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Genetic Diversity Studies for Yield and Yield Component Traits using Principal Component Analysis in Rice (*Oryza sativa* L.)

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ABSTRACT

The present investigation was carried out to assess the diversity among 107 rice genotypes with regards to yield and yield component traits. Principal component analysis was utilized to evaluate the variation and to estimate the relative contribution of various traits for total variability. Results revealed three principal components with eigen value > 1. These components contributed for a total variability of 69.412 per cent. Component 1 (PC 1) had contributed maximum of 33.594 per cent while PC 2 had contributed to 22.566 per cent and PC 3 had contributed to 13.251 per cent towards the total variability. The characters, namely, panicle length, days to 50 per cent flowering, ear bearing tillers per plant, plant height and test weight were observed to explain maximum variance in PC 1. The results of 2D scatter diagram revealed RTCNP 9 and MTU 1006 genotypes to be most diverse. Hybridization of these diverse genotypes is therefore predicted to result in desirable transgressive segregants.

Keywords: *Genetic Divergence, Principal Component, Rice, Yield*

INTRODUCTION

Rice is one of the most extensively cultivated cereal crops in the world and a primary source of food for more than half of the world's population. Among the rice growing countries, India has largest area in the world *i.e.* 43.86 million hectares and ranks second in production with 99.24 million tonnes and productivity of 2.49 t/ha next to wheat (Ministry of Agriculture, Government of India, 2018-19). With ever increasing population and plateauing trend in the yield coupled with declining natural resources like land and water, development of new high yielding rice varieties has become essential.

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In this context, multivariate analysis tools such as principal component analysis (PCA) and cluster analysis have been reported to be effective for evaluating the phenotypic diversity in addition to identifying genetically distant clusters of genotypes and selecting important traits contributing to the total variation in the genotypes. These analyses provide information that could help in better selection of parental genotypes with specific traits and in devising breeding strategies for trait improvement. Principal component analysis (PCA) allows natural grouping of the genotypes and is precise indicator of differences among genotypes. The main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only (Mohammadi, 2002). Principal component analysis (PCA) was used to identify redundancy of the genotypes with similar characters and their elimination (Adams, 1995), while two-way cluster analysis is useful for identification and separation of core subset of genotypes with distinct phenotypic traits. Principal component analysis (PCA) allows natural grouping of the genotypes and is precise indicator of differences among genotypes. Principal component analysis (PCA) and two-way cluster analysis are therefore two important statistical programs that aid in selecting elite genotypes. The present investigation was undertaken in this context to study the nature and magnitude of genetic diversity among 107 rice genotypes for yield and yield component traits using Principal Component Analysis (PCA).

MATERIALS AND METHODS

Experimental material for the present investigation comprised of 107 elite rice genotypes collected from Regional Agricultural Research Station (RARS), Maruteru; Agricultural Research station (ARS), Bapatla; and erstwhile, ARS, Pulla; Andhra Pradesh, India, in addition to germplasm obtained from International Rice Research Institute (IRRI), Phillippines (Table 1). These genotypes were sown during *Kharif* 2017 at RARS, Maruteru in a randomized block design with two replications. For transplanting, nursery was raised separately and 28 days old seedlings were transplanted in the main field with a spacing of 20×15 cm. Standard agronomic practices were followed to raise good crop. Observations were recorded on five randomly selected plants for grain yield per plant (g) and yield component characters, namely, days to 50 per cent flowering, plant height (cm), number of ear bearing tillers per plant, panicle length (cm), total number of grains per panicle, spikelet fertility (%) and test weight (g). However, days to 50 per cent flowering was recorded on plot basis. In contrast, observations for test weight were obtained from a random grain sample drawn from each plot in each genotype and replication. Principal component analysis was carried out using the software WindowStat Version 8.5.

RESULTS AND DISCUSSION

The results on analysis of variance (ANOVA) for yield and yield component traits revealed highly significant differences among the genotypes for all the characters studied, indicating the exsistence of sufficient variation among the genotypes and therefore opportunity for plant breeder to undertake further breeding activities like hybridization program. In the present study, first four principal components contributed to 81.328 per cent towards the total variability (Table 2). The first principal component (PC 1) contributed 33.594 per cent towards variability. The characters, namely, panicle length (0.478), days to 50% flowering (0.458), ear bearing tillers per plant (0.427), plant height (0.369), test weight (0.367) and grain yield per plant (0.312) explained maximum variance in this component. The second principal component (PC 2) contributed to 22.566 per cent of total variance. The characters namely spikelet fertility (0.600), grains per panicle (0.512), ear bearing tillers per plant (0.201), days to 50% flowering (0.140), panicle length (0.136) explained maximum loadings in this component. The third principal component was characterized by 13.251 per cent contribution towards the total variability. Characters, namely, ear bearing tillers per plant (0.357) and days to 50% flowering (0.319) explained maximum variance in this component. The fourth principal component was characterized by 11.915 per cent contribution towards the total variability. Characters namely, test weight (0.360), days to 50% flowering (0.359), ear bearing tillers per plant (0.316), spikelet fertility, grains per panicle showed maximum variance in this component.

The PCA analysis thus identified maximum contributing traits towards the exsisting variability as panicle length, days to 50% flowering, ear bearing tillers per plant, plant height and test weight. Similar results were reported earlier by Tiruneh et al. (2019) for panicle length, Prafull et al. (2015) for days to 50% flowering, Pachuari et al. (2015) for tillers per plant, Shaibu and Uguru (2017) for plant height and Ahmed *et al.* (2016) for test weight. The PCA scores for 107 rice genotypes in the first three principal components were computed and were considered as three axes as X, Y and Z and squared distance of each genotype from these three axes were calculated (Table 3). These three PCA scores for 107 genotypes were plotted in graph to get two dimensional scatter diagram (Fig. 1). A perusal of these results revealed genotypes number 74 (RTCNP 9) and 6 (MTU 1006) to be most diverse. Hybridization of these diverse genotypes is therefore predicted to result in desirable transgressive segregants.

Table 1: Details of the material studied

S.No.	Centre of Collection	Genotypes
1	Maruteru, Andhra Pradesh, India	MTU 1001, MTU 1006, MTU 1010, MTU 1031, MTU 1032, MTU 1061, MTU 1064, MTU 1071, MTU 1075, MTU 1078, MTU 1112, MTU 1121, MTU 1140, MTU 1153, MTU 1156, MTU 1166, MTU 1184, MTU 1187, MTU 1194, MTU 1210, MTU 1224, MTU 1226, MTU 1229, MTU 2067, MTU 2077, MTU 2716, MTU 3626, MTU 4870, MTU 5182, MTU 5249, MTU 5293, MTU 7029, RTCNP 1, RTCNP 3, RTCNP 4, RTCNP 5, RTCNP 6, RTCNP 7, RTCNP 8, RTCNP 9, RTCNP 10, RTCNP 12, RTCNP 13, RTCNP 14, RTCNP 15, RTCNP 17, RTCNP 18, RTCNP 20, RTCNP 21, RTCNP 23, RTCNP 28, RTCNP 29, RTCNP 31, RTCNP 33, RTCNP 34, RTCNP 35, RTCNP 36, RTCNP 37, RTCNP 38, RTCNP 39, RTCNP 40, RTCNP 41, RTCNP 42, RTCNP 43, RTCNP 44, RTCNP 45, RTCNP 46, RTCNP 47, RTCNP 48, RTCNP 49, RTCNP 50, RTCNP 52, SM-1, SM-2, SM-3, SM-4, SM-6, SM-7, SM-8, SM-9, SM-10, SM-11, SM-13, SM-14, SM-15, SM-16, SM-17, SM-18, SM-19, SM-23, SM-24, SM-25, SM-26, SM-27, SM-28, SM-29, SM-30, SM-31, SM-3-1
2	Bapatla, Andhra Pradesh, India	BPT 2231, BPT 3291, BPT 5204
3	Pulla, Andhra Pradesh, India	PLA-1100
4	IRRI, Phillipines	FL 478, NONA BOKRA, POKKALI

Table 2: Eigen values, proportion of the total variance represented by first four principal components, cumulative per cent variance and component loading of different characters in rice for yield and yield component traits

	PC 1	**PC 2**	**PC 3**	**PC 4**
Eigen Value (Root)	**2.687**	**1.805**	**1.060**	**0.953**
% Var. Exp.	**33.594**	**22.566**	**13.251**	**11.915**
Cum. Var. Exp.	**33.594**	**56.161**	**69.412**	**81.328**
Days to 50% Flowering	0.458	0.140	0.319	0.359
Plant Height (cm)	0.369	-0.036	0.085	-0.721
Ear bearing tillers per plant	0.427	0.201	0.357	0.316
Panicle length (cm)	0.478	0.136	0.043	-0.348
Grains per panicle	0.111	0.512	-0.528	0.021
Spikelet Fertility (%)	0.000	0.600	-0.312	0.030
Test Weight	0.367	-0.345	-0.371	0.360
Grain yield per plant	0.312	-0.423	-0.498	-0.006

Table 3: PCA scores for 107 rice genotypes

S.No.	**Genotype**	**PC I X vector**	**PC II Y vector**	**PC III Z vector**
1	BPT 5204	54.947	27.892	0.441
2	BPT 3291	53.933	22.749	1.057
3	BPT 2231	55.129	25.017	-0.061
4	FL 478	51.428	15.818	-3.832
5	MTU 1001	58.887	20.84	-0.59
6	MTU 1006	49.866	20.487	0.903
7	MTU 1010	55.543	22.784	-1.377
8	MTU 1031	61.824	23.985	2.972
9	MTU 1032	61.189	24.113	2.211
10	MTU 1061	62.1	25.679	2.124
11	MTU 1064	61.763	23.416	3.002
12	MTU 1071	64.535	22.986	3.391
13	MTU 1075	60.002	24.789	-0.141
14	MTU 1078	59.374	25.818	2.739
15	MTU 1112	62.958	24.276	5.428
16	MTU 1121	58.914	25.332	-3.622
17	MTU 1140	61.372	26.087	-0.813
18	MTU 1153	53.023	22.977	-4.923
19	MTU 1156	54.924	23.17	-4.673
20	MTU 1166	63.059	24.826	2.489
21	MTU 1184	62.413	26.983	3.278
22	MTU 1187	59.916	25.674	-1.074
23	MTU 1194	61.206	24.091	2.933
24	MTU 1210	57.954	25.811	0.503
25	MTU 1224	55.896	29.132	1.361

S.No.	Genotype	PC I X vector	PC II Y vector	PC III Z vector
26	MTU 1226	66.769	25.978	1.413
27	MTU 1229	63.63	31.279	4.179
28	MTU 2067	62.282	24.107	2.084
29	MTU 2077	58.286	25.294	-1.055
30	MTU 2716	58.544	23.407	1.004
31	MTU 3626	52.307	17.621	-3.148
32	MTU 4870	60.163	24.472	-0.021
33	MTU 5182	59.161	22.362	-1.149
34	MTU 5249	56.261	22.43	-0.408
35	MTU 5293	59.672	23.302	0.051
36	MTU 7029	56.524	23.566	-1.544
37	NONABOKRA	54.563	18.251	-3.399
38	PLA-1100	60.495	23.878	1.543
39	POKKALI	56.338	23.957	1.868
40	SM1	58.579	25.067	-3.257
41	SM2	57.058	24.333	0.355
42	SM 3	56.016	25.4	-2.508
43	SM 4	62.06	26.622	2.98
44	SM 6	62.246	26.576	-0.281
45	SM 7	58.92	25.016	-2.278
46	SM8	58.398	26.312	-0.451
47	SM 9	57.857	26.774	-0.699
48	SM 10	60.356	23.371	-0.182
49	SM 11	59.032	26.07	-0.048
50	SM 13	59.478	22.535	1.498
51	SM 14	57.978	27.103	0.612
52	SM 15	58.217	20.717	1.865
53	SM16	58.833	23.989	1.156
54	SM 17	58.542	25.6	-0.212
55	SM 18	58.57	23.591	0.199
56	SM 19	58.188	23.387	0.34
57	SM 23	60.821	26.805	-0.747
58	SM 24	60.775	23.842	0.243
59	SM 25	61.082	29.331	-1.594
60	SM 26	64.244	29.075	0.403
61	SM 27	57.445	27.476	-0.673
62	SM 28	62.44	27.411	-0.614
63	SM 29	59.452	26.634	-0.444
64	SM 30	61.823	25.593	-3.08
65	SM 31	58.077	27.751	0.979
66	SM 3-1	53.257	27.37	-3.582
67	RTCNP1	59.986	27.76	3.293
68	RTCNP 3	64.688	22.978	8.503
69	RTCNP 4	66.203	24.73	4.957
70	RTCNP5	61.956	31.393	-2.706
71	RTCNP 6	64.817	20.771	8.891
72	RTCNP 7	66.808	26.723	5.974
73	RTCNP 8	71.77	30.499	1.529
74	RTCNP 9	73.203	21.835	3.456
75	RTCNP 10	62.883	27.034	0.229
76	RTCNP 12	67.565	25.65	3.012
77	RTCNP 13	66.944	25.925	5.621
78	RTCNP 14	68.807	23.039	3.431

S.No.	**Genotype**	**PC I X vector**	**PC II Y vector**	**PC III Z vector**
79	RTCNP 15	67.776	23.877	2.111
80	RTCNP 17	68.531	25.968	0.978
81	RTCNP 18	65.107	25.066	2.184
82	RTCNP 20	67.748	28.518	3.937
83	RTCNP 21	68.106	26.066	5.306
84	RTCNP 22	69.867	22.467	2.51
85	RTCNP 23	66.049	26.795	1.076
86	RTCNP 28	66.33	27.617	-1.835
87	RTCNP 29	60.406	27.907	-0.789
88	RTCNP 31	67.343	26.235	3.253
89	RTCNP 33	60.696	28.291	2.01
90	RTCNP 34	66.009	24.415	3.129
91	RTCNP 35	67.191	29.339	4.054
92	RTCNP 36	62.107	25.425	2.638
93	RTCNP 37	68.636	25.046	1.036
94	RTCNP 38	66.475	27.177	-2.336
95	RTCNP 39	64.858	27.475	4.733
96	RTCNP 40	66.135	23.096	3.427
97	RTCNP 41	62.15	28.173	0.783
98	RTCNP 42	58.521	27.793	1.363
99	RTCNP 43	57.055	21.9	-3.659
100	RTCNP 44	60.501	29.33	1.439
101	RTCNP 45	65.431	27.911	4.514
102	RTCNP 46	67.512	24.62	1.101
103	RTCNP 47	63.468	26.209	-1.323
104	RTCNP 48	65.215	31.771	-4.081
105	RTCNP 49	63.605	28.416	0.499
106	RTCNP 50	65.777	22.603	0.982
107	RTCNP 52	65.207	34.819	-9.138

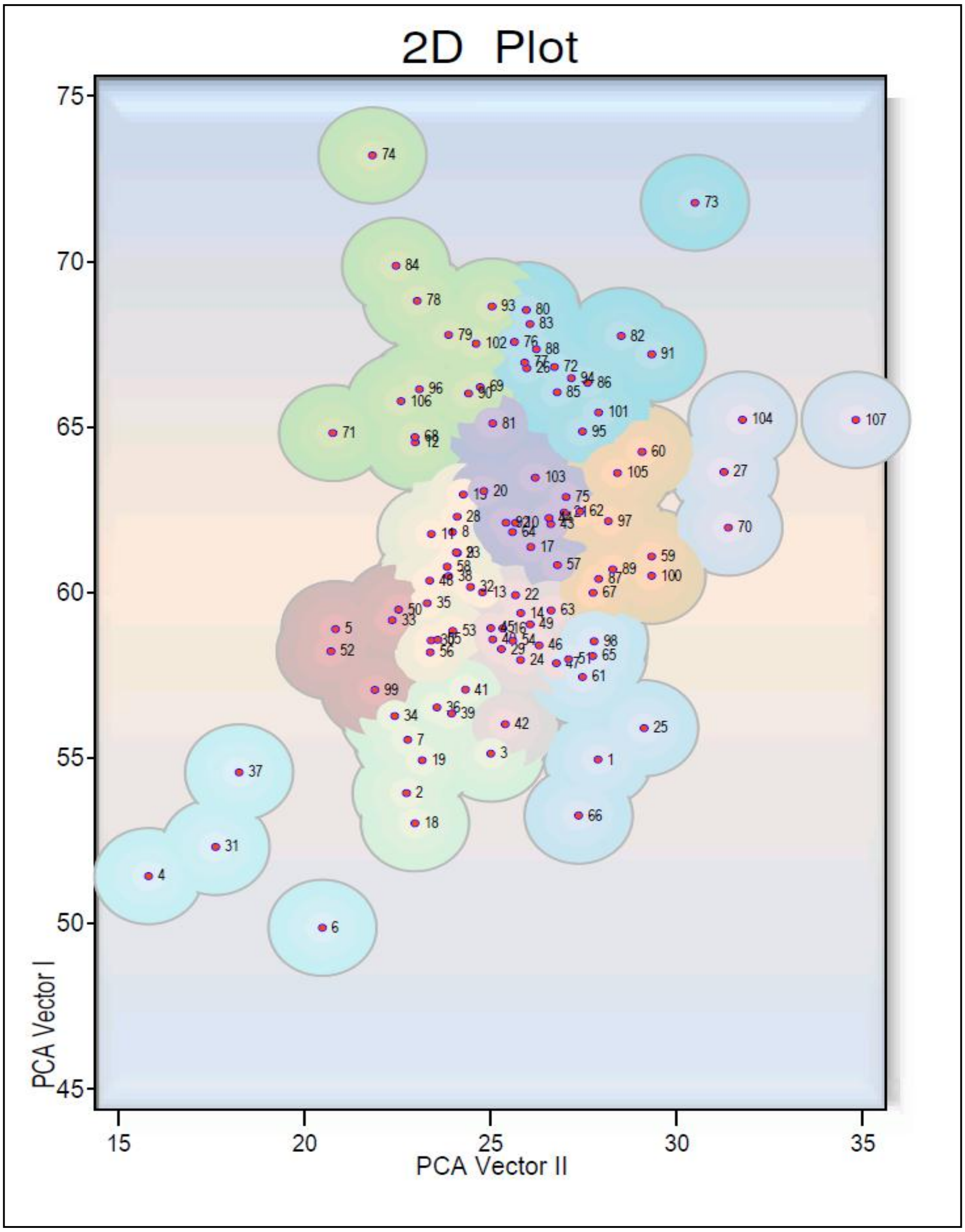

Fig. 1: Two dimensional graph showing relative positions of 107 rice genotypes based on PCA scores

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