Genetic divergence assessment in proso millet (*panicum milliaceum*)

A. Thanga Hemavathy, C. Priyadharshini

Department of Millets, Tamil Nadu Agricultural University (TNAU), Coimbatore.

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Abstract

An investigation was undertaken to determine the extent of genetic diversity present among 52 proso millet genotypes using D^2 statistic. Cluster analysis grouped 52 germplasm into six clusters based on the degree of divergence between the genotypes. Maximum number of 27 and 17 genotypes were grouped under cluster I and IV, respectively, while clusters III had three genotypes and clusters II and V consisting of 3 genotypes each and cluster VI had single genotype. Maximum inter cluster was observed between cluster V and VI (30.96) followed by cluster II and VI (28.47). The greater the distance between the two clusters indicates wider the genetic diversity between genotypes. Hence, the genotypes in cluster V viz., CO 5, 23/1 had wider diversity with PCGP 49 in cluster VI and these lines may be utilized in further breeding programme for the exploitation of hybrid vigour. The intra cluster distance was maximum in cluster V (13.77) followed by cluster I (11.40) indicates hybridization involving genotypes within the same clusters may result in good cross combinations. Among the six traits studied, maximum contribution was made by single plant grain yield (49.55%) followed by days to 50 per cent flowering (26.62%) and number of productive tillers (17.04%). Hence, grain yield, days to 50% flowering and number of productive tillers together contribute 93.21% towards total divergence. Therefore, these characters may be given importance during hybridization programme.

Introduction

Proso millet, also called broomcorn and common millet, was domesticated in Neolithic China as early as 10,000 years ago. Proso millet was important in the diets of human across India prior to the introduction of wheat, barley and potatoes. At present it is consumed in significant quantities in India (where it is known as *pani varagu* in Tamil), Nepal, western Myanmar, Sri Lanka, Pakistan, and South East Asian countries. In order to ensure food security in the fragile ecosystem, it is important to trap the available genetic diversity among the germplasm to select the superior highly diverged lines may be used as the parents for the crop improvement programmes. Despite very meager work only carried out in proso millet germplasm to study the genetic divergence, further work is necessary to understand the genetic basis of phenotypic variation among different genotypes.

Materials and Methods

The experiment for the present study were conducted during summer, 2014 at Department of Millets, Tamil Nadu Agricultural University, Coimbatore. The experimental material comprised of 52 proso millet entries and it was laid out in Randomised Block Design with two replications. The spacing between plant to plant, 7.5 cm and row to row, 22.5 cm was maintained. At the time of maturity

Corresponding Author: A. Thanga Hemavathy, Assistant Professor, Department of Millets, Tamil Nadu Agricultural University (TNAU), Lawley Road, Coimbatore-641003, Tamil Nadu.
E-mail: hemavathy.tnau@gmail.com

three plants selected at random from each genotype and that were tagged in each replication. Observations on quantitative traits were recorded and the average of these five plants for each quantitative character was made to compute mean for further analysis. Observations were recorded for six quantitative traits *viz.*, days to 50 % flowering, plant height, number of productive tillers per plant, length of peduncle, length of inflorescence and single plant grain yield. The quantitative measurement of genetic divergence among the genotypes was carried out by Mahalanobis D2 statistic (Rao, 1952).

Results and Discussion

The genotypes included in the study were from the different sources and were grouped into six clusters (Table 1). Cluster I was the largest with twenty seven genotypes followed by cluster IV with seventeen genotypes. The lowest single genotype was included in cluster VI. Clustering pattern under this study

reveals that the proso millet showed considerable genetic diversity among themselves by occupying six different clusters. As statement by Murthy and Arunachalam (1966), this none parallelism may be due to genetic drift and intense natural and human selection for diverse adaptive gene complexes under different environments causing greater diversity among genotypes rather than their geographic distances.

The intra and inter cluster distance are presented in Table 2. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. Cluster V (13.77) recorded the highest intra cluster distance followed by cluster I (11.40) and cluster IV (11.36). The inter cluster distance was maximum between cluster V and cluster VI (30.96) followed by cluster II and VI (28.47) indicating greater divergence belonging to these clusters. The crosses which involve parents from these more divergent clusters will yield relatively good amount of heterosis in F_1 and high frequency of transgressive segregants and genetic variability in subsequent generations. The minimum distance was

Table 1: Cluster composition of 52 proso millet germplasm

Cluster Number	No. of Accessions	Accession Number
I	27	PCGP 1, PCGP 2, PCGP 3, PCGP 4, PCGP 5, PCGP 6, PCGP 7, PCGP 8, PCGP 9, PCGP 10, PCGP 11, PCGP 12, PCGP 13, PCGP 14, PCGP 15, PCGP16, PCGP 17, PCGP 18, PCGP 19, PCGP 20, PCGP 21, PCGP 22, PCGP 23, PCGP 24, PCGP 25, PCGP 27, PCGP 50
II	2	PCGP 33, PCGP 41
III	3	PCGP 26, PCGP 30, PCGP 39
IV	17	PCGP 28, PCGP 29, PCGP 31, PCGP 32, PCGP 34, PCGP 35, PCGP 36, PCGP 37, PCGP 38, PCGP 40, PCGP 42, PCGP 43, PCGP 44, PCGP 45, PCGP 46, PCGP 47, PCGP 48
V	2	CO 5, 23/1
VI	1	PCGP 49

Table 2: Average intra (diagonal) and inter cluster distances in proso millet

Clusters	I	II	III	IV	V	VI
I	**11.40**	14.58	13.51	11.85	17.48	18.33
II		**1.47**	21.00	11.62	8.01	28.47
III			**10.89**	16.30	24.06	11.33
IV				**11.36**	14.53	21.96
V					**13.77**	30.96
VI						**0.00**

Table 3: Cluster mean values for six quantitative characters in proso millet

Clusters	Days to 50% Flowering	Plant Height	Number of Productive Tillers	Length of Peduncle	Length of Inflorescence	Single Plant Grain Yield
I	40.93	90.41	7.19	9.22	29.37	12.27
II	46.50	89.02	7.25	10.25	30.97	9.00
III	36.67	84.50	7.00	9.23	29.51	8.17
IV	42.97	88.64	7.21	9.02	30.52	12.83
V	47.25	88.43	3.75	9.93	33.27	11.74
VI	33.00	84.73	7.50	9.63	32.67	12.68

Table 4: Relative contribution of different characters towards divergence

S. No.	Characters	Number of first rank	Contribution (%)
1	Days to 50% flowering	353	26.62
2	Plant height	34	2.56
3	No. of productive tillers	226	17.04
4	Length of peduncle	43	3.24
5	Length of inflorescence	13	0.98
6	Single plant grain yield	657	49.55
	Total	1326	100

observed between clusters II and V (8.01) followed by cluster III and VI (11.33). The genotypes in these clusters are genetically very close and hence, hybridization among the varieties will not give fruitful result.

The cluster mean values are presented in Table 3. Among the characters, cluster V recorded the highest mean value for days to 50 percent flowering and length of inflorescence per plant. Cluster I had the lowest mean values for days to 50 percent flowering and the highest mean values for number of productive tillers per plant. Cluster IV had the highest mean values for single plant grain yield. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. Based on the per se performance of the best genotypes within the clusters, they may be directly selected or may be used as potential parents in hybridization programme.

The contribution of each trait to total divergence is presented in table 4. Among the traits studied, single plant grain yield contributed maximum divergence (49.55%) followed by days to 50 percent flowering (26.62%) and number of productive tillers (17.04%). The minimum percentage of contribution was observed in length of inflorescence (0.98%) followed by plant height (2.56%) and length of peduncle (3.24%). The traits viz., grain yield, days to fifty percent flowering and number of productive tillers contributed 93.21 per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population.

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