Research Article

Genetic Diversity Analysis among Maintainer Lines of Pearl Millet [*Pennisetum glaucum* (L.) R. Br.] Based on Grain Yield and Yield Component Characters

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Abstract

A field experiment was conducted to study genetic diversity among forty eight pearl millet genotypes at Chaudhary Charan Singh Haryana Agricultural University, Hisar using Principal Component Analysis (PCA) and Principal Factor Analysis (PFA). The first five principal components (PCs) having eigen values more than one accounted for 81.02% of the total variability attributable to grain yield. Most important traits in PF1 were 1000 grain weight, green fodder yield/plant, dry fodder yield/plant and grain yield/plant and captured 25.12% of the total variation. PF2 was represented by days to 50% flowering, panicle length, number of productive tillers/plant and plant height and contributed 19.9% of the total variation. PF3 represented panicle length with 13.8% and PF5 represented panicle diameter with 10.1% of the total variation. All genotypes were plotted for PF1 as X-axis and PF2 as Y-axis. Graphical display of genotypes indicated that genotypes HMS 7B, HMS 45B, HMS 49B, HMS 61B, ICMB 97111 were superior for grain yield, number of productive tillers/plant and panicle length.

Keywords: Pearl millet, PCA, principal factor analysis, genetic diversity, eigen value, principal components

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Introduction

Pearl millet which is grown as a staple food grain and is source of feed and fodder is the most drought tolerant warm season crop. It is grown on an area of about 26 million hectares in Asia, Africa and Latin America. In India, pearl millet is most widely cultivated cereal after rice and wheat. The grain production has increased from 3.5 to 9.5 million tones with 47.9% which is mainly due to adoption of high yielding hybrids and cultivars and suitable agro-production technologies. During last three decades, there is substantial increase in production of pearl millet in India. This additional pearl millet grain is being diverted to cattle feed in northern India, poultry feed in southern India and also in beverage industries. Though there are no base line surveys available but it is estimated that 40-50% of pearl millet grain is being diverted to be used in feed and other industries.

It is necessary to increase emphasis on development of dual purpose (grain cum fodder) pearl millet for ensuring high grain yield as well as high dry fodder yield under rainfed cultivation. Existence of genetic variability is necessary to develop an effective breeding programme. Pearl millet is considered as a rich reservoir of genetic variability in terms of yield components, adaptation and quality traits. Exploiting genetic variability in the available germplasm lines hold good promise for releasing hybrids having high grain and fodder yield [1]. It has been suggested to use genetic resources to develop sustainable solutions to basic crop constraints, but the main difficulty is that there is large number of variation effects and lack of sufficient evaluation and classification techniques. For grouping of the germplasm to select for diverse types, there are various first degree and second degree statistics are available. But sometimes there is a problem in interpreting the recorded data as it become unmanageable and complicated to interpret. So, it become necessary to reduce large number of germplasm lines up to a manageable source for identification of characters of significance to be used in breeding programme with a greater degree of reliance. For this, often PCA have been used [2].

The present investigation was undertaken to evaluate, categorize and classify for similarity and degree of diversity based on data recorded on nine morphological characters using Principal Component Analysis.

Materials and Methods

A number of 48 lines were sown in of pearl millet in randomized block design with three replications raised at the farm area of Department of Genetics and Plant Breeding, CCSHAU, Hisar during *Kharif*, 2014. The plot size was

1R×4m×0.45m. All recommended package of practices were adopted to raise a good crop. Observations were recorded on plot basis using five random plants per entry per replication at the designated stage for yield and its component traits *viz*., days to 50% flowering, panicle length, panicle girth, number of productive tillers/plant, plant height, 1000 grain weight, green fodder yield/plant, dry fodder yield/plant and grain yield/plant.

Statistical Analysis

Principal component and factor analysis was carried out on 48 genotypes using SPSS package. Principal component analysis reduce the data with large number of correlated variables into substantially smaller set of new variables, through linear combination of the variables that accounts for most of the variation present in the original variables. Generally either correlation matrix or variance-covariance matrix are used to estimate principal components. Anderson-Rubin method [3] is then used to determine principal factor scores which is a modification of Bartlett's method.

Results and Discussion

Analysis of variance was significant for all the nine characters studied at 5 per cent level of significance which indicate large variability present in the material. Thus, it was worthwhile to proceed further for multivariate diversity analysis.

Principal component analysis was done for dimensional reduction and to know the importance of different traits in explaining multivariate polymorphism.

Principal components having eigen values greater than one were selected for interpretation in the present investigation [4]. The first five principal components having eigen values greater than one altogether explained 81.021% of the total accumulated variability (**Table 1**). Out of five principal components, the first principal component explained 25.12% of the total variation. And 19.91%, 13.79%, 12.15% and 10.05% of the total variance was explain by second, third, fourth and fifth principal components, respectively. [5] reported that first three component together explained 86.63% of the total variability. Similarily, [2]; [6] and [7] reported that 77.7%, 81.03% and 70.97% of total variability was explained by first six, four and four principal components, respectively.

Table 1 Total variance explained by different principal components in pearl millet maintainer lines

Principal components	Eigen value	Variation explained (%)	Cumulative variation explained (%)
1	3.265	25.12	25.12
2	2.588	19.91	45.03
3	1.793	13.79	58.82
4	1.579	12.15	70.97
5	1.307	10.05	81.02

Principal component analysis does not assume a definite model. In this, the total variation contained in a set of variables is considered. Further, principal factor analysis was carried out which centers on that part of variance which is shared by common factors leaving aside the unique factor (including error) of the variable. This is considered as the most commonly used method and it can also be placed in a meaningful biological context [8]. First, principal factor analysis was carried out without any rotation to derive clear picture of interaction of variables among themselves and with the principal factors (**Table 2**). The results of Table 2 showed that eight variables viz., days to 50% flowering, panicle length, number of productive tillers/plant, plant height, 1000 grain weight, green fodder yield/plant, dry fodder yield/plant and grain yield/plant had very high loading on the first factor. One variable, panicle girth showed high loading on second and fifth factor. Third and fourth factor have no loading of a character. So, it did not derive clear picture of interaction as some factors had very high loading of variables and some have none. So, next alternative was used i.e. factor analysis with varimax rotation method as described in **Table 3** [4].

The results presented in Table 3 clearly indicated that, the first principal factor showed high loading for 1000 grain weight, green fodder yield/plant, dry fodder yield/plant and grain yield/plant. Similarily, days to 50% flowering, panicle length, number of productive tillers/plant were highly loaded on second and panicle length was highly loaded on third principal factor, respectively. The fifth principal factor enabled high loading for panicle girth. [2] reported that dry fodder weight, plant height and grain yield were highly loaded on same principal factor. Similarily, [7] found that days to 50% flowering, plant height, panicle length, grain yield/plant had high loading on first principal factor. Similarly, dry matter yield/plant had high loading on second and productive tillers/plant had high loading on third, fourth principal factor.

Table 2 Factor loading of different characters with respect to different principal factor (Unrotated)

Characters/Principal Factor	PF-1	PF-2	PF-3	PF-4	PF-5
Days to 50% flowering	.673*	.366	.200	-.012	-.237
Panicle length	.704*	-.116	.478	.145	-.327
Panicle girth	.218	.556*	.054	-.410	.556*
Number of productive tillers /plant	.729*	-.136	.100	-.393	-.191
Plant height	.751*	-.094	.156	-.514*	-.252
1000 grain weight	.725*	.022	-.289	-.040	.205
Green fodder yield/plant	.850*	-.138	-.342	-.038	.029
Dry fodder yield/plant	.721*	-.177	-.380	.298	.217
Grain yield/plant	.903*	-.106	-.311	.042	.078
*High loading					

Table 3 Factor loading of different characters with respect to different principal factor (Varimax rotation)

Characters/PF	PF-1	PF-2	PF-3	PF-4	PF-5
Days to 50% flowering	.224	.553*	.354	.435	.108
Panicle length	.173	.648*	.580*	.066	-.272
Panicle girth	.089	.072	.082	.112	.897*
Number of productive tillers /plant	.350	.785*	.060	-.069	.066
Plant height	.285	.910*	.029	-.050	.115
1000 grain weight	.728*	.259	.094	.064	.207
Green fodder yield/plant	.830*	.411	.045	.038	.011
Dry fodder yield/plant	.886*	.046	.200	.006	-.070
Grain yield/plant	.872*	.381	.146	.063	.026
*High loading					

Using the principal factor scores (PF scores), graph plotted to represent the position of genotypes on X and Y-axis taking two most important factors at one time and to chalk out the breeding plan for further improvement by identifying superior parents for hybridization/crossing programme. In **Figure 1**, all the genotypes were plotted for PF-1 (1000 grain weight, Green Fodder Yield, Dry Fodder Yield, Grain Yield) and PF-2 (DF, SL, NPT, PH).

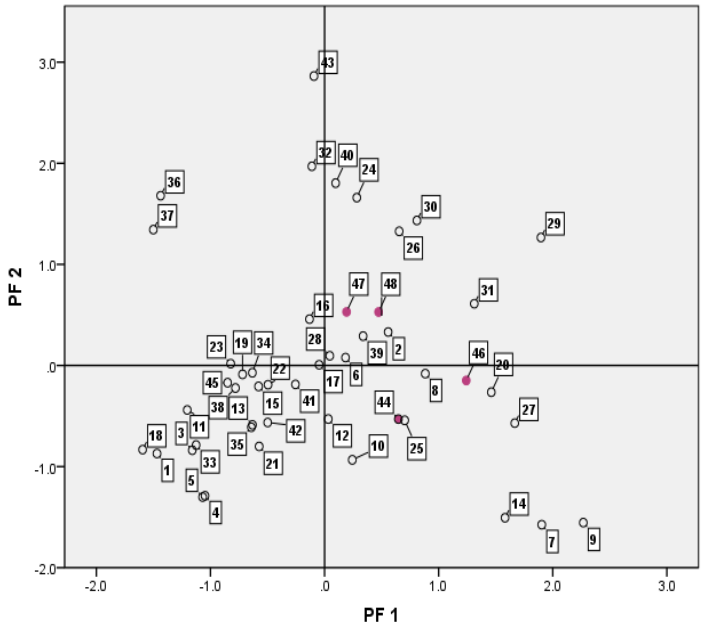

Figure 1 Distribution of Pearl millet genotypes based on Principal Factor 1 and 2
(1-HMS 6B, 2-HMS 7B, 3-HMS 13B, 4-HMS 16B, 5-HMS 18B, 6-HMS 20B, 7-HMS 21B, 8-HMS 22B, 9-HMS 23B, 10-HMS 26B, 11-HMS 28B, 12-HMS 29B, 13-HMS 30B, 14-HMS 32B, 15-HMS 33B, 16-HMS 34B, 17-HMS 36B, 18-HMS 37B, 19-HMS 38B, 20-HMS 39B, 21-HMS 40B, 22-HMS 41B, 23-HMS 42B, 24-HMS 43B, 25-HMS 44B, 26-HMS 45B, 27-HMS 46B, 28-HMS 47B, 29-HMS 48B, 30-HMS 49B, 31-HMS 51B, 32-HMS 52B, 33-HMS 53B, 34-HMS 54B, 35-HMS 55B, 36-HMS 56B, 37-HMS 58B, 38-HMS 59B, 39-HMS 60B, 40-HMS 61B, 41-HMS 62B, 42-HMS 63B, 43-HMS 64B, 44-81B, 45-ICMB 843-22, 46-ICMB 94555, 47-ICMB 97111, 48-Tift 23 D_2B)

In Figure 1, the genotypes HMS 21B, HMS 23B, HMS 39B, HMS 44B, HMS 46B, HMS 55B, HMS ICMB 94555, HMS 22B *etc.* were found to have high 1000 grain weight, dry fodder yield, green fodder yield and grain yield/plant stood out towards the positive portion of PF1 axis in the plot, whereas the genotypes which had high number of productive tillers/plant, spike length, plant height clustered towards the positive side of PF2 axis (Figure 1), such genotypes were HMS 52B, HMS 56B, HMS 58B, HMS 64B *etc.* The genotypes which found place towards the positive end of the PF-1 and PF-2 are supposed to be superior collectively both for high yield, high number of productive tillers/plant and spike length. On the basis of present investigation, genotypes HMS 7B, HMS 45B, HMS 49B, HMS 61B, ICMB 97111 *etc*. have been identified superior for both the characters collectively. HMS 6B, HMS 18B, HMS 37B, HMS 55B *etc*. were found to be separated on negative axis of PF1 and PF2 showing earliness of these varieties.

Conclusion

The present study was proved to be successful in classifying different genotypes based on various morphological characters. It reduces large number of variables into only five principal components and principal factors. It also helps in identifying different genotypes better for different combinations of characters. For evaluation and characterization of genetic variation in pearl millet, the results of the present study can be used as a stepping stone for evolving well defined approach. It can be utilized in various breeding programmes depending on their specific objectives.

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