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Research Article

Genetic analysis and diversity studies in pearl millet (*Pennisetum glaucum* (L.) R. Br.)

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Abstract
Hundred pearl millet genotypes were evaluated to understand their diversity and association among the yield and yield attributing traits. The PCV was higher than the GCV for all the characters studied indicating the influence of environment in expression of characters. High heritability along with high genetic advance as per cent of mean was observed in single earhead weight, grain yield per earhead, 1000 seed weight, spike girth and days to 50 per cent flowering indicated that additive gene action for these characters. Single earhead weight, 1000 seed weight and days to 50 per cent flowering possessed high direct effect on grain yield. Hence, direct selection for these characters could be rewarding for the improvement of grain yield. The estimation of genetic divergence based on D^2 value revealed that the 100 pearl millet genotypes can be grouped into 11 clusters. The distribution of genotypes into various clusters indicating the high divergence among the studied genotypes. The cluster VII had 41 genotypes followed by 28 genotypes in cluster III, 14 genotypes in cluster I and three genotypes in cluster XI. The highest inter cluster distance (39.0) was recorded between cluster VIII and cluster X. The genotypes, PT 2616 and PT 2656 had high mean value for plant height, spike length, 1000 seed weight, single earhead weight and grain yield / earhead.

Key words
Pearl millet, variability, correlation, diversity analysis

Introduction

Pearl millet [*Pennisetum glaucum* (L) R.Br.] is a fast growing and a drought tolerant crop. Even in marginal land the pearl millet can be successfully cultivated at rainfed condition where other cereal crops cannot be grown. Pearl millet was domesticated in Africa (west of the Nile), nearly 3000 to 5000 years ago and subsequently spread to southern Asia (Harlen 1975; Brunken *et al*., 1977). Pearl millet is one of the eight major world cereals and fourth in importance after rice, wheat and sorghum in India with an area of 7.89 million ha having 9.18 million tons of production and productivity of 1164 kg/ha (Agricultural Statistics at a Glance, 2014). In Tamil Nadu, pearl millet was cultivated around 0.43 lakhs hectares with productivity of 1316 kg/hectare (Statistical Handbook of Tamil Nadu, 2014). The past four decades witnessed significant advances in the productivity of major food crops, particularly the cereal grains. This improvement was mainly achieved through breeding of high yielding cultivars coupled with improved agronomic practices. The development of superior varieties / hybrids depends on the magnitude of genetic variability and heritability present in the source material. The extent of variability is measured by GCV and PCV which provides information about relative amount of variation in different characters. Since the estimates of heritability alone will not be of much use for selection based on phenotypic basis, genetic gain should also be considered. Selection on the basis of grain yield character alone is usually not very effective and efficient. However, selection based on its components and secondary characters could be more efficient and reliable. Knowledge on the yield and between yield and its components and among the component characters themselves can improve the efficiency of selection in plant breeding (Izge *et al*., 2006). Estimation of genetic diversity and identification of superior genotypes are some of the prime objectives of any crop improvement programme. The genotypes which are highly diverse can assessed as parents in hybridization programme to produce superior varieties/hybrids. Therefore there is a necessity to avail the genetic divergence among the germplasm. The present study was carried out to study the genetic variability, correlation and path analysis and also to know the genetic diversity for selecting the genotypes to develop a superior hybrid/variety.

Materials and methods

A total of 100 pearl millet genotypes maintained at Department of millets, Millet Breeding Station, TNAU, Coimbatore were used for this study. All these genotypes were raised during summer 2014 at Department of Millets under Randomized Completely Block Design with three replications in two rows of each genotype per replication. Nine quantitative characters *i.e*. days to 50 per cent flowering, days to maturity, number of tillers per plant, plant height (cm), spike length (cm), spike girth (cm), 1000 seed weight (g), single earhead weight (g) and grain yield / earhead (g) were recorded in randomly selected five plants in all the three replications. The recorded data were subjected to statistical analysis using mean values. Phenotypic and genotypic coefficients of variation were calculated based on the method advocated by Burton (1952). Heritability in broad sense was estimated as per Allard (1960) and expressed in percentage. Genetic advance was estimated by the method suggested by Johnson *et al*. (1955). Genotypic correlation coefficient was worked out using the formulae suggested by Falconer (1964). Path coefficient analysis suggested by Wright (1921) and elaborated by Dewey and Lu (1959) was used to calculate the direct and indirect contributions of various traits to yield. Genetic diversity among these genotypes can be calculated using D^2 statistic of Mahalanobis (1928).

Results and discussion

Analysis of variance resulted significant variance between the genotypes for all the characters except number of tillers and spike length. This shows that sufficient amount of variations was present among the genotypes.

Variability parameters: The PCV was higher than the GCV for all the characters studied indicating the influence of environment in expression of characters (Table 1).This result was in accordance with the findings of Sumathi *et al*. (2010) and Rachel (2014). Among all the characters, high PCV and GCV were recorded for single earhead weight and grain yield / earhead, indicating the presence of high amount of genetic variability for these two characters therefore selection for these characters would be effective because the response to selection is directly proportional to the variability present in the experimental material. Similar results were reported by Sumanth (2011) and Sowmiya (2012) for single earhead weight. Moderate PCV and GCV were observed for number of tillers per plant, 1000 seed weight, spike girth and days to 50 per cent flowering. Low PCV and GCV were observed in spike length, plant height and days to maturity. This result coincides with the findings of Sathya (2014) for spike length and days to maturity. Genetic coefficient of variance does not provide the clear indication on the proportion of heritable components of variation.

In this study, most of the characters *viz*., days to 50 per cent flowering, days to maturity, plant height, spike girth, 1000 seed weight, single earhead weight and grain yield / earhead showed high heritability (Table 1). Moderate heritability was recorded in number of tillers and spike length. Heritability estimates along with genetic advance were more useful than heritability estimates alone in predicting the response to selection. Also the heritability estimates alone do not provide reliable information about the gene governing the expression of a particular character. The high genetic advance as per cent of mean was recorded single earhead weight, grain yield / earhead, 1000 seed weight, spike girth and days to 50 per cent flowering. Moderate genetic advance was noticed in number of tillers per plant, plant height and days to maturity. Spike length alone had low genetic advance as per cent of mean.

High broad sense heritability along with high genetic advance as per cent of mean was observed in single earhead weight, grain yield / earhead, 1000 seed weight, spike girth and days to 50 per cent flowering, this indicated that these characters were governed by additive genes. Similar results were reported previously by Bhoite *et al*. (2008) for days to 50 per cent flowering and spike girth and Vagadiya *et al*. (2013) for 1000 seed weight and single earhead weight. Therefore, selection should be efficient using these characters for improving the genotypes. High heritability with moderate genetic advance was recorded in the characters plant height and days to maturity. This observation is in agreement with the results of Lakshmana *et al*. (2009) for plant height and days to maturity. Number of tillers showed moderate heritability and moderate genetic advance. Moderate heritability and low genetic advance were notice for spike length.

Correlation and path analysis: Genotypic correlation coefficients between all possible traits of characters are presented in Table 2. In the present study the characters *viz*., single earhead weight, 1000 seed weight, days to 50 per cent flowering, spike girth and days to maturity were exhibited significantly positive correlation with grain yield / earhead. The above results were supported by Meenakumari and Nagarajan (2008) and Sowmiya (2012) for earhead girth and single earhead weight. It would be inferred that, selection for high yield would be effective through selection for these characters.

The relationship existing between the pairs of characters were measured by using association analysis. But dependent characters are an interaction product of many mutually associated components. The path analysis takes into account the cause and effect relationship between the variables by partitioning the association into direct and indirect effects through other independent variables. The direct and indirect effects for the nine characters are given in Table 3. The path analysis revealed that, a very high positive direct effect on grain yield was observed by days to 50 per cent flowering and spike girth. Single earhead weight had high positive direct effect followed by 1000 seed weight on grain yield. These revealed the true relationship of these characters with grain yield. Direct selection for these characters could be rewarding for the improvement of grain yield.

Hence, it would be inferred that selection should be in positive side for the characters single earhead weight and 1000 seed weight and automatically increase the grain yield. Selection based on early

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maturity plants would be also effective because it shows highly negative direct effect on grain yield.

Diversity studies: The estimation of genetic divergence based on D^2 value revealed that the 100 pearl millet genotypes can be grouped into 11 clusters (Table 4) with cluster VII had more number of genotypes (41 genotypes) followed by 28 genotypes in cluster III, 14 genotypes in cluster I and three genotypes in cluster XI. The remaining seven clusters *i.e*. cluster II, IV, V, VI, XIII, IX and X had two genotypes each. Hence, the genotypes from these clusters may be selected for an effective breeding programme for grain yield improvement.

The irregular distribution of genotypes into various clusters indicating the high divergence among the genotypes of the cluster. While considered the inter cluster distance, it was ranged from 39.0 to 6.9 were presented in Table 5. The highest inter cluster distance was recorded between cluster VIII and cluster X (39.0) followed by cluster IX and cluster X (36.4), cluster VI and cluster X (35.5). Selection of parents for hybridization between the high inter cluster distance can give high amount of heterosis effect in F_1 generation and it generate useful recombinant in segregating population.
Considering the cluster mean performance (Table 6), cluster X containing the genotypes PT 2616 and PT 2656 had high mean value for plant height, spike length, 1000 seed weight, single earhead weight and grain yield / earhead. Selection of parental line from these clusters can be utilized for developing superior variety / hybrid / composites. Early flowering and early maturity was the most preferable type in crop plants for escape from severe drought condition. In this study utilizing genotypes from the cluster IV containing the lines *viz*., PT 2409 and PT 2533 may develop superior variety / hybrid with early flowering and early maturity helps cultivars more suitable by enabling them escape from terminal drought.

Conclusion

The traits namely 1000 grain weight and single earhead weight had high variation among the studied genotypes. Selection based on these traits would increase the grain yield in pearl millet genotypes. The genotypes, PT 2616 and PT 2656 had high performance for plant height, spike length, 1000 seed weight, single earhead weight and grain yield / earhead. So these genotypes could be used for effective hybridization programme to develop hybrid or variety or composites.

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Table 1. Genetic parameters for yield and yield components in pearl millet

Characters	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
Days to 50 % flowering	12.00	11.77	96.3	23.80
Days to maturity	6.33	6.10	92.8	12.11
Plant height (cm)	8.22	8.04	95.7	16.21
Number of tillers/plant	17.54	11.83	45.5	16.43
Spike length (cm)	9.29	5.94	40.8	7.81
Spike girth (cm)	15.05	14.05	87.1	27.01
1000 seed weight (g)	17.38	16.78	93.2	33.37
Single earhead weight (g)	34.63	34.29	98.1	69.94
Grain yield / earhead (g)	27.64	27.22	97.0	55.23

Table 2. Genotypic correlation coefficients among yield and its components in pearl millet

Traits	DFF	DM	PH	NPT	SL	SG	TSW	SEW	GY/E
DFF	1.000	0.987**	0.077	0.050	-0.053	0.040	0.141	0.381**	0.249*
DM		1.000	0.081	-0.036	-0.091	0.102	0.149	0.365**	0.208*
PH			1.000	0.014	0.216*	0.353**	0.047	0.123	0.100
NPT				1.000	-0.054	-0.291**	-0.134	-0.051	0.076
SL					1.000	0.089	0.196*	0.041	0.046
SG						1.000	0.284**	0.233*	0.219*
TSW							1.000	0.404**	0.547**
SEW								1.000	0.786**
GY/E									1.000

*, ** significant at 5 and 1 per cent level, respectively

Table 3. Direct (diagonal) and indirect effects of different characters in pearl millet

Characters	DFF	DM	PH	NPT	SL	SG	TSW	SEW
DFF	**1.423**	-1.478	0.000	0.002	0.006	0.004	0.043	0.248
DM	1.404	**-1.498**	0.000	-0.002	0.010	0.010	0.046	0.238
PH	0.110	-0.121	**0.005**	0.001	-0.023	0.035	0.014	0.080
NPT	0.071	0.055	0.000	**0.048**	0.006	-0.029	-0.041	-0.033
SL	-0.075	0.136	0.001	-0.003	**-0.108**	0.009	0.060	0.027
SG	0.057	-0.153	0.002	-0.014	-0.010	**1.000**	0.087	0.152
TSW	0.200	-0.223	0.000	-0.006	-0.021	0.028	**0.306**	0.263
SEW	0.542	-0.548	0.001	-0.002	-0.004	0.023	0.124	**0.651**

DFF – days to 50 per cent flowering; DM – days to maturity; PH – plant height (cm); NPT – number of productive tillers per plant; SL – spike length (cm); SG – spike girth; TSW thousand seed weight (g); SEW – single earhead weight (g); GY/E grain yield per earhead (g)

Table 4. Clustering of genotypes based on D^2 value

Cluster	No. of genotypes	Name of the genotypes
I	14	PT 2073, PT 2089, PT 2098, PT 2103, PT 2104, PT 2113, PT 2115, PT 2117, PT 2127, PT 2153, PT 2156, PT 2164, PT 2600, PT 2529
II	2	PT 2364, PT 2540
III	28	PT 2174, PT 2192, PT 2193, PT 2196, PT 2198, PT 2199, PT 2209, PT 2213, PT 2231, PT 2234, PT 2236, PT 2243, PT 2248, PT 2262, PT 2270, PT 2280, PT 2286, PT 2303, PT 2324, PT 2328, PT 2328/1, PT 2332, PT 2339, PT 2340, PT 2343, PT 2347, PT 2349, PT 2355
IV	2	PT 2409, PT 2533
V	2	PT 2655, PT 2659
VI	2	PT 2368, PT 2390
VII	41	PT 2392, PT 2393, PT 2394, PT 2410, PT 2423, PT 2425, PT 2459, PT 2473, PT 2481, PT 2482, PT 2484, PT 2487, PT 2497, PT 2518, PT 2528, PT 2530, PT 2532, PT 2534, PT 2551, PT 2552, PT 2556, PT 2557, PT 2558, PT 2563, PT 2568, PT 2573, PT 2574, PT 2576, PT 2577, PT 2578, PT 2581, PT 2582, PT 2584, PT 2589, PT 2590, PT 2593, PT 2596, PT 2598, PT 2602, PT 2610, PT 2360
VIII	2	PT 2617, PT 2619
IX	2	PT 2630, PT 2644
X	2	PT 2616, PT 2656
XI	3	PT 2616/1, PT 2631, PT 2655/1

Table 5. Intra (Diagonal) and inter cluster distance of pearl millet genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	17.9	14.6	16.9	15.0	17.0	18.9	17.9	18.9	15.5	31.7	19.8
II		3.9	13.9	6.9	13.4	13.5	14.6	10.6	8.3	35.1	17.4
III			16.5	14.9	15.4	16.9	17.6	17.4	15.3	31.9	19.6
IV				4.1	16.7	15.1	15.6	14.5	7.2	35.2	18.4
V					4.4	13.2	16.3	10.6	17.9	31.5	17.5
VI						4.4	19.6	11.7	16.6	35.5	21.2
VII							18.3	17.9	16.2	33.2	19.9
VIII								6.1	15.6	39.0	20.1
IX									8.7	36.4	19.6
X										19.4	31.4
XI											24.8

Table 6. Cluster mean for nine quantitative characters of pearl millet genotypes

Cluster	DFF	DM	PH	NPT	SL	SG	TSW	SEW	GY/E
I	46.0	86.0	181.2	3.7	22.3	8.2	9.3	19.4	12.2
II	45.7	86.3	176.9	3.6	22.1	6.8	9.0	13.4	11.7
III	46.5	87.6	175.3	3.8	22.5	8.3	9.6	19.2	12.4
IV	**41.3**	**81.8**	180.4	3.6	21.7	7.2	9.8	14.6	10.4
V	51.8	80.0	160.8	4.2	23.2	6.0	9.0	22.2	12.5
VI	44.5	85.7	143.9	4.1	22.1	7.3	11.2	16.4	12.7
VII	47.0	87.6	181.1	4.0	22.4	7.3	8.9	19.0	11.7
VIII	49.2	89.3	155.6	4.4	20.3	5.3	9.2	14.3	10.3
IX	43.5	83.8	184.3	4.6	22.5	**8.5**	9.9	13.0	9.9
X	47.5	87.3	**201.7**	4.3	**23.4**	7.8	**11.6**	**36.4**	**23.9**
XI	46.4	85.9	180.1	**5.1**	21.3	6.3	8.5	20.6	13.8

DFF – days to 50 per cent flowering; DM – days to maturity; PH – plant height (cm); NPT – number of productive tillers per plant; SL – spike length (cm); SG – spike girth; TSW thousand seed weight (g); SEW – single earhead weight (g); GY/E grain yield per earhead (g)