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Yield and yield stability of diverse genotypes of pearl millet (*Pennisetum glaucum* (L.) R. Br.)

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Abstract

Thirty-six genotypes of pearl millet (*Pennisetum glaucum*) differing greatly in the contribution from landraces in their parentage were evaluated in six environments in order to examine their yield and yield stability across changing environmental conditions. The test environments provided a good range of yield levels ranging from a low of 843 kg ha^{-1} at Jaipur to a high of 2860 kg ha^{-1} at Patancheru. The genotypes were grouped in five clusters. Clustering pattern did not give any clear indication of classification of genotypes according to the source they were derived from. Apparently clusters proved to be heterogeneous in their genotypic constitution. Performances of the individual group showed various pattern of adaptation to the test environments. Clusters 1 and 4 showed contrasting adaptation in certain environments because of significant difference in their phenology, which might have influenced their response to different environments. Cluster 3 containing 13 genotypes derived from landraces, improved germplasms and their crosses appeared to be the most stable group but at a relatively poor performance level as compared to cluster 5. Results indicated that sources of adaptation to range of environments are not exclusively found in landrace group, rather they can be identified in non-landrace materials through evaluation over variable environments.

Key words: *Pennisetum glaucum*, stress environments, stability, adaptation, germplasm

Introduction

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is an important cereal of traditional farming system in the hot and and semi-arid tropical areas of the Indian sub-continent and Africa. The major production constrains of these regions include highly variable and unpredictable drought, low soil fertility and poor stand establishment as the crop is grown as rainfed on marginal lands without the application of fertilizers.

Strong breeding programmes though have produced numerous high yielding crop cultivars [1-2] but environmental resources of marginal areas are often too insufficient to tap their yield potential resulting into low yield levels. Under these circumstances genotypes with a stable performance across changing environments, even with modest yield, are considered more relevant than high yielding cultivars with inconsistent performance across unpredictable crop seasons [3-5] in order to provide food security in fragile environments. For this, small and marginal farmers of and environments continue to rely heavily upon stress resistance and yield stability of local cultivars.

Some studies in pearl millet have been conducted to evaluate only a limited number of landraces and modern varieties [6-7]. The information on yield performance and stability over variable environments of cultivars differing widely in the genetic contribution is largely lacking. The present study was, therefore, designed to examine the yield levels and stability in cultivars that were developed either from pure landraces or had substantial contribution from adapted landraces in their parentage and then to identify the sources of adaptation to changing environmental conditions.

Materials and methods

The material consisted of 36 cultivars of pearl millet and details about their genetic composition are given in Table 1. The basic material consisted of landraces, improved germplasm or their crosses. Experiments were carried out during kharif 1996 at six locations viz., Jodhpur, Jaipur, Fatehpur, Hisar, Agra and Patancheru ranging in seasonal rainfall from 1062 mm at Patancheru to 363 mm at Hisar. The experimental design was a 6 x 6 lattice with three replications. Plots were 2.0 or 2.4 m wide and 4 m long giving the plot sizes between 8 and 9.6 m^2. Recommended packages of practices were followed to raise a good crop at all locations. Days to flower were recorded as number of days from sowing to a point when stigma emerged in

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main stem of 50% plants in a plot. Grain yield was recorded (kg ha^{-1}) on net area basis.

A cluster analysis of grain yield data was used to group genotypes. The similarity between two genotypes was expressed as the squared Euclidean distance. An agglomerative hierarchical procedure with an incremental sum of squares grouping strategy known as Ward's method [8] was employed for the purpose of grouping genotypes. To adjust for the differences in yield levels between different locations, data for each environment was standardized to a mean of zero and standard deviation of one as suggested by Fox and Rosielle [9]. A large distance between the last few clustering steps was an indicator of truncation of clustering. Stability analysis was carried out following the model of Eberhart and Russell [10]. The genotypes that had high mean performance, regression coefficient of unity and minimum deviation from regression are considered as most stable.

Results and discussion

Both genotypes and environments were significant (P = 0.01) sources of variation for grain yield and days to flower (data not presented). The average yields in environments ranged from 843 kg ha^{-1} at Jaipur to 2860 kg ha^{-1} at Patancheru. Mean squares due to genotype x environment interaction were also significant indicating differential response of genotypes to various test environments.

The classification of genotypes was truncated at five group levels (Fig. 1). The first cluster contained eight genotypes (Table 1). All but two of them were derived from the crosses of landraces and improved materials. Cluster 2 contained seven genotypes. All but one of them were developed either from landrace or their crosses with improved germplasm and yielded lesser than average. The third cluster included 13 genotypes characterized by above average mean grain yield (except ICMP 96830, ICMP 96840 and RCB-IC

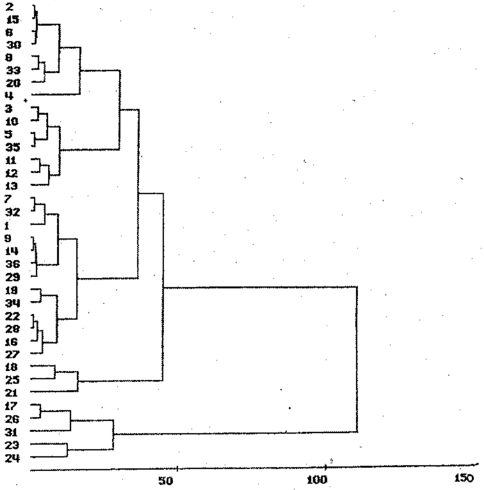

Fig. 1. Dendogram from average linkage cluster analysis of standardized grain yield of 36 pearl millet genotypes grown in six environments. The order of genotypes from top to bottom corresponds with the order in Table 1

Table 1. Origin, mean grain yield and days to flower of genotypes used in analysis, classified according to the results of cluster analysis

Entry	Origin	Grain yield (kg ha^{-1})	Days to flower
Cluster 1			
ICMV 96841	LR x IG	1565	46.8
ICNIV 95845	LR x IG	1546	46.0
ICMV 96845	LR x IG	1660	49.6
RCB-IC 525	LR x IG	1662	45.7
ICMV 96847	LR x IG	1587	47.0
ICMV 95835	LR	1645	48.0
MCB-IC 531	LR	1614	49.7
ICMV 96843	LR x IG	1397	46.7
Cluster 2			
ICMV 96842	LR x IG	1581	47.3
ICMV 96831	LR	1596	47.7
ICMV 96844	LR x IG	1608	47.0
ICMV 95846	LR x IG	1675	47.8
ICMV 96832	LR	1554	49.0
ICMV 96833	LR	1675	49.0
ICMV 221	IG	1731	47.3
Cluster 3			
ICMV 96846	LR x IG	1794	47.7
ICMV 95836	LR	1796	48.5
ICMP 96840	LR x IG	1776	46.0
ICMP 96830	LR	1634	46.5
RCB-IC 948	LR x IG	1682	48.5
ICMV 95837	LR x IG	1626	47.7
RCB-IC 325	LR	1724	49.0
CZP-IC 315	IG	1754	50.8
RCB-IC 944	LR x IG	1712	48.8
HHB 67	Hybrid	1804	44.6
RCB-IC 95	IG	1775	48.8
CZP-IC 416	LR x IG	1694	49.5
CZP-IC 923	IG	1862	50.3
Cluster 4			
ICMP 94852	LR	1418	51.7
ICTP 8203	IG	1582	48.7
Nokha local	LR	1094	51.0
Cluster 5			
CZH-IC 314	Hybrid	1941	45.7
CZP 9401	IG	2027	49.7
CZH-IC 511	Hybrid	2052	49.0
RCB-IC 9	IG	2188	51.7
ICMV 155	IG	2055	52.2

LR = Landrace; IG = Improved germplasm

948) and, on an average, early flowering. More than half of genotypes were derived from crosses of landraces and improved germplasm. Only three genotypes were grouped in Cluster 4 that had a characteristic low mean yield and late flowering (Table 1). On the contrary, cluster 5 contained five genotypes, all improved materials or hybrids with grain yield rather higher than the mean yield.

The classification of genotypes was somewhat related to flowering time: early to medium flowering were grouped in cluster 1, 2 and 3 and late flowering in clusters 4 and 5. Clustering pattern, however, did not give any clear indication of classification of genotypes according to the source they were derived from. For example, varieties derived from landraces were spread over first four clusters and landrace x improved germplasm derivatives scattered across clusters 1, 2 and 3. This might be due to the fact that very diverse open-pollinated landraces and improved germplasms were utilized in the development of genotypes tested in this study. Since the open-pollinated materials in outcrossed species like pearl millet are generally a mixture of several genotypes [11], the different varieties derived from a single source may still be markedly different. The clustering pattern in this study suggests that the genotypes tested in this study are genetically very diverse.

Performance plots of the individual entry group show various pattern of adaptation to the test environments (Fig. 2). Clusters 1 showed below average performance in all the test environments except the lowest yielding environment of Jaipur. Similarly cluster 4 which consisted of two local landraces and one improved cultivar showed below average performance in all test environments except Hisar. Clusters 1 and 4 showed contrasting adaptation in certain environments. For example, cluster 1 was relatively better adapted to high yielding location Agra and most stressful test location Jaipur, while cluster 4 showed negative interaction to these environments. Reverse adaptation pattern in these clusters was observed at Hisar test location as well. There was significant difference ($P < 0.05$) in flowering time of clusters 1 and 4 which might have influenced their response to different environments. This observation is supported by results of earlier studies [12-13] that phenology has a marked effect on yield response of millet across variable environments.

Cluster 2 showed contrasting adaptation in different test environments (Fig. 2). It showed positive interaction at Jodhpur, average at Jaipur and Patancheru and negative interaction at Fatehpur and Hisar. Adaptation to all environments was indicated for cluster 5 that contained improved cultivars including hybrids. This was the only group that showed high positive interaction at the two highest yielding sites but simultaneously showed a little more sensitivity to the lowest yielding site as compared to other sites. On the other hand, cluster 3 appeared to be the most stable group but at a relatively poor performance level throughout as compared to cluster 5 (Fig. 2). This can be best seen by comparing the regression coefficients and deviation from regression of different groups (Table 2). Cluster 3 had a regression coefficient of unity and a minimum value of deviation squares from regression. The regression coefficient of more than unity of cluster 5 indicated that this group of genotypes was better adapted to favourable environments.

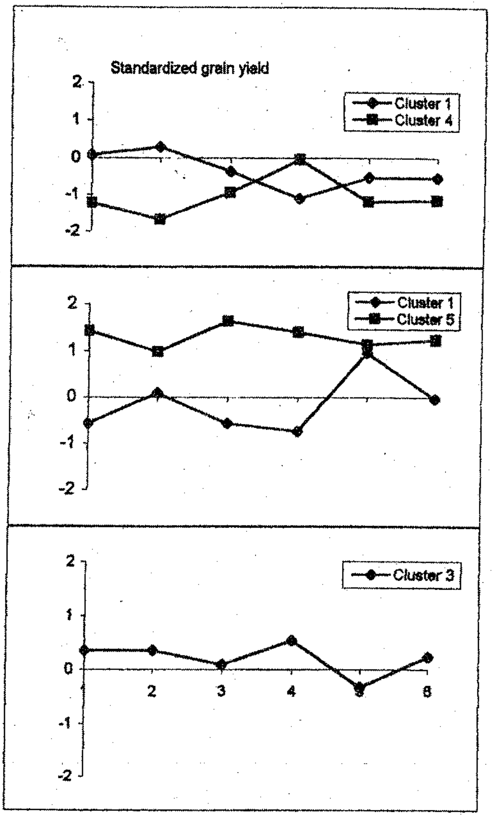

Fig. 2. Perofrmance plots of five entry groups at six locations (1 = Agra, 2 = Jaipur, 3 = Fatehpur, 4 = Hisar, 5 = Jodhpur and 6 = Patancheru)

The genotypes of cluster 3 are thus the most potential sources for developing the cultivars that would provide stable yield performance. This group contains landraces, improved materials and also their crosses.

Table 2. Mean performance, regression coefficients and deviation mean squares from regression of five groups of pearl millet genotypes for grain yield

Group	Mean grain yield (kg ha^{-1})	Regression coefficient	Deviation from regression
Cluster 1	1585	0.92	58844
Cluster 2	1631	0.92	39030
Cluster 3	1805	1.03	39591
Cluster 4	1413	0.82	59895
Cluster 5	2162	1.27	110068

This observation suggests that sources of adaptation, measured in terms of consistently higher grain yield, are not exclusively found in landrace group, as usually claimed, rather they are available in improved materials as well and can be identified through evaluation over variable environments.

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