

Identification of superior male sterile lines and landraces based on simultaneous selection indices and PCA analysis among pearl millet [*Pennisetum glaucum* (L.) R. Br.] genotypes

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ABSTRACT

Two male sterile lines and thirty pearl millet genotypes were evaluated to identify potential genotypes based on their selection indices and spatial distances. The traits grain number per panicle recorded maximum expected genetic advance, followed by plant height, leaf length, green fodder yield, grain number per unit structural panicle mass, total biomass and days to 50% flowering. The first six principal components with more than one eigen value contributed 83.7% of variability in the studied genotypes. Based on simultaneous selection indices and PCA analysis the landraces 2348, 2325, 2328, 2370, 2382, 2368 and male sterile line ICMA 97111 recorded highest selection index values and were also spatially diverse in 2D and 3D scatter diagrams. Hence, the cross combinations resulted from these genotypes may result in the development of superior hybrids. The identified landraces will also be improved as new inbred lines by population improvement methods.

Key words : Selection index, PCA analysis, Eigen value and pearl millet

Introduction

Pearl millet is an important drought tolerant food and fodder crop widely grown under the harsh climatic conditions of arid and semi-arid regions of India and Africa. Because of its well adoptive and growing nature in adverse conditions, traditionally it has been considered as poor man's bread (Sharma, *et al.*, 2020). In India, it occupies fourth place in its importance as stable food after rice, wheat and sorghum with 10.36 million tones of production from 7.54 million hectares of area and with 1373.86kg/ha of unit production (Ministry of Agriculture, 2019-

2020).

The success of any hybridization programme depends on selection of superior plants with diverse gene complexes. The superior plants would be not only with respect to improved yield but also contain other improved traits. As the yield is a complex quantitative character and is always depends on several other traits. Hence in breeding programmes, for phenotypic selection of a desirable plant from any population or segregating material aimed at simultaneous improvement of several characters. The rapid improvement in the economic value is expected from simultaneous selection applied to all

the characters, which will determine the economic value of a plant (Dabhulkar, 1992). Smith (1937) proposed the concept of selection index based on the discrimination function of Fisher (1936). An index or score was constructed by combining the component characters by providing appropriate weights to each character according to their relative importance, heritability and correlations between characters and the selection based on the index of each genotype will result in improvement of the economic value.

The desirable plants with diverse nature can be identified by multivariate analysis. Differentiation among genotypes was resulted from gradual divergence accumulated over time at different stages during evolution. Principal component analysis is eigen vector based multivariate analysis, measures the divergence among genotypes in terms of spatial distances and also indicate the characters contribute at each axes of differentiation (Sharma, 1988). PCA along with 2D cluster analysis helps in identification of few variables which contribute maximum towards genetic diversity by reducing dimensionality of large data and in selection of diverse clusters of genotypes, respectively. To identify the diverse plants with superior characters and the traits that contribute maximum variability, the present study contained 32 genotypes which were evaluated by simultaneous selection indices and PCA analysis.

Materials and Methods

Two male sterile lines (ICMA 97111 and ICMA 04999) developed by ICRISAT, Hyderabad and thirty landraces collected from four different states comes under two zones of India *viz.*, Madhya Pradesh (A zone) and; Maharashtra, Tamilnadu and Andhra Pradesh (B zone) were evaluated at Indian Institute of Millets Research, Hyderabad during *Kharif*, 2019. The genotypes were planted in alpha lattice design with three replications. Each genotype was sown in two rows of four meter length with 45 × 15 cm spacing between and within rows, respectively. The yield component traits *ie.*, 18 quantitative traits *viz.*, days to 50% flowering, plant height, leaf length, leaf width, stem width, tillers/plant, productive tillers/plant, panicle length, panicle width, panicle weight, 1000-grain weight, grain number/panicle, grain number per unit structural panicle mass, fresh fodder yield, dry fodder yield, total biomass, harvest index and grain yield and four grain quality traits *viz.*, iron content, zinc content, protein

and rancidity were recorded. Days to 50% flowering, panicle weight, fresh fodder yield, dry fodder yield, total biomass, harvest index, grain yield, iron content, zinc content, protein content and rancidity were recorded on plot basis; while the remaining traits were recorded on five competitive plants selected randomly in each replication. In the present study, selection index or score was constructed by giving inverse mean of each character as their appropriate economic weights. PCA analysis transforms all possible correlated variables into few uncorrelated variables called principle components. The number of principle components formed will be equal to the number of variables studied, here PCI, PCII, PCIII, ..., PC XXII. In each principal component the loadings of each character represents their contribution at that axis of differentiation. Loadings sign (+,-) indicate the direction of contribution. The first principal loadings were chosen so as to make its variance as large as possible. Loadings of second PC were chosen such that the variance of PCII is large as possible and with a constraint that PC I and PC II are uncorrelated. This process was continued to create 22 principle components. But the eigen values less than one are practically not significant (Legendre and Legendre, 1984). From the results of PCA, the PCA scores of each genotype under first two axes with maximum percent of variation and with more than one eigen value were used for clustering of genotypes as suggested by Anderberg (1993).

Results and Discussion

Simultaneous selection indices

Selection index scores can be constructed by assigning equal economic weights as well as by inverse means as economic weights, both the methods are almost equally efficient in identifying superior genotypes (Pavani ana Babu, 2020). The economic weights (a_i values) for all the characters were taken as inverse of means in the present study. From a_i values weighing coefficients (b_i values) were calculated and these were used for the estimation of expected genetic advance for each character. The economic weights (a_i), weighing coefficients (b_i) and expected genetic advance for all the traits under study were presented in Table. 1. Rancidity (6.430) recorded maximum economic weight, followed by harvest index (5.40), stem width (1.163), grain yield

(0.5693), panicle width (0.417), zinc content (0.319), panicle weight (0.294), leaf width (0.286), tillers per plant (0.280), iron content (0.173), dry fodder yield (0.128) and test weight (0.111). Among the 22 traits Grain number per panicle (376.891) recorded maximum expected genetic advance, followed by plant height (12.918), leaf length (5.086), green fodder yield (4.374), Grain number per unit structural panicle mass (3.948), total biomass (2.638) and days to 50% flowering (2.270).

Simultaneous selection index values or scores were constructed for all the genotypes by considering all the 22 characters using weighing coefficients (b_i values) (Table 2). Among the landraces, 2348

(24.003) recorded highest index value followed by 2325 (24.00), 2332 (22.902), 2370 (22.343), 2328 (22.242) and 2382 (22.085) while, 2318 (16.801), 2329 (14.583) and 2309 (14.261) recorded least index values. The male sterile line ICMA 97111 (21.117) recorded highest selection index value than ICMA 04999. The graphical representation of genotypes based on their selection index values in descending order are shown in Fig. 1. Similar technique was employed earlier to identify superior genotypes in different crops; Pavani and Babu (2020) in foxtail millet; Srilakshmi *et al.* (2017) in finger millet and Kumar *et al.* (2012) in sorghum.

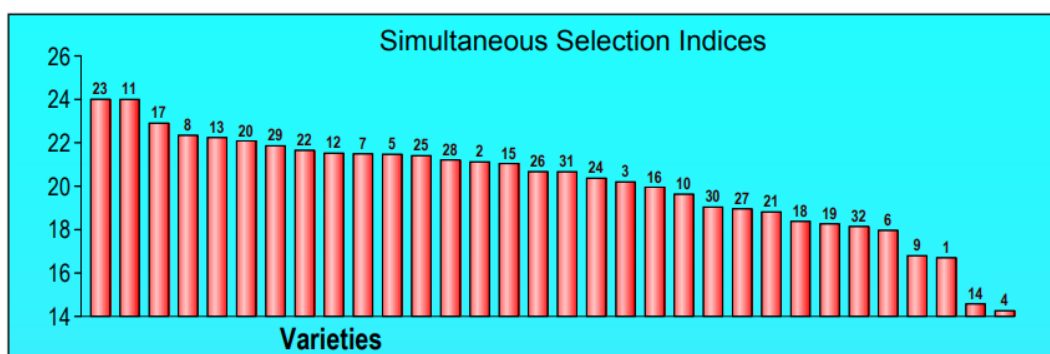


Fig. 1. Selection index values of 32 pearl millet genotypes

Table 1. Economic weights, weighing coefficients and genetic advance of different characters in pearl millet

S. No.	Characters	Economic weights (a_i values)	Weighing coefficients (b_i values)	Expected genetic advance
1.	Days to 50% flowering	0.0180	0.0137	2.2704
2.	Plant height	0.0058	0.0025	12.9176
3.	Leaf length	0.0165	0.0148	5.0856
4.	Leaf width	0.2857	0.2410	0.2318
5.	Stem width	1.1630	1.4982	0.0694
6.	Tillers per plant	0.2798	0.3718	-0.1314
7.	Productive tillers per plant	0.4174	0.3056	-0.0520
8.	Panicle length	0.0471	0.0228	1.8394
9.	Panicle width	0.4136	0.5222	0.2661
10.	Panicle weight	0.2937	0.3289	0.5961
11.	Test weight	0.1105	0.0675	0.3014
12.	Green fodder yield	0.0503	0.0520	4.3743
13.	Dry fodder yield	0.1282	0.3021	2.0311
14.	Grain number per panicle	0.0008	0.0009	376.8907
15.	Total biomass	0.0893	-0.0624	2.6378
16.	Harvest index	5.2399	5.4590	0.0286
17.	Grain number per unit structural panicle mass	0.0592	0.0533	3.9484
18.	Grain yield	0.5693	0.6217	0.5886
19.	Zinc content	0.3188	0.3533	-0.1984
20.	Iron content	0.1727	0.1587	-0.1448
21.	Protein	0.0943	0.0382	-0.1438
22.	Rancidity	6.4296	6.3924	0.0094

Principal Component Analysis

Among the 22 principal components formed, the first six PC's or vectors were significant with eigen value more than one and contribute 83.7 % of cumulative variation towards the total variability in the studied genotypes (Table 3). The heritable variation contributed by first PC (PC I) was 29.164 %. The characters accounted maximum variance in this component are panicle length (0.332), grain number per panicle (0.320), stem width (0.306) and grain yield (0.300). The second principal component (PC II) accounted for 21.108 % and the maximum variation in this component was due to the traits *viz.*, days to 50 % flowering (0.360), leaf length (0.321), protein content (0.249) and leaf width (0.247). The genetic variation explained though the PC III was 12.500% with the highest loadings of plant height (0.469), rancidity (0.437), tillers per plant (0.303) and productive tillers per plant (0.301). Similarly, the percent of variation contributed by PC IV, PC V and PC VI were 8.934%, 6.668% and 5.333%, respectively. The percent of cumulative variances explained by the first six components were 29.164%, 50.273%, 62.772%, 71.706%, 78.375 and 83.707, respectively.

The PCA scores of 32 pearl millet genotypes in the first three PC's as X, Y and Z axes (Table 4) were plotted in a graph to get two dimensional (2D) and three dimensional scatter (3D) diagrams (Fig. 2&3). The genotypes numbered 23 (2348), 11 (2325), 13 (2328), 2 (ICMA 97111), 8 (2370), 20 (2382) and 7

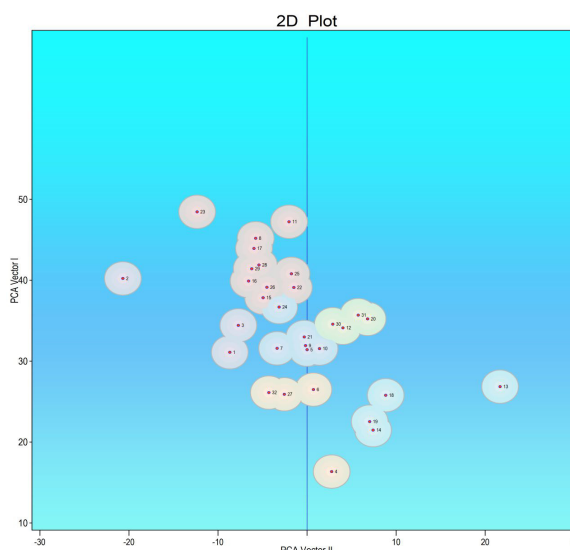


Fig 2. Two dimensional graph showing relative positions of 32 pearl millet genotypes based on PCA scores

(2368) are far apart from each other and falls under different clusters in 2D and 3D scatter diagrams. Further, the genotypes originated from same state were grouped under different clusters and also the genotypes explored from different states were falls under same cluster. This indicating that there is lack of correlation between geographical diversity and genetic diversity. In 2D scatter diagram solitary clusters were formed which may be due to geographic barriers preventing gene flow or intense natural and

Table 2. Selection index values of 32 pearl millet genotypes

S. No.	Genotype	Selection index or score	S. No.	Genotype	Selection index or score
1.	ICMA 04999	16.704	17.	2332	22.902
2.	ICMA 97111	21.117	18.	2333	18.379
3.	2306	20.194	19.	2337	18.269
4.	2309	14.261	20.	2382	22.085
5.	2310	21.467	21.	2342	18.809
6.	2311	17.964	22.	2386	21.650
7.	2368	21.486	23.	2348	24.003
8.	2370	22.343	24.	2352	20.370
9.	2318	16.801	25.	2364	21.401
10.	2381	19.629	26.	2365	20.667
11.	2325	24.000	27.	2387	18.959
12.	2327	21.515	28.	2394	21.212
13.	2328	22.242	29.	2395	21.860
14.	2329	14.583	30.	2396	19.033
15.	2330	21.040	31.	2346	20.662
16.	2331	19.954	32.	2349	18.140

Table 3. Eigen values, percent of variances, cumulative percent of variances and component loadings of first six principal components of pearl millet genotypes

	PC I	PC II	PC III	PC IV	PC V	PC VI
Eigene Value (Root)	6.416	4.644	2.750	1.966	1.467	1.173
% Var. Exp.	29.164	21.108	12.499	8.934	6.668	5.333
Cum. Var. Exp.	29.164	50.272	62.772	71.706	78.375	83.707
Days to 50% flowering	0.138	0.360	0.154	0.136	0.130	0.114
Plant height	0.152	0.073	0.469	-0.111	0.092	-0.061
Leaf length	0.240	0.321	0.058	0.049	0.085	0.090
Leaf width	0.249	0.247	-0.131	0.010	0.135	0.317
Stem width	0.306	0.127	-0.085	-0.050	0.302	0.171
Tillers per plant	-0.120	-0.277	0.303	-0.059	0.240	0.319
Productive tillers /plant	-0.156	-0.262	0.301	-0.011	0.185	0.258
Panicle length	0.332	0.114	-0.039	0.009	0.200	0.009
Panicle width	0.228	-0.006	-0.185	0.207	0.097	-0.271
Panicle weight	0.228	-0.212	-0.248	-0.297	0.025	0.056
Test weight	0.097	-0.145	0.150	0.108	0.074	-0.574
Green fodder yield	0.118	-0.172	0.299	-0.031	0.308	-0.288
Dry fodder yield	0.201	0.195	0.297	-0.269	0.001	-0.285
Grain number per panicle	0.320	0.040	0.151	-0.036	-0.276	0.124
Total biomass	0.044	0.068	-0.122	-0.584	-0.311	-0.145
Harvest index	0.223	-0.330	-0.023	0.158	0.011	0.088
Grain number per unit structural panicle mass	-0.024	0.215	0.071	0.513	-0.299	-0.064
Grain yield	0.299	-0.255	-0.073	-0.024	-0.125	-0.017
Zinc content	-0.293	0.240	0.057	0.029	0.004	-0.124
Iron content	-0.226	0.205	-0.077	-0.095	0.410	-0.107
Protein	-0.213	0.249	-0.013	-0.314	0.081	0.023
Rancidity	0.044	0.068	0.437	-0.066	-0.404	0.177

human selection for diverse and adaptable gene complexes. Similarly for identification of genotypes based on their spatial distances by PCA analysis were earlier reported by Chaudhary *et al.* (2015), Kumar *et al.* (2015), Rakesh *et al.* (2015), Verma *et al.* (2015) and Verma *et al.* (2016).

The hybrids developed from the cross combinations of male sterile lines and landraces may not maximize hybrid vigour but can increase yield potential than open pollinated varieties and also provide broad genetic base. The resultant hybrids also contain the agronomic characters of landraces preferred by farmers and provide more genetic diversity for diverse environmental conditions. In the present study the genotypes with highest selection index value *ie.*, 2348, 2325, 2328, ICMA 97111, 2370, 2382 and 2368 were also showed as diverse genotypes as they fell under different clusters in the scatter diagrams. Hence, the cross combinations ICMA 97111 × 2348, ICMA 97111 × 2325, ICMA 97111 × 2328, ICMA 97111 × 2370, ICMA 97111 × 2382 and

ICMA 97111 × 2368 may result in potential high yielding hybrids. The diverse landraces with more selection index value may also be used in development of improved inbred lines by following population improvement methods.

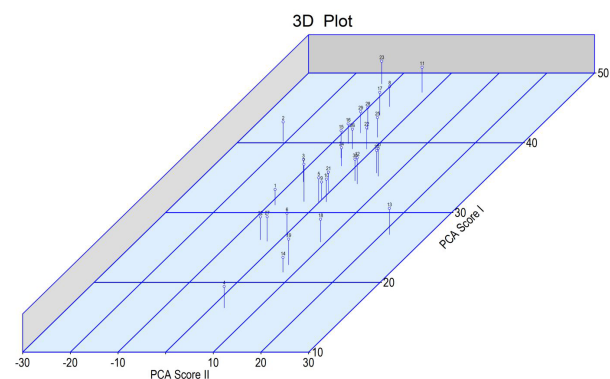


Fig. 3. Three dimensional graph showing relative positions of 32 pearl millet genotypes based on PCA scores

Table 4. PCA scores of respective vectors for 32 pearl millet genotypes

S. No.	Genotype	PCA I X Vector	PCA II Y Vector	PCA III Z Vector
1	ICMA 04999	31.091	-8.673	18.236
2	ICMA 97111	40.221	-20.681	22.791
3	2306	34.418	-7.713	26.125
4	2309	16.347	2.766	25.202
5	2310	31.412	0.008	29.358
6	2311	26.483	0.723	27.968
7	2368	31.581	-3.36	43.776
8	2370	45.177	-5.768	23.6
9	2318	31.922	-0.166	20.167
10	2381	31.546	1.401	26.659
11	2325	47.22	-2.023	29.525
12	2327	34.11	4.031	30.804
13	2328	26.847	21.68	30.726
14	2329	21.468	7.421	17.258
15	2330	37.835	-4.931	31.962
16	2331	39.898	-6.558	23.163
17	2332	43.928	-5.96	27.098
18	2333	25.778	8.836	26.773
19	2337	22.524	7.037	30.064
20	2382	35.216	6.806	32.665
21	2342	32.981	-0.314	23.067
22	2386	39.101	-1.478	25.027
23	2348	48.449	-12.343	26.59
24	2352	36.682	-3.133	21.483
25	2364	40.795	-1.756	23.162
26	2365	39.127	-4.504	23.121
27	2387	25.897	-2.547	28.784
28	2394	41.879	-5.4	26.096
29	2395	41.417	-6.209	25.038
30	2396	34.563	2.891	25.226
31	2346	35.682	5.747	26.306
32	2349	26.111	-4.285	26.853

References

- Anderberg, M.R. 1993. *Cluster Analysis for Application*. Academic Press, New York.
- Chaudhary, S., Sagar, P., Hooda, B.K. and Arya, R.K. 2015. Multivariate analysis of pearl millet data to delineate genetic variation. *For. Res.* 40(4): 201-208.
- Dabholkar, A.R. 1992. *Elements of Biometrical Genetics*. Concept Pub. Com. New Delhi.
- Fisher, R.A. 1936. The use of multiple measurements in taxonomic problems. *Ann. Eugen.* 7: 179-189.
- Kumar, C.V.S., Sreelakshmi, C.H. and Shivani, D. 2012. Selection indices for yield in *rabi* sorghum (*Sorghum bicolor* L. Moench.) genotypes. *Electron. J. Plant Breed.* 3(4) : 1002-1004.
- Kumar, R., Verma, U., Malik, V. and Vart, D. 2015. Multi-variate analysis for selection of diverse genotypes in pearl millet germplasm. *For. Res.* 41 (2): 73-77.
- Legendre, L. and Legendre, P. *Ecologia Numerique*. Presses de l'Universite du Quebec 1984;Xv+260p, viii+335.
- Ministry of Agriculture, 2019-2020. Government of India. <http://www.indiaagristat.com>
- Pavani, A. and Babu, D.R. 2020. Simultaneous selection for improvement of yield and nutritional components using classical selection index in foxtail millet [*Setaria italica* (L.) Beauv.]. *J. Pharmacogn. Phytochem.* 9(1) : 1502-1506.
- Rakesh, G., Shashibhushan, D., Reddy, T.D. and Nagesh, J.U. 2015. Evaluation of bajra [*pennisetum glaucum* (L.) R. Br.] germplasm lines for yield and yield related traits using principal component analysis. *Progress. Res. J.* 10 (Special-VII): 3885-3887
- Sharma, B., Ahugh, L., Singh, V.K, Sekhar, C. and Tanwar, N. 2020. Characterization of rancidity indicators in selected pearl millet genotypes by multivariate analysis. *Plant Archives*. Special Issue (AIAAS-2020): 229-235
- Sharma, J.R. 1988. *Statistical and Biometrical Techniques in Plant Breeding*. New Age Int. Pvt. Limt. Pub.
- Smith, F. 1937. A discriminant function for plant selection. *Ann. Eugen.* 7: 240-250.
- Srilakshmi, P., Babu, D.R., Kumar, P.V.R. and Kumar, P.A. 2017. Simultaneous selection for nutritional and yield components using classical selection index in finger millet [*Eleusine coracana* (L.) Gaertn.]. *Environment and Ecology.* 35(3C): 2380-2384.
- Verma, U., Kumar, R. and Dalal, M.S. 2015. Genetic diversity analysis in pearl millet germplasm. *Int. J. Agric. Stat.* 11(2): 335-340.
- Verma, U., Kumar, R. and Dalal, M.S. 2016. An application of multivariate techniques for divergence study in pearl millet germplasm. *Statistics and Applications.* 14 (1&2): 63-73.