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Research Article

Genetic variability, trait association and diversity study in proso millet (*Panicum miliaceum* L.)

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Abstract

Proso millet, being the climate-resilient crop among cereals can be grown for food and fodder purposes. The current study was carried out to assess the variability, association, and divergence for 15 biometrical traits among 72 Proso millet accessions. The traits *viz*., number of basal tillers, flag leaf blade width, peduncle length, number of grains per panicle, dry fodder yield and single plant yield contributed maximum for the variability among the genotypes. High heritability with high genetic advance were recorded for the traits namely plant height, number of basal tillers, flag leaf blade length, flag leaf blade width, peduncle length, panicle length, number of grains per panicle, number of primary inflorescence branches, crude protein, dry fodder yield and single plant yield. Therefore selection based on these traits will be rewarding in future proso millet breeding programs. The traits such as plant height, number of basal tillers, flag leaf blade width, peduncle length, number of grains per panicle, and number of primary inflorescence branches were positively and significantly correlated with single plant yield, indicating the importance of these traits while improving the yield. High positive direct effect in path coefficient analysis for the traits plant height, flag leaf sheath length, panicle length, peduncle length, and thousand-grain weight indicated that yield improvement can be accomplished by direct selection based on these characters. Divergence by using Mehalanobis D^2 analysis resulted in ten clusters. High inter cluster distance was observed between the clusters VII and X, VI and X, VI and X, and XII and I. Therefore, hybridization between the genotypes among the respective pair of clusters would be desirable to have high heterotic crosses.

Keywords: Proso millet, germplasm, variability, association, divergence

INTRODUCTION

Millets are designated as "Nutri-cereals" since they are rich in macro and micronutrients, minerals protein, and dietary fiber and play a significant role in nutritional requirement of the humans. This, in turn, reduces the risk of inflammatory bowel disease and acts as a natural cleansing agent for the body. The protein content in millets ranges from 7% to 12%, lipid content from 2% to 5%, carbohydrate content from 60% to 70%, and dietary fiber content from 15% to 20%. Furthermore, millets contain approximately 2% to 4% of minerals (Annor *et al.,* 2017). Proso millet (*Panicum miliaceum* L.) an allotetraploid with a chromosome number of 36 (2n = 4x = 36) is one of the hardy millet crops belonging to the family Poaceae. It is also known as common millet, broom millet, broomcorn millet, white millet, Russian millet, ersey millet and hog millet. It is vernacularly called '*Panivaragu*' in Tami and Chenna or Barri in Hindi (Lu *et al.,* 2009). It is comparable to wheat in terms of protein (12.5 %) and essential amino acids (leucine, isoleucine, methionine) content. The proso grain contained about 3.3 g kg^{-1} of the amino acid-lysine (Nithiyanandham *et al.*, 2019).

Coeliac disease is one of the most common intestinal diseases in humans (Das *et al.,* 2019). For such patients, proso millet is a suitable food since it contains the specific prolamin fraction is under the permitted level. Though this crop has great potential as a good contingency crop and also a crop of nutritional importance, the availability of information on variability in germplasm for important traits such as yield and quality enables the effective utilization of genetic resources in crop improvement programs is very limited (Vetriventhan *et al*., 2019). Hence a study was carried out to estimate the genetic variability, nature and degree of association among the yield contributing traits and the extent of genetic diversity among germplasm accessions in prosomillet.

MATERIALS AND METHODS

The experimental material used for the study comprised of 70 germplasm lines raised along with the checks ATL-1 and CO (Pv) 5. The germplasm were sourced from the Gene banks of ICRISAT, Hyderabad, Dr. Ramaiah gene bank, Tamil Nadu Agricultural University, Coimbatore and Centre of Excellence for Millets, Athiyandal. This study was carried out during *Rabi*, 2022-23 at the Centre of Excellence in Millets, Tamil Nadu Agricultural University, Athiyandal, Tiruvannamalai. The genotypes were raised in Randomised Block Design (RBD) with two replications. Each accession was sown in rows of 3m length rows with a spacing of 30cm between rows and 10cm between plants. Recommended agronomic packages were followed for maintenance of good plant stand.

The observations were recorded on five randomly selected plants from each replication for various biometrical traits namely plant height (PH), number of basal tillers (NBT), flag leaf blade length (FLBL), flag leaf blade width (FLBW), peduncle length (PED L), panicle length (PL), number of grains per panicle (NGP), number of primary inflorescence branches (NPIB), thousand-grain weight (TGW), crude protein (CP), dry fodder yield (DFY) and single plant yield (SPY), while observations on days to first flowering (D 1^{ST} F), days to fifty percent flowering (DFF), days to maturity (DM) were recorded on a plot basis.

The magnitude of variation available in the germplasm accessions was estimated by the coefficient of variation. The genotypic and phenotypic coefficients of variation (GCV & PCV) were calculated using the method derived by Burton (1952). The variability was classified into three classes *i.e.*, low (20%) as proposed by Sivasubramanian and Madhavamenon (1973). Broad sense heritability (h^2b) was computed as per the method suggested by Lush (1940) and was classified as high (> 60%), moderate (30-60%), and low (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 genetic divergence study D^2 statistics was developed by Mahalanobis, (1928) and used in plant breeding by Rao (1952). The statistical analyses were carried out using R software .

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). In the present study, days to first flowering ranged from 30 to 39 days, whereas, days to 50% flowering ranged from 32 to 41 days. The days to maturity among the genotypes ranged from 61 to 73 days. The plant height ranged from 58.5 cm to 143.15 cm with a mean of 88.92 cm. The number of basal tillers varied from 2 to 7 with a mean of 3.7 tillers. The flag leaf blade length varied from 15.1 cm to 30.75 cm with a mean value of 21.36 cm and the flag leaf blade width from 0.45 cm to 1.7 cm with a mean value of 0.89 cm. Peduncle length ranged from 5.75 cm to 18.7 cm with an average of 9.3 cm and the panicle length from 18.3 cm to 35.95 cm with an average of 23.47 cm. The number of grains per panicle varied from 92.67 to 286.72 with a mean 187.23 grains per panicle. The number of primary inflorescence branches ranged from 4.45 to 8.2 with a mean of 5.92. The thousand-grain weight ranged from 3.3 g to 6.75 g with a mean of 5.33 g. The crude protein ranged from 6.95% to 13.2% with a mean of 10.07%. The dry fodder yield varied from 9.05 gram to 35.05 gram with an average of 21.2 gram. Single plant yield ranged from 5.6 g to 21.2 g with a mean of 9.89 g. This suggested existence of wide variability among the prosomillet accessions under study for the traits under study.

Analysis of variance and Variability measures: The analysis of variance (ANOVA) revealed that the mean sum of squares for all the 15 biometrical traits tested was found to be significant (**Table 1**) which also specifies the prevalence of considerable variation among the 72 proso millet genotypes, thus presenting sufficient scope for selection among the germplasm accessions involved in this study.

Phenotypic and Genotypic coefficient of variation: The variability measures such as Vg, Vp, PCV, GCV, h^2b and GAM for different traits are presented in **Table 2**. The PCV values were greater than that of the GCV values for all the traits studied indicating that the apparent variation was due to environment influence. However, the differences in PCV and GCV are very narrow, which is an indication of the least influence of the

Table 1. ANOVA for 15 biometrical traits in prosomillet

	df	D 1st F	DFF	DM	PH	NBT	FLBL	FLBW	PED L	PL	NGP	N PIB	TGW	CP	DFY	SPY
Replication	**1**	2.507	0.03	0.69	3.80	4.08	0.30	0.31	0.02	2.75	1.58	0.01	1.56	0.0001	0.61	0.25
Treatment	**71**	7.65 **	7.16 **	8.52 **	594.79 **	11.87 **	23.89 **	17.31 **	10.35 **	19.99 **	4573.06 **	5.6903 **	7.91 **	4.1473 **	67.28 **	21.47 **
Error	**71**	0.70	0.79	3.58	6.27	7.41	1.64	4.37	0.15	1.22	75.43	1.43	0.76	0.08	3.68	1.35

*Significance at 5% level, ** Significance at 1% level

D 1st F - Days to first flowering, DFF - Days to fifty percent flowering, DM - Days to maturity , PH - Plant height, NBT - Number of basal tillers, FLBL - Flag leaf blade length, FLBW - Flag leaf blade width, PED L - Peduncle length, PL - Panicle length, NGP - Number of grains per panicle, N PIB - Number of primary inflorescence branches, TGW - Thousand grain weight, CP - Crude protein, DFY - Dry fodder yield, SPY - Single plant yield.

Table 2. Estimates of variability parameters and mean for 15 biometrical traits in prosomillet

Character	Grand Mean	Minimum	Maximum	PCV(%)	GCV(%)	h^2bs(%)	GAM(%)	PV	GV
D 1st F	34.8	30	39	5.87	5.35	83.15	10.06	4.18	3.48
DFF	36.8	32	41.5	5.42	4.85	80.17	8.95	3.98	3.19
DM	66.8	61.5	72.5	3.68	2.35	40.85	3.1	6.06	2.47
PH	88.92	58.5	143.15	19.5	19.29	97.91	39.33	300.53	294.26
NBT	3.7	2.2	6.6	29.09	25.35	75.98	45.53	1.16	0.88
FLBL	21.36	15.1	30.75	16.39	15.96	94.81	32.02	12.27	11.63
FLBW	0.89	0.45	1.7	35.97	29.65	67.93	50.34	0.10	0.07
PED L	9.3	5.75	18.7	24.64	24.28	97.1	49.28	5.25	5.10
PL	23.47	18.3	35.95	13.87	13.05	88.48	25.29	10.61	9.39
NGP	187.23	92.67	286.72	22.06	21.69	96.75	43.96	24.25	22.81
N PIB	5.92	4.45	8.2	15.94	15.12	89.96	29.54	0.89	0.80
TGW	5.33	3.3	6.75	10.7	10.26	91.91	18.26	0.33	0.30
CP	10.07	6.95	13.2	14.43	14.16	96.25	28.62	2.11	2.03
DFY	21.2	9.05	35.05	28.1	26.61	89.62	51.88	35.48	31.80
SPY	9.89	5.6	21.2	34.16	32.08	88.21	62.07	11.41	10.06

D 1st F - Days to first flowering, DFF - Days to fifty percent flowering, DM - Days to maturity , PH - Plant height, NBT - Number of basal tillers, FLBL - Flag leaf blade length, FLBW - Flag leaf blade width, PED L - Peduncle length, PL - Panicle length, NGP - Number of grains per panicle, N PIB - Number of primary inflorescence branches, TGW - Thousand grain weight, CP - Crude protein, DFY - Dry fodder yield, SPY - Single plant yield.

environment on the expression of the traits. Therefore, the variability observed for most of the traits in this study is due to the influence of both the genetic constitution of the genotypes as well as the influence of the environment and hence selection based on the traits could yield desirable results. Days to first flowering (5.87, 5.35), days to fifty percent flowering (5.42, 4.85) and days to maturity (3.68, 2.35) expressed low PCV and GCV indicating the presence of low variability among accessions. Similar results were reported by Anilkumar *et al.*, (2022) for days to 50% flowering and days to maturity and Salini *et al.,* (2010), Verulkar *et al.*, (2014), Anuradha *et al.*, (2020) and Anilkumar *et al.*, (2022) for days to maturity. The traits number of basal tillers (29.09, 25.35), flag leaf blade width (35.97, 29.65), peduncle length (24.64, 24.28), number of grains per panicle (22.06, 21.69), dry fodder yield (28.10, 26.61) and single plant yield (34.16, 32.08) recorded high PCV and GCV indicating high variability for these traits. These findings are in alignment with the previous reports by Salini *et al.* (2010) and Verulkar *et al.* (2014) for the trait number of basal tillers. Similar findings of high PCV and GCV was also reported by Anilkumar *et al.*, (2022) for the traits peduncle length and number of basal tillers. Plant height (19.50, 19.29), flag leaf blade length (16.39, 15.96), panicle length (13.87, 13.05), number of primary inflorescence branches (15.94, 15.12), thousand grain weight (10.70, 10.26) and crude protein (14.43, 14.16) recorded moderate PCV and GCV indicating the presence of moderate variability for these traits. Salini *et al.* (2010) and Verulkar *et al.* (2014) also reported moderate PCV and GCV for the traits plant height and panicle length. Whereas, independent reports by Anuradha *et al.* (2020) and Anilkumar *et al.* (2022) suggested moderate PCV and GCV for panicle length and for all the above mentioned traits respectively. In the present study, the traits number of basal tillers, flag leaf blade width, peduncle length, number of grains per panicle, dry fodder yield and single plant yield recorded high PCV and GCV indicating the lesser influence of environment on the expression of these traits and selection based on these traits would be rewarding

Heritability and genetic advance: **I**n this study, plant height (97.91, 39.30), number of basal tillers (75.98, 49.53), flag leaf blade length (94.81, 32.02), flag leaf blade width (67.93, 50.34), peduncle length (97.10, 49.28), panicle length (88.48, 25.29), number of grains per panicle (96.75, 43.96), number of primary inflorescence branches (89.96, 29.54), crude protein (96.25, 28.62) dry fodder yield (89.62, 51.88) and single plant yield (88.21, 62.07) recorded the high heritability and high GAM. Calami *et al.*, (2020), Anuradha *et al.*, (2020) reported similar findings as that of the results obtained in this study. Salini *et al.*, (2010) and Anilkumar *et al.*, (2022) also reported high heritability for all the traits reported in this study. The traits days to maturity (3.10 %) and single plant yield (62.07%) recorded low and high genetic advance as percent of mean respectively. In this study majority of the traits except days to 50 % flowering and days to maturity showed high heritability and a substantial genetic advance as percent of mean, indicating a probability of additive gene action influence in their inheritance. This suggest that early selection based on these traits could be beneficial for their improvement. These results are in conformity with the findings of Salini *et al.* (2010), Verulkar *et al.* (2014), Anuradha *et al.* (2020) and Anilkumar *et al.* (2022) for the traits such as plant height, panicle length, single plant yield, thousand-grain weight, and the number of basal tillers.. The traits days to 50% flowering and days to maturity exhibited high heritability and low GAM and revealed the possibility of non-additive gene action in the expression of these two traits. Verulkar *et al.* (2014) and Anilkumar *et al.* (2022) also reported similar results for these two traits. Based on heritability and genetic advance estimates in the current study, priority may be given for the traits, number of basal tillers, flag leaf blade width, peduncle length, number of grains per panicle, dry fodder yield and single plant yield for effective selection.

Association studies: Genotypic correlation:Association of single plant yield with 15 different yield attributing traits was studied. It revealed that the traits *viz.,*plant height (0.3278), number of basal tillers (0.7829), flag leaf blade width (0.4469), peduncle length (0.4544), number of grains per panicle (0.773) and number of primary inflorescence branches (0.369) exhibited highly positive significant correlation with single plant yield. Significant direct correlation was recorded for flag leaf blade length (0.2695), panicle length (0.2138), crude protein (0.2541) and dry fodder yield (0,270). Thus, direct selection based on these traits would result in increased yield (**Table 3**).

Thousand grain weight (0.0455) exhibitted positive non-significant correlation with single plant yield. Negative correlation with single plant yield was recorded by the traits, days to first flowering (-0.138), days to 50% flowering (-0.1196) and days to maturity (0.2215). This was in accordance with the findings of Salini *et al.* (2010), Calami *et al.* (2020) for these traits. In the findings of Anilkumar *et al.*, (2022) the traits plant height, and panicle length, flag leaf blade width, panicle length, thousand grain weight were identified to be exhibiting significant correlation to single plant yield. The findings of Anilkumar *et al.*, (2022) revealed significant correlation among the traits plant height, flag leaf blade width, panicle length and peduncle length. Thus, it can be inferred that selection based on the traits, plant height, number of basal tillers, flag leaf blade width, peduncle length, number of grains per panicle, and number of primary inflorescence branches could be effective in improving plant yield as they expressed significant and positive association with single plant yield.

Path co-efficient analysis: Path analysis is a statistical technique that breaks down the correlation coefficient into separate estimates for the direct and indirect impacts of independent variables on the dependent variable. In the present study, the direct and indirect influence of the 14 yield contributing traits over the dependent variable is single plant yield was analyzed and the results are furnished in **Table 4.**

Days to 50% flowering (-0.4635) showed highly negative direct effect on yield followed by thousand grain weight (-0.1294), flag leaf blade width (-0.0984), flag leaf blade length (-0.0776) and plant height (-0.0715). whereas, number of grains per panicle (0.6078) and number of basal tillers (0.3491) exhibited high positive direct effect on yield. The trait, days to first flowering (0.2631) had the moderate to low direct effect on dry fodder yield (0.1453), days to maturity (0.187) and peduncle length (0.147). It could be concluded that direct selection based on number of basal tillers and number of grains per panicle will result in the elimination of undesirable effects of the component traits on grain yield The results are in alignment with the findings of Anilkumar *et al.* (2022), Sasamala *et al.* (2011) and Salini *et al.* (2010) regarding association of plant height and thousand-grain weight with grain yield in proso millet. Similar findings were reported by previous workers in different minor millets [Amarnath *et al.* (2018) - fox tail millet; Sreeja *et al.*, (2015) - kodo millet; Amaravel *et al.*, (2023) - little millet]. Based on the results of path analysis, it could be concluded that grain yield in proso millet can be improved through indirect selection based on the traits such as plant height, flag leaf sheath length, panicle length, peduncle length, and thousand-grain weight.

Table 3. Genotypic correlation between 15 biometrical traits in proso millet

Characters	D 1st F	DFF	DM	PH	NBT	FLBL	FLBW	PED L	PL	NGP	N PIB	TGW	CP	DFY	SPY
D 1st F	1	1.057**	1.278**	-0.0458	-0.0846	-0.1469	0.0277	-0.1805	-0.132	-0.1468	-0.1244	0.0001	-0.2165	0.0352	-0.138
DFF		1	1.198**	-0.0423	-0.1429	-0.1827	-0.009	-0.1974	-0.1397	-0.1287	-0.1261	0.0088	-0.236	0.0611	-0.1196
DM			1	-0.0014	-0.0848	-0.154	0.0196	-0.2416	-0.2302	-0.2361	-0.0992	-0.032	-0.21	0.2083	-0.2215
PH				1	0.315**	0.6556**	0.5497**	0.4241**	0.6718**	0.2973**	0.458**	0.0471	0.3235**	0.4875**	0.3278**
NBT					1	0.3308**	0.4241**	0.4668**	0.3797**	0.599**	0.3603**	0.1939	0.2252	0.2205	0.7829**
FLBL						1	0.6965**	0.5028**	0.6801**	0.2106	0.4683**	0.1126	0.2941**	0.4336**	0.2695*
FLBW							1	0.6336**	0.5877**	0.4203**	0.5117**	-0.1341	0.1304	0.2429*	0.4469**
PED L								1	0.365**	0.3108**	0.2951**	-0.1084	0.1681	0.184	0.4544**
PL									1	0.151	0.4601**	0.164	0.2155	0.286*	0.2138*
NGP										1	0.227	0.222	0.114	0.0691	0.773**
N PIB											1	-0.1003	0.2016	0.2626*	0.369**
TGW												1	0.1008	-0.0209	0.0455
CP													1	0.5257**	0.2541*
DFY														1	0.276*
SPY															1

**Significance at 5% level, ** Significance at 1% level*

Table 4. Genotypic path analysis for 15 biometrical traits in proso millet

Characters	D 1st F	DFF	DM	PH	NBT	FLBL	FLBW	PED L	PL	NGP	N PIB	TGW	CP	DFY	SPY
D 1st F	**0.2631**	-0.4874	0.239	0.0033	-0.0296	0.0114	-0.0027	-0.0266	-0.0047	-0.0892	-0.0117	0	-0.008	0.0051	-0.138
DFF	0.2768	**-0.4635**	0.2241	0.003	-0.0499	0.0142	0.0009	-0.0291	-0.005	-0.0782	-0.0118	-0.0011	-0.0087	0.0089	-0.1196
DM	0.3363	-0.5553	**0.187**	0.0001	-0.0296	0.0119	-0.0019	-0.0357	-0.0082	-0.1435	-0.0093	0.0041	-0.0078	0.0303	-0.2215
PH	-0.0121	0.0196	-0.0003	**-0.0715**	0.11	-0.0509	-0.0541	0.0626	0.024	0.1807	0.043	-0.0061	0.012	0.0709	0.3278**
NBT	-0.0223	0.0662	-0.0159	-0.0225	**0.3491**	-0.0257	-0.0417	0.0689	0.0136	0.3641	0.0338	-0.0251	0.0083	0.0321	0.7829**
FLBL	-0.0386	0.0847	-0.0288	-0.0469	0.1155	**-0.0776**	-0.0685	0.0742	0.0243	0.128	0.0439	-0.0146	0.0109	0.063	0.2695*
FLBW	0.0073	0.0041	0.0037	-0.0393	0.1481	-0.0541	**-0.0984**	0.0935	0.021	0.2555	0.048	0.0173	0.0048	0.0353	0.4469**
PED L	-0.0475	0.0915	-0.0452	-0.0303	0.163	-0.039	-0.0623	**0.1476**	0.013	0.1889	0.0277	0.014	0.0062	0.0267	0.4544**
PL	-0.0347	0.0647	-0.0431	-0.048	0.1325	-0.0528	-0.0578	0.0539	**0.0357**	0.0918	0.0432	-0.0212	0.008	0.0416	0.2138*
NGP	-0.0386	0.0596	-0.0442	-0.0212	0.2091	-0.0163	-0.0414	0.0459	0.0054	**0.6078**	0.0213	-0.0287	0.0042	0.01	0.773**
N PIB	-0.0327	0.0584	-0.0185	-0.0327	0.1258	-0.0363	-0.0503	0.0436	0.0164	0.138	**0.0938**	0.013	0.0075	0.0382	0.369**
TGW	0	-0.0041	-0.006	-0.0034	0.0677	-0.0087	0.0132	-0.016	0.0059	0.1349	-0.0094	**-0.1294**	0.0037	-0.003	0.0455
CP	-0.057	0.1094	-0.0393	-0.0231	0.0786	-0.0228	-0.0128	0.0248	0.0077	0.0693	0.0189	-0.013	**0.0371**	0.0764	0.2541*
DFY	0.0093	-0.0283	0.0389	-0.0348	0.077	-0.0336	-0.0239	0.0272	0.0102	0.042	0.0246	0.0027	0.0195	**0.1453**	0.276**

Residual effect: 0.4637, *'*' Significance at 5% level*, *'**' Significance at 1% level*

D 1st F - Days to first flowering, DFF - Days to fifty percent flowering, DM - Days to maturity , PH - Plant height, NBT - Number of basal tillers, FLBL - Flag leaf blade length, FLBW - Flag leaf blade width, PED L - Peduncle length, PL - Panicle length, NGP - Number of grains per panicle, N PIB - Number of primary inflorescence branches, TGW - Thousand grain weight, CP - Crude protein, DFY - Dry fodder yield, SPY - Single plant yield.

The residual effect of the path analysis for 15 quantitative traits is 0.4637. Hence, it can be inferred that the traits chosen for the study influenced about 63 percent of the variability in dependent traits .

Genetic divergence – quantitative traits: Genetic diversity of 72 germplasm accessions were worked out based on their quantitative characters by Tocher's value (**Table 5**). Divergence among genotypes within the clusters showed high variation in germplasm accessions which can be utilized in future breeding programs. Mehalonobis D^2 statistics analysis grouped the 72 genotypes into 12 clusters based on yield and its attributing traits. The highest number of germplasm accessions were grouped in cluster I, followed by Cluster II and Cluster IV. The accessions PRO-348, PRO-801, CO (Pv)-5, TNAU-145 found in clusters VIII, IX, XI and XII showed that these accessions were highly divergent from other accessions for various traits observed.

Highest and lowest intra cluster distances were recorded in Cluster XI, Cluster VIII respectively (**Table 6**). The inter cluster distances were higher than the intra cluster distance. The inter cluster D^2 values ranged from 382.68 (distance between cluster II & III) to 2690.36 (distance between cluster VII & X). The highest distance was recorded between the clusters VII to X (2690.36) followed by clusters VII to X (2535.28), clusters VII to XII (2521.10), cluster VI to XII (2059.27) and clusters I to XII (1805.77). Bharathi *et al.,* (2023) in finger millet; Nirmalakumari and Vetriventhan (2010) in foxtail millet also reported similar results.

Table 5. Clustering of 72 germplasm accessions

Clusters	Proso millet germplasm accessions
Cluster – I	PRO – 685, PRO – 688, PRO – 832, PRO – 691, PRO – 875, PRO – 692, PRO – 706, PRO – 881, PRO – 715, PRO – 885, PRO – 883, PRO – 735, PRO – 887, PRO – 737, PRO – 905, PRO – 738, PRO – 906, PRO – 907, PRO – 256, PRO – 755, PRO – 919, PRO – 989, PRO – 873, PRO – 1013, PRO – 874, PRO – 455, PRO – 571, PRO – 595, PRO – 652, GPUP – 8, PRO – 656, PRO – 660, PRO – 1091, PRO – 658, PRO – 671, PRO – 674, PRO – 676, PRO – 683, PRO – 205, PRO - 204
Cluster – II	PRO – 173, PRO – 174, PRO – 189, PRO – 734, PRO – 198, PRO – 199, PRO – 207, PRO – 1139, ATL – 1, PRO – 649, PRO – 944, PRO - 987
Cluster – III	PRO – 38, PRO – 190, PRO - 661
Cluster – IV	PRO – 356, PRO – 354, PRO - 1193
Cluster – V	TNAU – 164, TNAU – 202, PRO – 953, PRO - 14
Cluster – VI	PRO – 876, PRO - 751
Cluster – VII	PRO – 662, PRO - 675
Cluster – VIII	PRO - 348
Cluster – IX	PRO - 801
Cluster – X	PRO – 28, PRO - 331
Cluster – XI	CO (Pv) 5
Cluster - XII	TNAU - 145

Table 6. Average inter and intra cluster D^2 values of prosomillet

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**305.66**	584.19	796.63	537.45	571.49	449.72	602.15	605.12	727.21	1952.91	1051.57	1850.77
II		**266.08**	382.68	476.19	489.37	849.38	1202.81	435.17	588.61	923.29	436.44	792.49
III			**365.97**	468.69	702.76	972.57	1270.74	625.04	993.50	839.00	606.25	634.86
IV				**372.41**	462.84	451.37	754.92	518.49	1024.36	1532.02	682.80	1057.27
V					**372.41**	635.24	907.72	671.56	957.79	1734.23	711.97	1158.99
VI						**332.20**	472.44	662.34	1341.53	2535.28	1253.37	2059.27
VII							**399.04**	1271.13	1560.88	2690.36	1595.78	2521.10
VIII								**172.52**	737.07	1439.61	898.49	1343.57
IX									**0.00**	1299.52	774.31	1623.81
X										**0.00**	826.49	640.10
XI											**422.67**	591.92
XII												**0.00**

Table 7. Mean values of clusters over fifteen biometrical traits of proso millet

Clusters\ traits	D 1st F	DFF	DM	PH	NBT	FLBL	FLBW	PED L	PL	NGP	N PIB	TGW	CP	DFY	SPY
I	34.99	37.01	66.98	79.87	3.54	19.97	0.78	8.31	22.38	212.38	5.59	5.48	9.59	19.25	9.19
II	34.75	36.71	66.67	102.34	4.21	24.22	1.06	10.28	25.73	254.57	6.36	5.52	10.85	24.92	11.96
III	32.83	34.50	65.33	97.67	4.22	25.63	0.85	11.58	25.85	188.93	6.88	5.63	11.83	25.78	8.63
IV	35.00	37.00	66.83	93.72	3.22	20.30	0.80	9.68	22.85	177.80	6.72	4.78	11.52	20.10	7.93
V	35.25	37.25	68.00	113.13	3.19	22.50	1.01	7.86	24.40	207.34	6.16	4.76	9.78	24.64	7.65
VI	36.00	38.00	67.25	74.45	2.68	17.18	0.83	7.95	21.03	171.33	5.00	4.88	11.40	22.45	6.63
VII	36.50	38.00	67.50	67.33	2.60	19.65	0.85	11.05	22.08	127.40	4.93	3.75	7.55	17.13	6.80
VIII	30.00	33.00	62.50	82.15	3.55	20.75	0.85	8.50	21.55	282.20	5.50	4.60	12.60	24.90	16.95
IX	33.50	35.50	66.50	94.80	4.85	18.10	0.75	10.85	20.50	317.15	7.70	5.55	7.90	21.15	17.30
X	31.75	33.50	63.00	115.25	5.33	29.28	1.70	16.73	31.30	294.73	6.83	5.08	10.55	19.15	16.20
XI	39.00	41.50	71.00	118.40	6.60	21.95	1.55	13.25	28.80	247.50	7.40	5.40	10.75	28.95	15.80
XII	34.50	36.50	67.00	143.15	2.95	27.80	1.25	14.65	23.05	225.05	6.75	5.35	12.15	28.60	9.35

D 1st F - Days to first flowering, DFF - Days to fifty percent flowering, DM - Days to maturity , PH - Plant height, NBT - Number of basal tillers, FLBL - Flag leaf blade length, FLBW - Flag leaf blade width, PED L - Peduncle length, PL - Panicle length, NGP - Number of grains per panicle, N PIB - Number of primary inflorescence branches, TGW - Thousand grain weight, CP - Crude protein, DFY - Dry fodder yield, SPY - Single plant yield.

Table 8. Percent contribution of characters in genetic divergence of germplasm accessions

Source	D 1st F	DFF	DM	PH	NBT	FLBL	FLBW	PED L	PL	NGP	N PIB	TGW	CP	DFY	SPY
Number of times ranked first	12	0	0	564	2	154	1	316	29	408	161	155	663	78	13
per cent contribution	0.47	0.00	0.00	22.07	0.08	6.03	0.04	12.36	1.13	15.96	6.30	6.06	25.94	3.05	0.51

D 1st F - Days to first flowering, DFF - Days to fifty percent flowering, DM - Days to maturity , PH - Plant height, NBT - Number of basal tillers, FLBL - Flag leaf blade length, FLBW - Flag leaf blade width, PED L - Peduncle length, PL - Panicle length, NGP - Number of grains per panicle, N PIB - Number of primary inflorescence branches, TGW - Thousand grain weight, CP - Crude protein, DFY - Dry fodder yield, SPY - Single plant yield.

It is expected that, utilization of genotypes from these distant clusters for hybridization would result in desirable variation for traits in a segregating population and breaking of undesirable linkage and release of hidden variability.

Cluster X (PRO-28, PRO-331) showed high cluster mean for flag leaf blade width, peduncle length, panicle length, number of grains per panicle, number of primary inflorescence branches and single plant yield (**Table 7**). Cluster III (PRO–38, PRO–190, PRO-661) expressed high mean for thousand grain weight. In this study, crude protein was observed to play a major contribution in cluster diversity up to 25.94% followed by plant height, number of grains per panicle, peduncle length, and number of primary inflorescence branches, flag leaf blade length and thousand grain weight (Table. 8). Verulkar *et al.* (2014) in his study grouped 39 genotypes into nine clusters based on D^2 values and reported the inter cluster distance of 10.90 to 32.59 in total genetic divergence. The germplasm taken for the study showed a wide range of variation for the characters number of basal tillers, flag leaf blade width, peduncle length, number of grains per panicle, dry fodder yield and single plant yield. In this study majority of the traits excepting days to 50 % flowering and days to maturity showed high heritability and a substantial genetic advance as percent of mean, indicating a probability of additive gene action influence in their inheritance. This suggested that early selection based on these traits could be beneficial for their improvement. The association studies revealed that the primary selection of the characters plant height, number of basal tillers, flag leaf blade width, peduncle length, number of grains per panicle, and number primary inflorescence branches may be given paramount importance for the direct selection for yield enhancement in proso millet.

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