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Principal component analysis for yield and quality traits of coloured rice (*Oryza sativa* L.)

Kumar Saurabh Singh, Y Suneetha, D Sandeep Raja and T Srinivas

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Abstract

The present investigation was undertaken with 33 coloured and white rice genotypes to estimate genetic divergence of the genotypes for yield and quality traits. The study involved seven red pericarp, eight black pericarp and 17 white rice genotypes, in addition to the check, BPT 5204. Principal component analysis was utilized to evaluate the variation and to estimate the relative contribution of various traits for total variability. Results revealed five principal components with eigen value > 1. These components contributed for a total variability of 78.2632 per cent. Component 1 (PC 1) had contributed maximum of 34.9423 per cent while PC 2 had contributed to 18.7909 per cent, PC 3 had contributed 11.2637 per cent, PC 4 had contributed 6.9756 and PC 5 had contributed to 6.2906 per cent towards the total variability. The characters, namely, milling per cent, iron content, plant height and head rice recovery were observed to explain maximum variance in PC 1. The results of 2D scatter diagram revealed Kakirekalu and BPT 5204 genotypes to be most diverse. Hybridization of these diverse genotypes is therefore predicted to result in desirable coloured transgressive segregants.

Keywords: Coloured rice, genetic divergence, grain yield, nutritional quality, principal component analysis

Introduction

'Rice is Life' for most of the World population and cultivation of rice has shaped culture, diet and economic status of millions of people. Rice is grown in more than 100 countries across the globe. It is an important staple food for more than half of the world's population and hence, is referred to as "Global Grain" (Prasad *et al.*, 2018) [9]. Rice is the predominant staple food in at least fifteen countries in Asia and the pacific, ten countries in Latin America and the Caribbean, one country in North Africa and seven countries in sub-Saharan Africa (FAOSTAT, 2005) [3]. In Asia, nearly two billion people depend on rice for their 60-70 percent calories (Diouf 2003; Khush 2005) [2] [6]. Further, rice is the only cereal, cooked and consumed as a whole grain and quality considerations in rice are therefore much more important than for any other food crop (Hossain *et al.*, 2009) [5]. Whole grain pigmented rice has been categorized as one of the potent functional foods since it contains high amounts of phenolic compounds (Yawadio *et al.*, 2007) [14]. In addition, coloured rice contains higher levels of proteins, vitamins and minerals than common white rice, while red rice is good source of fibre, antioxidants, zinc and iron (Sridevi *et al.*, 2019) [10]. Therefore, increased health consciousness among the rice consumers in the recent years has resulted in greater attention to rice genotypes with red and black pericarp colour containing high levels of antioxidants (Tian *et al.*, 2004) [13] and these genotypes are in increasing demand. However, the yields of coloured rice need to be improved and high yielding slender grain coloured rice varieties with good nutritional quality are required to meet the increasing demand for coloured rice. In this context, information on genetic divergence in coloured rice genotypes plays a key role in analyzing of diversity among the genotypes and aids in the selection of parents towards realization of enhanced levels of heterosis in addition to wide range of variability for effective selection. Multivariate analysis tools such as principal component analysis (PCA) has 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. Principal component analysis (PCA) allows natural grouping of the genotypes and is precise indicator of differences among genotypes. The main advantage of using PCA is that each genotype can be assigned to one group only.

Kumar Saurabh Singh
Department of Genetics and Plant Breeding, Agricultural College, Bapatla, Andhra Pradesh, India

Y Suneetha
Agricultural Research Station, Bapatla, Andhra Pradesh, India

D Sandeep Raja
Post-Harvest Technology Centre, Bapatla, Andhra Pradesh, India

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

Corresponding Author:
Kumar Saurabh Singh
Department of Genetics and Plant Breeding, Agricultural College, Bapatla, Andhra Pradesh, India

Principal component analysis (PCA) has been used to identify redundancy of the genotypes with similar characters and their elimination (Adams, 1995) [1]. The present investigation was undertaken in this context to study the nature and magnitude of genetic diversity among 33 coloured rice genotypes for yield, yield component and quality traits using Principal Component Analysis (PCA).

Material and Methods

The experimental material consisted of 33 white and coloured rice genotypes obtained from Agricultural Research Station, Bapatla, Andhra Pradesh state in addition to collections from Telangana and Tamil Nadu states. Among the 33 genotypes, 15 genotypes were coloured, of which, seven were with red pericarp and eight genotypes were with black pericarp, while remaining 18 genotypes had brown pericarp and were white rice genotypes including, BPT 5204, a popular high yielding white rice genotype with excellent cooking quality traits, which was used as check variety in the present study. Details of the genotypes studied in the present investigation are presented in Table 1.

All the 33 genotypes were sown at Agricultural College Farm, Bapatla during *Kharif* 2019 on separate raised nursery beds. All recommended package of practices were adopted to raise a healthy nursery and thirty days old seedlings were transplanted in the main field laid out in Randomized Block Design (RBD) with three replications. Each genotype was transplanted separately in 5 rows of 4.5 m length by adopting a spacing of 20 cm between rows and 15 cm between plants. All the recommended package of practices was adopted throughout the crop growth period and need based plant protection measures were taken up to raise a healthy crop. Observations were recorded on five randomly selected plants for grain yield per plant, days to 50 per cent flowering and the quality characters, namely, head rice recovery per cent, amylose content, alkali spreading value, protein content, total phenol content, total antioxidant activity, zinc and iron content in addition to grain type were recorded. However, days to 50 per cent flowering was recorded on plot basis. In contrast, observations for the quality traits studied were obtained from a random grain sample drawn from each plot in each genotype and replication using standard procedures. The data collected was subjected to standard statistical procedures given by Panse and Sukhatme (1967) [8]. Principal component analysis was carried out using the software Window Stat Version 8.5.

Results and Discussion

The results on principal component analysis are presented in Tables 2-3 and Fig.1-2. The eigen values, proportion of total variance represented by principal components of importance and the component loading of different characters for the principal components are presented in Table 2 and Fig. 1. A perusal of these results revealed first five principal components with eigen value more than one. These principal components were observed to contribute to 78.2632 per cent towards the total variability. Similar results were reported earlier in rice by Gana *et al.* (2013) [4] and Nachimuthu *et al.* (2014) [7]. The first principal component (PC 1) contributed was noticed to contribute maximum towards divergence (34.9423 %). The characters, milling per cent (0.3384), head rice recovery (0.2790), days to 50 per cent flowering (0.2235), hulling per cent (0.2213), length/breadth ratio (0.1630), amylose content (0.1541), productive tillers per plant (0.1256), days to maturity (0.0430) had contributed positively for the variation in the principal component (Fig.1), while the other characters studied had contributed negatively. The second principal component (PC 2) contributed to 18.7909 per cent of total variance. Grains per panicle (0.4395), panicle length (0.4080), length/breadth ratio (0.3775), days to 50 per cent flowering (0.3270), kernel length (0.2311), total antioxidant activity (0.1938), grain yield per plant (0.1922), days to maturity (0.1910), head rice recovery (0.1559), total phenol content (0.1631), iron content (0.1422), zinc content (0.1344), plant height (0.1102), protein content (0.0969), amylose content (0.0952), hulling per cent (0.0784) and productive tillers per plant (0.0101) were noticed to be positively loaded for the principal component, while other traits were noticed to be negatively loaded. The third principal component (PC 3) was characterized by 11.2637 per cent contribution towards the total variability. The characters, alkali spreading value (0.4505), grain yield per plant (0.3596), hulling per cent (0.3291), plant height (0.2304), grains per panicle (0.2251), amylose content (0.1261), kernel breadth (0.1226), panicle length (0.1218), total antioxidant activity (0.1100) had contributed positively for the variation in the principal component, while other characters studied had contributed negatively. The fourth principal component (PC 4) described 6.9756 per cent of the total variability and it reflected positive loading for the characters, namely, days to maturity (0.4841), protein content (0.2926), days to 50 per cent flowering (0.2250), panicle length (0.1547), zinc content (0.1114), total antioxidant activity (0.1056), amylose content (0.0857), kernel breadth (0.0080), test weight (0.0371) and alkali spreading value (0.0355), while the other traits recorded negative loadings. The fifth principal component (PC 5) was characterized by 6.2906 per cent contribution towards the total variability and the characters, namely, test weight (0.3634), days to maturity (0.3628), kernel breadth (0.2694), productive tillers per plant (0.2065), panicle length (0.1687), days to 50 per cent flowering (0.1629), plant height (0.1539), head rice recovery (0.0958), grain yield per plant (0.0766), kernel length (0.0468), milling per cent (0.0402) and length/breadth ratio (0.0317) were noticed to contribute positively for the variability explained by the principal component, while other traits studied recorded negative loadings for the principal component. The PCA analysis thus identified maximum contributing traits towards the existing variability (Fig. 1) as milling per cent, head rice recovery per cent, days to 50 per cent flowering and hulling per cent. Sudeepthi *et al.* (2020a) [11] in her studies on principal component analysis in rice also reported days to 50 per cent flowering as one of the maximum contributors for variability.

The PCA scores for 33 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 and are presented in Table 3. These PCA scores for 33 genotypes were plotted in a graph to get the two dimensional scatter diagram (Fig. 2). A perusal of these results revealed nine different clusters. Among these, four clusters were noticed to be monogenotypic. The pattern of distribution of the genotypes in these clusters was observed to be at random with no reference to geographical diversity as genotypes from different geographical regions were grouped in the same as well as different clusters. The results are in agreement with the findings of Sudeepthi *et al.* (2020b) [12]. The results also revealed maximum diversity between Kakirekalu (Genotype 23), a black pericarp genotype with high levels of total phenol content, total antioxidant activity, protein content, zinc and iron content and BPT 5204 (Genotype 9), the white rice variety with high yield and excellent grain and cooking quality. Hybridization of these diverse genotypes is therefore suggested for obtaining of desirable coloured transgressive segregants towards development of coloured rice varieties with high yield, in addition to grain, cooking and nutritional quality.

Table 1: Details of the rice genotypes studied in the present investigation

S. No.	Genotype	Origin
Red pericarp genotypes		
1.	Apputhokal	Telangana
2.	Asandi	Telangana
3.	Chittiga	Telangana
4.	BPT 3111	Andhra Pradesh
5.	BPT 3139	Andhra Pradesh
6.	BPT 3178	Andhra Pradesh
7.	Hallabhatta	Telangana
Black pericarp genotypes		
8.	BPT 2841	Andhra Pradesh
9.	BPT 2848	Andhra Pradesh
10.	BPT 3136	Andhra Pradesh
11.	BPT 3140	Andhra Pradesh
12.	BPT 3141	Andhra Pradesh
13.	BPT 3145	Andhra Pradesh
14.	BPT 3165	Andhra Pradesh
15.	Kakirekalu	Telangana
Brown pericarp white coloured genotypes		
16.	ADT 49	Tamil Nadu
17.	BPT 2411	Andhra Pradesh
18.	BPT 2507	Andhra Pradesh
19.	BPT 2595	Andhra Pradesh
20.	BPT 2615	Andhra Pradesh
21.	BPT 2660	Andhra Pradesh
22.	BPT 2766	Andhra Pradesh
23.	BPT 2776	Andhra Pradesh
24.	BPT 2782	Andhra Pradesh
25.	BPT 2846	Andhra Pradesh
26.	BPT 3173	Andhra Pradesh
27.	BPT 5204	Andhra Pradesh
28.	JKRH 3333	Telangana
29.	PHI 17108	Telangana
30.	WGL 14	Andhra Pradesh
31.	MTU 1281	Andhra Pradesh
32.	27 P 63	Telangana
33.	US 301	Telangana

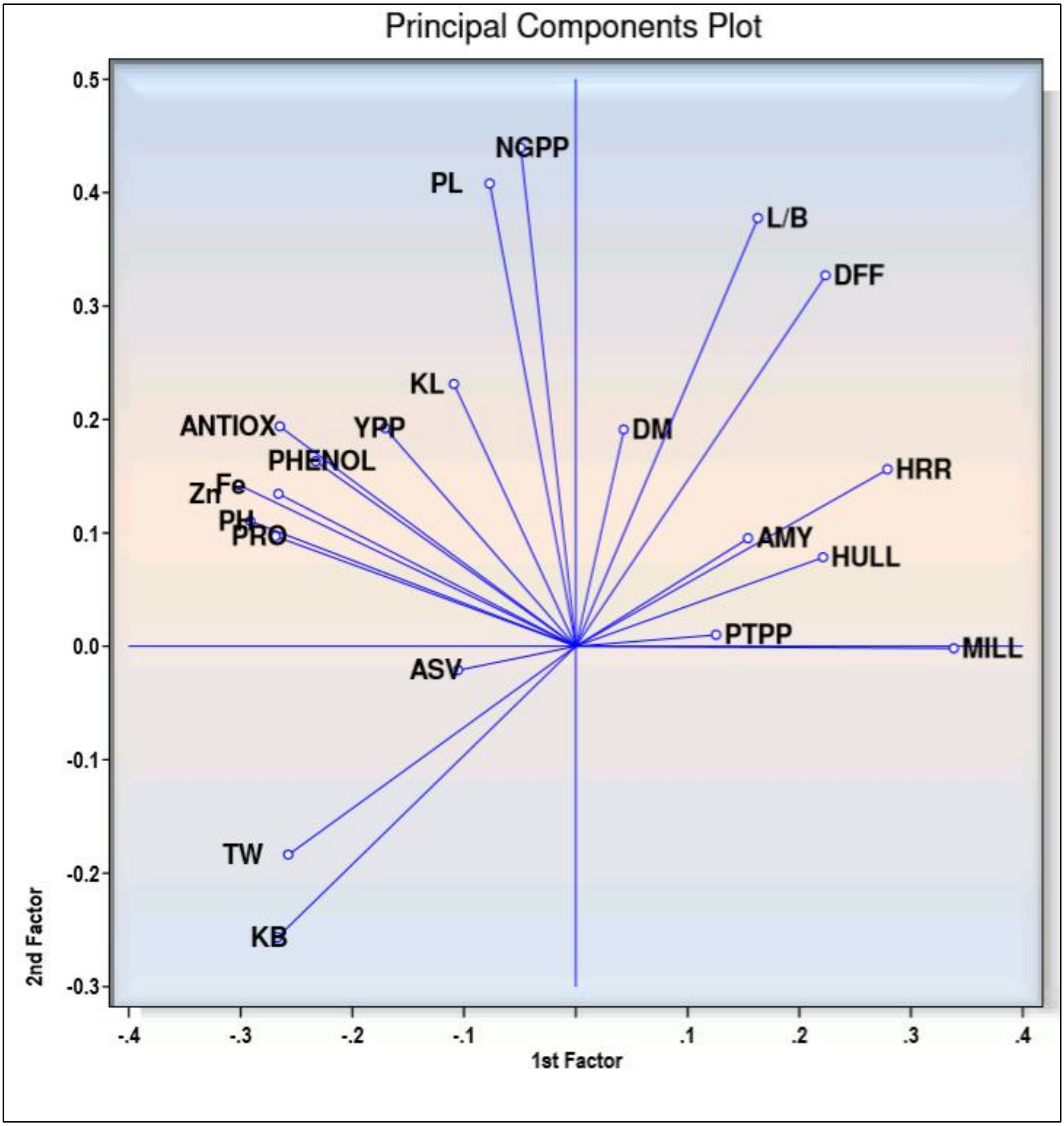
Table 2: Eigen values, proportion of total variance represented by first five principal components, cumulative per cent variance and component loading of different characters in rice.

Components	PC 1	PC 2	PC 3	PC 4	PC 5
Eigen Value	7.3378	3.9460	2.3653	1.4648	1.3210
% Variance	34.9423	18.7909	11.2637	6.9756	6.2906
Cumulative %	34.9423	53.7332	64.9969	71.9726	78.2632
Characters	**PC 1**	**PC 2**	**PC 3**	**PC 4**	**PC 5**
Days to 50% flowering	0.2235	0.3270	0.01455	0.2250	0.1629
Days to maturity	0.0430	0.1910	-0.07602	0.4841	0.3628
Plant height (cm)	-0.2911	0.1102	0.2304	-0.1474	0.1539
Productive tillers per plant	0.1256	0.0101	-0.1827	-0.2502	0.2065
Panicle length (cm)	-0.0769	0.4080	0.1218	0.1547	0.1687
Grains per panicle	-0.0493	0.4395	0.2251	-0.0035	0.0826
Test Weight (g)	-0.2572	-0.1837	-0.0461	0.0371	0.3634
Grain yield per plant (g)	-0.1706	0.1922	0.3596	-0.2476	0.0766

Kernel length (mm)	-0.1089	0.2311	-0.1573	-0.5735	0.0468
Kernel breadth (mm)	-0.2671	-0.2568	0.1226	0.0080	0.2694
Length/Breadth ratio	0.1630	0.3775	-0.2011	-0.0284	0.0317
Hulling percentage	0.2213	0.0784	0.3291	-0.0559	-0.035
Milling percentage	0.3384	-0.0018	-0.0095	-0.0450	0.0402
Head Rice Recovery (%)	0.2790	0.1559	-0.1395	-0.2476	0.0958
Amylose Content (%)	0.1541	0.0952	0.1261	0.0857	-0.5980
Alkali Spreading Value	-0.1052	-0.0209	0.4505	0.0355	-0.1900
Protein Content (%)	-0.2685	0.0969	-0.2218	0.2926	-0.1919
Total Phenol Content (mg/100g)	-0.2326	0.1631	-0.3203	0.1326	-0.1639
Total Antioxidant Activity (mg AAE/100g)	-0.2647	0.1938	0.1100	0.1056	-0.1110
Zinc content (ppm)	-0.2660	0.1344	-0.3443	0.1114	-0.1684
Iron content (ppm)	-0.3013	0.1422	-0.0303	-0.1104	-0.1267

Table 3: PCA scores of 33 rice genotypes

S. No.	**Genotypes**	**PCA I**	**PCA II**	**PCA III**
		X Vector	**Y Vector**	**Z Vector**
1	PHI 17108	8.901	38.099	-8.835
2	WGL 14	9.541	36.973	-10.811
3	MTU 1281	7.438	41.761	-7.198
4	BPT 2507	12.142	37.042	-12.889
5	ADT 49	8.713	38.451	-4.868
6	JKRH 3333	9.943	35.950	-8.684
7	27 P 63	10.424	36.760	-10.941
8	US 301	11.093	34.964	-7.272
9	BPT 5204	11.719	36.338	-8.483
10	BPT 2841	-2.664	43.720	-9.591
11	BPT2848	-2.544	48.548	-14.893
12	BPT3111	-1.119	44.773	-12.899
13	BPT3136	-6.143	42.932	-12.719
14	BPT 3139	1.442	45.224	-9.426
15	BPT 3140	-6.082	49.368	-18.455
16	BPT 3141	-5.530	49.775	-21.281
17	BPT 3145	-8.144	46.931	-12.881
18	BPT 3165	-9.627	49.085	-10.343
19	BPT 3173	8.053	39.639	-3.943
20	BPT 3178	0.173	47.700	-7.642
21	Asandi	-9.079	35.290	-4.500
22	Chittiga	-13.763	35.849	-14.763
23	Kakirekalu	-17.219	46.361	-28.670
24	Apputhokal	-4.044	40.248	-10.677
25	Hallabhatta	-8.075	36.948	-1.575
26	BPT 2411	9.973	38.231	-9.906
27	BPT 2615	9.750	38.797	-6.368
28	BPT 2595	5.883	39.151	-10.434
29	BPT 2660	7.665	42.776	-9.066
30	BPT 2776	10.540	39.756	-0.800
31	BPT 2766	11.281	41.303	-2.597
32	BPT 2782	8.871	40.481	-3.990
33	BPT 2846	11.88141	39.728	-6.025



DFF=Days to 50 per cent flowering, **DM**=Days to maturity, **PH**=Plant height, **PTPP**=Productive tillers per plant, **PL**= Panicle length, **NGPP**= Grains per panicle, **TW**=Test Weight, **KL**=Kernel length, **KB**=Kernel breadth, **L/B**=Length/Breadth ratio, **HULL**= Hulling percentage, **MILL**= Milling percentage, **HRR**=Head rice recovery, **AMY**=Amylose content, **ASV**=Alkali spreading value, **PRO**=Protein content, **PHENOL**=Total phenol content, **ANTIOX**=Total antioxidant activity, **Zn**=Zinc content, **Fe**=Iron content, **YPP**=Yield per plant.

Fig 1: Biplot diagram of principal components

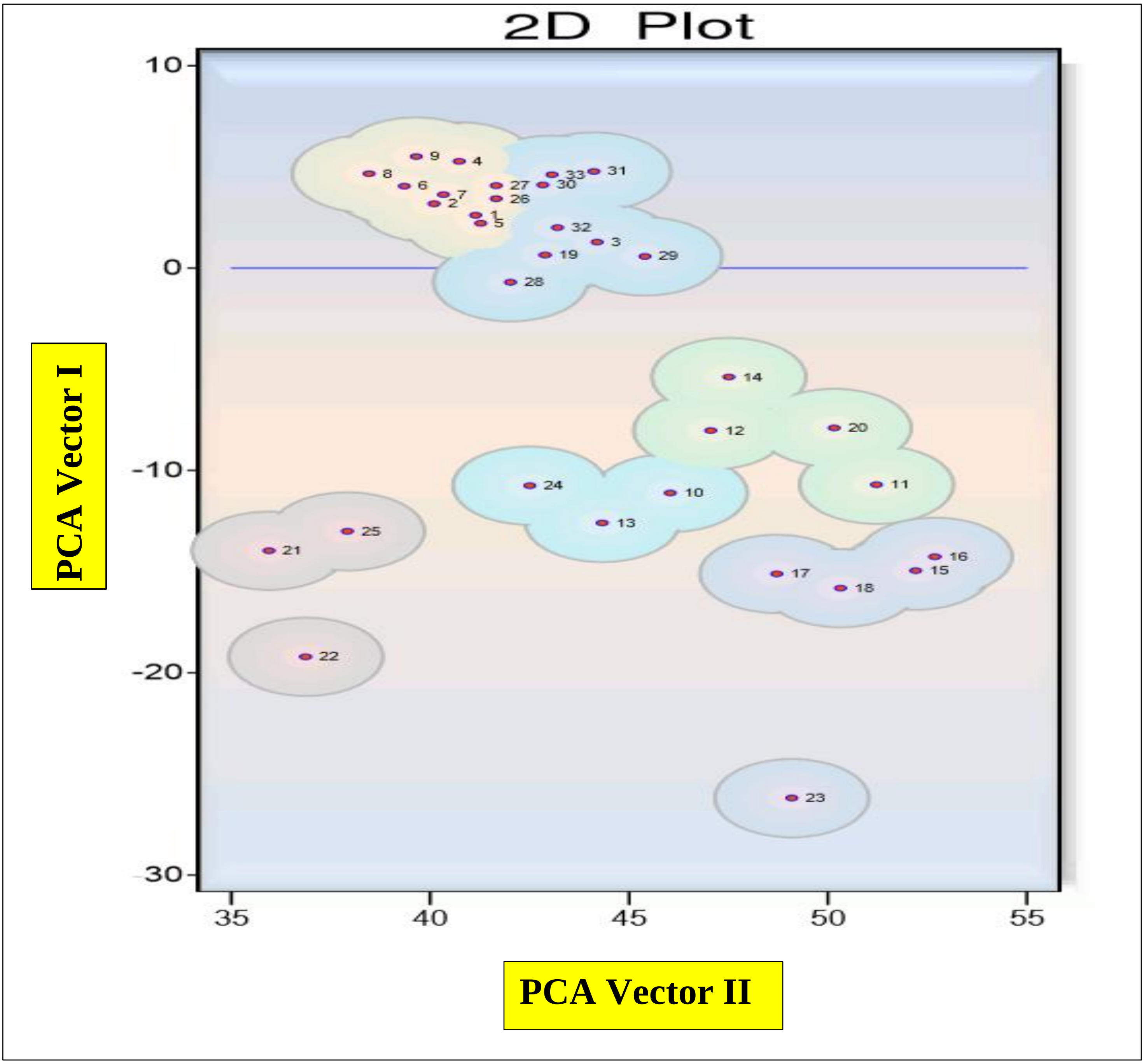


Fig 2: Two dimensional graphs showing relative position of 33 Rice genotypes based on PCA scores

1.	PHI 17108	12.	BPT 3111	23.	Kakirekalu
2.	WGL-14	13.	BPT 3136	24.	Apputhokal
3.	MTU 1281	14.	BPT 3139	25.	Hallabhatta
4.	BPT 2507	15.	BPT 3140	26.	BPT 2411
5.	ADT 49	16.	BPT 3141	27.	BPT 2615
6.	JKRH 3333	17.	BPT 3145	28.	BPT 2595
7.	27 P 63	18.	BPT 3165	29.	BPT 2660
8.	US 301	19.	BPT 3173	30.	BPT 2776
9.	BPT 5204	20.	BPT 3178	31.	BPT 2766
10.	BPT 2841	21.	Asandi	32.	BPT 2782
11.	BPT 2848	22.	Chittiga	33.	BPT 2846

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