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Clustering of upland rice genotypes by different biometrical methods

***A. SOHARU, S. K. SANADYA, A. DWIVEDI AND D. P. PANDEY**

Department of Genetics and Plant Breeding, College of Agriculture, Chaudhary Sarwan Kumar Himachal Pradesh Agricultural University, Palampur- 176062 (H. P.) India

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ABSTRACT

The type and level of genetic divergence in thirty-three advance lines of rice was estimated by various clustering approaches. Analysis of variance revealed considerable amount of variability present in the material. High estimates of the coefficient of variation were observed for seed yield per plant followed by the grains per panicle, which were used to plot a graph. Based on their total index score highly diverse germplasms were HPR2839, HPR2845, HPR2847, HPR2866 and HPR2875. Based on D^2 analysis, genotypes were divided into eleven clusters. Cluster II constituted eight genotypes and only single genotype consisted from VII to XI clusters. The maximum inter-cluster value was observed between cluster X and V (110.40) followed by cluster X and XI (95.83) suggesting that the genotypes HPR 2839, HPR 2883, HPR 1156, HPR 2656 and HPR2889 constituted in these clusters may be used as parents for future hybridization programs. It can be concluded that characters contributed more towards divergence in D^2 analysis were loaded in principal component1. Hence, the results of cluster analysis were supported by principal component analysis.

Keywords: Clustering, ordination, scoring, screening and upland rice

Rice (2n = 24) is an important self-pollinated crop belongs to family *Poaceae*. It is being cultivated almost across the world. It is the staple food for half of the world's population. In Asia alone, more than 2 billion people obtain 60-70% of caloric intake from rice and its derived products. It is a major source of employment for nearly a billion of families throughout the world furthermore relies on rice based cropping systems for their livelihood. With the gradual increase in population its demand is also rising day by day and keeping this in view, there is a tangible need to develop new varieties, which have the ability to break the yield plateau. One of the prerequisites for a successful breeding programme is the information on the nature and magnitude of genetic variability in selecting genotypes with desirable characters (Dudly and Moll, 1969). The knowledge of the genetic divergence is of great importance for breeders, based on a set of dissimilar variables it categorized the samples of a subjects into different groups thus allowing similar subjects to fall in same group (Fellahi *et al.,* 2013). However, several methods have been introduced for diversity analysis but if large number of germplasms to be assessed than metroglyph approach would be more suitable than D^2 statistic approach and Principal Component Analysis. Therefore, assessed genetic diversity of the rice germplasm for yield and related traits was assessed using different clustering approaches such as Metroglyph method, D^2 statistic approach and Principal Component Analysis and was compared them. Therefore, rice germplasm could be selected for further hybridization programme to develop varieties.

MATERIALS AND METHODS

The present investigation was carried out at the experimental farm of Rice and Wheat Research Centre (RWRC), Malan during *Kharif*-2017 under upland condition. Thirty-three advanced breeding lines (Table 1) of rice including two checks were planted in Randomized Block Design (RBD) with three replications. For the present study, rice germplasms were taken from CSKHPKV, Palampur India. The data were collected on different yield contributing traits like days to 50% flowering (DF), days to 75% maturity (DM), plant height (PH), panicle length (PL), spikelet per panicle (SP), grains per panicle (GP), grain yield per plant (GY), yield per plot (YP), 1000-grain weight (TW), grain length (GL), grain breadth (GB) and L:B ratio (LBR). The experimental material was sown in a single row during the *Kharif* 2017 with 25 cm x 10 cm spacing. Germplasms were subjected to recommended packages of agronomical and plant protection to obtain a healthy crop. Observation was recorded for all the traits on plant basis (averaged of five randomly selected plants) except days to 50 % flowering and days to maturity which were taken on plot basis. The collected data were subjected to statistical analysis by Metroglyph method Anderson (1957), D^2 statistics technique Mahalanobis (1928) and Principal Component Analysis Pearson (1901).

Email: alkasoharu5@gmail.com

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA)

Analysis of variance (Table 2) showed significant difference for all the characters under study indicating sufficient amount of variability present in experimental material and could be exploited for further analysis such as Metroglyph approach, D^2 analysis and PCA.

Metroglyph analysis

Coupled with an index score, metroglyph could be of great use in preliminary screening and classification of genotypes when a large number of germplasms are available. This approach was found to be useful for preliminary classification of germplasm and its divergence study (Anderson ,1957). Still this approach is popular. The genotypes were plotted a graph between seed yield per plant on X-axis and grains per panicle on Y-axis as these two characters exhibited high coefficient of variation. The range of each character divided into three equal classes (low, medium and high, respectively) and each character was represented by different length of the ray depending on their index score. Low, medium and high scores were represented with 1, 2 and 3 respectively according to their range of mean values (Table 3). The thirty-three advance lines of rice were graphically represented as metroglyph (Fig. 1) following Anderson (1957). Group I containing the line HPR1156 was placed farthest from the group VI with HPR2839. HPR2839 and HPR1156 had contrasting mean values for both the axes. Distributions of genotypes of rice have been given in Table 5. Thirty-three advance lines of rice were grouped into six clusters among group VI, containing only one advance line, groups III and IV contain two advance lines each, group V, containing six advance lines, group I, with ten advance lines and II, comprising of twelve advance lines were placed closely on the scattered plot (Table 5). The advance lines of group IV had medium values for both axes. The total index score values recorded for 30 germplasms ranged from 17 to 27 (Table 4). Five genotypes showed the highest score (27), while HPR 2878 showed the lowest score (17). The germplasm, which had the index score from 22 to 27, constituted the upper superior class and the germplasms that were between the index score of 17 to 22 constituted the lower (inferior) class. Several workers had suggested metroglyph analysis for preliminary classification of genotypes (Gomathinayagam and Natarajan, 1988; Mahapatra *et al.,* 1995, Bharadwaj *et al.,* 2001, Cheema *et al.,* 2004; Rashid *et al.,* 2007) in rice or other species such as Aslam *et al.* (2014) in cotton, Jha *et al.* (2013) in chickpea, Sanadya *et al.* (2018) in sewan grass and Jakhar *et al.* (2020) in groundnut. Pictorial representation of genotypes (Fig. 1) as brought about by the scattered plot of metroglyph analysis can be used as a measure of relative genetic distance among the genotypes. Highly diverse germplasms based on their total index score were HPR2839, HPR2845, HPR2847, HPR2866 and HPR2875 and less diverse germplasms were HPR2878 followed by HPR2883, HPR2869, HPR2884 and HPR1156. It can be also inferred that the scoring procedure would be utilized in the preliminary screening of a large number of genotypes for selection of germplasm with a desirable combination of various characters influencing the seed yield per plant with grains per panicle in rice.

D^2 Statistic analysis

D^2 statistic approach is another popular method to quantify the degree of genetic divergence amongst populations/germplasm/elite varieties (Mahalanobis, 1936). Previously workers had also noted the presence of steady genetic diversity in rice (Ahmed *et al.,* 2014; Sandhya *et al.,* 2015, Sowmiya and Venkatesan, 2017). The random distribution of 33 genotypes into 11 clusters, five of them having solitary genotypes each was presented in Table 6. The uniqueness of these latter five genotypes placed them separately. Among the 11 clusters, cluster II accommodated maximum of eight genotypes.

Cluster I were found to be second largest cluster with seven genotypes and cluster IV comes at number three position with five genotypes followed by cluster V and VI with three genotypes each whereas cluster III contained two genotypes and remaining clusters are monotypic due to only single genotype accommodated. The genotypes included in cluster II indicating that there was no parallelism between clustering pattern and geographic distribution of genotypes (Soni *et al.,* 2014).

The maximum intra-cluster distance was observed in cluster VI (151.76) followed by cluster IV (144.22), cluster V (107.65), cluster II (105.27), cluster I (90.35), cluster III (22.84) indicating limited genetic diversity among genotypes representing these clusters (Table 7). The clusters VII, VIII, IX, X and XI consisted of only one genotype hence, they lack of intra-cluster distance. The relative divergence of each cluster from other cluster (inter-cluster distance) indicated greater divergence between cluster V and X (12187.77) followed by cluster X and XI (9182.43). Thus the selection of divergent genotypes from these clusters might be used in the hybridization programme. These crosses would produce high heterotic F_1 lines and in advance generation broad spectrum variability could be achieved from the recombinants. The smallest inter-cluster distance was recorded between cluster II and VII (241.28) followed by cluster III and XI (283.62). The lines belonging to

Table 1: Experimental materials used in present study

S. No.	Germplasm	Parentage
1	HPR 2839	Kalizini/HPR2143// HPR2143
2	HPR 2840	Kalizini/HPR2143// HPR2143
3	HPR 2841	Kalizini/HPR2143// HPR2143
4	HPR 2842	Kalizini/HPR2143// HPR2143
5	HPR 2843	Kalizini/HPR2143// HPR2143
6	HPR 2845	Kalizini/HPR2143// HPR2143
7	HPR 2846	Kalizini/HPR2143// HPR2143
8	HPR 2847	Kalizini/HPR2143// HPR2143
9	HPR 2866	HPR 2143/AC 19146//VL 30424
10	HPR 2867	HPR 2143/AC 19146//VL 30424
11	HPR 2868	HPR 2143/AC 19146//VL 30424
12	HPR 2869	HPR 2143/AC 19146//VL 30424
13	HPR 2870	HPR 2143/AC 19146//VL 30424
14	HPR 2871	HPR 2143/AC 19146//VL 30424
15	HPR 2872	HPR 2143/AC 19146//VL 30424
16	HPR 2873	HPR 2143/AC 19146//VL 30424
17	HPR 2874	HPR 2143/AC 19146//VL 30424
18	HPR 2875	HPR 2143/AC 19180//VL 30424
19	HPR 2876	HPR 2143/AC 19180//VL 30424
20	HPR 2877	HPR 2143/AC 19180//VL 30424
21	HPR 2878	HPR 2143/AC 19180//VL 30424
22	HPR 2879	HPR 2143/AC 19180//VL 30424
23	HPR 2881	HPR 2143/AC 19180//VL 30424
24	HPR 2882	HPR 2143/AC 19180//VL 30424
25	HPR 2883	HPR 2143/AC 19180//VL 30424
26	HPR 2884	HPR 2143/AC 19180//VL 30424
27	HPR 2885	HPR 2143/AC 19180//VL 30424
28	HPR 2886	HPR 2143/AC 19180//VL 30424
29	HPR 2887	HPR 2143/AC 19180//VL 30424
30	HPR 2888	HPR 2143/AC 19180//VL 30424
31	HPR 2889	HPR 2143/AC 19180//VL 30424
32	**Sukara Dhan1(HPR 1156) ©**	**IR 32429-122-3-1-2/IR 31868-64-2-3-3-3**
33	**Him Palam Dhan-1 (HPR 2656) ©**	**RP 2421/VL Dhan 221**

Table 2: Estimates of mean sum of squares due to replications, genotypes and error for twelve characters of rice

Source of variation	df	DF	DM	PH	PL	GP	SP	GY	TW	GL	GB	LBR	YP
RMS	**2**	0.98	0.04	8.91	4.62	290.28	701.66	9.227	26.75	0.13	0.015	0.22	0.02
GMS	**32**	84.45*	73.97*	126.77*	6.79*	1311.76*	3538.04*	8.20*	18.13*	0.42*	0.07*	0.27*	0.08*
EMS	**64**	0.48	0.04	3.77	0.34	63.76	224.29	0.57	1.38	0.04	0.01	0.03	0.004

these clusters were found relatively closer to each other, thus selection of genotypes from these clusters must be avoided because of the presence of homozygosity among the genotypes to maintain the broad genetic base. Other researcher (Yadav *et al.,* 2011) reported similar results.

Cluster mean analysis revealed a wide range of variation for all the traits under study (Table 8) which can be used to assess the superiority of clusters, which could be considered in the improvement of various characters through hybridization programme. Cluster XI showed earliness in maturity, minimum cluster mean for plant height and higher cluster mean for yield per plot. Whereas, cluster III was reported for higher cluster mean for panicle length, grain length and L:B ratio.

The preference and choice of parents mainly depends upon contribution of characters towards divergence.

Table 3. Index score and signs used for ten characters for metroglyph analysis of thirty-three genotypes of rice

S. No.	Character	Range	Score1		Score2		Score3	
			Value less than	Sign	Value from - to	Sign	Value more than	Sign
1	**DOF**	76-99	83.67		83.68-91.33		91.34	
2	**DOM**	106-123	111.67		111.68-117.33		117.34	
3	**PH**	88.13-112.83	96.36		96.37-104.6		104.61	
4	**PL**	22.03-27.60	23.89		23.90-25.74		25.75	
5	**YPP**	6.97-13.27	9.07		9.08-11.17		11.18	
6	**GW**	21.24-31.89	24.79		24.80-28.34		28.35	
7	**GL**	6.53-7.72	6.93		6.94-7.32		7.33	
8	**GB**	1.66-2.22	1.85		1.86-2.03		2.04	
9	**LBR**	2.8-4.11	3.24		3.25-3.67		3.68	
10	**PC**	6.57-11.85	8.33		8.34-10.09		10.10	

Among the 12 characters studied, days of 75% maturity contributed maximum of 82.39 per cent, followed by days of 50% flowering 8.52 per cent, yield per plot 2.65 per cent, grains per panicle 2.08 per cent, grain length 1.33 per cent towards genetic divergence. Previously Sandhyakishore *et al.* (2007) has been noticed parallel results. Hence, these characters can be given due concern for selection of genotypes for further improvement. Clustering of genotypes through D^2 statistic had been suggested by earlier workers in rice (Roy *et al.,* 2002; Bose and Pradhan *et al.,* 2005; Hosan *et al.,* 2010; Chakravorty and Ghosh, 2012; Perween *et al.,* 2020).

Principal component analysis

PCA was performed using yield and its component traits on rice genotypes. Out of 12 (Table 9), only four principal components (PCs) exhibited more than one eigenvalue and showed about 79.22% total variability among the characters were studied. The PC1 displayed

Table 4: Total index score of rice genotypes for twelve traits

Genotypes	Symbol	DOF	DOM	PH	PL	GPP	SPP	YPP	GW	GL	GB	LBR	PC	Total
HPR 2839	1	3	3	3	3	3	3	3	1	1	1	2	1	27
HPR 2840	2	2	3	1	3	3	2	2	2	2	2	2	1	25
HPR 2841	3	2	3	2	3	3	2	2	2	1	3	1	1	25
HPR 2842	4	2	2	2	2	2	1	2	1	3	2	3	1	23
HPR 2843	5	2	3	2	2	3	2	3	1	3	1	3	1	26
HPR 2845	6	2	3	2	3	3	1	3	2	2	2	3	1	27
HPR 2846	7	2	3	2	3	2	1	3	2	1	2	2	2	25
HPR 2847	8	2	2	2	3	2	2	3	2	3	2	3	1	27
HPR 2866	9	2	2	2	3	3	2	3	1	3	2	3	1	27
HPR 2867	10	1	1	1	1	2	1	3	3	2	3	2	2	22
HPR 2868	11	2	2	1	2	3	1	3	2	1	3	2	1	23
HPR 2869	12	1	1	1	1	2	1	2	3	1	3	1	1	18
HPR 2870	13	1	2	3	2	3	2	2	3	1	2	2	1	24
HPR 2871	14	1	2	2	3	1	1	2	3	2	3	2	1	23
HPR 2872	15	2	2	2	2	1	1	1	3	2	3	2	2	23
HPR 2873	16	1	2	3	2	2	1	2	2	2	2	3	2	24
HPR 2874	17	2	2	2	3	2	1	1	2	2	1	3	1	22
HPR 2875	18	3	3	2	2	2	1	3	3	1	3	2	2	27
HPR 2876	19	3	3	2	3	2	1	2	3	1	2	2	2	26
HPR 2877	20	2	1	1	2	3	2	2	1	1	2	2	2	21
HPR 2878	21	1	2	1	1	1	1	1	2	2	1	3	1	17
HPR 2879	22	1	3	2	2	1	1	2	2	2	2	3	1	22
HPR 2881	23	2	1	2	2	3	1	3	3	2	3	2	1	25
HPR 2882	24	2	1	2	1	1	1	2	3	3	1	3	2	22
HPR 2883	25	1	1	3	1	1	1	1	3	1	3	1	1	18
HPR 2884	26	2	2	2	2	2	1	1	1	1	2	2	1	19
HPR 2885	27	1	2	2	2	1	1	3	2	2	2	3	2	23
HPR 2886	28	2	3	2	3	3	2	3	1	1	2	2	1	25
HPR 2887	29	3	3	1	2	2	1	1	1	1	2	2	3	22
HPR 2888	30	3	3	1	2	1	1	1	1	1	1	2	3	20
HPR 2889	31	2	1	1	2	1	1	2	2	3	1	3	2	21
HPR 1156	32	1	1	3	1	1	1	2	2	1	2	2	2	19
HPR 2656	33	1	1	3	1	2	2	3	2	2	2	1	2	20
Total		60	69	63	70	67	44	72	67	57	68	74	49	**758**

Table 5: Distribution of rice genotypes into different clusters

Cluster	Number of genotypes	Composition of cluster	Distribution
I	10	14, 15, 27, 21, 22, 24, 25, 31, 32 and 30	Low GPP and Low SPP
II	12	18, 4, 33, 18, 29, 17, 16,10, 19, 7, 26 and 5	Low GPP and Medium SPP
III	2	23 and 11	Low GPP and High SPP
IV	2	8 and 15	Medium GPP and Medium SPP
V	6	20, 28, 2, 13, 8 and 3	Medium GPP and High SPP
VI	1	1	High GPP and High SPP

Table 6: Based on D^2 analysis distribution of rice genotypes in different clusters

Cluster no.	No. of genotypes	List of the genotypes
CLUSTER 1	4, 8, 26, 9, 15, 11,14	HPR 2842, HPR 2847, HPR 2884, HPR 2866, HPR 2872, HPR 2868, HPR 2871
CLUSTER 2	6, 28, 5, 3, 19, 7, 29,2	HPR 2845, HPR 2886, HPR 2843, HPR 2841, HPR 2876, HPR 2846, HPR 2887, HPR 2840
CLUSTER 3	10, 12	HPR 2867, HPR 2869
CLUSTER 4	13, 16, 27, 17, 21	HPR 2870, HPR 2873, HPR 2885, HPR 2874, HPR 2878
CLUSTER 5	25, 32, 33	HPR 2883, HPR 1156, HPR 2656
CLUSTER 6	20, 24, 23	HPR 2656, HPR 2882, HPR 2881
CLUSTER 7	18	HPR 2875
CLUSTER 8	30	HPR 2888
CLUSTER 9	22	HPR 2879
CLUSTER 10	1	HPR 2839
CLUSTER 11	31	HPR 2889

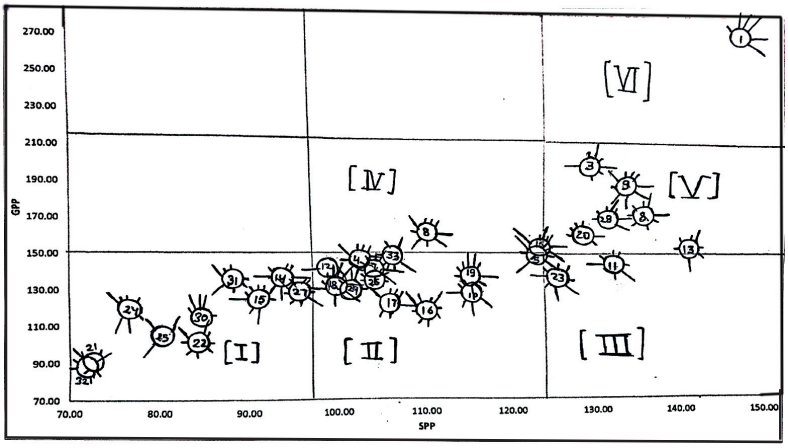

Fig. 1. Scattered diagram of metroglyph analysis of rice germplasm

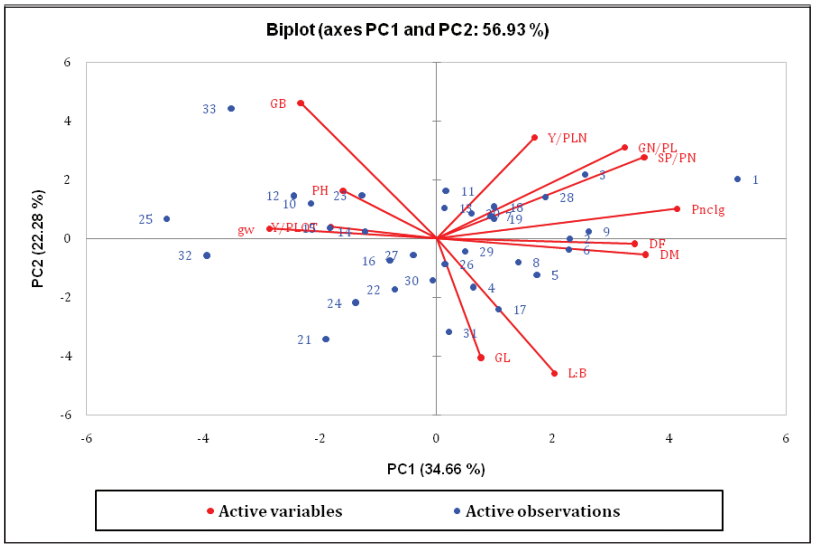

Fig. 2: Distribution of different upland rice genotypes in the biplot

Table 7: Intra (bold) and inter cluster (unbold) D^2 values of various clusters in rice

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**90.35**9.51	1231.7935.10	1714.1741.40	326.5718.07	3492.7459.10	676.4026.01	1260.8535.51	472.7421.74	1359.0736.87	2862.1853.50	1996.7244.68
II		**105.27**10.26	5566.2774.61	741.6327.23	8448.4191.92	3430.1458.57	241.2815.53	356.2718.88	268.8216.40	485.4022.03	6036.0577.69
III			**22.84**4.78	2780.7852.73	562.4723.72	461.0621.47	5580.4374.70	3618.8560.16	5581.5274.71	8726.1293.41	283.6216.84
IV				**144.22**12.01	4678.0068.40	1500.0538.73	1009.3131.77	325.0818.03	587.4224.24	2041.1645.18	3325.2857.67
V					**107.65**10.38	1468.7338.32	8458.9391.97	6003.0077.48	8105.5590.03	12187.77110.40	897.4029.96
VI						**151.76**12.32	3258.8057.09	1955.5744.22	3608.6060.07	5901.7976.82	584.0524.17
VII							**0.00**0.00	390.3619.76	625.7625.02	662.4225.74	5811.3376.23
VIII								**0.00**0.00	489.1622.12	1358.7536.86	3865.3262.17
IX									**0.00**0.00	804.9928.37	6278.0079.23
X										**0.00**0.00	9182.4395.83
XI											**0.00**0.00

Table 8: Cluster mean and contribution of various characters towards diversity in rice

Clusters	DF	DM	PH	PL	GP	SP	GY	TW	GL	GB	LBR	YP
I	87.76	115.00	96.63	0.95	25.57	109.83	148.42	10.67	27.09	7.20	1.99	3.62
II	90.42	120.42	95.02	0.91	**26.27**	120.81	156.42	10.90	25.41	6.90	1.94	3.55
III	82.00	109.00	90.12	**1.15**	23.80	107.25	134.92	11.50	**30.47**	6.87	**2.17**	3.26
IV	82.20	117.00	100.78	0.96	24.88	105.19	122.53	9.68	26.98	7.12	1.84	3.76
V	**76.67**	106.33	110.76	0.96	22.58	86.20	113.96	9.80	26.66	**6.51**	2.18	3.13
VI	89.00	111.22	100.74	0.99	24.28	110.44	**139.08**	10.54	27.70	7.06	1.96	3.53
VII	99.00	120.00	100.23	0.80	24.86	99.83	131.73	**12.70**	25.36	6.76	2.05	3.31
VIII	92.00	118.00	88.47	0.79	24.11	84.53	114.93	7.33	24.06	6.64	1.85	3.38
IX	82.00	120.67	101.47	0.89	24.12	84.27	101.07	10.43	26.58	7.18	1.87	3.83
X	92.00	123.00	104.57	0.56	27.60	149.03	274.47	12.57	21.24	6.75	1.85	3.66
XI	89.00	**108.00**	88.13	0.65	24.79	88.17	136.03	9.00	27.40	**7.72**	1.81	**4.11**
Contribution towards divergence (%)	8.52	82.39	0.95	0.57	2.08	0.19	0.57	0.76	1.33	0.00	0.00	2.65

Table 9: Eigen values, percent variance and cumulative variance values of rice genotypes

Traits	DF	DM	PH	YP	PL	GP	SP	GY	TW	GL	GB	Eigen value	Variability (%)	Cumulative (%)
PC1	12.65	14.03	2.82	3.58	18.59	11.37	13.85	3.11	8.96	0.64	5.94	4.16	34.66	34.66
PC2	0.03	0.31	2.92	0.18	1.13	10.46	8.33	12.91	0.13	17.74	23.14	2.67	22.28	56.93
PC3	1.30	1.13	0.28	22.58	3.13	4.37	0.02	18.39	17.70	23.74	0.49	1.56	12.99	69.93
PC4	16.61	0.48	57.48	4.71	0.02	0.07	2.13	1.24	9.33	0.50	2.04	1.11	9.29	79.22

maximum contribution toward variability *i.e.,* 34.66% while PC2, PC3 and PC4 showed 22.28%, 12.99%, and 9.29% respectively for the traits under study among the genotypes. Several scientists (Ashfaq *et al.,* 2012; Anyaoha *et al.,* 2018) reported almost similar findings.

PC1 that accounted for the maximum variability (34.66%), were highly loaded with characters such as panicle length (18.59), days to 75% maturity (14.02), spikelets per panicles (13.85), days to 50% flowering (12.64), grains per panicle (11.37), 1000-grain weight (8.96) and grain breadth (5.94). Therefore, it clearly revealed that the variation in PC1 is mainly accounted by yield contributing characters. PC2 accounted (22.29%) of total variability and filled with the characters like L:B ratio (22.73), grain length (17.74), yield per plant (12.91), grains per panicle (10.46) and spikelets per panicle (8.33) indicated that variation is contributed by both yield contributing and quality traits. Characters like grain length (23.74), yield per plot (22.58), yield per plant (18.39), 1000-grain weight (17.70) and L: B ratio (6.87) had contributed (12.99%) of the total variation. PC4 had the contribution from the traits like plant height (57.49), days of 50% flowering (16.61), 1000- grain weight (9.33), L: B ratio (5.40) and yield per plot (4.71) which accounted for (9.29%) of total variation. Researcher Ravi *et al.*(2018) observed similar results.

Comparison of Mahalanobis's D^2 method and metroglyph technique

Comparisons between the results of the three analyses revealed the striking diversity as regards to group arrangement. Earlier it has been suggested that the metroglyph technique would be suitable for preliminary grouping prior to undertaking D^2 analysis if large number of germplasm were taken for study of diversity. However, after the association of PCA with D^2 statistic method results would be reliable because it reduces the dimensionality of the data set by creating significant principal components that contributed towards maximum variability of the genotypes. In metroglyph method, higher amount of variability among traits reported for the length breath ratio, yield per plot, panicle length, days to 75 % maturity and grain breath. In D^2 analysis, days to 75 % maturity, days of 50% flowering, yield per plot, grains per panicle contributed maximum towards divergence. In PCA the characters *viz.,* panicle length, days to 75% maturity, spikelets per panicles, days to 50% flowering, grains per panicle, 1000-grain weight and grain breadth loaded significantly and contributed more towards variability. The data were analyzing using these three methods, which show comparable results for contribution of the main traits for variance. However, rice germplasm fallen into the different clusters using Metroglyph method and D^2 analysis associated with PCA. Based on Mahalanobis D^2 analysis, maximum diverse germplasm fallen into the cluster X (HPR 2839), cluster V (HPR 2883, HPR 1156, HPR 2656) and cluster XI (HPR2889), while metroglyph analysis revealed that germplasm HPR2839, HPR2845, HPR2847, HPR2866 and HPR2875 were more divergent. However, in the context of variability, all the three methods showed comparable result, while in the context of divergence, results are highly variable. Therefore, D^2 method associated with PCA should be followed for the selection of desirable germplasm for hybridization programmes and development of varieties.

AUTHORS' CONTRIBUTION

Conceptualization of research; designing of the experiments; execution of field experiments and data collection; analysis of data and interpretation; preparation of the manuscript.

DECLARATION

The authors declare no conflict of interest.

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