Biological Forum – An International Journal **14(3): 208-214(2022)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Association and Variability Studies of Quantitative Traits in Proso Millet (*Panicum miliaceum* L.)

***G. Anil Kumar*[1], *C. Vanniarajan*[2*], *M. Vetriventhan*[3], *R. Sudhagar*[4] *and S. Saravanan*[5]**
[1]Department of Plant Breeding and Genetics, Agricultural College and Research Institute-Madurai,
Tamil Nadu Agricultural University (Tamil Nadu), India.
[2]Anbil Dharmalingam Agricultural College and Research Institute -Trichy,
Tamil Nadu Agricultural University (Tamil Nadu), India.
[3]International Crop Research Institute for Semi-Arid Tropics (ICRISAT), Patancheru (Telangana), India.
[4]Tamil Nadu Agricultural University-Coimbatore (Tamil Nadu), India.
[5]Department of Biotechnology, Agricultural College and Research Institute-Madurai,
Tamil Nadu Agricultural University (Tamil Nadu), India.

(Corresponding author: C. Vanniarajan)*
(Received 09 May 2022, Accepted 30 June, 2022)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Proso millet, being the climate-resilient crop among cereals can be grown for food, feed, and fodder purposes. Comparatively, Proso millet grains are higher in protein, vitamins, minerals, and micronutrients like iron, zinc, copper, and manganese. The current study was carried out to assess the variability and association analysis for 13 biometrical traits in 20 Proso millet accessions. High variability was noticed in the traits namely number of basal tillers, peduncle length, and flag leaf sheath length and moderate variability were recorded for the traits namely plant height, panicle length, flag leaf blade length, flag leaf blade width, thousand-grain weight, and single plant yield. High heritability with high genetic advance were recorded for the traits namely plant height, number of basal tillers, peduncle length, panicle length, flag leaf blade length, flag leaf blade width, flag leaf sheath length, thousand-grain weight, and single plant yield. The association analysis revealed significant phenotypic correlation for panicle length and flag leaf blade width while thousand-grain weight, plant height, and flag leaf sheath length, exhibited significance in both phenotypic and genotypic correlation analysis besides possessing a high positive direct effect in path coefficient analysis inferring that yield improvement can be accomplished by direct selection of these characters.

Keywords: Proso millet, germplasm, variability, association analysis.

INTRODUCTION

The term ‘millet’ refers to the small-grained, annual cereal grasses which are cultivated in low-input agricultural conditions, where major cereal crops usually return low yields. On marginal soils with low fertility, millets are typical for sustainable agriculture and food security. Proso millet (*Panicum miliaceum* L.) an allotetraploid with a chromosome number of 36 ($2n = 4x = 36$) is an annual herbaceous plant that can be easily grown in marginally fertile soils of arid and semi-arid regions. It is also known as common millet, hersey millet, broom corn millet, broom millet, white millet, russian millet and hog millet. It is predominantly a self-pollinated crop however natural cross-pollination of more than 10 % is also reported. Though cultivated principally for bird seed in the USA, the crop is widely cultivated across the countries like India, China, Russia, Ukraine, Turkey, Romania, Sri Lanka, Pakistan, Nepal, Western Burma, and a few other South-East Asian countries for food, feed and fodder purposes. Proso millet grains are nutritionally rich in protein, vitamins, minerals, and micronutrients including iron, zinc, copper, and manganese, compared to other staple cereals (Saleh *et al.,* 2013). It is also a low-maintenance and stress-resistant crop capable of evading drought due to its short life cycle and producing an acceptable yield, making it appropriate for crop production in inhospitable climates.

Despite Proso millet’s nutritional superiority and climatic resilience, it is an under-utilized crop. Global warming, changing environmental conditions, and erratic rainfall behaviour pose a serious threat to global food security in near future. Hence, there is a dire need for research on millets like Proso millet, which ensures food and nutritional security in mere future. Germplasm refers to the total of all the hereditary material available in a particular crop species. The information of variability in germplasm for important traits such as yield and quality enables the effective utilization of genetic resources in crop improvement programs (Vetriventhan *et al.,* 2019). Estimation of the nature and degree of association among the yield contributing traits is essential to identify the direction of selection and to maximise yield in the shortest time possible.

MATERIALS AND METHODS

The current study mainly aims the assessment of the genetic variability and association of various quantitative traits for the complex trait yield in Proso millet. The experimental material used for the study comprises 18 germplasm lines raised along with the checks ATL-1 and CO-5. This study was carried out during Rabi, 2021 at Agricultural College and Research Institute, Madurai, TNAU. The germplasm was procured from the Gene bank- ICRISAT, and the check varieties from the Centre of Excellence for Millets, Athiyandal. The total plot size adopted was $298m^2$ and the genotypes were raised in Randomised Block Design (RBD) with 3 replications. Each accession was sown in 3 rows of row length 3m with a spacing of 30×10 cm in each replication and standard agricultural management practices were carried out for the proper growth and establishment of the crop stand.

The observations were taken on five randomly selected plants from each replication for various biometrical traits namely plant height (cm), number of basal tillers, peduncle length (cm), panicle length (cm), flag leaf blade length (cm), flag leaf blade width (cm), flag leaf sheath length (cm), grain length (mm), grain width (mm),thousand-grain weight (g) and single plant yield (g)while the days to 50% flowering and days to maturity were recorded on a whole plot basis.

The magnitude of variation available in the germplasm accessions studied can be estimated by the coefficient of variation. The genotypic and phenotypic coefficients of variation (GCV & PCV) were calculated using the method devised by Burton (1952). The variability was classified into three classes *i.e.,* low (<10%), moderate (10 - 20%), and high (>20%) as proposed by Sivasubramanian and Madhavamenon (1973). Broad sense heritability (h^2_b) was computed as per the method suggested by Lush (1940) and was classified as high (> 60%), moderate (30-60%), and low (<30%). By using the method developed by Johnson (1955), the genetic advance was evaluated and categorised into low (<10 %), moderate (10- 20 %), and high (> 20 %). The correlation coefficients were computed using the method suggested by Falconer (1960) and the path coefficient analysis was worked out using the method specified by Dewey and Lu (1959).

The collected data were subjected to statistical analyses for the computation of genotypic variance (V_g), phenotypic variance (V_p), genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), Broad sense heritability(h^2_b), genetic advance as percent of mean (GAM), correlation and path analysis were carried out using the "variability" package in R software. The correlogram (Fig. 1) was constructed using the "Corrplot" package in R.

RESULTS AND DISCUSSION

Mean performance

The estimation of mean values (Table 2) serves as a basis for selecting the desirable genotypes (Salini *et al.,* 2010). The plant height ranged from51.74 cm to 104.64 cm with a mean of 68.20 cm. The number of basal tillers varied from 3 to 12 with a mean of 7 tillers. The germplasm evaluated attained the days to 50% flowering stage at a range of 34 to 41 days. Peduncle length ranged from 6.25 cm to 22.14 cm with an average of 14.91 cm and the panicle length from 16.21 cm to 31.25 cm with an average of 20.97 cm. The flag leaf blade length varied from 17.12 cm to 31.52 cm with a mean value of 22.79 cm and the flag leaf blade width from 0.86 cm to 2.79 cm with a mean value of 1.39 cm. The days to maturity among the genotypes ranged from 64 to 73 days. The grain length and grain width recorded a range of 2.62 mm – 3.19 mm and 1.85 mm – 2.30 mm and mean values of 2.88 mm and 2.05 mm respectively. The thousand-grain weight ranged from 4.02 g to 8.06 g with a mean of 5.29 g. Single plant yield ranged from 6.24 g to 12.56 g with a mean of 8.2 g.

Analysis of variance and Measures of variability. The analysis of variance (ANOVA) revealed that the mean sum of squares for all the 13 biometrical traits tested among 20 accessions was found to be significant (Table 1) which specifies the prevalence of large variation. The variability measures such as V_g, V_p, PCV, GCV, h^2_b and GAM for different traits are presented in Table 2. The PCV values are greater than that of the GCV values for all the traits studied indicating that the apparent variation is not only due to genotypes but also due to the influence of the environment. However, the differences in PCV and GCV are very narrow which is an indication of least influence of environment on the expression of the traits studied. Therefore, the variability observed among the genotypes under this study is due to the genetic constitution only.

The traits namely number of basal tillers, peduncle length and flag leaf sheath length have higher estimates of PCV and GCV indicating high variability. The results aligned with Salini *et al.* (2010); Verulkar *et al.* (2014) for the trait number of tillers. The features namely plant height, panicle length, flag leaf blade length, flag leaf blade width, thousand-grain weight and single plant yield recorded the moderate PCV and GCV values indicating moderate variability. Similar results were reported by Salini *et al.* (2010); Verulkar *et al.* (2014) for plant height and panicle length and panicle length by Anuradha *et al.* (2020). The characters such as days to 50% flowering, days to maturity, grain length and grain width recorded the lower estimates of PCV and GCV values indicating low variability in accordance with Anuradha *et al.* (2020); Verulkar *et al.* (2014); Salini *et al.*(2010) for days to maturity by Anuradha *et al.* (2020).

In the current study, estimates of broad sense heritability (h^2_b) were found to be high for all the 13 biometrical traits ranging from 67.95% (for grain width) to 99.17% (for the number of basal tillers), inferring that selection maybe effective since the environmental influence is low. The results obtained concurred with the findings reported by Calamai *et al.* (2020); Anuradha *et al.* (2020); Verulkar *et al.* (2014); Salini *et al.* (2010).

Out of the 13 biometrical characters studied 9 characters exhibited high genetic advance percent of mean (GAM) ranging from4.50% for days to maturity to 71.88% for the number of basal tillers. The characteristics days to 50% flowering, days to maturity, grain length and grain width showed low genetic advance as a percent of the mean.

Association analysis -Correlation and Path analysis. The yield is a complex trait governed by the interplay of numerous component characters. Understanding the complex relationships between various yield and yield-contributing characters is crucial for increasing the efficiency of selection in the process of aiming for the genetic improvement of yield. The estimation of correlation coefficients determines the nature and degree of association of various plant characters for yield. Phenotypic correlation denotes the observable correlation between two traits and it includes both genotypic and environmental effects and thus tends to vary under different environmental conditions. Genotypic correlation denotes the inherent association between two traits at the genetic level which was more stable and reliable thereby having principal importance in selecting the yield contributing characters. The estimates of genotypic correlation coefficient values (Table 4) were found to be greater than that of phenotypic correlation coefficient values (Table 3) for all the 13 biometrical characters studied which implies that the stronger association between the traits was mainly governed by the genetic factors.

Phenotypic and genotypic correlation. The phenotypic correlation analysis (Table 3) revealed that the independent variables *i.e.,* plant height (0.4517), panicle length (0.3406), flag leaf blade width(0.3754), flag leaf sheath length (0.5898) and thousand-grain weight (0.5777)had exhibited a highly significant positive relationship with single plant yield. Similar results were observed by Manimozhi *et al.* (2014) for the flag leaf sheath and panicle length. The genotypic correlation analysis (Table 4) exposed that 3 of the 5 variables which were significant in phenotypic correlation expressed the genotypic correlation *i.e.,* plant height (0.4672), flag leaf sheath length (0.6118) and thousand-grain weight (0.6213).The above traits exhibited a highly significant positive relationship with single plant yield. The obtained results concurred with Dikshit and Sivaraj (2013) for plant height, flag leaf sheath length and thousand-grain weight and also with Yazdizadeh *et al.* (2020) who reported a significant positive correlation of plant height and thousand-grain weight with yield in both normal and salinity stress conditions. Salini *et al.* (2010) also witnessed a positive correlation between plant height with grain yield per plant.

The number of basal tillers recorded a significant negative correlation with peduncle length, panicle length, flag leaf blade length, flag leaf blade width, flag leaf sheath length and days to maturity.

Many of the traits expressed significant positive intercorrelation among themselves, the trait plant height exhibited a positive correlation with days to 50 % flowering, peduncle length, panicle length, flag leaf blade length, flag leaf blade width, flag leaf sheath length and days to maturity. Similar inter-correlation results were reported by Vetriventhan *et al.* (2019). A correlogram (Fig. 1) was constructed for depicting the association of various biometrical traits studied. The associations among the traits - days to 50% flowering, peduncle length, panicle length, flag leaf blade length and flag leaf sheath length were significant and positively correlated with each other both in genotypic and phenotypic correlations. From the above results, it is evident that the selection of plant height from the above-mentioned traits will simultaneously lead to an increase in other traits due to significant inter-correlations. Therefore, the characters *i.e.,* plant height, flag leaf sheath length and thousand-grain weight were given prior importance for primary selection.

Path co-efficient analysis. Path analysis enables the partition of correlation coefficients into direct and indirect effects and thus helps in determining the actual contribution of the yield attributing component. The path coefficients along with correlation coefficients are essential to study the association among variables. The direct and indirect effects of phenotypic path analysis for the 13 biometrical traits are shown in Table 5. The character panicle length had a high negative direct effect (-0.43) and positive indirect effects of high, moderate and low via flag leaf sheath, plant height and thousand-grain weight respectively. The character flag leaf blade width has a moderate positive direct effect (0.256) and a moderate positive indirect effect via flag leaf sheath length and low positive indirect effects via plant height and thousand-weight. The traits flag leaf sheath length (0.52) had the highest positive direct effect followed by a high direct effect of thousand-grain weight (0.47) and a moderate direct effect of plant height (0.27). As these characters possess a high positive direct effect, implies that yield enhancement can be achieved by direct selection of these traits.

The direct and indirect effects of genotypic path analysis for the 13 biometrical traits are shown in Table 6. Panicle length has the highest negative direct effect (-0.78) followed by flag leaf blade length (-0.458) and days to 50% flowering (-0.333). The traits thousand-grain weight (0.655) had the highest positive direct effect followed by a high direct effect of flag leaf sheath length (0.631), a high direct effect of plant height (0.623), and a moderate direct effect of days to maturity (0.463). Salini *et al.* (2010) also witnessed a high positive direct effect of plant height with grain yield per plant. The characters mentioned above possess a high positive direct effect and positive correlation with single plant yield, inferring that yield improvement can be accomplished by direct selection of these characters.

Table 1: ANOVA for 13 biometrical traits in Proso millet.

Source of Variation	df	PH	NBT	DTFF	PEDL	PANL	FLBL	FLBW	FLSL	DTM	GL	GW	TGW	SPY
RMSS	2	10.23	0.0052	1.8167	0.433	2.034	0.2634	0.00075	0.0384	0.95	0.00511	0.00025	0.00201	0.0103
TMSS	19	482.61**	17.3391**	7.4737**	47.4734**	38.177**	28.3451**	0.72881**	3.6825**	9.9114**	0.04527**	0.01841**	1.95693**	5.9551**
EMSS	38	6.74	0.0478	0.5711	0.937	1.442	1.4698	0.00251	0.0793	0.9325	0.00479	0.00248	0.06048	0.0475

Table 2: Estimates of mean and variability parameters for 13 biometrical characters in Proso millet.

Character	Minimum	Maximum	Grand mean	V_g	V_p	GCV%	PCV%	h^2_b%	GAM
PH	51.74	104.64	68.2023	158.6234	165.3598	18.4665	18.8545	95.93	37.2581
NBT	3.2	11.2	6.8517	5.7638	5.8116	35.0395	35.1845	99.18	71.8832
DTFF	34	41	37.6667	2.3009	2.872	4.0271	4.4992	80.11	7.4254
PEDL	6.25	22.14	14.191	14.5144	15.4513	26.8464	27.6993	93.94	53.6009
PANL	16.21	31.25	20.9733	12.2449	13.6874	16.6844	17.6398	89.46	32.5084
FLBL	17.12	31.52	22.7903	8.9584	10.4282	13.133	14.1695	85.91	25.0751
FLBW	0.86	2.79	1.3958	0.2421	0.2446	35.2504	35.4319	98.98	72.2436
FLSL	5.02	9.27	6.571	1.2011	1.2804	16.6785	17.2203	93.81	33.2765
DTM	64	73	69.15	2.993	3.9255	2.5018	2.8652	76.25	4.5002
GL	2.624	3.191	2.8855	0.0135	0.0183	4.0266	4.6881	73.77	7.1252
GW	1.85	2.301	2.0588	0.0053	0.0078	3.536	4.2897	67.95	6.0034
TGW	4.024	8.062	5.2953	0.6322	0.6927	15.0153	15.7173	91.27	29.5505
SPY	6.247	12.564	8.5233	1.9692	2.0167	16.464	16.6614	97.64	33.5139

Table 3: Phenotypic correlation between 13 biometrical traits of Proso millet.

	PH	NBT	DTFF	PEDL	PANL	FLBL	FLBW	FLSL	DTM	GL	GW	TGW	SPY
PH	1												
NBT	-0.4091 **	1											
DTFF	0.5923 **	-0.2012 NS	1										
PEDL	0.7567 **	-0.5904 **	0.5063 **	1									
PANL	0.8275 **	-0.4597 **	0.5175 **	0.676 **	1								
FLBL	0.6023 **	-0.5253 **	0.4392 **	0.6646 **	0.652 **	1							
FLBW	0.5746 **	-0.5946 **	0.284 *	0.5654 **	0.6048 **	0.6447 **	1						
FLSL	0.7735 **	-0.2893 *	0.5119 **	0.4996 **	0.6959 **	0.5119 **	0.4792 **	1					
DTM	0.5745 **	-0.2545 *	0.8501 **	0.5842 **	0.4158 **	0.4819 **	0.2059 NS	0.4062 **	1				
GL	-0.3522 **	-0.1052 NS	-0.4279 **	-0.2548 *	-0.2819 *	-0.182 NS	0.0652 NS	-0.2149 NS	-0.3745 **	1			
GW	-0.066 NS	-0.0874 NS	0.089 NS	-0.0584 NS	0.0033 NS	0.3478 **	0.3873 **	-0.0303 NS	0.0061 NS	-0.0967 NS	1		
TGW	0.2182 NS	0.1104 NS	0.0818 NS	0.0621 NS	0.3297 *	0.0718 NS	0.2367 NS	0.276 *	0.0557 NS	-0.0929 NS	-0.0965 NS	1	
SPY	0.4517 **	-0.1275 NS	0.1915 NS	0.2302 NS	0.3406 **	0.1441 NS	0.3754 **	0.5898 **	0.1725 NS	0.036 NS	-0.1733 NS	0.5777 **	1

`*'Significant at $P \leq 0.05$; `**'Significant at $P \leq 0.01$; `NS' Non-Significant

PH- Plant height; NBT-Number of basal Tillers; DTFF- Days to fifty % flowering; PEDL- Peduncle length: PANL- Panicle length: FLBL-Flag leaf blade length; FLBW- Flag leaf blade width; FLSL- Flag leaf sheath length; DTM- Days to Maturity; GL- Grain length; GW- Grain width; TGW- Thousand-grain weight; SPY-Single plant yield

Table 4: Genotypic correlation between 13 biometrical traits of Proso millet.

	PH	NBT	DTFF	PEDL	PANL	FLBL	FLBW	FLSL	DTM	GL	GW	TGW	SPY
PH	1												
NBT	-0.4194 NS	1											
DTFF	0.6798 **	-0.24 NS	1										
PEDL	0.7789 **	-0.6146 **	0.5763 **	1									
PANL	0.8933 **	-0.482 *	0.6172 **	0.7302 **	1								
FLBL	0.6535 **	-0.5607 *	0.603 **	0.7114 **	0.6902 **	1							
FLBW	0.5871 **	-0.6023 **	0.2971 NS	0.5898 **	0.6453 **	0.7068 **	1						
FLSL	0.8152 **	-0.2904 NS	0.5795 **	0.5312 *	0.7513 **	0.5698 **	0.4942 *	1					
DTM	0.65 **	-0.3018 NS	0.947 **	0.6756 **	0.4889 *	0.6261 **	0.2359 NS	0.4672 *	1				
GL	-0.381 NS	-0.1079 NS	-0.5689 **	-0.2722 NS	-0.3574 NS	-0.2582 NS	0.0779 NS	-0.2849 NS	-0.4825 *	1			
GW	-0.1179 NS	-0.1013 NS	0.12 NS	-0.0904 NS	0.0167 NS	0.4191 NS	0.474 *	-0.0264 NS	-0.0734 NS	-0.081 NS	1		
TGW	0.2262 NS	0.1093 NS	0.101 NS	0.0432 NS	0.3828 NS	0.0779 NS	0.2605 NS	0.3196 NS	0.0268 NS	-0.1296 NS	-0.0966 NS	1	
SPY	0.4672 *	-0.1292 NS	0.2275 NS	0.2451 NS	0.3507 NS	0.1505 NS	0.3798 NS	0.6118 **	0.2159 NS	0.043 NS	-0.2277 NS	0.6213 **	1

`*'Significant at P ≤ 0.05; `'Significant at P ≤ 0.01; `NS' Non-Significant**

PH- Plant height; NBT-Number of basal Tillers; DTFF- Days to fifty % flowering; PEDL- Peduncle length: PANL- Panicle length: FLBL-Flag leaf blade length; FLBW- Flag leaf blade width; FLSL- Flag leaf sheath length; DTM- Days to Maturity; GL- Grain length; GW- Grain width; TGW- Thousand-grain weight; SPY-Single plant yield

Table 5: Phenotypic path analysis between 13 biometrical traits of Proso millet.

	PH	NBT	DTFF	PEDL	PANL	FLBL	FLBW	FLSL	DTM	GL	GW	TGW	SPY
PH	**0.27351**	0.03078	-0.03459	-0.05804	-0.35614	-0.08377	0.14711	0.40682	0.0453	-0.03225	0.01012	0.10285	0.4517 **
NBT	-0.11189	**-0.07525**	0.01175	0.04528	0.19784	0.07308	-0.15228	-0.1521	-0.02007	-0.00956	0.01367	0.05213	-0.1275 NS
DTFF	0.162	0.01514	**-0.05839**	-0.03884	-0.22276	-0.0611	0.07272	0.26907	0.06702	-0.03918	-0.01332	0.03875	0.1915 NS
PEDL	0.20696	0.04441	-0.02956	**-0.07671**	-0.29093	-0.09244	0.14475	0.26287	0.04606	-0.02327	0.00883	0.02922	0.2302 NS
PANL	0.22633	0.03459	-0.03022	-0.05185	**-0.43038**	-0.09068	0.15492	0.36595	0.03278	-0.02582	-0.00048	0.15536	0.3406 **
FLBL	0.16473	0.03953	-0.02565	-0.05098	-0.28061	**-0.13909**	0.16513	0.26918	0.038	-0.01678	-0.05321	0.03384	0.1441 NS
FLBW	0.15713	0.04475	-0.01658	-0.04336	-0.26038	-0.0897	**0.25647**	0.25188	0.01625	0.00548	-0.05967	0.11223	0.3754 **
FLSL	0.21156	0.02176	-0.02987	-0.03834	-0.29946	-0.07118	0.12263	**0.52579**	0.03204	-0.01976	0.0046	0.13015	0.5898 **
DTM	0.15713	0.01916	-0.04963	-0.04481	-0.17895	-0.06703	0.05277	0.21369	**0.07884**	-0.0342	-0.00087	0.0263	0.1725 NS
GL	-0.09622	0.00785	0.02496	0.01948	0.12124	0.02547	0.01531	-0.11339	-0.02942	**0.09016**	0.01283	-0.04186	0.036 NS
GW	-0.01805	0.00671	-0.00507	0.00442	-0.00133	-0.04828	0.09966	-0.01578	0.00045	-0.00767	**-0.13758**	-0.04487	-0.1733 NS
TGW	0.05968	-0.00832	-0.0048	-0.00476	-0.14185	-0.00999	0.06097	0.14521	0.0044	-0.00814	0.01459	**0.4709**	0.5777 **

`*'Significant at P ≤ 0.05; `**'Significant at P ≤ 0.01; `NS' Non-Significant

Residual effect: 0.3411

PH- Plant height; NBT-Number of basal Tillers; DTFF- Days to fifty % flowering; PEDL- Peduncle length: PANL- Panicle length: FLBL-Flag leaf blade length; FLBW- Flag leaf blade width; FLSL- Flag leaf sheath length; DTM- Days to Maturity; GL- Grain length; GW- Grain width; TGW- Thousand-grain weight; SPY-Single plant yield

Table 6: Genotypic path analysis between 13 biometrical traits of Proso millet

	PH	NBT	DTFF	PEDL	PANL	FLBL	FLBW	FLSL	DTM	GL	GW	TGW	SPY
PH	**0.62305**	0.08383	-0.22665	0.02195	-0.69701	-0.29956	0.0777	0.51503	0.30142	-0.06452	-0.01632	0.14827	0.4672 *
NBT	-0.26132	**-0.19987**	0.08002	-0.01732	0.37604	0.25702	-0.07972	-0.18345	-0.13997	-0.01828	-0.01402	0.07167	-0.1292 NS
DTFF	0.42357	0.04797	**-0.33339**	0.01624	-0.48158	-0.27641	0.03933	0.36613	0.43917	-0.09635	0.01661	0.06624	0.2275 NS
PEDL	0.48532	0.12284	-0.19213	**0.02818**	-0.5697	-0.32611	0.07806	0.33562	0.31329	-0.04611	-0.01251	0.02834	0.2451 NS
PANL	0.55658	0.09633	-0.20578	0.02058	**-0.78024**	-0.31642	0.08541	0.47469	0.22675	-0.06053	0.00231	0.25101	0.3507 NS
FLBL	0.40714	0.11206	-0.20103	0.02005	-0.53856	**-0.45842**	0.09355	0.36001	0.29035	-0.04372	0.05799	0.05109	0.1505 NS
FLBW	0.36577	0.12037	-0.09905	0.01662	-0.50348	-0.32401	**0.13236**	0.31222	0.1094	0.01319	0.06557	0.17081	0.3798 NS
FLSL	0.50788	0.05803	-0.19319	0.01497	-0.5862	-0.26121	0.06541	**0.63182**	0.21665	-0.04825	-0.00366	0.20952	0.6118 **
DTM	0.40495	0.06032	-0.31572	0.01904	-0.38149	-0.28701	0.03122	0.29516	**0.46376**	-0.08172	-0.01016	0.01759	0.2159 NS
GL	-0.23737	0.02158	0.18969	-0.00767	0.27888	0.11836	0.01031	-0.18003	-0.2238	**0.16934**	-0.01128	-0.08498	0.043 NS
GW	-0.07348	0.02024	-0.04002	-0.00255	-0.01301	-0.19211	0.06272	-0.01669	-0.03406	-0.01381	**0.13837**	-0.06337	-0.2277 NS
TGW	0.1409	-0.02185	-0.03368	0.00122	-0.29872	-0.03572	0.03448	0.20191	0.01244	-0.02195	-0.01338	**0.65563**	0.6213 **

`*'Significant at $P \leq 0.05$; `**'Significant at $P \leq 0.01$; `NS' Non-Significant

Residual effect: 0.1746

PH- Plant height; NBT-Number of basal Tillers; DTFF- Days to fifty % flowering; PEDL- Peduncle length: PANL- Panicle length: FLBL-Flag leaf blade length; FLBW- Flag leaf blade width; FLSL- Flag leaf sheath length; DTM- Days to Maturity; GL- Grain length; GW- Grain width; TGW- Thousand-grain weight; SPY-Single plant yield

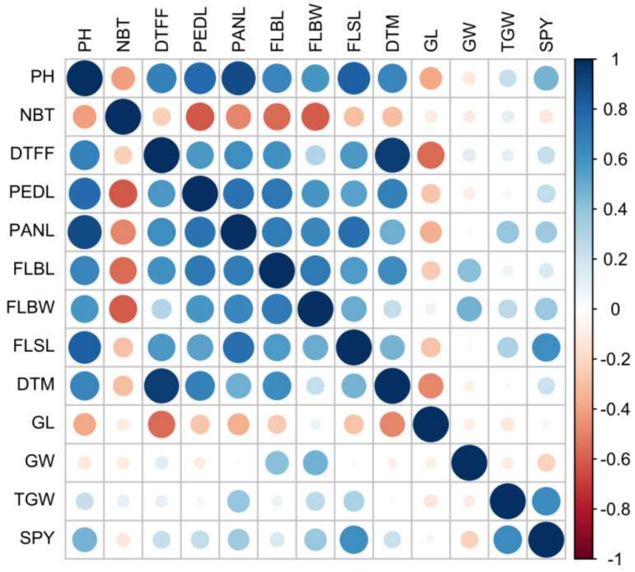

Fig. 1. Correlogram - association between 13 biometrical traits.

CONCLUSION

The germplasm taken for study showed a wide range of variation for the characters number of basal tillers, peduncle length and flag leaf sheath length had high variability. Moderate variability was recorded for the traits of plant height, panicle length, flag leaf blade length, flag leaf blade width, thousand-grain weight and single plant yield. Plant height, number of basal tillers, peduncle length, panicle length, flag leaf blade length, flag leaf blade width, flag leaf sheath length, thousand-grain weight and single plant yield exhibited high genetic advance as per cent of mean indicating the additive nature of gene action. The association studies revealed that the primary selection of the characters- plant height, flag leaf sheath length and thousand-grain weight may be given paramount importance for the direct selection for the enhancement of yields.

Effective utilisation of the trait-specific genetic resources will play a vital role in crop improvement. For the upcoming scenarios of global warming and scanty rainfall to ensure nutritional and food security, the cultivation and consumption of Proso millet, which is a source of micronutrients and protein along with yield will contribute to crop and diet diversification and thus helps in mitigating the future thrust.

Acknowledgment. The current research work was supported by the Department of Plant Breeding and Genetics, Agricultural College and Research Institute-Madurai, Tamil Nadu Agricultural University, Tamil Nadu, India.

Conflict of interest. None.

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How to cite this article: G. Anil Kumar, C. Vanniarajan, M. Vetriventhan, R. Sudhagar and S. Saravanan (2022). Association and variability Studies of Quantitative Traits in Proso Millet (*Panicum miliaceum* L.). *Biological Forum – An International Journal*, *14*(3): 208-214.