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Genetic diversity analysis of Pearl Millet germplasm by cluster analysis

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Abstract

There are 40 genotypes of pearl millet that were gathered from ICRISAT in Hyderabad for the study. The experiment was performed in triplicate using Randomized Block Design. With an average D^2 value of 398.08, the experimental material was divided into seven clusters, indicating the presence of diversity across the lines for the attributes being studied. Among different clusters the maximum cluster lines i.e., ten lines were observed in cluster V followed by cluster IV, cluster III, cluster I, cluster II, cluster VII, and cluster VI. Cluster V has the greatest intra cluster distance, followed by Cluster II, Cluster IV, and Cluster I. As a result, within these clusters, selection might be based on the greatest mean for desirable characteristics. The relative divergence shows the degree to which each cluster differs. The highest order of divergence was observed in cluster VIII and cluster X, followed by cluster V and cluster VIII. The results revealed that the parents are genetically heterogeneous in these clusters. The high heterotic response may have been achieved when used in a hybridization programme. Cluster VI and Cluster VII had the shortest inter-cluster distance, indicating low genetic diversity. Plant height had the highest cluster value in cluster VIII and the lowest in cluster X, whereas phenological parameters like days to flowering and days to maturity had the highest cluster value in cluster II. Days to flowering were the most important factor in genetic divergence, followed by the number of panicle length, fodder yield per plot, and productive tillers per plant.

Keywords cluster analysis, intra and inter cluster distance, pearl millets, RBD

Introduction

Pearl millet, also known as bajra, is a monocotyledonous C4 crop that belongs to the Poaceae family. It's the warm-season cereal crop with the highest drought tolerance, and it's mostly used as staple food grain, feed, and forage. Pearl millet is an appropriate crop for different agro-climatic environments as it efficiently uses moisture in the soil and has greater heat tolerance than sorghum and maize [1]. The protein content of the grain is higher, and the amino acids are well-balanced, CHO, as well as fat, are all vital components of the human diet, and it has the same nutritional value as rice and wheat. Because it has no HCN, pearl millet green fodder is more appealing. Around the world, the pearl millet crop is grown in dry and semi-arid climates, such as West Africa, India, and Pakistan, where rainfall is around 150 and 700 mm. India is a major pearl millet producer, with 43.3 percent of the world's acreage and 42 percent of global production. It is cultivated predominantly on 9.16 million hectares of land in the states of Rajasthan, Maharashtra, Gujarat, Madhya Pradesh, Karnataka, Andhra Pradesh, Uttar Pradesh, and

Table 1. Analysis of variance for yield and its component traits in Pearl millet

	DF	Days to 50% flowering	Days to maturity	Plant height (cm)	Productive tillers per plant	Panicle Diameter (cm)	Panicle Length (cm)	Yield/plant (gm)	Fodder yield/plot (Kg)
Replicates	2	2.57	9.05	74.25	0.175	0.007	0.51	26.43	0.005
Genotype	39	34.73	39.36	1531.37	4.64	0.07	78.43	153.85	0.387
Error (A)	78	1.73	4.15	66.10	0.07	0.01	0.98	9.67	0.009
Total	119	12.56	15.77	546.45	1.57	0.03	26.36	57.20	0.133
Mean		51.65	87.41	135.21	4.20	2.37	19.54	42.89	1.275
C.V		2.55	2.33	6.01	6.01	5.29	7.25	42.89	7.433

Tamil Nadu, with an annual yield of 8.01 million tones. In order to meet the needs of the rural poor and subsistence farmers, pearl millet varieties and hybrids with a disease and pest resistance, as well as high yield and tolerance to environmental challenges, are all necessary.

As a result, both national and international institutions and breeders continue to focus on developing new kinds or hybrids [2]. The amount of variety in a crop species determines how far it progresses genetically in its gene pool for economically significant features. As a result, estimating genetic diversity and identifying superior genotypes is the first and most critical stage in crop development. To profit from transgressive segregation, parents must have a genetic gap [3]. The greater the genetic distance between parents, the greater the heterosis in offspring [4]. In bajra breeding operations, one of the most useful tools for parental selection is genetic distance estimation. It is critical to choose the right parents for use in crossing nurseries in order to maximize genetic recombination and potentially increase yield [5].

Table 2. D^2 values among the seven clusters formed based on the 40 pearl millet genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	26.53	49.32	36.53	57.79	80.8	41.23	74.41	58.78	51.66	93.33
Cluster II	49.32	31.11	67.31	135.09	139.82	61.21	102.25	107.61	53.48	106.44
Cluster III	36.53	67.31	0	46.58	106.52	56.18	105.23	93.07	82.44	107.98
Cluster IV	57.79	135.09	46.58	29.27	85.35	64.98	104.46	85.34	131.76	149.83
Cluster V	80.8	139.82	106.52	85.35	48.25	78.8	71.04	151.7	99.74	76.18
Cluster VI	41.23	61.21	56.18	64.98	78.8	0	25.7	102.9	104	134.75
Cluster VII	74.41	102.25	105.23	104.46	71.04	25.7	0	142.01	125.04	143.11
Cluster VIII	58.78	107.61	93.07	85.34	151.7	102.9	142.01	0	87.12	203.75
Cluster IX	51.66	53.48	82.44	131.76	99.74	104	125.04	87.12	0	44.8
Cluster X	93.33	106.44	107.98	149.83	76.18	134.75	143.11	203.75	44.8	0

Identification of genetic diversity, parental selection, following the path of crop evolution, center of origin, and diversity, and studying the interface between the environments, certain applicable approaches like cluster analysis, PCA, and factor analysis are already available [6]. Researchers can use cluster analysis to identify significant relationships between phenotypes and genotypes. Cluster analysis reveals the type of link between samples specified by different descriptors. It can be used as a preliminary step in selecting parental type which will produce better hybrids. The purpose of present study was to investigate the genetic diversity of pearl millet cultivars in terms of morpho-physiological characteristics. The goal of this research is to evaluate 40 pearl millet lines for eight quantitative features and to investigate genetic diversity

Methodology

For the study, 40 pearl millet genotypes were collected from ICRISAT in Hyderabad. On the Palem Farm of the Regional Agricultural Research Station, PJTSAU, the field trial was conducted. Table 4 shows the genotypes studied. Randomized Block Design was used to conduct the experiment in triplicate. Pearl millet seeds were instantly sown in the field at 45 x 15 cm spacing. Six different rows, six meters long represent each genotype. Conventional agronomic methods were used to cultivate the crop. Ten pearl millets plants were randomly selected at different growing stages. The economically important biometric traits such as 50% flowering, plant height, days to maturity, panicle diameter, productive tillers per plant, fodder yield per plot, panicle length, and yield per plant were observed. Statistical analysis of the mean values of individual genotypes was performed using the statistical programme OPSTAT

Table 3. Means of the quantitative traits in different clusters

Char.	Days to 50% flowering	Days to Maturity	Plant height	Productive tillers per plant	Panicle diameter	Panicle length	Yield per plant	Fodder yield per plant
Cluster I	58.10	93.83	139.17	2.50	2.41	17.65	33.26	0.98
Cluster II	66.00	102.11	141.22	2.33	2.61	15.00	29.44	0.86
Cluster III	50.67	86.00	89.00	2.00	2.30	14.00	24.00	0.58
Cluster IV	47.50	83.61	138.22	2.33	2.38	17.99	33.83	0.95
Cluster V	54.55	90.39	120.21	3.82	2.73	19.82	45.82	1.39
Cluster VI	59.00	94.00	150.00	2.00	3.50	19.00	35.00	1.12
Cluster VII	64.00	101.00	129.67	2.00	3.80	24.00	45.67	1.61
Cluster VIII	59.67	95.00	180.00	2.00	2.00	24.00	35.00	1.05
Cluster IX	62.00	95.67	107.00	4.00	2.00	18.00	36.00	0.86
Cluster X	56.67	92.33	80.00	5.00	2.00	13.00	39.67	0.96

Results and Discussion

The results of an analysis of variance for eight quantitative factors for 40 Pearl millet genotypes are shown in Table 1. The results express substantial variations across the inbred lines for the traits tested ($p \leq 0.01$), indicating a high level of genetic diversity and hence the need for divergence study.

The genetic diversity prevalent among the pearl millet lines was investigated using cluster analysis and the ward approach. With an average D^2 value of 398.08, the experimental material was divided into seven clusters, demonstrating the presence of diversity among the lines for the features under investigation. Cluster V has the most lines, with ten, followed by cluster IV, cluster III, cluster I, cluster II, cluster VII, and cluster VI, each with eight, six, five, three, and two lines. Table 2 shows the cluster distances between the seven clusters. These findings revealed that pearl millet lines may be differentiated clearly. The use of phenotypic data to screen breeding material for effective parents for hybridization programs is a quick and simple technique to measure genetic diversity among genetically distinct lines. Different authors also explain the clustering of genetic material in pearl millet, based on quantitative data [7-14]. Table 3 shows the average D^2 values between (intra cluster) and between (inter cluster) clusters. Cluster V (48.25) had the greatest intra cluster distance, followed by Cluster II (31.11), Cluster IV (29.27), and Cluster I (26.53). As a result, within these clusters, selection might be based on the greatest mean for desired qualities. It's possible that heterogeneity, pedigree, and the degree of general combining ability are responsible for such intra cluster genetic variability among lines within the same group. The inter cluster distance (relative divergence among different clusters) revealed a high level of divergence between cluster VIII and cluster X (203.75), followed by cluster V and cluster VIII (151.7). As a result, the parents in these clusters are genetically heterogeneous, and when utilized in a hybridization programme, they may have a high heterotic response. The specified lines might be intercrossed to create a base population with desirable traits [14] papers backed up these findings. Cluster VI and Cluster VII had slight genetic diversity as they have the shortest inter-cluster distance (25.7). Table 3 explains the cluster mean and every character

Table 4. Pearl millet lines tested in the study

SN.	Millet lines	SN.	Millet lines	SN.	Millet lines	SN.	Millet lines
1	Fe-101-1	11	Fe-111-30	21	Fe-121-34	31	Fe-131-29
2	Fe-102-37	12	Fe-112-9	22	Fe-122-20	32	Fe-132-2
3	Fe-103-28	13	Fe-113-16	23	Fe-123-11	33	Fe-133-4
4	Fe-104-24	14	Fe-114-6	24	Fe-124-35	34	Fe-134-36
5	Fe-105-17	15	Fe-115-18	25	Fe-125-39	35	Fe-135-31
6	Fe-106-15	16	Fe-116-10	26	Fe-126-26	36	Fe-136-19
7	Fe-107-27	17	Fe-117-25	27	Fe-127-12	37	Fe-137-38
8	Fe-108-3	18	Fe-118-32	28	Fe-128-8	38	Fe-138-13
9	Fe-109-23	19	Fe-119-33	29	Fe-129-14	39	Fe-139-22
10	Fe-110-5	20	Fe-120-40	30	Fe-130-7	40	Fe-140-21

contribution to genetic diversity. For the majority of the traits studied, the cluster mean values showed a broad range of variance. Plant height had the maximum cluster value in cluster VIII and the minimum in cluster X, whereas phonological characteristics, days to flowering, and days to maturity had the highest cluster value in cluster II. In order to ensure the effective selection and the selection of parents for hybridization, the features that contribute to the majority of the divergence should be given more weight. Table 3 shows the means of the quantitative features investigated in different groups. Days to flowering were the most important factor in genetic divergence (18.71%), followed by productive tillers per plant (18.46%), fodder yield per plot (18.20%), and panicle length (17.30%). The remaining characteristics contributed less genetic difference, indicating that they had little genetic diversity. In Pearl millet, [12] and [9] showed comparable results

Conclusion

The pearl millet lines that have been evaluated have a lot of variation that may be used in breeding programmes. The genotypes of Pearl millet were divided into 10 groups in this study. The lines of cluster VIII, VII, and IV might be employed in the crop enhancement programme to generate potential hybrids based on genetic distances.

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