Electronic Journal of Plant Breeding, 6(4): 1052- 1059 (Dec- 2015)

ISSN 0975-928X

Research Article

Principal component analysis for assessment of genetic diversity in upland paddy for Bastar plateau

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(Received: 27th May 2015; Accepted: 18th Aug 2015)

Abstract
An experiment was conducted with 18 IRRI and Raipur originated rice genotypes to assess the heritable diversity among the parent lines during Kharif 2013 and 2014. First five principal components exhibited more than one eigen values and accounted for 82 percent of total variation, comprised of 38.95 (PC I), 20.80 (PC II), 14.67 (PC III) and 10.69 (PC IV). The genotypes viz., R-1570-2649-1-1546-1 and IR-83381-B-B-137-3 scored maximum in PCA I and II, respectively. On the basis of Ward's linkage cluster analysis, five clusters were formed to identify relative genetic closeness among test genotypes. Cluster II and III harboured maximum of five genotypes while cluster V with two IRRI genotypes assuring comparative diversity of exotic material. Combined analysis of principal components showed scattered position of genotypes across the plot which indicated that accessions have sufficient genetic diversity. Genotypes IR-83381-B-B-137-3, IR-1570-2649-1-1546-1 and R-RF-65 had maximum distance from other genotypes were found to be more divergent and can be utilized for future upland rice breeding programmes.

Keywords: Upland rice, water stress, genetic diversity, genotypic clustering.

Introduction

Rice is cultivated in highly diverse situations that range from flooded wetland to rainfed dryland (Degenkolbe *et al*., 2009). Irrigated rice, which accounts for 55% of the global rice area, provides 75% of production and consumes about 90% of the freshwater resources, used for agriculture in Asia. Water requirement for rice cultivation is quite higher i.e. 2500 litres to produce 1 kg of grain (Bouman *et al*., 2007), and is expected that rice production will be decreased due to water stress in many Asian countries (Shrawan *et al*., 2012; Guimarães *et al*., 2013), affecting more than 19 million ha (Lifitte *et al*., 2006). Upland rice ecology is much harsh environment for rice production where intermittent moisture deficit is the major constraint and cause a yield penalty from 12 to 46 per cent. It is grown with little or no fertilizer input with direct seeded methodology in moisture deficit unsaturated soils (Aditya and Bhartiya, 2013). Further, poor ability of varieties to produce economic quantity of grain, due to the concomitant poor panicle yield, caused by varying degrees of water stress, makes rice production risky and unattractive due to low yield of 1 to 2 tones/hectare (Adewusi and Nassir, 2011). Moreover, development of variety from limited genetic resource have laid the lowering down of genetic diversity in modern cultivars (Guang and Xiong-Ming, 2006; Ahmad *et al*., 2012). Earlier workers have reported the presence higher diversity in exotic germplasm (Lacap *et al*., 2007). Therefore, entries from diverse geographical origin viz., IRRI, Phillipines, IGKV, Raipur and other sources were incorporated in upland research programme. To discern pattern of variation, PCA was performed in all genotypes simultaneously so as to identify potential parental population rice improvement.

Materials and methods

The experiment was undertaken with 18 genotypes under rainfed conditions during Kharif, 2013 and Kharif, 2014 at Upland Rice Breeding Block of S. G. College of Agriculture and Research Station, Jagdalpur, IGKV, Raipur, Chhattisgarh. Sowing was completed by just onset of monsoon by direct seeding in agronomically standardized geometry in 10sq M plot with two replications. Trench was made in periphery of experimental plot to avoid water stagnation. The data was recorded for 10 quantitative characters namely days to flowering, crop duration, plant height, and panicles per square meter, panicle length, spikelets per panicle, spikelet fertility, grain yield, biological yield and harvest index. The mean over replication of each character were subjected to statistical analysis. Cluster analysis and Principal component analysis were performed to detect the diversity of the genotypes and the contribution of traits to the total divergence respectively using the software WindowStat Version 9.1.

Results and discussion

Principal component Analysis – Environment I :

The breeders are interested to evaluate morphological markers based genetic diversity because they are inexpensive, rapid and simple to score. Further, study of these traits needs neither sophisticated methods nor complicated equipments and these traits can be inherited without specific biochemical and molecular techniques (Sahrobi *et al*., 2012). In the present study, the first principal component accounted for 56.43 per cent variation in the population. The traits such as days to

flowering (0.396), panicles per square meter (0.396) followed by crop duration (0.377) and panicles per square meter (0.347) contributed more towards total variation, while plant height (-0.196), grain yield (-0.228) and harvest index exhibited negative contribution. Second principal component contributed 17.84 per cent of total variation and major share was come from plant height (0.529), spikelet fertility (0.549), biological yield (0.173), panicles per square meter (0.129) and panicle length (0.117). The third principal component accounted for 10.15 of total variation which was chiefly contributed by panicle length (0.445). For the fourth principal component most traits contributed negatively making a total of 8.067 percent variation.

In genotype scoring, in PCA I the genotype R-1570-2649-1-1546-1 scored the maximum and R-RF-84 was minimum while, in PCA II IR-86857-46-1-1-2 scored minimum and IR-83381-B-B-137-3 scored maximum (Table 2). However, in PCA III, IR-848-87-B-15 and IR-88287-677-60-3 was reported to carry maximum and minimum score, respectively. All principal components exhibited low level of diversity except PCA III, which was contributed chiefly by IRRI and Raipur bred entries. In Wards Linkage Cluster Analysis, two clusters were formed each composed of two subclusters i.e. 1a, 1b and 2a, 2b. Sub-cluster 1a comprised of maximum of six genotypes and five genotypes each formed the subcluster 2a and 2b. The sub-cluster 1b was unique with only one genotype namely IR-86857-46-1-1-2. Cluster analysis revealed that almost all IRRI and Raipur originated entries scattered based on the geographical origin, this may be due to common ancestral background of these genotypes (Figure 1). Genotypes of distantly located clusters are suggested to use in crop improvement programmes for obtaining a wide spectrum of variation among the segregants (Yadav *et al*., 2011; Vennila *et al*., 2011; Latif *et al*., 2011). In other studies, Ahmad *et al*. (2012) also have reported cluster analysis to separate genotypes based on origin and suggested to opt distance cluster parents in crop improvement programmes. The characters with high variability are expected to provide high level of genetic gain during further breeding programs. Days to flowering, panicles per square meter, spikelet fertility and biological yield were identified as traits for maximum variability. Among the genotypes, 1st PC was related to days to flowering, panicle per unit area and spikelet fertility while 2nd PC was associated with plant height, panicle length and spikelet per panicle. The previous reports also suggest incorporation of characters with high variability in breeding programmes (Aliyu *et al*., 2000; Gana, 2006, 2013).

Principal component Analysis – Environment II :
First three principal components exhibited more than one eigen value and accounted for 86 percent of total variation (Table 1). The first PCA displayed 36.38 % variation, brought about by days to flowering (0.504), crop duration (0.508) and grain yield (0.302). However, all the reproductive units i.e. panicle per square meter, panicle length, spikelet per panicle and spikelet fertility contributed negatively. The second component (PCA II) has 29.45 percent contribution towards total variation and major role was played by panicle per square meter (0.424), biological yield (0.356) and harvest index (0.291). The third component shared 21.6 percent variation with plant height (0.534), harvest index (0.465), spikelet fertility (0.426) to be major components. In earlier studies, Lasalita-Zapico *et al*. (2010) computed approximately 82.7% of total variation among 32 upland rice varieties, 66.9% variation for PC1 and 15.87% for PC2. This suggested a strong correlation among characters being examined. Rajiv et al. (2010) have also reported the first two principal components accounting for 82.1% of total variation in control and 68.6% in the stress-induced genotypes. In varietal scoring, IR-83383-B-B-141-1 showed maximum score in PC I, whereas minimum score was reported in R-RF-95 (Table 2). Similarly, IR-88287-677-53-3 and Sahbhagidhan was found to be maximum and minimum scorers in PCA II. In wards linkage cluster analysis, two major clusters were formed of which cluster II comprised of two major subclusters i.e. IIa and IIb. IIb which was further partitioned into two divisions, one of which harboured maximum of six genotypes followed by cluster Ia having five genotypes (Figure 2). Eighteen accessions of upland rice were clustered into five main groups. To achieve wide spectrum of variation in the segregating generations, genotypes from distance origin namely R-RF-69, R-RF-95, IR-1570-2649-1-1546-1, IR-83381-B-B-137-3 should be deployed.

Pooled over environments:First four components having eigen value more than one and offered 82 percent of total variation (Table 1). Days to flowering (0.432), plant height (0.548), crop duration (0.627) and spikelet per panicle had greater contribution in PCs I, II, III and IV. Spikelet per panicle contributed negatively in all components except for PCA II, similarly grain yield was found to partition negatively in all components except for PCA II. In components based genotype scoring IR-83383-B-B-141-1 (PCA I), PM 2004 (PCA II) and R-RF-65 was showed maximum score and IR-86857-46-1-1-2 (PCA I), R-RF-95 (PCA II) and IR-88287-677-53-3 (PCA III) had minimum scores (Table 2). In genotype clustering, two major clusters were

formed (I and II), of which further partitioning was made to separate five distinct genotypes. Cluster II was further portioned into two subclusters which comprised of five and two components respectively (Figure 3). Principal component analysis is valuable technique to quantify relationship among traits and for pattern of data by reducing dimensions. An insight into the process contributing in yield is essential for recognition of potential genotypes among diverse base. The PCA technique has retrospect been applied for rice workers namely Uga et al. (2003); Zamira et al. (2003); and Rashid et al. (2008).

The parents for hybridization program should be selected based on the magnitude of genetic distance, contribution of different characters towards the total divergence and magnitude of cluster means for different characters performance having maximum heterosis. Genotypes of distantly located clusters were suggested to use in hybridization programs for obtaining a wide spectrum of variation among the segregates. Current study reports days to 50 percent flowering, biological yield and grain yield are greater contributors of variability and due weightage should be given while formulating breeding schedule. Among genotypes, IR-1570-2649-1-1546-1 and IR-83381-B-B-137-3 are considered as most diverse among population studied.

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Table 1. Eigen values and contribution first four principal components axes to variation

	Kharif 2013				Kharif 2014				Pooled over environments			
	PCA I	PCA II	PCA III	PCA IV	PCA I	PCA II	PCA III	PCA IV	PCA I	PCA II	PCA III	PCA IV
Eigene Value (Root)	5.64	1.78	1.015	0.807	3.639	2.946	2.160	0.661	3.896	2.080	1.467	1.069
% Var. Exp.	56.43	17.84	10.151	8.067	36.387	29.456	21.600	6.611	38.958	20.804	14.671	10.690
Cum. Var. Exp.	56.43	74.27	84.429	92.497	36.387	65.843	87.444	94.054	38.958	59.762	74.433	85.123
Days to Flowering	0.396	0.042	0.076	0.121	0.505	0.073	0.112	0.089	0.432	0.052	0.230	0.233
Crop Duration	0.377	-0.130	0.244	-0.033	0.508	0.056	0.111	0.055	0.222	0.130	0.628	-0.274
Plant Height (cm)	-0.177	0.530	0.535	-0.100	0.024	-0.332	0.534	-0.084	0.149	0.549	-0.222	-0.069
Panicles Per M²	0.365	0.130	-0.239	-0.177	-0.211	0.424	0.109	-0.518	0.337	-0.137	-0.004	-0.434
Panicle Length (cm)	0.347	0.118	0.445	-0.214	-0.087	-0.407	0.358	-0.504	0.134	0.476	-0.024	-0.549
Spikelets Per Panicle	0.229	-0.566	-0.121	-0.158	-0.399	-0.359	0.005	0.160	-0.313	0.376	-0.387	-0.006
Spikelet Fertility (%)	0.045	0.540	-0.600	-0.017	-0.288	0.025	0.424	0.638	0.319	0.373	-0.102	0.394
Grain Yield (kg/Plot)	-0.229	-0.052	-0.067	-0.920	0.302	-0.443	0.043	-0.074	-0.432	-0.015	0.076	-0.331
Biological Yield (kg/Plot)	0.396	0.173	-0.113	-0.092	-0.199	0.353	0.389	-0.116	0.253	-0.349	-0.465	-0.333
Harvest Index (%)	-0.390	-0.160	0.028	0.130	0.247	0.292	0.466	0.093	-0.400	0.176	0.348	-0.010

Table 2. Rice data genotype scoring derived from first four principal components

	Kharif 2013				*Kharif* 2014				Pooled over environments			
Genotype	Vector 1	Vector 2	Vector 3	Vector 4	Vector 1	Vector 2	Vector 3	Vector 4	Vector 1	Vector 2	Vector 3	Vector 4
R-RF-69	240.054	90.427	-5.706	-59.826	151.733	10.468	85.204	5.014	31.832	27.215	13.202	6.242
R-RF-84	237.882	90.042	-6.484	-59.495	164.147	10.171	87.625	5.027	32.296	28.517	14.577	6.905
R-RF-95	239.981	89.376	-6.810	-63.902	147.686	12.550	89.382	2.824	31.852	26.959	12.292	4.379
R-RF-65	245.132	88.995	-3.293	-61.087	165.166	7.716	92.103	3.173	32.534	29.894	14.929	6.112
IR 84887-B-15	241.494	93.309	0.304	-62.558	154.878	7.500	92.559	3.996	32.576	29.702	13.251	5.338
IR 83929-B-B-132-2	239.753	91.616	-3.033	-61.093	158.819	1.927	89.951	5.999	32.666	30.235	12.943	6.986
IR 86857-46-1-1-2	251.274	92.380	-4.671	-64.981	160.909	11.559	91.262	4.010	32.988	28.885	13.560	5.802
R-RF-45	254.197	98.585	-3.445	-64.364	160.653	15.479	99.518	4.307	35.061	28.845	11.589	5.306
PM 6004	252.346	95.985	-5.145	-66.481	156.440	9.092	96.464	7.455	33.582	30.648	13.212	6.645
IR 83381-B-B-137-3	255.873	99.357	-6.271	-64.744	163.686	13.813	98.124	6.233	35.368	29.455	12.361	6.466
Sahbhagidhan	241.691	93.471	-7.411	-61.036	162.084	3.021	89.743	5.480	33.729	30.035	12.567	7.146
IR 88287-677-60-3	258.203	93.307	-8.512	-63.569	164.717	11.286	90.624	1.883	34.772	28.411	13.594	6.042
IR 84852-B-12-1-4	262.053	96.484	-7.916	-66.618	165.688	15.141	98.068	2.355	35.697	28.696	13.320	5.836
IR 88287-677-53-3	260.555	97.355	-7.869	-63.660	165.632	21.947	98.494	6.585	35.988	27.199	12.246	6.821
IR 83383-B-B-141-1	260.260	95.064	-3.859	-62.013	174.796	14.573	89.367	4.441	36.396	28.426	13.124	7.330
IR 84859-B-41-1-2	254.204	92.176	-4.989	-62.661	167.463	12.778	94.315	6.366	33.695	28.628	13.962	6.705
IR 86857-46-1-1-2	247.837	86.152	-3.685	-62.649	154.082	9.920	89.072	3.511	31.208	27.605	13.797	5.051
R-1570-2649-1-1546-1	266.665	96.231	-5.218	-66.884	166.355	9.181	93.082	2.582	35.247	28.861	12.817	5.460

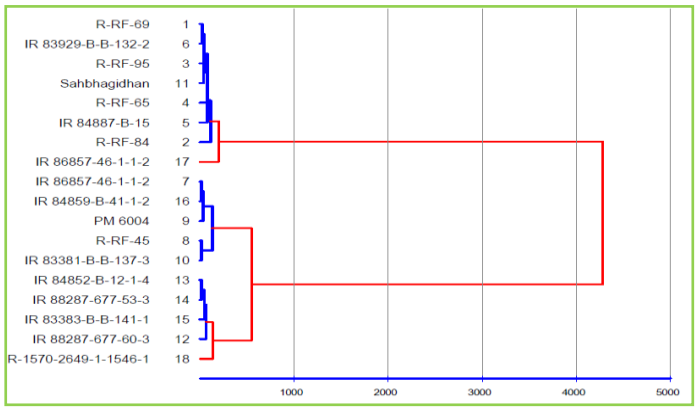

Figure 1. Dendrogram of 18 genotypes Kharif - 2013

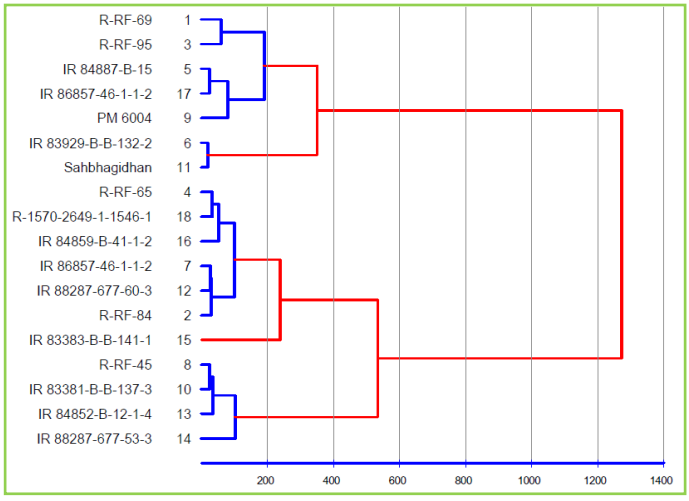

Figure 2. Dendrogram of 18 genotypes Kharif - 2014

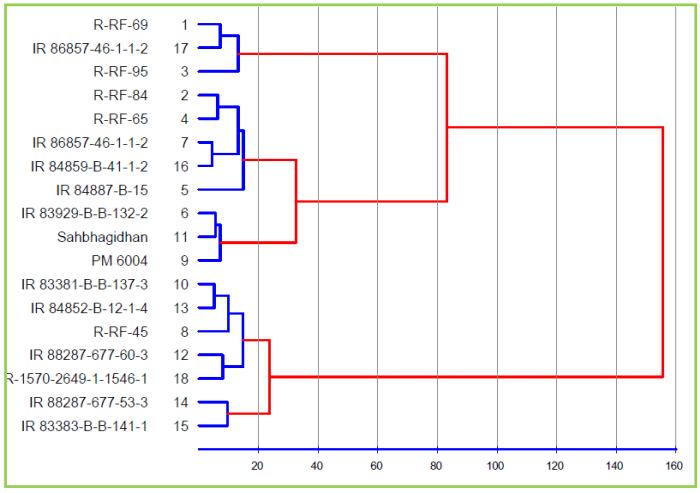

Figure 3. Dendrogram of 18 genotypes pooled over environments