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

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A B S T R A C T

The present investigation was undertaken with 30 rice genotypes to estimate the nature and magnitude of genetic divergence for yield and nutritional traits. The 30 genotypes were categorized into six clusters based on D^2 values using agglomerative hierarchical clustering complete linkage based on Mahalanobis distance. Cluster I was largest comprising of nine genotypes followed by cluster III and IV comprising of seven and six genotypes respectively. Maximum intra cluster distance was observed in cluster IV (95.017) followed by cluster VI (79.535) indicating greater genetic diversity among the genotypes present in these clusters. The highest inter cluster distance (213.16) was observed between cluster IV and V, followed by cluster I and V (173.93). Genotypes present in the cluster IV recorded highest mean values for the number of productive tillers plant-1, panicle length, 100 grain weight, total antioxidant activity, total soluble phenol content and amylose (intermediate). Hence, the genotypes from these clusters may be considered as parents in hybridization programme for obtaining superior transgressive segregants with respect to yield and nutritional content. Principal component analysis was utilized to evaluate the variation and to estimate the relative contribution of various traits towards total variability. The results revealed five principal components with Eigen value more than one contributed 75.56% towards the total variability. The traits contributing maximum towards the existing variability were plant height, panicle length, spikelet fertility, yield plot-1, 100 grain weight, iron content, antioxidant activity and phenol

Introduction

Rice is the second most important cereal crop of the world and is staple food for majority 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). Diversity in rice can be well utilized to resolve the present scenario of food problems. Arunachalam (1981) stated that chance of getting high variability in segregating population and superior heterotic hybrids mostly depends on genetic divergence of the parents utilized in the hybridization programme. The novel characters and existing

variability in the germplasm should be exploited to develop the need based varieties and hybrids using crop improvement programmes. A thorough knowledge on nature and magnitude in the genetic variability and association of characters of a species is a pre-requisite for an effective breeding programme. The quantification of the degree of divergence in a given experimental materials of immense value in the identification of divergent genotypes for future use in hybridization to create new variability. Mahalanobis D^2 statistic has been proven to be powerful tool for the plant breeder in selecting the right type of parents among the genotypes having wider variability for different traits (Shivani *et al.,* 2018). 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. Therefore, development of improved genotypes is the ultimate goal of any plant breeding programme, which is better than the prevailing genotypes for producing the economic yield. This necessitates genetic improvement through maximum exploitation of allelic resources in developing ideal genotype (Pratap*et al*., 2012).

In view of the above, present investigation was undertaken to study the nature and magnitude of genetic diversity among 30 rice genotypes for yield, yield components and nutritional traits for rice improvement programmes using both Mahalanobis D^2 statistics and Principal Component Analysis (PCA) for selection of parents for future rice breeding programme.

Materials and Methods

Experimental material for the present investigation comprised of 30 rice genotypes collected from collected from farmers of different districts of Telangana (Table 1). These genotyupes were sown during *Kharif* 2018 in a randomized complete block design (RBD) with three replications at Agricultural College Farm, Bapatla, Guntur district of Andhra Pradesh. All the 30 genotypes were sown separately in the raised nursery beds. Thirty days old seedlings of each genotype was transplanted separately in 5 rows of 3m length by adopting a spacing of 20cm between rows and 15cm between plants with in a row. All the necessary precautions were taken to maintain uniform plant population of each genotype per replication. The intercultural operations were done at regular intervals and necessary plant protection measures were adopted during the crop growth. Observations were recorded on five randomly chosen plants of each genotype per replication for the characters Plant height (cm), days to 50% flowering**,** number of productive tillers plant^{-1}**,** panicle length (cm), spikelet fertility (%), yield plot^{-1} (Kg), 100 grain weight (g), kernal length/breadth ratio, protein content (%), Zn content (µgg^{-1}), Fe content (µgg^{-1}), total starch content (%), amylose content (%), total antioxidant activity (mg AAE 100g^{-1}), total soluble phenol content (mg 100g^{-1}), glycemic indexand phytate content (mg 100g^{-1}).The data obtained was subjected to standard statistical procedures. Genetic divergence analysis was done following the D^2 statistics proposed by Mahalanobis (1936) described by Rao (1952) and Principal Component Analysis (PCA). The analysis was carried out using the software WindowStat Version 8.5.

Results and Discussion

Analysis of variance showed significant differences for yield and nutritional traits in

the present investigation indicating existence of sufficient variation among the genotypes and therefore an ample scope for effective selection.

Grouping of genotypes into various clusters

A perusal of the results on grouping of genotypes (Fig.1 and Table 2) revealed that the 30 genotypes were grouped into six clusters based on the relative magnitude of D^2 values using agglomerative hierarchical clustering complete linkage based on Mahalanobis distance Berkhin *et al.,* (2006).

The genotypes belonging to same cluster had an average smaller D^2 value than those belonging to different clusters. Among the six clusters, cluster I was largest comprising of nine genotypes (Narayanakamini, Chintalurisannalu, Selamsanna, Ambemohar, Pancharatna, Kalajira, Ramsri, Ramyagali, Ratanachudi) followed by cluster III with seven genotypes (Sammelbhog, Ghani, Parimalasanna, Mappilllai samba, Bahurupi, Madumurangi, Mysore malliga), cluster IV with six genotypes (Arakuloya, Kalabhatt, Burma black, Kulakar, Navara, Pathariya), four genotypes (Tulasibaso, Doddiga, Illapaipu samba, Karuppukavuni) in cluster VI, three genotypes (Ranikanda, Poongar, Sannajajulu) in cluster II and cluster V with one genotype (Badshabhog).

The genotypes present in different clusters showed high degree of diversity than the genotypes present in the same cluster.

Genotypes from same geographic location fell into different clusters indicating that clustering of genotypes did not follow their geographic or location distribution. These findings are in conformity with the reports of Ashok *et al.,* (2017), Prasad *et al.,* (2018), Sri Devi *et al.,* (2019) and Sudeepthi *et al.,* (2020).

Average intra and inter-cluster D^2 value

An analysis of inter- and intra- cluster distances (Table 3) revealed that the inter-cluster D^2 values ranged from 34.51 (cluster II and III) to 213.16 (clusters IV and V) indicating presence of broad spectrum of genetic diversity among the genotypes present in the clusters. Maximum inter cluster distance was observed between cluster IV and V(213.16), followed by cluster I and V (173.93) indicating that genotypes from these clusters were highly divergent and holds great promise as parents for hybridization. The greater the distance between two clusters, the wider would be the genetic diversity between the genotypes. Therefore, hybridization between the genotypes of the above clusters is expected to result in greater variability and transgressive segregants. Minimum inter-cluster distance was observed between cluster II and III (34.51), indicating their close relationship and similarity with regards to the characters studied for the genotypes in these two clusters. The inter-cluster distances were higher than the intra-cluster distances which indicate the existence of substantial diversity among the genotypes. Similar results of inter and intra cluster distances in rice were reported earlier by Behra *et al.,* (2018).

Intra cluster D^2 values ranged from 0.000 (cluster V) to 95.017 (cluster IV). Maximum intra cluster distance was observed in cluster IV (95.017) followed by cluster VI (79.535). It reveals that genotypes present in the same cluster have low level of diversity and selection of parents with in the cluster for hybridization programme may not be considered promising. The nearest and the farthest clusters from each cluster based on D^2 value given in Table 4.

Cluster means

Cluster means represent average performance of all genotypes present in that particular cluster. Cluster means provides information

on suitable parents for improvement of particular traits. In the present study cluster means revealed considerable variation between the clusters for all the characters. The cluster mean for grain yield and nutritional characters are presented in Table 5. A perusal of these results revealed considerable differences between the clusters for all characters under study. Cluster mean values for plant height were highest in cluster III (152.59 cm) and lowest in cluster V (124.87 cm). Cluster mean for number of productive tillers plant^{-1} was highest in cluster IV (13.9) and lowest in cluster II (10.9), while for days to 50% flowering it was highest in cluster V (95.00) and lowest in cluster I (85.33days). Panicle length was highest in cluster III (27.90) and lowest in cluster IV(21.63). Similarly, spikelet fertility was highest in cluster VI (87.01%) and lowest in cluster V (73.20%), while yield plot^{-1}was highest in cluster VI (2.66 kg) and lowest in in cluster V (1.72 kg). Further, 100 seed weight was highest incluster IV (2.20g) and lowest in cluster V(1.40g). Kernel length/ breadth was highest in cluster II (3.28) and lowest cluster V (1.90). Protein content was highest in cluster III (11.95%) and lowest in cluster II (7.76%). Similarly, zinc content was highest in cluster V (35.45µgg^{-1}) and lowest in cluster III (22.27µgg^{-1}). Iron content was highest in cluster VI (35.09µgg^{-1}) and lowest in cluster V (15.66 µgg^{-1}). Total starch content was highest in cluster II (70.12%) and lowest in cluster V (57.12%). Amylose content was highest in cluster II (26.58%) and lowest in cluster VI (19.62%) While, total antioxidant activity was highest in cluster IV (90.61 mg 100g^{-1}) and lowest in cluster VI (44.95 mg 100g^{-1}). Total phenol content was highest in cluster IV (187.42) and lowest in in cluster I (78.52). Glycemic Index was highest in cluster III (62.58) and lowest in cluster V (54.19). Phytate content was highest in in cluster IV (497.91mg) and lowest in cluster V (308.96mg). Similarly, Supriya *et al.,* (2017), Sridhar *et al.,* (2016) and Rathod *et al.,* (2017) also reported varied cluster means for yield and related characters in rice genotypes.

Genotypes present in the cluster IV recorded maximum for number of productive tillers plant-1, panicle length, 100 grain weight, total antioxidant activity, total soluble phenol content and intermediate amylose content. Whereas, the cluster VI recorded maximum for spikelet fertility, yield plot^{-1} and iron content. Further, cluster III recorded maximum for the nutritional as well as yield characters viz., protein content, zinc, phenol content, low glycemic index, 100 grain weight and yield per plant. Selection of genotypes from clusters with high mean for the respective traits is suggested for utilization in hybridization programmes aimed at improvement of the respective traits. A perusal of these results also revealed that there was no single cluster with all the desirable traits, which ruled out the possibility of direct selection of genotypes for immediate use. Therefore, judicious combination of selected genotypes from the above divergent clusters may be carried out to obtain desirable segregants with respect to nutritional properties coupled with high yield potential. The results are in broad agreement with the reports of Sudeepthi *et al.,* (2020) and Singh *et al.,* (2020).

Principal Component Analysis (PCA)

In the present study, the first five principal components with eigen value more than one contributed 75.56% towards the total variability. 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 6 and Fig. 2.

The first principal component (PC1) contributed 31.74 per cent towards variability.

The characters namely, yields/plot (0.37) and 100 grain weight (0.37) antioxidants (0.28), phenols (0.29), plant height (0.28) explained maximum variance in this component. The second principal component (PC2) contributed 16.46% of total variation. The characters namely productive tillers/plant (0.43), 100 grain weight (0.16) protein content (0.22), glycemic index (0.19) and phytate content (0.16) explained maximum loadings in this component. Likewise, the third principal component (PC3) contributed 13.54% of total variability. The characters namely plant height (0.36), 50% flowering (0.36), panicle length (0.48) and glycemic index (0.30) yield plot-1 (0.22), l/b ratio (0.24), explained maximum variance in this component. Similarly the fourth principal component (PC4) contributed 7.45% of total variation and the characters namely, spikelet fertility (0.44), protein content (0.55), amylose content (0.48) and phytate content (0.36) showed maximum variance in this component. The fifth principal component (PC5) contributed 6.35% of total variation and the characters namely,100 grain weight (0.26), zinc content (0.11), iron content (0.52), starch content (0.23), amylose content (0.14), glycemic index (0.32) contributed maximum towards variance.

Among all the principal components, PC1 showed maximum variability of 31.74% with high Eigen value 5.39, which decreased gradually indicating that maximum variation was observed in PC1 an comparison to the other PC's. Variation in PC1, PC2 and PC3 is mainly contributed by the yield and its component characters whereas, in PC3, PC4, PC5 variation is mainly due to the nutritional characters. The PCA analysis identified that maximum contributing traits towards the existing variability are plant height, panicle length, spikelet fertility, yield per plot, 100 grain weight, iron content, antioxidant activity and phenol content. Hence, these characters may be considered as principal discriminatory traits for this germplasm indicating that selection is effective in favour of these traits. Similar results were reported by Beevi and Venkatesan (2015) and Archana *et al.,* (2018) for number of filled spikelets per panicle, Prasad *et al.*, 2018 for spikelet fertility and 1000 seed weight, for grain yield per plant and 1000 grain weight by Sowmiya and Venkatesan (2017) for plant height, spikelet per panicle and grain yield /plant by Raghavendra *et al.,* (2018).

The PCA scores for 30 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 7. These PCA scores for 30 genotypes were plotted in a graph to get the three dimensional scatter diagram (Fig. 2).

A perusal of these results revealed genotypes Chintalurisannalu and Burmablack to be most diverse. It is also evident form the Tocher's method proving that these genotypes are more divergent and belongs to two different clusters i.e., cluster I and cluster IV with an inter cluster distance of 120.261. Further the genotype Chintalurisannalu recorded low glycemic index, high spikelet fertility and high number of productive tillers whereas, the other genotype Burmablack recorded high soluble phenol content and yield per plant. Hence, hybridization between these two diverse genotypes is therefore predicted to result in desirable transgressive segregants with respect to yield and nutrition.

Table.1 List of genotypes studied in the present investigation

S.No.	Genotype	Place of collection
1	Ambemohar	Kamanpur (Village), Peddapalli (District), Telangana
2	Arakuloya	Ranga Reddy, Hyderabad, Telangana
3	Badshabhog	Kamanpur (Village), Peddapalli (District), Telangana
4	Bahurupi	Gummakonda (Village), Nagarkurnool (District), Telangana.
5	Burma black	Ranga Reddy, Hyderabad, Telangana
6	Chintalurisannalu	Kamanpur (Village), Peddapalli (District), Telangana
7	Doddiga	Kamanpur (Village), Peddapalli (District), Telangana
8	Ghani	Gummakonda (Village), Nagarkurnool (District), Telangana
9	Illapaipu samba	Gummakonda (Village), Nagarkurnool (District), Telangana
10	Kalabhatt	Ranga Reddy, Hyderabad, Telangana
11	Kalajira	Kamanpur (Village), Peddapalli (District), Telangana
12	Karuppukavuni	Ranga Reddy, Hyderabad, Telangana
13	Kulakar	Kamanpur (Village), Peddapalli (District), Telangana
14	Madumurangi	Gummakonda (Village), Nagarkurnool (District), Telangana.
15	Mappillai samba	Ranga Reddy, Hyderabad, Telangana
16	Mysore malliga	Ranga Reddy, Hyderabad, Telangana.
17	Narayanakamini	Kamanpur (Village), Peddapalli (District), Telangana
18	Navara	Ranga Reddy, Hyderabad, Telangana.
19	Pancharatna	Kamanpur (Village), Peddapalli (District), Telangana
20	Parimalasanna	Gummakonda (Village), Nagarkurnool (District), Telangana
21	Pathariya	Gummakonda (Village), Nagarkurnool (District), Telangana.
22	Poongar	Kamanpur (Village), Peddapalli (District), Telangana
23	Ramsri	Gummakonda (Village), Nagarkurnool (District), Telangana
24	Ramyagali	Kamanpur (Village), Peddapalli (District), Telangana
25	Ranikanda	Kamanpur (Village), Peddapalli (District), Telangana.
26	Ratnachudi	Ranga Reddy, Hyderabad, Telangana.
27	Sammelbhog	Gummakonda (Village), Nagarkurnool (District), Telangana
28	Sannajajulu	Kamanpur (Village), Peddapalli (District), Telangana
29	Selamsanna	Kamanpur (Village), Peddapalli (District), Telangana
30	Tulasibaso	Kamanpur (Village), Peddapalli (District), Telangana

Table.2 Clustering pattern of 30 rice genotypes for yield and nutritional characters

S. No.	Clusters	No.	Genotypes names
1	Cluster 1	9	Narayanakamini, Chintalurisannalu, Selamsanna, Ambemohar, Pancharatna, Kalajira, Ramsri, Ramyagali, Ratanachudi
2	Cluster 2	3	Rani kanda, Poongar, Sannajajulu
3	Cluster 3	7	Sammelbhog, Ghani, Parimalasanna, Mappilllai samba, Bahurupi, Madumurangi, Mysore malliga
4	Cluster 4	6	Arakuloya, Kalabhatt, Burma black, Kulakar, Navara, Pathariya
5	Cluster 5	1	Badshabhog
6	Cluster 6	4	Tulasibaso, Doddiga, Illapaipu samba, Karuppukavuni

Table.3 Average intra-and inter –cluster D2 values among seven clusters of 30 rice genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	**54.476**	81.826	72.449	120.261	173.931	47.133
Cluster 2	81.826	**43.992**	34.514	130.323	98.961	60.399
Cluster 3	72.449	34.514	**59.385**	134.845	112.563	54.094
Cluster 4	120.261	130.323	134.845	**95.017**	213.162	99.343
Cluster 5	173.931	98.961	112.563	213.162	**0.000**	152.790
Cluster 6	47.133	60.399	54.094	99.343	152.790	**79.535**

Table.4 Nearest and the farthest cluster from each cluster based on D^2 value

S. No.	Clusters	Farthest cluster	Nearest cluster
1	**Cluster 1** (54.476)	**Cluster 5** (173.931)	**Cluster 6** (47.133)
2	**Cluster 2** (43.992)	**Cluster 4** (130.323)	**Cluster 3** (34.514)
3	**Cluster 3** (59.385)	**Cluster 4** (134.845)	**Cluster 6** (54.094)
4	**Cluster 4** (95.017)	**Cluster 5** (213.162)	**Cluster 6** (99.343)
5	**Cluster 5** (0.000)	**Cluster 4** (213.162)	**Cluster 2** (98.961)
6	**Cluster 6** (79.535)	**Cluster 5** (152.790)	**Cluster 2** (60.399)

Table.5 Mean values of six clusters by Tocher's method for 30 rice genotypes (*Oryza sativa* L.)

S. No.	Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
1	Plant height (cm)	127.111	130.144	152.59	139.811	124.867	147.933
2	Days to 50% flowering	85.333	91.444	87.476	85.778	95	94.083
3	Number of productive tillers per plant	12.378	10.989	12.338	13.956	11.3	11.458
4	Panicle length (cm)	21.826	27.189	27.905	21.633	26.867	26.325
5	Spikelet fertility (%)	86.701	75.374	83.468	85.845	73.208	87.015
6	Yield per plot (Kg)	2.008	2.116	2.472	2.431	1.726	2.66
7	100 grain weight (g)	1.758	2.095	1.977	2.202	1.408	2.029
8	Kernal Length / Breadth ratio	2.931	3.289	2.292	2.372	1.9	2.262
9	Protein content (%)	9.354	7.767	11.957	10.332	7.927	10.536
10	Zn content (µg g^{-1})	25.045	24.392	22.277	23.506	35.453	24.005
11	Fe content (µg g^{-1})	27.762	28.764	20.186	19.866	15.66	35.091
12	Total starch content (%)	68.791	70.123	61.309	66.069	57.125	65.36
13	Amylose content (%)	22.001	26.581	20.669	21.522	20.499	19.624
14	Total antioxidant activity (mg AAE/100g)	45.858	59.945	58.035	90.615	49.366	44.945
15	Total soluble phenol content (mg/100g)	78.529	104.472	87.768	187.422	102.392	112.032
16	Glycemic Index	58.481	59.861	62.589	61.551	54.193	56.454
17	Phytate content (mg/100g)	479.105	404.341	414.554	497.911	308.964	457.01

Table.6 Eigen values, proportion of total variance represented by the first six principal components, cumulative per cent variance and component loading of different characters

S. No.		PC I	PC II	PC III	PC IV	PC V
	Eigen Value (Root)	5.39736	2.79831	2.30315	1.26747	1.08030
	% var. Exp	31.74915	16.46064	13.54794	7.45568	6.35470
	Cum. Var. Exp.	31.74915	48.20979	61.75772	69.21341	75.56811
1	Plant height	0.28767	0.06593	0.36690	0.02166	0.05799
2	50% flowering	0.06392	-0.43739	0.36126	0.19756	0.02309
3	Productive tillers per plant	0.05605	0.43927	-0.11719	-0.06005	-0.03815
4	Panicle length	0.14170	0.06839	0.48011	-0.19104	-0.20733
5	Spikelet fertility	0.10309	-0.35537	-0.01951	0.44361	0.09018
6	Yield per plot	0.37958	0.03870	0.22938	0.08090	0.18201
7	100 grain weight	0.37027	0.16220	-0.08627	0.07354	0.26325
8	l/b ratio	-0.28550	-0.25490	0.24083	-0.03592	-0.17067
9	Protein content	0.01451	0.22378	0.19726	0.55907	-0.36913
10	Zn content	-0.22272	-0.35175	0.02965	-0.00902	0.11571
11	Fe content	0.31344	-0.07470	0.01877	0.04938	0.52226
12	Starch content	-0.09050	-0.26280	-0.25442	-0.15622	0.23800
13	Amylose content	-0.09463	0.07606	-0.23469	0.48496	0.14576
14	Anti-oxidant activity	0.28212	-0.11265	-0.27702	0.00379	-0.28543
15	phenols content	0.29854	-0.23850	-0.19824	-0.01958	-0.34495
16	Glycemic Index	-0.31580	0.19307	0.30713	-0.04367	0.32414
17	Phytate content	-0.28807	0.16296	-0.04335	0.36522	0.07844

Table.7 PCA scores of divergence in 30 rice genotypes

S. No.	Genotype	PCA I	PCA II	PCA III
		X Vector	Y Vector	Z Vector
1	Narayanakamini	69.786	-96.524	**-70.635**
2	Ranikanda	98.251	-109.254	**-76.554**
3	Sammelbhog	147.290	-137.009	**-99.767**
4	Chintalurisannalu	24.739	-69.194	**-66.505**
5	Selamsanna	80.218	-108.784	**-77.669**
6	Arakuloya	108.041	-86.828	**-90.266**
7	Ambemohar	84.130	-110.869	**-89.688**
8	Pancharatna	217.779	-159.653	**-200.768**
9	Kalajira	68.773	-80.439	**-84.144**
10	Kalabhatt	364.586	-284.085	**-261.100**
11	Badshabhog	136.563	-137.518	**-92.153**
12	Poongar	228.370	-161.210	**-182.505**
13	Ghani	84.668	-81.331	**-80.826**
14	Parimalasanna	60.424	-89.406	**-70.041**
15	Tulasibaso	67.899	-89.201	**-71.455**
16	Ramsri	73.989	-94.933	**-102.562**
17	Doddiga	127.286	-96.518	**-78.580**
18	Mappillai samba	242.439	-127.708	**-152.472**
19	Sannajajulu	104.418	-126.360	**-86.894**
20	Illapaipu samba	77.176	-100.009	**-67.439**
21	Burma black	384.587	-273.791	**-236.320**
22	Ramyagali	56.193	-45.470	**-60.714**
23	Karuppukavuni	297.785	-218.352	**-195.857**
24	Kulakar	195.159	-149.539	**-187.251**
25	Bahurupi	75.270	-58.602	**-48.074**
26	Ratnachudi	74.464	-90.519	**-53.254**
27	Madumurangi	201.619	-121.723	**-114.167**
28	Navara	289.865	-233.628	**-244.976**
29	Mysore malliga	62.309	-83.505	**-67.486**
30	**Pathariya**	**261.996**	**-174.410**	**-214.509**

Fig.1 Dendrogram showing relationship among 30 rice genotypes in 6 clusters based on Mahalanobis distance

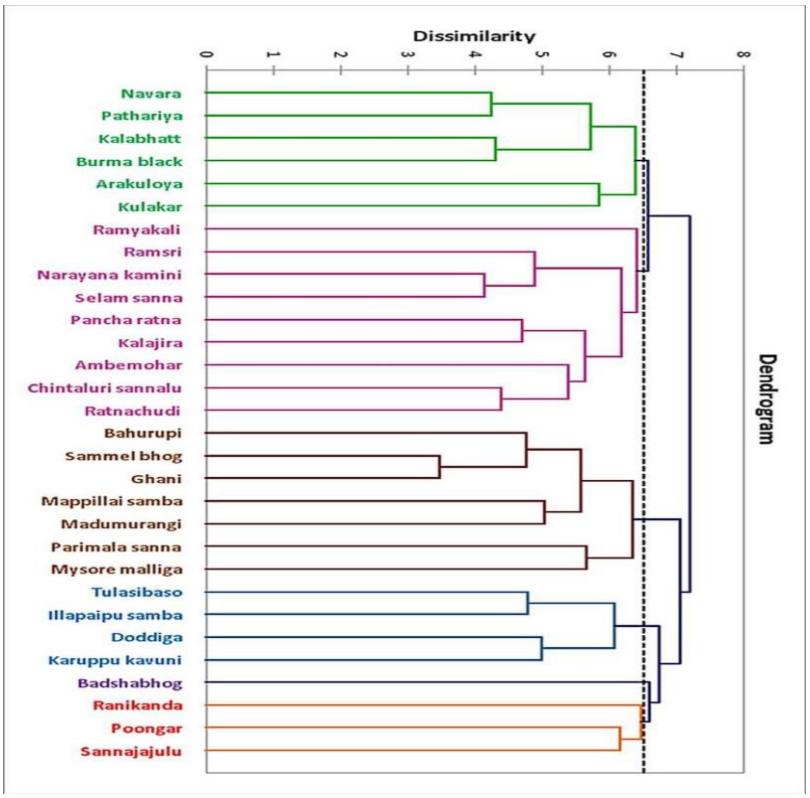
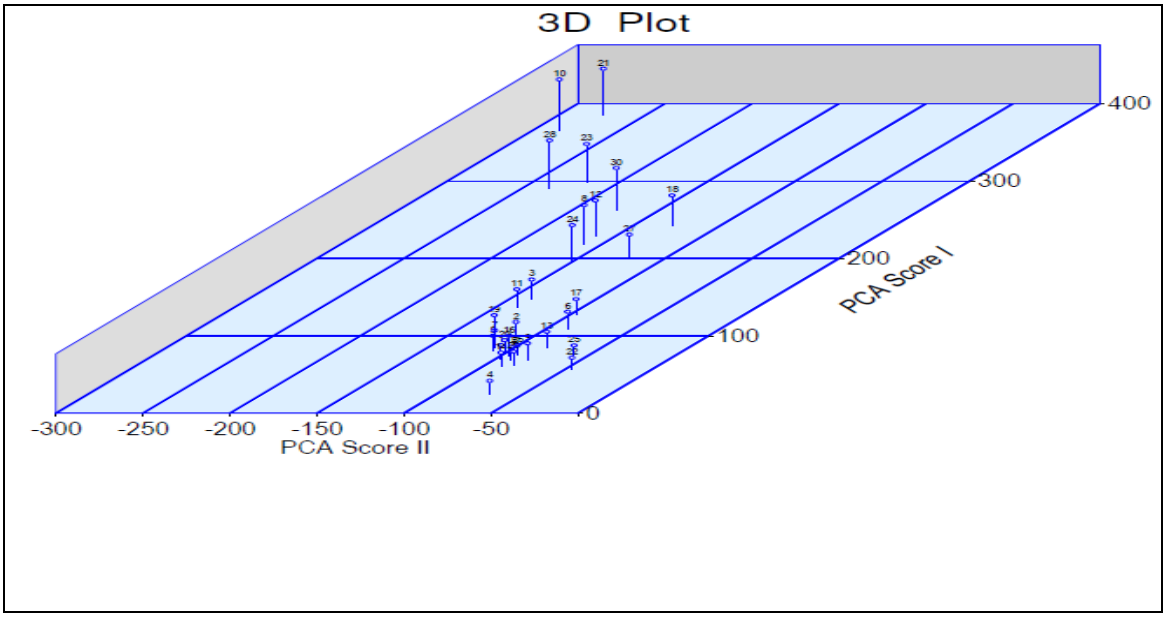


Fig.2 Three dimensional graph showing relative position of 30 rice genotypes based on PCA score



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