



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.03
TPI 2018; 7(4): 661-664
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www.thepharmajournal.com
Received: 15-02-2018
Accepted: 17-03-2018

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Evaluation of rice germplasm for genetic diversity on yield characters by principal component analysis

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Abstract

A population comprising 98 rice genotypes were evaluated for 13 agro - morphological traits by principal component analysis for determining the pattern of genetic diversity and relationship among individuals. Thirteen quantitative characters *i.e.* plant height, leaf length, leaf width, number of productive tillers per plant, panicle per plant, panicle length, number of grains per panicle, days to 50% flowering, days to harvest maturity, biological yield, harvest index, test weight and single plant yield were measured. Maximum variation was observed for flag leaf width followed by number of panicles per plant, tillers per plant, test weight and flag leaf length. Days to maturity has shown the least variation. In PCA, Component 1 had the contribution from the traits such as days to maturity and harvest index which accounted 25.34% of the total variability. Plant height, biological yield per plant and grain yield per plant has contributed 19.30% of total variability in component 2. The remaining variability of 11.86%, 10.26%, 7.61% and 5.64% was consolidated in component 3, component 4, component 5 and component 6 by various traits such as flag leaf width, number of productive tillers per plant, days to 50% flowering, spikelets per plant, flag leaf length, panicles per plant, test weight and panicle length. The cumulative variance of 80.04% of total variation among 13 characters was explained by the first six axes. Thus the results of principal component analysis used in the study have revealed the high level of genetic variation and the traits contributing for the variation was identified. Hence this population can be utilized for trait improvement in breeding programs for the traits contributing major variation.

Keywords: genetic diversity, principle component analysis, rice

1. Introduction

Rice is a major agriculture crop in India grown under diverse ecological conditions (Gopikanan *et al.*, 2013), with varied phenology and yield. History shows that technological advancement and its applications in agricultural crop plants brought great respite at times when burgeoning population desperately needed security in food fronts (Shetty *et al.*, 2014) [7]. The success of plant breeding depends on the availability of genetic variation, knowledge about desired traits, and efficient selection strategies that make it possible to exploit existing genetic resource (Rai *et al.*, 2013).

Before exploiting a population for trait improvement, it is necessary to understand the magnitude of variability in the population which is fundamental for genetic improvement in all crop species. Genetic distance estimates for population grouping can be estimated by different methods as it is crucial to understand the usable variability existing in the population. One of the approaches is to apply is multivariate analysis. Multivariate statistical tools include Principal Component Analysis (PCA), Cluster analysis and discriminate analysis (Oyelola *et al.*, 2004). Principal Component Analysis (PCA) can be used to uncover similarities between variable and classify the cases (genotypes), while cluster analysis on the other hand is concerned with classifying previously unclassified materials (Leonard *et al.*, 2009) [4]. Principal Component Analysis (PCA) is a multivariate technique that analyzes a data table in which observations are described by several inter-correlated quantitative dependent variables. Proper values measure the importance and contribution of each component to total variance, whereas each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated. The higher the coefficients, regardless of the direction (positive or negative), the more effective they will be in discriminating between accessions.

The study is aimed to identify and classify variation for grouping the genotypes by taking into account several characteristics and relationship between them.

2. Material and Methods

The experiment was conducting during *kharif 2013* at the field Experimentation Centre, Department of Genetics and Plant Breeding, SHUATS, Allahabad. The Experimental material comprised 98 rice genotypes and it was laid out in randomized block design with the gross plot area of 2260 m² and net plot area of 1800 m² with three replications. Observations were recorded for 13 quantitative traits viz., days to 50% flowering, days to maturity, flag leaf length, flag leaf width, panicle length, tillers per Plant, panicle per plant, plant height, test weight, spikelets per panicle, biological yield per plant, harvest index and grain yield per plant. Genetic diversity analysis was conducted by NTSYS-PC software (version 2.1) and Minitab software (version 15).

3. Results and Discussion

Maximum variation was observed for flag leaf width with CV of 13.09% followed by panicles per plant (CV= 10.95), number of tillers per plant (CV= 10.82) and test weight (CV= 7.24). Days to maturity has shown the least variation with the CV of 2.72%. Number of spikelets per panicle ranged from (260.00) in the variety SHIATS DHAN 1 to (101.00) in the variety PAU 3842-59-7-1-1. The variety PAU 3842-59-7-1-1 took maximum days for 50% flowering (118.66 days) while the variety BPT-2615 took minimum days (80.89 days) and variety 102 (33.53 g) recorded high and variety PAU 3842-59-7-1-1 recorded low (9.33 g) grain yield per plant.

For selection of parents, genetic diversity is one of the important decisive factors (Mazid *et al* 2013) [5]. Euclidean distance was calculated using standardized morphological data and a UPGMA dendrogram was constructed using these values for 98 rice genotypes. Cluster I contained maximum number of genotypes (19), which consisted of 18% of all genotypes, cluster III consist of 13 genotypes and cluster IX and X, consists 12 genotypes. In Principal component analysis, cumulative variance of 80.04% by the first six axes with Eigen value of > 1.0 indicates that the identified traits within the axes exhibited great influence on the phenotype of population panel (Table 2). Principal Component Analysis measures the importance and contribution of each component to total variance. It can be used for measurement of independent impact of a particular trait to the total variance whereas each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated. Higher the coef-

ficients, regardless of the sign, the more effective they will be in discriminating between accessions. The different morphological traits contribute for total variation calculated for each component. For Component 1 which has the contribution of days to maturity (0.341) and harvest index (0.427) for 25.35% of the total variability. For component 2, plant height (0.42), biological yield per plant (0.19) and grain yield per plant (0.33) has contributed 19.30% of total variability. Similarly flag leaf width (0.62) and number of tillers per plant (0.40) has contributed for the total variation of 11.86% for component 3, days to 50% flowering (0.51), spikelets per plant (0.43) and flag leaf length (0.37) for component 4, panicle per plant (0.50) and test weight (0.18) for component 5 and panicle length (0.46) for component 6.

The first four components in the PCA analysis with eigen values >1 contributed 67.76 per cent of the variability among genotypes evaluated for different agro-morphological traits. Other PCs (5 & 6) had eigen values less than 1. Thus, the prominent characters coming together in a particular principal component by contributing towards variability has the tendency to hang together offer opportunity for its utilization in crop breeding. Similarly, Worede *et al* (2014) [2] explained 61.2% of the total variability using the first and second PCs. Approximately, 82.7% of the total variation among 32 upland rice varieties was also noted by Lasalita-Zapico *et al.* (2013).

Table 1: Characteristic means and variations of 98 accessions

Variable	Mean	C.V	CD 5%	Range lowest	Range highest
DFP	94.61	3.94	6.01	80.89	118.66
PH (cm)	107.41	6.25	10.82	78.00	127.72
FLL (cm)	32.03	6.78	3.50	19.96	47.66
FLW(cm)	1.25	13.09	0.26	0.90	1.75
TPP	12.43	10.82	2.16	8.00	16.66
PPP	10.64	10.95	1.87	7.33	13.66
PL (cm)	24.51	5.52	2.18	16.66	28.96
DM	129.73	2.72	5.70	115.89	153.66
SPP	170.81	3.60	9.92	101.00	260.00
TW (g)	20.28	7.24	2.36	15.06	27.47
BYPP (g)	57.40	3.57	3.30	21.66	96.66
GYPP (g)	21.48	5.69	1.96	9.33	33.53
HI %	38.13	6.55	4.02	22.17	50.51

DFP- Days to 50% percent Flowering, FLL- Leaf Length, FLW- Flag leaf width, PH- Plant Height, NTPP- Number of Tiller per plant, PL- Panicle Length, DM- Days to Maturity, GYPP – Grain yield per plant, HI- harvest index, SPPP- spikelet per panicle, BYPP- biological yield per plant, TW- test weight, PPP- panicle per plant.

Table 2: Eigen value and percent of total variation and component matrix for the principal component axes

	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
Eigene Value (Root)	3.295	2.510	1.542	1.335	0.990	0.734
% Var. Exp.	25.346	19.305	11.864	10.267	7.615	5.643
Cum. Var. Exp.	25.346	44.652	56.516	66.783	74.397	80.04
DFP	0.161	0.385	0.161	0.512	0.148	0.209
PH (cm)	-0.048	0.425	0.303	0.397	0.181	0.136
FLL (cm)	-0.196	0.165	-0.271	0.379	-0.519	-0.438
FLW(cm)	-0.160	-0.241	0.625	0.004	-0.180	0.079
TPP	-0.285	-0.251	0.403	0.193	-0.293	-0.255
PPP	-0.190	-0.359	-0.079	0.137	0.501	-0.122
PL (cm)	-0.235	0.329	0.035	-0.365	-0.302	0.469
DM	0.341	0.236	0.180	-0.135	0.212	-0.487
SPP	-0.098	-0.254	-0.377	0.437	-0.056	0.335
TW (g)	-0.413	0.124	0.131	-0.010	0.183	-0.114
BYPP (g)	-0.442	0.192	-0.070	-0.169	0.134	-0.011
GYPP (g)	-0.248	0.335	-0.225	-0.098	0.008	-0.277
HI %	0.427	0.007	0.030	-0.017	-0.341	-0.018

Note: PC1, first principle component; PC2, second principle component; PC3, third principle component; PC4, four principle component and PC5 fifth principle component.

Table 3: Cluster analysis of 98 rice genotypes based on yield and yield associated characters

Group	Cluster Members
1	8 9 14 15 16 17 20 22 23 26 38 39 40 47 48 50 72 85 87
2	18 35 80 86 88 94 97
3	27 45 61 66 67 68 82
4	30 43 57 58 59 60 71
5	11 13 32 44 52 77 78
6	19 24 28 29 33 34 36 69
7	42 62 63 64 65 70
8	1 2 3 4 5 6 7 10 51 73 74 75 76
9	12 41 46 49 53 55 56 81 83 84 92 93
10	21 25 31 37 54 79 89 90 91 95 96 98

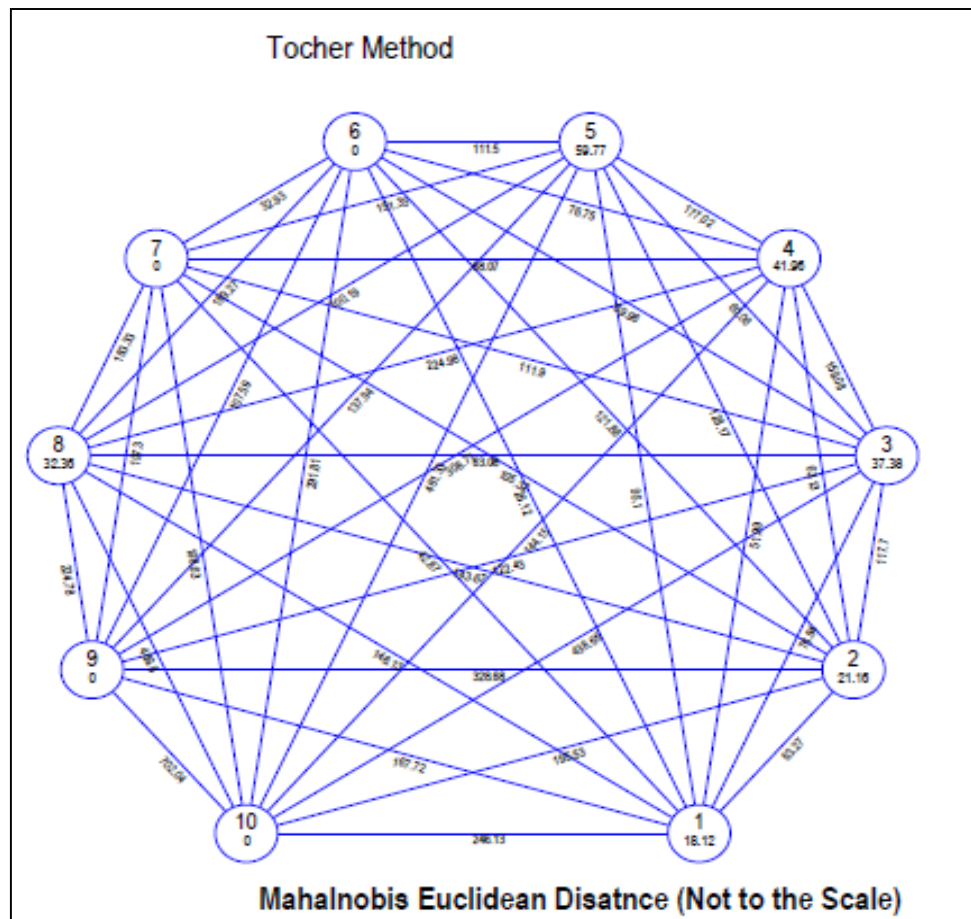


Fig 1: Cluster analysis of 98 rice genotypes based on yield and yield associated characters

5. Conclusions

The present study showed the existence of a considerable level of diversity among 98 rice genotypes. Principal component analysis has identified few characters that plays prominent role in classifying the variation existing in the germplasm set. The analysis identified days to 50% flowering, days to maturity, test weight, biological yield, flag leaf length and grain yield per plant in different principal components are the most important characters for classifying the variation. Thus the results of principal component analysis used in the study have revealed the high level of genetic variation existing in the population panel and explains the traits contributing for this diversity. Hence the results will be of greater benefit to identify parents for improving various morphological traits analyzed in this study.

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