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Principal component analysis for anaerobic germination traits in rice (*Oryza sativa* L.)

K Sudeepthi, T Srinivas, BNVSR Ravi Kumar, Jyothula DPB and SK Nafeez Umar

K Sudeepthi
Research Scholar, Department of Genetics & Plant Breeding, Agricultural College, Bapatla, Andhra Pradesh, India

T Srinivas
Professor, Department of Genetics & Plant Breeding, Agricultural College, Bapatla, Andhra Pradesh, India

BNVSR Ravi Kumar
Senior Scientist, Department of Genetics & Plant Breeding, Regional Agricultural Research Station, Maruteru, Andhra Pradesh, India

Jyothula DPB
Associate Professor· Department of Genetics & Plant Breeding, Administrative office, LAM, Guntur, Andhra Pradesh, India

SK Nafeez Umar
Assistant Professor, Department of Statistics and Computer Application, Agricultural College, Bapatla, Andhra Pradesh, India

Corresponding Author:
K Sudeepthi
Research Scholar, Department of Genetics & Plant Breeding, Agricultural College, Bapatla, Andhra Pradesh, India

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Abstract

Principal component analysis was carried out to assess the diversity among 107 rice genotypes with regards to anaerobic germination tolerance traits. Results revealed three principal components with eigen value > 1. These components contributed for a total variability of 75.780 per cent. Component 1 (PC 1) had contributed maximum 27.288 per cent while PC 2 had contributed to 26.060 per cent and PC 3 had contributed to 22.331 per cent towards the total variability. The characters, namely, anaerobic response index and germination per cent explained maximum variance in PC 1. The results of 2D scatter diagram revealed maximum diversity for MTU 1140. Hybridization of MTU 1140 with MTU 1010, identified as widely diverse genotypes in the study is expected to result in high yielding transgressive segregants with high yield and tolerance for germination under anaerobic conditions.

Keywords: Anaerobic response index, eigen value, genetic divergence, principal component, rice

Introduction

Rice production in the recent years is increasingly shifting from transplanting to direct seeding, due to reduction in cost of cultivation and early maturity of the direct sown crop (Pandey and Valesco, 2002) [9]. However, poor seedling establishment under direct seeding in standing water has prevented its large-scale adoption. It is attributed to the lack of tolerance to anaerobic germination (AG) caused by submergence and is identified as the main limiting factor for popularisation of direct seeding in rice (Yang *et al.*, 2019) [10]. However, varietal differences for anaerobic germination were observed by Ismail *et al.* (2009) [5]. Studies on genetic diversity for anaerobic germination traits are therefore essential for devising effective breeding strategies aimed at the development of rice varieties tolerant to anaerobic conditions during germination for wet direct seeding under puddled conditions.

In this context, multivariate analysis tools such as principal component analysis (PCA) have been reported to be effective for evaluating the phenotypic diversity 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) [7]. Principal component analysis (PCA) was used to identify redundancy of the genotypes with similar characters and their elimination (Adams, 1995) [2]. Therefore, Principal component analysis (PCA) is an important statistical program that aids in selection of elite genotypes. The present investigation was undertaken in this context to study the nature and magnitude of genetic diversity for anaerobic germination traits using Principal Component analysis towards development of anaerobic germination tolerant varieties.

Material and Methods

The experimental material comprised of 107 rice genotypes collected from Regional Agricultural Research Station (RARS), Maruteru; Agricultural Research Station (ARS), Bapatla; and erstwhile, ARS, Pulla of Andhra Pradesh, India, in addition to germplasm obtained from International Rice Research Institute (IRRI), Phillippines (Table 1). Screening of these genotypes for tolerance to anaerobic conditions during germination was undertaken at

Regional Agricultural Research Station, Maruteru during *Kharif* 2017 with test tube method detailed by Hsu and Tung (2015) [4] in completely randomized design with two replications.

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

Screening for tolerance to anaerobic conditions during germination with test tube method was undertaken with three days pre-germinated rice seeds at pigeon breast stage in glass test tubes of 25 mm in diameter and 150 mm in height and filled with distilled water to 10 cm depth (Plate 1). Observations were recorded after seven days. Data on number of seedlings survived after seven days of submergence was recorded as germination percentage (%). In addition, shoot length (cm), root length (cm) and seedling dry weight (mg) were recorded for each variety in both the methods in each replication. Further, seedling vigour index (Kharb *et al.*, 1994) [6] and anaerobic response index (Hsu and Tung, 2015) [4] were estimated as per the standard procedures suggested by earlier workers. The data obtained was subjected to standard statistical procedures. Principal component analysis was carried out using the software Window Stat Version 8.5.

Results and Discussion

Principal component analysis (PCA) was performed with the objective to identify the main components of anaerobic germination tolerance, namely, germination per cent, shoot length, root length, seedling dry weight, seedling vigour index and anaerobic response index that would reveal best response of different genotypes to tolerance during anaerobic conditons. The results on analysis of variance (ANOVA) for anaerobic germination traits revealed highly significant differences among the genotypes for all the anaerobic germination 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.

The presence of broad morphological differences among genotypes was confirmed by principal component analysis, which indicated that the overall diversity observed could be elucidated by a few Eigen vectors. In the present study, first three principal components with eigen value > 1 contributed to 75.780 per cent towards the total variability (Table 2). The first principal component (PC 1) contributed maximum (27.388) per cent towards total variability. The characters, namely, anaerobic response index (0.191) and germination per cent (0.074) were positively loaded while seedling vigour index (-0.683), root length (-0.547), seedling dry weight (-0.427) and shoot length (-0.088) were negatively loaded for the first principal component.

The second principal component (PC 2) contributed to 26.060 per cent of variance and the characters, namely, germination per cent (0.683), anaerobic response index (0.620) and root length (0.379) contributed positively to the variation while seedling vigour index (-0.044) and seedling dry weight (-0.021) contributed negatively to the variation. The third principal component was characterized by 22.331 per cent contribution towards the total variability. The characters, namely, shoot length (0.741), seedling dry weight (0.381) and germination per cent (0.347) were positively loaded while anaerobic response index (-0.307), seedling vigour index (-0.250) and root length (-0.164) were negatively loaded.

The PCA analysis thus identified the principal discriminatory characteristics as anaerobic response index (ARI), germination per cent, shoot length and seedling dry weight in diverse PCs which are responsible for the observed genotypic variation within a group of genotypes. Important characters coming together in different PCs have tendency to remain together, which may be kept into consideration during utilization of these characters in breeding programme for development of anaerobic germination tolerant varieties and to bring about rapid improvement for anaerobic germination tolerance and other associated traits (Ojha *et al.*, 2017) [8].

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 genotype number 17, *i.e.*, MTU 1140, a known anaerobic germination tolerant genotype to be widely diverse from other genotypes studied in the present investigation. The results also revealed the genotypes, 7 (MTU 1010), 66 (SM 3-1) and 48 (SM 10) to be most diverse from MTU 1140 (genotype number 17).

MTU 1010 (genotype number 7) is a short duration, mega rice variety with high yield potential (Anila *et al.*, 2018) [1], while MTU 1140 (genotype number 17) is a flood and submergence tolerant variety also reported to possess tolerance for germination under anaerobic conditions (Girijarani *et al.*, 2014) [3]. Hybridization of these diverse genotypes is therefore predicted to result in transgressive segregants with high yield and tolerance to germination under anaerobic conditions for use in the breeding programmes aimed at the development of high yielding varieties coupled with anaerobic germination tolerance for wet direct seeding under puddled conditions.

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 anaerobic germination traits

	PC 1	**PC 2**	**PC 3**	**PC 4**
Eigen Value (Root)	1.643	1.563	1.339	0.810
% Var. Exp.	27.388	26.060	22.331	13.509
Cum. Var. Exp.	27.388	53.448	75.780	89.289
Germination (%)	0.074	0.683	0.347	0.035
Shoot length	-0.088	0.017	0.741	-0.417
Root length	-0.547	0.379	-0.164	-0.403
Seedling dry weight	-0.427	-0.021	0.381	0.775
Seedling vigour index	-0.683	-0.044	-0.250	-0.036
Anaerobic response index	0.191	0.620	-0.307	0.243

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	-0.619	21.004	22.633
2	BPT 3291	2.523	23.276	20.619
3	BPT 2231	6.136	19.116	22.876
4	FL 478	0.981	21.452	24.939
5	MTU 1001	3.232	22.726	21.518
6	MTU 1006	7.104	23.763	18.679
7	MTU 1010	8.363	3.281	20.123
8	MTU 1031	9.698	12.825	30.038
9	MTU 1032	5.365	22.774	20.185
10	MTU 1061	3.190	22.281	19.922
11	MTU 1064	2.435	21.850	23.019
12	MTU 1071	11.373	18.264	26.037
13	MTU 1075	1.786	19.971	19.896
14	MTU 1078	11.795	17.460	25.675
15	MTU 1112	11.045	18.898	26.862
16	MTU 1121	-1.007	21.753	24.778
17	MTU 1140	-3.893	23.953	29.974
18	MTU 1153	-3.960	14.797	28.834
19	MTU 1156	1.004	4.160	18.354
20	MTU 1166	10.313	10.645	17.335
21	MTU 1184	5.546	20.876	20.650
22	MTU 1187	12.180	17.850	25.446
23	MTU 1194	4.353	10.397	30.267
24	MTU 1210	3.248	22.228	22.500
25	MTU 1224	11.736	19.193	25.402
26	MTU 1226	-1.751	15.174	26.728
27	MTU 1229	7.754	15.726	28.852
28	MTU 2067	-0.878	18.329	21.947
29	MTU 2077	10.732	19.731	22.929
30	MTU 2716	-1.258	17.439	26.842
31	MTU 3626	0.201	17.264	27.019
32	MTU 4870	6.677	7.560	29.153
33	MTU 5182	-0.582	15.799	26.417
34	MTU 5249	8.764	19.040	27.590
35	MTU 5293	6.917	11.706	30.452
36	MTU 7029	8.433	10.219	20.699
37	NONABOKRA	4.030	9.367	23.913
38	PLA-1100	9.834	19.632	25.755
39	POKKALI	11.212	18.457	24.955
40	SM1	4.638	6.280	33.456
41	SM2	4.419	19.753	27.565
42	SM 3	10.272	13.551	19.997
43	SM 4	9.344	18.612	22.616
44	SM 6	4.354	19.817	26.165
45	SM 7	6.233	6.419	17.470
46	SM8	8.835	14.909	24.953
47	SM 9	8.871	11.670	18.830
48	SM 10	8.071	1.964	25.967
49	SM 11	8.373	17.334	24.302

50	SM 13	6.061	17.677	19.490
51	SM 14	2.888	5.493	17.700
52	SM 15	8.052	17.936	27.656
53	SM16	4.719	20.721	24.189
54	SM 17	1.913	7.770	29.427
55	SM 18	7.299	16.868	27.280
56	SM 19	8.286	18.159	28.159
57	SM 23	5.676	15.746	27.392
58	SM 24	3.993	18.617	27.695
59	SM 25	9.083	19.905	24.560
60	SM 26	6.361	12.884	23.894
61	SM 27	2.822	10.150	21.007
62	SM 28	2.256	9.760	35.628
63	SM 29	10.789	12.494	18.294
64	SM 30	12.814	16.327	25.189
65	SM 31	4.106	11.611	29.592
66	SM 3-1	8.502	2.651	23.145
67	RTCNP1	2.314	4.950	18.186
68	RTCNP 3	7.081	19.406	22.038
69	RTCNP 4	10.838	24.390	21.207
70	RTCNP5	9.311	20.645	26.767
71	RTCNP 6	7.466	17.020	23.438
72	RTCNP 7	6.085	19.414	21.273
73	RTCNP 8	8.039	22.657	20.013
74	RTCNP 9	6.911	22.174	23.336
75	RTCNP 10	2.888	4.577	22.663
76	RTCNP 12	4.993	13.494	23.859
77	RTCNP 13	4.276	22.740	24.235
78	RTCNP 14	10.543	13.245	21.763
79	RTCNP 15	-1.576	16.160	32.563
80	RTCNP 17	10.509	17.113	27.434
81	RTCNP 18	5.800	12.253	31.981
82	RTCNP 20	10.584	11.279	25.850
83	RTCNP 21	8.188	14.508	27.861
84	RTCNP 22	9.445	5.614	28.894
85	RTCNP 23	-3.196	8.363	31.607
86	RTCNP 28	3.338	16.622	30.260
87	RTCNP 29	8.560	18.366	22.790
88	RTCNP 31	8.540	9.661	26.379
89	RTCNP 33	9.035	17.799	24.029
90	RTCNP 34	-0.286	13.331	33.087
91	RTCNP 35	2.714	18.019	28.118
92	RTCNP 36	1.467	11.130	29.439
93	RTCNP 37	-1.225	15.957	27.965
94	RTCNP 38	1.170	10.589	32.211
95	RTCNP 39	1.236	19.276	28.330
96	RTCNP 40	9.990	15.757	26.118
97	RTCNP 41	5.392	21.257	22.438
98	RTCNP 42	8.062	21.382	26.797
99	RTCNP 43	3.790	18.116	29.603
100	RTCNP 44	7.918	13.978	20.569
101	RTCNP 45	2.635	13.054	27.203
102	RTCNP 46	4.059	8.245	29.473
103	RTCNP 47	1.461	20.554	26.819
104	RTCNP 48	-0.753	13.538	28.980
105	RTCNP 49	4.420	13.330	27.240
106	RTCNP 50	3.555	12.695	31.243
107	RTCNP 52	9.229	16.637	18.647

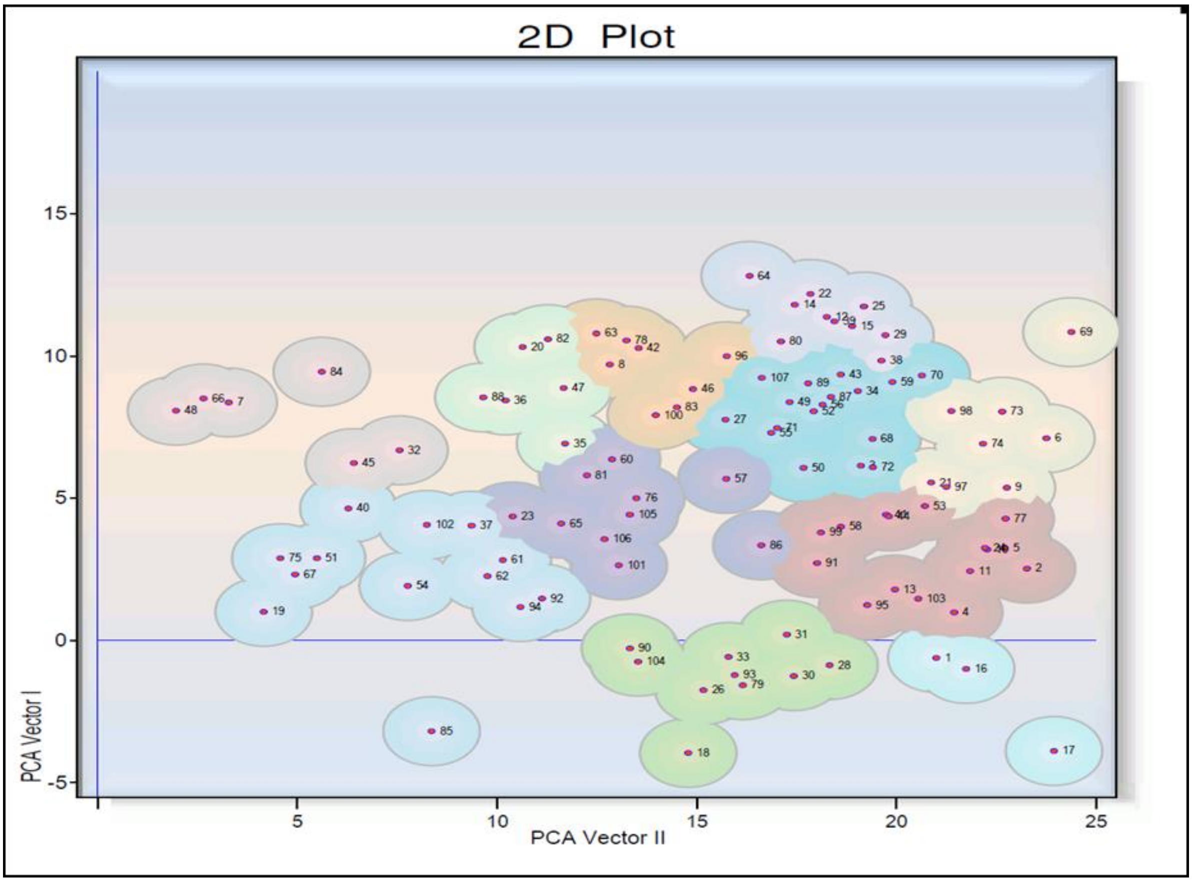

Fig 1: Two dimensional graph showing relative positions of 107 rice genotypes based on PCA scores

Plate 1: Test tube bioassay method for evaluating anaerobic germination tolerance

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