

# Electronic Journal of Plant Breeding



## Research Article

### Genetic variability and association analysis of yield and yield attributing traits in little millet (*Panicum sumatrense* Roth. ex. Roem. and Schultz.)

M. Amaravel<sup>1</sup>, A. Nirmalakumari<sup>1\*</sup>, S. Geetha<sup>2</sup>, K. Sathya<sup>1</sup> and R. Renuka<sup>3</sup>

<sup>1</sup>Centre of Excellence in Millets, Tamil Nadu Agricultural University, Tiruvannamalai- 606 603.

<sup>2</sup>Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore- 641003.

<sup>3</sup>Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai-625 104.

\*E-Mail: animalakumari@yahoo.com

#### Abstract

Three hundred and twenty seven germplasm accessions of little millet (*Samai*) including four checks were evaluated in augmented RCBD design. The analysis of variance (ANOVA) revealed the presence of significant variability for all the traits under study except days to fifty per cent flowering and days to maturity among the little millet genotypes. The mean phenotypic distribution displayed a wide range, with a near normal distribution for most of the traits. The traits like days to fifty percent flowering, days to maturity, plant height, flag leaf length, flag leaf breadth, peduncle length, number of node/plant, dry fodder weight/plant and single plant yield were significantly positively skewed, which indicated the presence of non-additive gene action. Thus, while choosing genotypes for heterosis breeding, these traits could be taken into consideration as selection criteria. Single plant grain yield (g) recorded high genetic coefficient variation (GCV) and phenotypic coefficient variation (PCV), while days to fifty per cent flowering and days to maturity had low PCV and GCV. Heritability ranged from 62.63 (plant height) to 98.85 (single plant grain yield) per cent. Genetic advance as percentage of mean ranged from 10.72 (days to maturity) to 178.21 (single plant grain yield). In correlation studies, days to fifty per cent flowering, days to maturity, plant height, flag leaf breadth, number of nodes/plant, peduncle length and dry fodder weight/plant showed high positive correlation with single plant grain yield. These traits would be effective for direct selection for crop improvement. The current results showed that yield and yield attributing traits had large variations and high heritability, which could be used for improvement of little millet.

**Keywords:** PCV, GCV, Heritability, Correlation, augmented RCBD, GAM

#### INTRODUCTION

Little millet (*Panicum sumatrense* Roth. ex. Roem. and Schultz) ( $2n=4x=36$ ) is an allotetraploid and climate resilient crop. Origin of little millet is India (De wet *et al.*, 1983) and mostly cultivated as a rain-fed crop by tribal farmers in hilly regions. Presently, the yield stability has been attained in field crops such as wheat and rice which have greater role to reduce hunger and poverty. But they have less amount of nutrient contents. Very little efforts are being made to increase the nutrient content of high

yielding varieties. Little millet is one of the important nutri-cereals which consists of protein, mineral nutrients such as iron, zinc and vitamins. (Selvi *et al.*, 2015 and Kundgol *et al.*, 2014). It is grown under poor soil and climatic conditions with minimal inputs. In Tamil Nadu, many land races of little millet are traditionally cultivated in hilly tracts of Javvadhu Hills, Kolli Hills, Servarayan Hills, Karumanthurai, Vellimalai and Sitheri. In crop breeding, it is essential to utilize the genetic variability

inherent in a crop to develop improved varieties that can meet the growing demands of the population. Hence the unexplored land races such as the ones indicated above could be beneficial. To accomplish this, plant breeders need to understand the heritability of the traits. Knowing the heritability of a trait, along with genetic advancements, can help predict the potential gain under selection (Johnson *et al.*, 1955). Additionally, the correlation study is used for the assessment of relationship between yield and yield attributing traits, which is used for direct and indirect selection of traits for crop improvement.

Skewness is a statistical tool that is widely used in plant breeding to better understand the characteristics of quantitative traits (Fisher, 1932). One of the primary advantages of skewness is that it can help breeders to determine the type of gene action responsible for a particular trait, as positive skewness often suggests additive gene action while negative skewness is more indicative of non-additive gene action (Vanniarajan and Chandrakala, 2020)

The aim of this study was to investigate the variability that existed within the little millet germplasm. In addition, the relationship between yield and yield attributing traits was explored through correlation analysis. Efforts were also made to understand the gene action for yield and yield attributing traits utilized skewness and kurtosis.

## MATERIALS AND METHODS

Totally 327 little millet germplasm accessions including four checks *viz.*, OLM203, BL6, CO4 (Samai) and ATL1 were evaluated in augmented randomized complete block design (ARCB) (Federer *et al.*, 1975). Little millet accessions were collected from International Crop Research Institute for Semi-Arid Tropics (ICRISAT) and Ramiah Gene Bank, Department of Plant Genetic Resources, Tamil Nadu Agricultural University, Coimbatore. The experiment was conducted at Centre of Excellence in Millets, Athiyandal during *rabi* season of 2019-2020. The accessions were sown with a spacing of 30 cm x 20 cm. Recommended agronomic practices were followed to raise a good crop. Eleven quantitative traits were observed *viz.*, days to fifty per cent flowering (DFF), days to maturity (DM), plant height (cm) (PH), flag leaf length (cm) (FLL), flag leaf breadth (cm) (FLB), number of productive tiller/plant (NPT), panicle length (cm) (PL), number of nodes per plant (NN), peduncle length (cm) (PEL), dry fodder weight/plant (g) (DFW) and single plant grain yield (g) (SPY). The analysis of variance was estimated in "R" tool using "augmented RCBD" package (Aravind *et al.*, 2020). The ANOVA and variability parameters such as genotypic coefficient variation (GCV), phenotypic coefficient variation (PCV), heritability and genetic advance were estimated. Based on the augmented block design, the phenotypic correlation analysis was estimated in "R" tool using "Performance Analytics" package.

## RESULTS AND DISCUSSION

ARCB is used for evaluating a large number of germplasm accessions. In the present study, little millet the accessions showed highly significant differences in ANOVA for both block adjusted and treatment adjusted values for all traits except days to maturity (**Table 1**). Checks provided stabilized performance, because the mean sum of square of checks were same in adjusted treatment and adjusted block. The critical difference of checks revealed the similar expression for all the traits across blocks (**Table 2**). The critical difference (CD) for any two test treatments of the same block showed marginally higher values than that same two test treatments for different blocks. Based on CD of the treatments, the environmental heterogeneity was non-significant for all the traits within blocks and between the blocks. In their study, Suman *et al.* (2019) found that there was no significant effect of environmental heterogeneity on all the traits for both within blocks and between blocks in finger millet landraces.

Coefficients of variation of more than six per cent were observed for all traits except days to fifty per cent flowering, days to maturity and flag leaf length. This suggested that higher variability was observed in plant height, dry fodder weight, flag leaf breadth, single plant grain yield, number of productive tiller/plant, peduncle length, number of node/plant and panicle length.

Mean values were statistically analyzed in order to investigate descriptive statistics such as range, standard deviation, standard error, coefficient of variation and skewness (**Table 2**). Almost all of the traits analyzed had a high level of phenotypic variability. On average, the collection of accessions studied flowered 58 days after sowing; however, the flowering time could range from as early as 43 days to as late as 77 days. For days to maturity, mean days to maturity was 83 and ranged from 71 to 105 days. The mean plant height was 70 cm, with a height range of 45 to 126 cm. The average number of productive tillers per plant was 2.9, ranging from 1 to 7.5. Flag leaf length ranged from 11.58 to 37.22 cm, with a mean measurement of 23.57 cm. The average flag leaf breadth was 0.65 cm, and it ranged from 0.31 to 1.36 cm. The average length of a panicle was 29.09 cm, with a length range of 12.19 to 48.74 cm. The peduncle length ranged from 5.32 cm to 17.73 cm with mean of 9.83 cm. The average number of nodes per plant was 4.08 and it ranged from 2.36 to 7.49. The range of dry fodder weight was 0.58 to 19.98 g, with a mean of 3.7g. The range of single plant grain yield was 0.19 to 9.94 g, with a mean of 1.49g.

Days to 50% flowering, days to maturity, plant height, flag leaf length, flag leaf breadth, peduncle length, number of nodes/plant, number of productivetiller/plant, dry fodder yield, and single plant grain yield/plant all showed positive skewness, with the majority of genotypes distributed to

**Table 1. ANOVA for treatment adjustment and block adjustment**

ANOVA - treatment adjusted												
Source	Df	DFF	DM	FLB	FLL	DFW	NN	PEL	PH	PL	NPT	SPY
Block (ignoring treatments)	12	140.5 **	155.75 **	0.02 **	41.16**	15.08 **	0.66 **	5.65 **	892.43 **	68.19 **	5.73 **	2.27 **
Treatment (eliminating blocks)	326	40.54 **	63.21 **	0.02 **	19.71**	7.69 **	0.81 **	4.55 **	264.21 **	49.83 **	1.23 **	1.64 **
Treatment: Check	3	1.95 ns	42.42 ns	0.17 **	374.34**	13.09 **	6.54 **	71.22 **	108.31 ns	544.91 **	3.28 **	4.51 **
Treatment: Test and Test vs. Check	323	40.9 **	63.41 **	0.02 **	16.39**	7.64 **	0.76 **	3.93 **	265.67 **	45.2 **	1.21 **	1.61 **
Residuals	36	7.38	16.43	0.0039	0.62	0.15	0.08	0.54	66.58	3.03	0.05	0.02
ANOVA - block adjusted												
Source	Df	DFF	DM	FLB	FLL	DFW	NN	PEL	PH	PL	NPT	SPY
Treatment (ignoring Blocks)	326	45.33 **	66.19 **	0.02 **	21.2 **	8.24 **	0.83 **	4.73 **	272.61 **	52.28 **	1.44 **	1.72 **
Treatment: Check	3	2.18 ns	42.23 ns	0.17 **	372.3 **	13.23 **	6.54 **	71.25 **	110.36 ns	548.71 **	3.25 **	4.49 **
Treatment: Test vs. Check	1	2.53 ns	6631.28 **	0.00053 ns	119.57 **	14.95 **	1.57 **	16.39 **	30978.96 **	2.28 ns	0.11 ns	0.05 ns
Treatment: Test	322	45.87 **	45.9 **	0.02 **	17.6 **	8.17 **	0.77 **	4.07 **	178.18 **	47.78 **	1.43 **	1.7 **
Block (eliminating Treatments)	12	11.14 ns	75.26 **	0.01 *	0.84 ns	0.13 ns	0.12 ns	0.86 ns	665.66 **	1.95 ns	0.12 *	0.06 **
Residuals	36	7.38	16.43	0.0039	0.62	0.15	0.08	0.54	66.58	3.03	0.05	0.02

ns P > 0.05; \* P ≤ 0.05; \*\* P ≤ 0.01

DFF- Days to fifty per cent flowering, PH-plant height (cm), FLL-Flag leaf length (cm), FLB- Flag leaf breadth (cm), DFW-Dry fodder weight (g)/plant, PEL-Peduncle length (cm), NN-Number of node/plant, PL-panicle length (cm), NPT-Number of productive tiller/plant and SPY-Single plant grain yield (g).

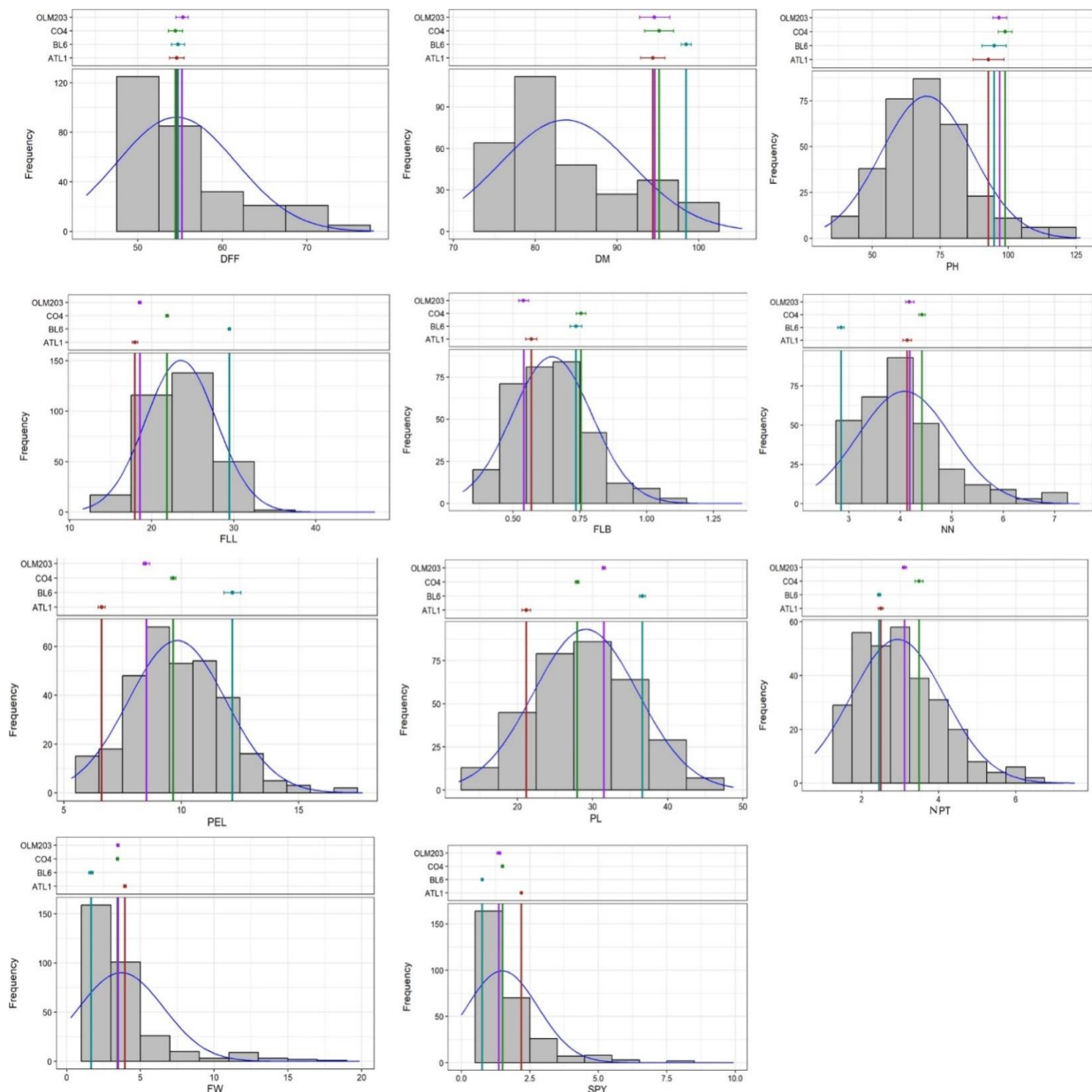
**Table 2. Critical difference and Coefficient of Variation**

Critical difference											
	DFF	DM	FLB	FLL	DFW	NN	PEL	PH	PL	NPT	SPY
A test treatment and a control treatment	6.38	9.52	0.15	1.85	0.9	0.68	1.72	19.16	4.09	0.54	0.33
Control treatment means	2.16	3.22	0.05	0.63	0.3	0.23	0.58	6.48	1.38	0.18	0.11
Two test treatments (Different blocks)	8.69	12.97	0.2	2.52	1.22	0.92	2.35	26.12	5.57	0.74	0.45
Two test treatments (Same block)	7.77	11.6	0.18	2.26	1.09	0.82	2.1	23.36	4.98	0.66	0.4
Descriptive statistics											
Mean	54.58	83.69	0.65	23.57	3.7	4.08	9.83	70.03	29.09	2.93	1.49
Std.Error	0.39	0.45	0.01	0.24	0.16	0.05	0.12	0.93	0.39	0.07	0.07
St. Deviation	7.03	8.04	0.15	4.31	2.87	0.91	2.08	16.74	6.95	1.21	1.3
Minimum	43.93	71.15	0.31	11.58	0.58	2.36	5.32	32.5	12.19	0.79	0.19
Maximum	77.94	105.32	1.36	47.22	19.88	7.49	17.73	126.6	48.74	7.54	9.94
CV	4.97	4.75	9.71	3.37	10.57	7.09	7.53	11.12	6.03	7.89	9.4
Skewness	1.1 **	0.76 **	0.77 **	0.49 **	2.54 **	1.21 **	0.42 **	0.76 **	0.09 ns	0.89 **	2.44 **

CD-Critical difference, CV-Coefficient variation, DFF- Days to fifty per cent flowering, PH-plant height (cm), FLL-Flag leaf length (cm), FLB- Flag leaf breadth (cm), DFW-Dry fodder weight (g)/plant, PEL-Peduncle length (cm), NN-Number of node/plant, PL-panicle length (cm), NPT-Number of productive tiller/plant and SPY-Single plant grain yield (g)

the left on the frequency distribution curve (**Table 2**) (**Fig. 1.**) It demonstrated the presence of non-additive gene action, which was necessary for exploiting hybrid vigour through heterosis breeding. As a result, by using different genotypes as parents to create hybrids, these features could be improved. Similar results were revealed by Vanniarajan and Chandirakala (2020) in Barnyard millet.

The estimation of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability ( $h^2$ ) and genetic advance (GA) are presented in **Table 3** and **Fig. 2**. The difference between PCV and GCV were minimal for flag leaf length followed by single plant yield and panicle length. The maximum difference for PCV and GCV was observed for plant height followed by flag leaf breadth and days to maturity. The PCV was



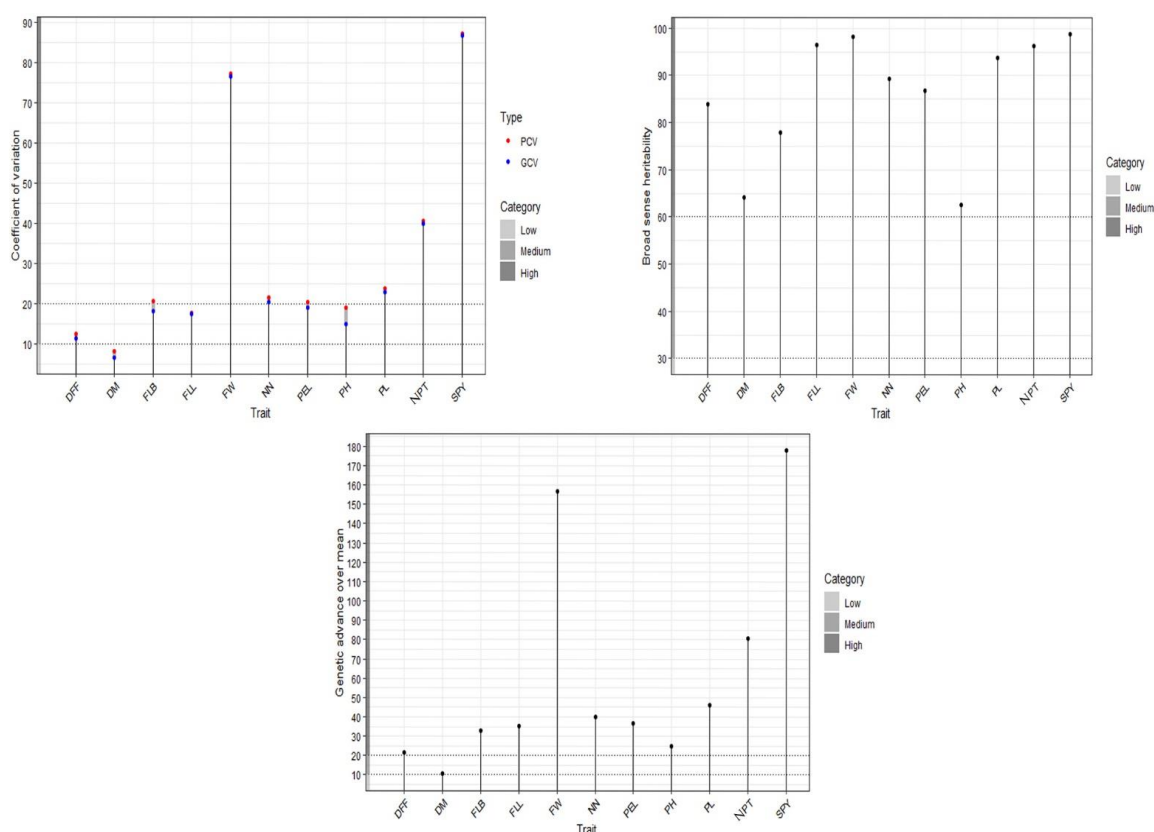
**Fig 1. Estimation of frequency distribution**

DFF- Days to fifty per cent flowering, PH-plant height (cm), FLL-Flag leaf length (cm), FLB- Flag leaf breadth (cm), DFW-Dry fodder weight (g)/plant, PEL-Peduncle length (cm), NN-Number of node/plant, PL-panicle length (cm), NPT-Number of productive tiller/plant and SPY-Single plant grain yield (g)

**Table 3. Estimation of mean, variance, coefficients of variability, heritability and genetic advance as per cent of mean (GAM) for 11 Quantitative traits of little millet**

Trait	Mean	PV	GV	EV	GCV		PCV		ECV	$h^2_b$		GA	GAM	
					Values	Category	Values	Category		Values	Category		Values	Category
DFF	54.58	45.87	38.49	7.38	11.37	Medium	12.41	Medium	4.98	83.92	High	11.73	21.48	High
DM	83.69	45.9	29.47	16.43	6.49	Low	8.1	Low	4.84	64.21	High	8.97	10.72	Medium
SPY	1.49	1.7	1.68	0.02	86.88	High	87.39	High	9.35	98.85	High	2.66	178.21	High
PH	70.03	178.18	111.6	66.58	15.08	Medium	19.06	Medium	11.65	62.63	High	17.25	24.63	High
FLL	23.57	17.6	16.98	0.62	17.49	Medium	17.8	Medium	3.34	96.47	High	8.35	35.43	High
FLB	0.65	0.02	0.01	0.0039	18.2	Medium	20.63	High	9.71	77.83	High	0.21	33.12	High
NPT	2.93	1.43	1.37	0.05	39.93	High	40.7	High	7.86	96.27	High	2.37	80.83	High
PEL	9.83	4.07	3.53	0.54	19.13	Medium	20.53	High	7.47	86.78	High	3.61	36.76	High
PL	29.09	47.78	44.75	3.03	23	High	23.76	High	5.98	93.66	High	13.36	45.91	High
NN	4.08	0.77	0.69	0.08	20.39	High	21.58	High	7.05	89.34	High	1.62	39.77	High
DFW	3.7	8.17	8.03	0.15	76.63	High	77.32	High	10.34	98.21	High	5.79	156.66	High

PV- Phenotypic Variance, GV- Genotypic Variance, EV-Environmental Variance, GCV- Genotypic Coefficient Variation, PCV-Phenotypic Coefficient Variation,  $h^2_b$  – Heritability in a Broad Sense, GA-Genetic Advance and GAM-Genetic Advance Mean



**Fig. 2. Estimation of coefficients of variability, heritability and genetic advance as per cent of mean (GAM)**

DFF- Days to fifty per cent flowering, PH-plant height (cm), FLL-Flag leaf length (cm), FLB- Flag leaf breadth (cm), DFW-Dry fodder weight (g)/plant, PEL-Peduncle length (cm), NN-Number of node/plant, PL-panicle length (cm), NPT- Number of productive tiller/plant and SPY-Single plant grain yield (g)

found to be slightly higher than the GCV, suggesting that environmental factors may have influenced the expression of the traits. These findings are consistent with those of Ganapathy *et al.* (2011). In the current analysis the single plant grain yield has high PCV and GCV followed by dry fodder weight/plant, number of productive tiller/plant, panicle length and number of node indicating that the germplasm has wide range of variability in the germplasm. Selvi *et al.* (2014) reported that high PCV and GCV estimated for dry fodder weight, panicle length, number of productive tiller and single plant grain yield/plant in little millet. Madhavi lath *et al.* (2020), Anuradha *et al.* (2017) and Nirmalakumari *et al.* (2010) reported similar results of high PCV and GCV for single plant grain yield and number of productive tiller/plant in little millet.

The days to fifty per cent flowering, plant height, flag leaf length and flag leaf breadth had medium PCV and GCV. The days to maturity had low PCV and GCV. Nirmalakumari *et al.* (2010) reported that days to fifty per cent flowering and flag leaf length had medium PCV and GCV in little millet. Patel *et al.* (2018) and Lule *et al.* (2012) observed that days to maturity had low PCV and GCV in little millet and finger millet respectively. Anuradha *et al.* (2017) reported that plant height and flag leaf length had medium PCV and GCV in little millet.

Heritability is predicted to know the transmission and expression of traits from parents to off springs. In the present study, heritability ranged from 62.63 (plant height) to 98.85 (single plant grain yield) per cent. Genetic advance as per cent of mean ranged from medium 10.72 (plant height) to 178.21 (single plant grain yield). In general, combined genetic advance and heritability are better used to predict the gain under selection than heritability alone. Based on the combined results of genetic advance and heritability, traits such as days to

maturity, plant height, flag leaf length, flag leaf breadth, number of productive tiller/plant, panicle length, number of nodes per plant, peduncle length, dry fodder weight/plant and single plant grain yield had high genetic advance and heritability indicating the presence of additive gene action. Hence, selection of these traits would increase the scope of little millet improvement. In little millet, Madhavalatha *et al.* (2020) reported that single plant grain yield and number of productive tiller/plant had high heritability and high genetic advance. Suryanarayana and Sekhar (2018) reported that plant height, single plant grain yield and number of productive tiller/plant were observed to show high heritability and high genetic advance in little millet. The high genetic advance and high heritability indicated that the traits were mostly influenced by additive genetic variance. Similar results of heritability and genetic advance were reported by Anuradha *et al.* (2017) in little millet and Patil *et al.* (2017) in finger millet.

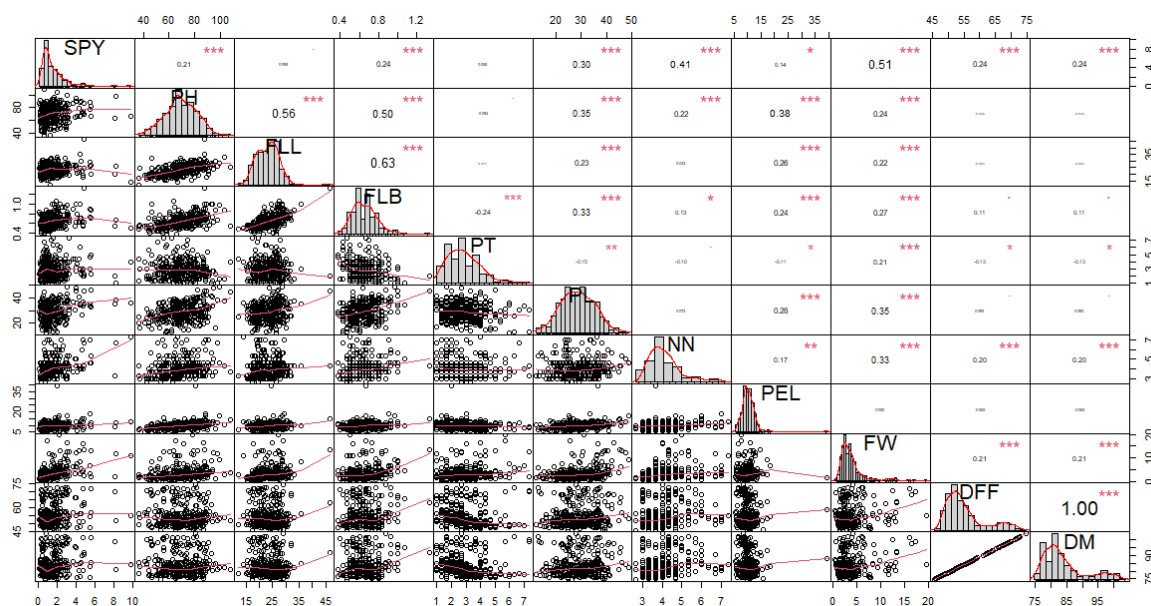
The correlation analysis is used to assess the relationship between yield and yield attributing traits which enables the breeder to identify the accession that has desired traits to improve the yield. In this study, single plant grain yield was significantly and positively correlated with days to fifty per cent flowering, days to maturity, plant height, flag leaf breadth, number of node/plant, panicle length, peduncle length and dry fodder weight/plant. Hence selection based on the above traits would increase the single plant grain yield (Table 4) (Fig. 3.). Similar results were reported by Gopikrishnan *et al.* (2021) and Anuradha *et al.* (2017) in little millet and Jyothsna *et al.* (2016) in finger millet. Venkataratnam *et al.* (2019) reported that positive correlation occurred between plant height and single plant grain yield in little millet. Sasamala *et al.* (2011) reported positive correlation among the traits such as plant height, flag leaf breadth, dry fodder weight

**Table 4. Estimation of phenotypic correlation between yield and yield attribute traits**

	SPY	PH	FLL	FLB	NPT	PL	NN	PEL	FW	DFF	DM
SPY	1.00	0.21**	0.10	0.24**	0.05	0.30**	0.41**	0.14*	0.51**	0.24**	0.24**
PH		1.00	0.56**	0.50**	-0.09	0.35**	0.22*8	0.38**	0.24**	-0.04	-0.04
FLL			1.00	0.63**	0.01	0.23**	0.04	0.26**	0.22**	-0.05	-0.05
FLB				1.00	-0.24**	0.33**	0.13*	0.24**	0.27**	0.11	0.11
PT					1.00	-0.15*	-0.10	-0.11	0.21**	-0.13*	-0.13*
PL						1.00	0.07	0.28**	0.35**	0.09	0.09
NN							1.00	0.17*	0.33**	0.20**	0.20**
PEL								1.00	0.05	-0.06	-0.06
DFW									1.00	0.21**	0.21**
DFF										1.00	1.00**
DM											1.00

ns P > 0.05; \* P <= 0.05; \*\* P <= 0.0

DFF- Days to fifty per cent flowering, PH-plant height (cm), FLL-Flag leaf length (cm), FLB- Flag leaf breadth (cm), DFW-Dry fodder weight (g)/plant, PEL-Peduncle length (cm), NN-Number of node/plant, PL-panicle length (cm), NPT-Number of productive tiller/plant and SPY-Single plant grain yield (g)



**Fig 3. Estimation of phenotypic correlation between yield and yield attribute traits**

DFF- Days to fifty per cent flowering, PH-plant height (cm), FLL-Flag leaf length (cm), FLB- Flag leaf breadth (cm), DFW-Dry fodder weight (g)/plant, PEL-Peduncle length (cm), NN-Number of node/plant, PL-panicle length (cm), NPT-Number of productive tiller/plant and SPY-Single plant grain yield (g)

/plant and single plant grain yield /plant in little millet. In little millet, Selvi *et al.* (2014) reported that plant height, panicle length, peduncle length and flag leaf breadth were positively correlated with grain yield/plant. Patel *et al.* (2019) reported that plant height and dry fodder weight /plant had positive correlation with single plant grain yield in little millet. The study suggests that traits such as days to fifty per cent flowering, days to maturity, plant height, flag leaf breadth, number of node/plant, panicle length, peduncle length, and dry fodder weight could be considered as selection criteria for improving single plant grain yield.

The results of ANOVA revealed presence of sufficient variability for all traits under study except days to fifty per cent flowering and days to maturity among the little millet germplasm accessions. In this study, all traits except panicle length exhibited significant positive skewness indicating the predominance of non-additive gene action. These could be useful for heterosis breeding. Single plant grain yield revealed high PCV and GCV followed by dry fodder weight /plant, number of productive tiller/plant, panicle length and number of node/plant. These traits would be effective for direct selection little millet improvement. Based on the combined results of genetic advance and heritability, the traits such as days to fifty per cent flowering, days to maturity, plant height, flag leaf length, flag leaf breadth, number of productive tiller/plant, panicle length, number of nodes per plant, peduncle length, dry fodder weight/plant and single plant grain yield had high genetic advance and heritability indicating

the presence of additive gene action. Hence, selection of these traits would increase the scope of little millet improvement. The correlation analysis indicated that traits such as plant height, flag leaf breadth, number of node/plant, panicle length, peduncle length and dry fodder weight /plant revealed significant association with single plant grain yield.

#### ACKNOWLEDGEMENT

The authors wish to express their gratitude to the Ramiah Gene Bank, and the Department of Plant Genetic Resources at Tamil Nadu Agricultural University, Coimbatore, International Crop Research Institute for Semi-Arid Tropics (ICRISAT) at Hyderabad, as well as the CEM-Centre of Excellence in Millets, TNAU, for providing the germplasm resources and the opportunity to carry out this research.

#### REFERENCES

- Anuradha, N., Patro, T. S. S. K., Divya, M., Rani, Y. S. and Triveni, U. 2017. Genetic variability, heritability and correlation of quantitative traits in little millet genotypes. *Journal of pharmacognosy and phytochemistry*, 6(6): 489-492.
- Aravind, J., Sankar, S. M., Wankhede, D. P. and Kaur, V. Package 'augmentedRCBD'.
- De Wet, J. M. J., Prasada Rao, K. E. and Brink, D. E. 1983. Systematics and domestication of *Panicum*

- sumatrense* (Graminae). *Journal d'agriculture traditionnelle et de botanique appliquée*, **30**(2): 159-168. [Cross Ref]
- Federer, W. T. and Raghavarao, D. 1975. On augmented designs. *Biometrics*, 29-35. [Cross Ref]
- Fisher, R. A., Immer, F. R. and Tedin, O. 1932. The genetical interpretation of statistics of the third degree in the study of quantitative inheritance. *Genetics*, **17**(2): 107. [Cross Ref]
- Ganapathy, S., Nirmalakumari, A. and Muthiah, A. R. 2011. Genetic variability and interrelationship analyses for economic traits in finger millet germplasm. *World Journal of Agricultural Sciences*, **7**(2): 185-188.
- Gopikrishnan, A., Pandiyan, M., Thilagam, P., Veeramani, P. and Nanthakumar, S. 2021. Characterization of little millet (*Panicum sumatrense*) genetic diversity in Yelagiri Hills of Tamil Nadu. [Cross Ref]
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimate of genetic and environmental variability in Soybeans. *Agronomy Journal*, **47**:341 – 318. [Cross Ref]
- Jyothsna, S., Patro, T. S. S. K., Ashok, S., Rani, Y. S. and Neeraja, B. 2016. Studies on genetic parameters, character association and path analysis of yield and its components in finger millet (*Eleusine coracana* L. Gaertn). *International Journal of Theoretical and Applied Sciences*, **8**(1): 25.
- Kundgol, N. G., Kasturiba, B., Math, K. K. and Kamatar, M. Y. 2014. Effect of preliminary processing on antiradical properties of little millet landraces. *International Journal of Farm Sciences*, **4**(2): 148-154.
- Lule, D., Tesfaye, K., Fetene, M. and De Villiers, S. 2012. Inheritance and association of quantitative traits in finger millet (*Eleusine coracana* Subsp. *Coracana*) landraces collected from eastern and south eastern Africa. *International journal of genetics*, **2**(2): 12-21.
- Madhavilatha, L., Rao, M. S., Priya, M. S. and Kumar, M. H. 2020. Variability, character association and path analysis studies in little millet (*Panicum sumatrense*). *Andhra Pradesh J Agril. Sci.*, **6**(1): 49-54
- Nandini, C., Bhat, S., Saritha, H. S., Pandey, C. D., Sushil Pandey, P., Bai, L. and Gowda, J. 2020. Characterization of barnyard millet (*Echinochloa frumentaceae* (Roxb.) Link) germplasm for quantitative traits to enhance its utilization. *Electronic Journal of Plant Breeding*, **11**(04): 1066-1072. [Cross Ref]
- Nirmalakumari, A., Salini, K. and Veerabhadhiran, P. 2010. Morphological characterization and evaluation of little millet (*Panicum sumatrense* Roth. ex. Roem. and Schultz.) germplasm. *Electronic Journal of Plant Breeding*, **1**(2): 148-155.
- Patel, S. N., Patil, H. E., Modi, H. M. and Singh, T. J. 2018. Genetic variability study in little millet (*Panicum miliare* L.) genotypes in relation to yield and quality traits. *Int. J Curr. Microbiol. App. Sci*, **7**(6): 2712-2725. [Cross Ref]
- Patel, S. N., Patil, H. E., Singh, S. and Gandhi, K. 2019. Association studies in relation to yield and quality traits in little millet (*Panicum sumatrense* L.). *IJCS*, **7**(5): 2725-2730. [Cross Ref]
- Patil, H. E., Patel, B. K. and Patel, S. N. 2017. Assessment of genetic diversity in finger millet (*Eleusine coracana* L.) through multivariate analysis approach. *International Journal of Economic Plants*, **4**(4): 148-151.
- Sasamala, A. C., Sahoo, L. P., Mahapatra, K. C. and Pandey, S. 2011. Genetic variability and character association in common millet germplasm of Odisha. *Indian Journal of Plant Genetic Resources*, **24**(1): 81-85.
- Selvi, V. M., Nirmalakumari, A. and Subramanian, A. 2014. Genetics and interrelationships of yield traits for enhancing productivity of little millet. *Electronic Journal of Plant Breeding*, **5**(1): 82-86.
- Suman, A., Surin, S. and Ahmad, E. 2019. Finger millet germplasm characterization and evaluation using principal component analysis. *Intl J Chem Stud*, **7**: 1002-1005.
- Suryanarayana, L. and Sekhar, D. 2018. Studies on genetic variability, character association and path analysis in little millet (*Panicum sumatrense* L.) genotypes. *The Pharma Innovation Journal*, **7**(7): 908-910.
- Vanniarajan, C. and Chandirakala, R. 2020. Descriptive statistical analysis and variability studies in germplasm collections of barnyard millet (*Echinochloa frumentacea* L.). *Electronic Journal of Plant Breeding*, **11**(04): 1240-1245. [Cross Ref]
- Venkataratnam, T., Latha, L. M., Sekhar, M. R. and Kumar, A. N. 2019. Studies on correlation and path analysis in little millet (*Panicum sumatrense*). *Green Farming*, **10**(6): 679-682. [Cross Ref]