to maturity. Plant height exhibited limited genetic variability, as reflected by the relatively low GCV value of 7.37%. The CV and PCV values suggest a moderate degree of variation among the tested genotypes. While the scope for significant improvement may be limited, selection for optimal plant height can still contribute to achieving desirable plant architecture, such as improved lodging resistance and efficient resource utilization.

Number of productive tillers per plant demonstrated high genetic variability, with a GCV of 21.49% and a heritability of 61.90. The relatively high CV and PCV values indicate substantial variation in expression of tiller number among genotypes to different placements in a location. Selection for higher tillers numbers can offer increased yield potential and promote greater productivity, leading to a genetic advance of 34.82%. 1000-grain weight revealed moderate genetic variability, supported by the GCV value of 14.17% and a high heritability of 79.90. The CV and PCV values indicate moderate variation in grain weight. Selection for increased grain weight can contribute to higher yields and improved market value, with a genetic advance of 26.10%. Fodder yield and grain yield exhibited high genetic variability, as evidenced by the GCV values of 25.68% and 25.73%, respectively. The CV and PCV values highlight considerable variability in grain yield among the tested genotypes. Selecting for higher yield can provide substantial genetic advances of 43.72% and 43.01% for fodder yield and grain yield, respectively.

The range of heritability for the investigated traits varied from high to moderate and their genetic advance expressed as a percentage of the mean (GAM) ranged from moderate to high, indicating a strong genetic influence on those traits expression. High heritability in conjunction with strong genetic advance reveals the low environmental effect and a predominance of additive gene action in their expression. Reduced genetic advance values indicate a high $G \times E$ interaction (non-additive gene action) and prevalence of narrow ranges of variability. The majority of the studied attributes showed high heritability coupled with high genetic advance except for plant height with moderate heritability and low genetic advance, indicating little environmental influence and the traits are controlled by additive genes and that phenotypic selection may be effective for these traits, making them particularly suitable for targeted breeding programs aimed at enhancing their expression. Regarding the plant height, moderate heritability with low genetic advance accompanied by low PCV and GCV were observed. This suggested the preponderance of non-additive gene action for the above trait and selection for this trait will not be rewarding. Overall, these genotypes may be used effectively for selection and improving yield attributing traits like number of productive tillers per plant, 1000-

grain weight, fodder yield, days to 50% flowering and days to maturity.

The correlation analyses find significant associations between various traits, providing meaningful conclusions for further investigation and understanding (Table 2). Grain yield and the number of productive tillers (0.527**) and 1000-grain weight (0.508**) reveal a significant positive correlation. On the other hand, this study found a significant negative association between grain yield and plant height (-0.284**), days to 50% flowering (-0.615***), and days to maturity (-0.614***). Similar findings were reported by Amaravel *et al.* (2023) and Gopikrishnan *et al.* (2021). The inter-association analyses confirmed a high positive correlation between days to 50% flowering and days to maturity (0.99***), as recent findings in little millet by Amaravel *et al.* (2023). The strong negative association (-0.77***) between the number of productive tillers and the days to maturity is another interesting finding. Furthermore, the moderately positive association between plant height and days to 50% flowering (0.36*), emphasises the importance of future studies into the genetic and physiological variables that affect plant height and flowering duration in little millet. The positive association between 1000-grain weight and number of productive tillers (0.68**), indicating that genotypes with more productive tillers also have larger seeds. Similar results were reported for the number of productive tillers per plant and 1000-grain weight Jyothsna *et al.* (2016). Additionally, a marginal positive association between fodder yield and grain yield suggests that increasing biomass may also increase grain yield. This study highlights the possibility of selecting genotypes that have the dual benefits of increased fodder production without compromising grain yield.

In conclusion, the seven qualitative traits showed a great deal of variation across the genotypes of little millet with varied genotypic makeup. The estimated phenotypic coefficient of variation was marginally larger than the genotypic coefficient of variation, indicating little environmental effect on the expression of all the traits. The number of productive tillers per plant, 1000-grain weight, fodder yield, days to 50% flowering and days to maturity are the yield-attributing traits that may be used as selection criteria to increase grain yield in little millet.

Table 1. Mean, range, coefficients of variation, heritability (broad sense) and genetic advance as per cent of mean for yield attributing traits in 28 little millet genotypes

Characters	Mean	Range	CV (%)	Coefficient of		Heritability (broad sense %)	Genetic advance % of mean
				PCV	GCV		
Days to 50% flowering	64	46 - 87	6.74	24.63	23.69	92.5	46.93
Days to maturity	95	76 - 117	4.26	16.67	16.12	93.5	32.1
Plant height (cm)	126.46	99.93 - 143.27	9.02	11.65	7.37	40.1	9.61
No. of productive tillers per plant	5	03-Jul	16.86	27.31	21.49	61.9	34.82
1000-Seed weight (g)	1.99	1.53 - 2.57	7.1	15.85	14.17	79.9	26.1
Fodder yield (kg/ha)	6442	3148 - 9679	17.5	31.08	25.68	68.3	43.72
Grain yield (kg/ha)	1288	758 - 1996	18.53	31.71	25.73	65.8	43.01

Table 2. Genotypic correlation for yield and yield attributing traits in 28 little millet genotypes

	DFF	DM	PH	NPT	1000 GW	FY	GY
DFF	1	0.999***	0.377*	-0.769***	-0.715***	-0.256	-0.615***
DM	0.999***	1	0.363	-0.771***	-0.729***	-0.269	-0.614***
PH	0.377*	0.363	1	-0.319	0.05	0.512**	-0.284
NPT	-0.769***	-0.771***	-0.319	1	0.684***	0.327	0.527**
1000 GW	-0.715***	-0.729***	0.05	0.684***	1	0.692***	0.508**
FY	-0.256	-0.269	0.512**	0.327	0.692***	1	0.168
GY	-0.615***	-0.614***	-0.284	0.527**	0.508**	0.168	1

DFF: Days to 50% flowering, DM: Days to maturity PH: Plant height, NPT: Number of productive tillers per plant, 1000 GW: 1000-Grain weight, FY: Fodder yield, GY: Grain yield

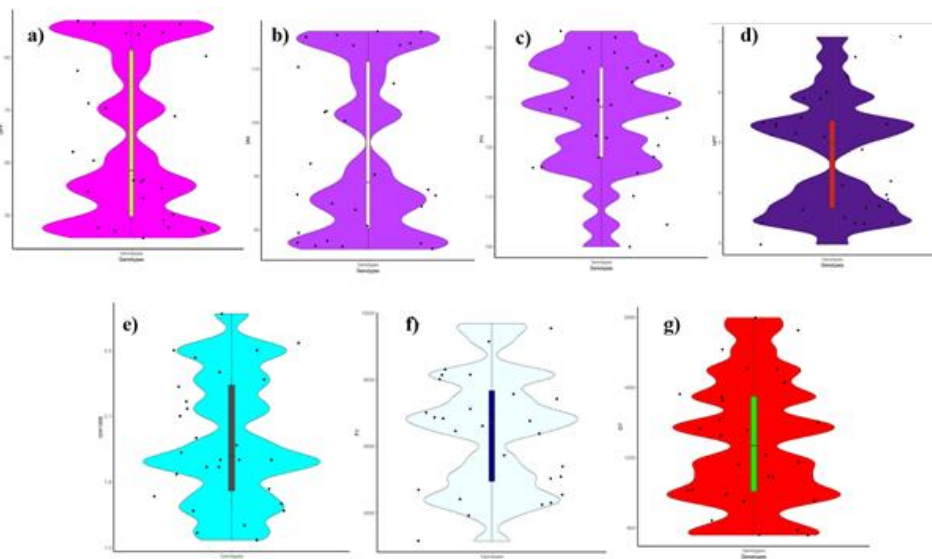


Figure 1. Frequency distribution in little millet genotypes for various traits a) Days to 50% flowering, b) Days to maturity, c) Plant height, d) Number of productive tillers per plants, e) 1000-grain weight, f) Fodder yield, g) Grain yield

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