

Original Research Article

Hierarchical clustering of pearl millet (*Pennisetum glaucum* (L.) R.Br) inbreds for morpho-physiological traits

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ABSTRACT

The present investigation was carried with an objective to assess the extent of genetic diversity with relation to morpho-physiological traits viz., days to 50 % flowering, plant height (cm), number of tillers, ear head length (cm), ear head breadth (cm), root length (cm), shoot length (cm), root-shoot ratio and grain yield (g/plant) of 47 pearl millet accessions (44 inbred lines and 3 checks) at Department Of Millets, Tamil Nadu Agricultural University, Coimbatore. The data on nine traits for all the forty seven accessions were subjected to multivariate hierarchial cluster analysis. A phenetic tree was constructed using the TREEPLOT program of NTSYS pc after standardization of the data. The hierarchial cluster analysis resulted in the formation of eight clusters indicating the presence of high level of genetic diversity among forty seven genotypes. Among eight clusters, cluster IV had highest number of inbreds (18) followed by cluster I and cluster VI (9). Similarity co-efficient value ranges from 1.00 to 9.96. The results indicated that the inbreds TNBI 9 and TNBI 21 and TNBI 15 and TNBI 22 were closely related. The dissimilarity was highest between the inbreds TNBI 30 and TNBI 39 (9.96) followed by TNBI 44 and TNBI 9 (9.95) and TNBI 29 and TNBI 1 (9.93) for yield and yield component traits which showed that they are highly divergent among the forty seven genotypes. It was found that the inbred TNBI 43 in cluster V recorded early flowering and highest mean value for ear head length, number of tillers, ear head breadth, root length, root-shoot ratio and grain yield among the 47 genotypes which can be used as a parent in hybridization programme to enhance yield potential of the pearl millet genotypes under moisture stress condition.

Keywords

Pearl Millet;
morpho-physiological traits;
Inbreds;
Genetic diversity;
Hierarchial cluster analysis.

Introduction

Pearl Millet [*Pennisetum glaucum* (L.) R.Br.] commonly known as bajra, cat tail millet, and bulrush millet in different parts

borne pollination mechanism, which fulfils one of the essential biological requirements for hybrid development.

Pearl millet is the most drought tolerant warm-season cereal crop predominantly grown as a staple food grain and source of feed and fodder. Infact, Pearl millet is the only suitable and efficient crop for arid and semiarid conditions because of its efficient utilization of soil moisture and higher level of heat tolerance than sorghum and maize (Shah *et al.*, 2012). The grain has higher levels of protein content with balanced amino acids, CHO and fat which are important in the human diet, and its nutritive value is considered to be comparable to rice and wheat. The green fodder of pearl millet is more palatable because it does not have HCN content as that of sorghum. The success of any breeding method depends on the availability of genetic diversity in the base population. Highly diverse genotypes or accessions can be utilized as parents in hybridization programmes to produce superior varieties/hybrids. Therefore there is a need to evaluate available genotypes for their genetic diversity. Hierarchical cluster analysis highlights the nature of relationship between any type of samples described by any type of descriptors. It could serve as a basis for selection of parental types that could result to superior hybrids. The objective of this study therefore was to analyze the genetic diversity among the pearl millet genotypes for morpho-physiological traits.

Materials and Methods

The experimental material comprised of forty seven genotypes (44 inbreds and 3 checks) collected from Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, India. The genotypes were evaluated in a replicated yield trial with two replications during kharif, 2010 at Department of Millets,

Tamil Nadu Agricultural University, Coimbatore. Data was recorded for the nine characters *viz.*, days to 50 % flowering, plant height (cm), number of tillers, ear head length (cm), ear head breadth (cm), root length (cm), shoot length (cm), root-shoot ratio and grain yield (g/plant) on five randomly selected plants in two replications. The statistical analysis was carried out for estimating analysis of variance as suggested by Panse and Sukhatme (1967). The data on nine traits for all the forty seven accessions were subjected to multivariate hierarchial cluster analysis. The mean data over two replications were computed for hierarchial cluster analysis. A phenetic tree was constructed using the TREEPLOT program of NTSYS pc (Rohlf, 1992) after standardization of the data.

Results and Discussion

Genetic diversity is the basic requirement for successful breeding programme. Collection and evaluation of genotypes of any crop is a pre-requisite for any programme, which provides a greater scope for exploiting genetic diversity. The importance of genetic diversity among parents to be crossed, whether aimed at heterosis breeding or recombination breeding, has long been realized (Ogunbayo *et al.*, 2005). With increased diversity between parental varieties, higher level of heterosis is expected in F₁ hybrids and larger variance and transgressive segregants in the F₂ and later generations. The hierarchial cluster analysis is a powerful tool to measure the genetic divergence within a set of genotypes (Loumerem *et al.*, 2008). The present study was planned to examine the trend of genetic divergence in forty seven genotypes of pearl millet for nine morpho-physiological traits. The presence of high

variability among the genotypes studied for different characters were confirmed from the pattern of distribution of these forty seven genotypes into eight clusters (Table 1; Fig 1).

Among eight clusters, cluster IV had highest number of inbreds (18) followed by cluster I and cluster VI (9). The inbreds TNBI 36, TNBI 43, TNBI 42 and TNBI 23 were grouped in separate clusters of II, V, VII and VIII respectively. Shah *et al.* (2012) grouped forty two and twenty seven pearl millet genotypes into nine and five clusters respectively. This grouping of accessions in to different clusters gives an opportunity to select the elite genotypes, which can be used as the donors in pearl millet hybridization programme. Similarity co-efficient value ranges from 1.00 to 9.96. The results indicated that the inbreds TNBI 9 and TNBI 21 and TNBI 15 and TNBI 22 were closely related. The dissimilarity was highest between the inbreds TNBI 30 and TNBI 39 (9.96) followed by TNBI 44 and TNBI 9 (9.95) and TNBI 29 and TNBI 1 (9.93) for morpho-physiological traits showed that they are highly divergent among the forty seven genotypes. These genotypes can be used as the potential parents in pearl millet hybridization programme for evolving superior varieties/hybrids.

The cluster mean performance of eight clusters for nine traits of forty seven pearl millet genotypes was given in Table 2. Cluster VII recorded the highest mean value for days to 50 % flowering (53.00) followed by cluster III (50.00) and clusters II and VI (49.00). Cluster V containing the inbred TNBI 43 recorded the lowest mean value for days to 50 % flowering (45.00) which was found to be early flowering. According to Vadez *et al.* (2012), earliness is an important drought escape attribute of

pearl millet, where the early cultivar has the more chance to escape drought stress, whereas the late cultivar is likely to suffer the stress before or during reproduction. Thus this inbred can be used as a parent in drought tolerant breeding programme. Cluster means for plant height ranged from 141.00 (cluster VIII) to 186.00 (cluster VII) Tillering in pearl millet is an important attribute that contributes to increased grain yield and fodder yield. In this study the genotypes in the clusters I, III, IV and V and XII had the highest mean value for total number of tillers (5) followed by the clusters II, VI, VII and VIII. Because of this high tillering ability and because the length of the period between floral initiation and flowering is similar, plants have tillers at all stages of apical development at all times. According to Mahalakshmi and Bidinger (1985), the developmental plasticity of pearl millet compensates for potential failure of the main and primary tillers in the case of a mid-season drought.

Earhead length and ear head breadth plays a vital role maximization of grain yield. The highest mean for ear head length was recorded by cluster VII (44.00 cm) followed by cluster V (33.00 cm), while the lowest mean for ear head length was recorded by cluster I and II (21.00 cm). The highest mean value for ear head breadth was recorded by cluster VI and V (9.00 cm) and other clusters recorded the lowest mean (8.00 cm). Both ear head length and breadth was found to be good in Cluster V containing the genotype TNBI 43. This genotype can be utilized as a elite parent in pearl millet improvement programme. Roots appear to play an important role in pearl millet genotypes that differ in the presence or absence of a major terminal drought tolerance (Vadez *et al.*, 2012).

Table.1 Cluster composition of 47 pearl millet genotypes for morpho-physiological traits

Clusters	Number of genotypes	Name of the genotypes
I	9	CO 7, CO (cu) 9, TNBI 9, TNBI 21, TNBI 20, TNBI 3, TNBI 10, TNBI 11 and TNBI 13
II	1	TNBI 36
III	7	ICMV 221, TNBI 5, TNBI 38, TNBI 40, TNBI 34, TNBI 35 TNBI 44
IV	18	TNBI 1, TNBI 2, TNBI 6, TNBI 7, TNBI 12, TNBI 41, TNBI 15, TNBI 22, TNBI 18, TNBI 19, TNBI 16, TNBI 17, TNBI 4, TNBI 8, TNBI 14, TNBI 37, TNBI 39, TNBI 33
V	1	TNBI 43
VI	9	TNBI 24, TNBI 28, TNBI 32, TNBI 25, TNBI 30, TNBI 26, TNBI 27, TNBI 29, TNBI 31
VII	1	TNBI 42
VIII	1	TNBI 23

Fig.1 Dendrogram showing the grouping of forty seven pearl millet genotypes in to different clusters. (Rohlf FJ. 1992. NTSYS)

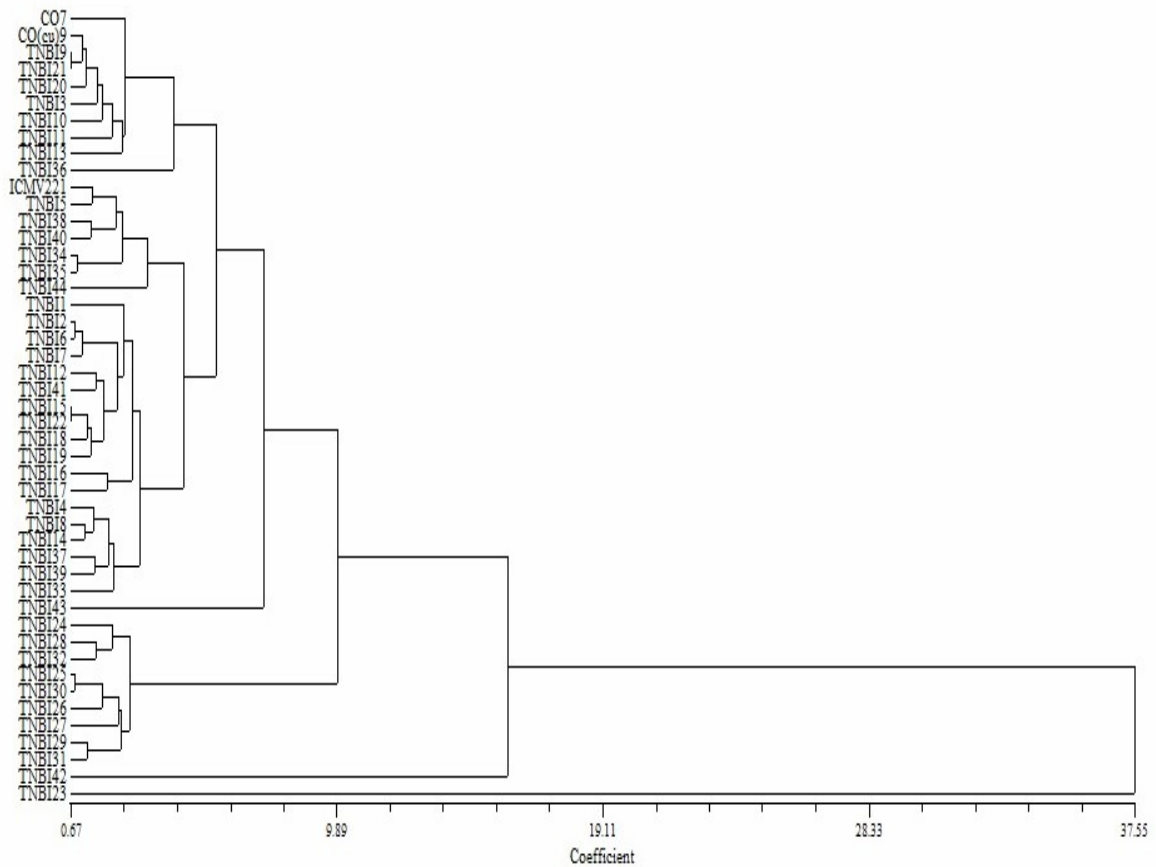


Table.2 Cluster mean composition of 47 pearl millet genotypes for recorded morphophysiological traits

Cluster	DTF	PH	TT	EHL	EHB	RL	SL	RSR	GY
Cluster 1	48	142	5	21	8	19	121	0.17	1.22
Cluster 2	49	151	4	21	8	25	114	0.21	0.99
Cluster 3	50	164	5	22	8	23	132	0.17	1.19
Cluster 4	49	161	5	22	9	23	126	0.17	1.16
Cluster 5	45	168	5	33	9	27	122	0.22	1.50
Cluster 6	49	128	4	22	8	23	116	0.20	1.39
Cluster 7	53	186	4	44	8	24	138	0.17	1.13
Cluster 8	46	141	4	23	8	27	120	0.18	1.14

DTF-Days to 50% flowering, PH – Plant height (cm), TT – Total tillers (no), EHL- Ear head length (cm), EHB-Ear head breadth (cm), RL-Root length(cm) (cm), SL-Shoot lengt(cm),h, RSR-Root shoot ratio, GY-Grain yield (g/plant)

Pearl millet is known to be deep and profusely rooted, with the ability to match its rooting to water availability in a very plastic manner, leading to a highly varying root growth to shoot growth ratio, depending on the intensity of water limitation. Deeper or more profuse rooting would allow the crop to sustain water uptake and continue grain filling in the latest part of the grain-filling period (Vadez *et al.* 2012). Cluster V containing the genotype TNBI 43 and cluster VIII containing the genotype TNBI 23 recorded the maximum root length (27.00 cm) while Cluster VII containing the genotype TNBI 42 recorded the maximum shoot length (138.00 cm). The inbred TNBI 43 in cluster V recorded the maximum root-shoot ratio (0.22). This inbred with the highest root- shoot ratio maintain greater growth rates which gives higher grain yield under moisture stress condition (Sashidhar *et al.*, 2000). Thus this inbred can be better utilized as the parent for drought improvement programme.

Grain yield character in pearl millet and as in all crop plants is quantitative in nature and is polygenically controlled. The major thrust in pearl millet improvement

programme is to improve yield potential in fragile arid regions. This may be achieved either through direct selection of landraces/ germplasm lines or by developing populations/hybrids that are adapted to such environments and provide higher grain yield. In this study, of all the clusters, the highest mean for the grain yield was recorded by cluster V containing the genotype TNBI 43 which can be chosen as the parent for pearl millet improvement programme.

It was evident from this study that of all the genotypes grouped in different clusters, cluster V containing the genotype TNBI 43 excelled over the checks and other inbreds which recorded early flowering and highest mean value for number of tillers, ear head length, ear head breadth, root length, root-shoot ratio and grain yield. Hence this inbred can be included in the hybridization programme as a parent to enhance yield potential of the pearl millet genotypes under moisture stress condition.

India has a rich source of pearl millet germplasm which might play a major role in breeding programs to address current

challenges of food security, biotic and abiotic stress and biofuel demands. The agromorphological characterization through hierarchical clustering in this study showed that the pattern of distribution of the forty seven genotypes into eight clusters that showed variability in most of the lines for nine characters viz., days to 50 % flowering, plant height (cm), number of tillers, ear head length (cm), ear head breadth (cm), root length (cm), shoot length (cm), root-shoot ratio and grain yield (g/plant). Of all the inbreds, TNBI 43 excelled over the checks and other inbreds which recorded early flowering and highest mean value for number of tillers, ear head length, ear head breadth, root length, root-shoot ratio and grain yield. This inbred can be included in the hybridization programme as a parent to enhance yield potential of the pearl millet genotypes under moisture stress condition. Pearl millet germplasm of this study representing a wide range of genetic variability can be used as a starting basis for breeding programmes to select high yielding varieties tolerating adverse arid conditions.

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