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Multivariate Analysis in Diverse Rice (*Oryza sativa* L.) Genotypes under Reproductive Stage Drought Stress

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ABSTRACT: The use of multivariate analyses to determine the nature and magnitude of genetic divergence, to identify potential parents for hybridisation, to examine the variation explained by each trait and to estimate the relative contribution of different traits governing total variability is a common practice in plant breeding activities. A study was conducted with set of 46 rice genotypes at Banaras Hindu University during *Kharif*-2018 under drought stress. A significant variation has been explained by the 46 genotypes for all the traits included in the study and further analysis using D^2 statistic revealed considerable amount of diversity in the material and grouped them into five clusters based on their performance with cluster I being the largest with 26 genotypes consisting mostly of high yielding rice varieties with poor performance under drought stress. The maximum inter cluster distance was observed between clusters II and III followed by clusters I and V indicating wider genetic diversity between these clusters, and hence, crosses involving parents belonging to these clusters are likely to produce wide variability and transgressive segregants with high heterotic effects. Principal Component Analysis revealed first six Principal Components (PCs) having eigen value more than 1, contributing 75.30% of total variance. PC1 and PC2 accounted for 23.49% and 20.09% of total variance respectively with different traits performing exceptionally well. Hence, trait improvement will be more effective if selection is made based on this trait combinations that contributes to substantial variance. The remaining variability was consolidated in the remaining components with different traits in each component. A similarity in the grouping can be observed in both the multivariate techniques and the most diverse genotypes obtained in the study can be used for the development of high yielding drought tolerant rice cultivars.

Keywords: Clusters, Drought, Genetic distance, Multivariate analysis, Principal Components, Rice.

INTRODUCTION

Rice (*Oryza sativa* L.) is an important staple food that constitutes a dominant portion of a world standard diet (Ashkani *et al*., 2015). Among the rice growing countries in the world, India has the largest area under rice cultivation and ranks second in production next to China. Rice occupies a pivotal place in Indian agriculture and has been grown under diverse ecological conditions. It gets exposed to various abiotic and biotic stresses *viz*., drought, flood, salinity, alkalinity, insect pests and pathogens. These stresses directly cause great loss in the production and productivity of rice. Among the various abiotic stresses affecting rice, drought is the toughest constraint, affecting nearly a third of the total rice area in Asia and causing significant economic losses (Kasyap and Yadav, 2020). Reproductive stage of the crop is most vulnerable to drought stress among all the stages. Approximately 42 million hectares of rice is subjected to occasional or frequent drought stress in Asia, resulting in yield losses (Venuprasad *et al.*, 2009). As it has been estimated that the world will have to produce 60% more rice by 2030 than what it produced in 1995 (Khush, 2005), an increase in the production of rice plays a very important role in food security and poverty alleviation.

A vast amount of germplasm is available in rice that still needs to be exploited and can be used for screening by various methods, including morphological, physiological, biochemical and molecular to attain some individuals with better performance. This screening also provides the knowledge of the extent and pattern of diversity and interrelationship between the germplasm accessions in the crop (Bailey-Serres *et al*., 2019). It further helps in grouping of genotypes based on their performance and specific traits which further can be used for trait specific breeding programs like abiotic or biotic stress breeding.

The germplasm available in any crop species provides the scope of wide variability and is a valuable source of the base population (Jovovic *et al.*, 2020). Information on the genetic diversity and distance among the breeding lines is important for determining breeding strategies, classifying the parental lines and predicting future hybrid performance. By and large, crossings between parents with the greatest genetic divergence are the most responsive to genetic improvement. Genetic distance estimates for population grouping can be estimated by different methods and one of them is to apply multivariate analysis. Various multivariate statistical tools include Mahalanobis D^2 statistic, Principal Component Analysis (PCA), Cluster analysis and discriminant function analysis (Oyelola, 2004; Henderson and Seaby, 2008). Among these, Mahalanobis D^2 statistics is widely used and a powerful tool to analyse the relative contribution of various yield components to total divergence and also classifies different genotypes into suitable clusters based on their genetic distances (D^2 values) (Awan *et al*., 2015). This study estimates the relative contribution of several components at the intra- and inter-cluster levels, and genotypes derived from widely divergent clusters are likely to form heterotic combinations, with a large range of variability expected in segregating generations. The other technique *viz.*, Principal component analysis (PCA) is a procedure which is commonly used for compression, reduction and transformation of data. It transforms a number of possibly correlated variables into a smaller number of uncorrelated variables called principal components (Jolliffe *et al*., 2016). This technique assists in identification of traits that help in distinguishing selected genotypes based on similarities in one or more traits and classify the genotypes into separate groups. With this background, the present study was conducted to group 46 rice genotypes of rice based on their distances and behaviour under drought stress.

MATERIAL AND METHODS

The present investigation was carried out at Agricultural Research Farm, Banaras Hindu University, Varanasi during *Kharif* 2018 with a set of 46 rice genotypes consisting of local drought donors, advanced varietal lines for reproductive stage drought tolerance, high yielding drought susceptible varieties and high yield drought tolerant varieties. The genotypes used in the present study were obtained from IRRI-South Asia Hub, Hyderabad (Table 1). These genotypes were evaluated in an Alpha Lattice Design with three replications. All the recommended package of practices were followed to grow the crop until harvest except irrigation, so as to provide proper drought stress. Appropriate measures were taken to impose reproductive stage drought stress at peak tillering stage.

Table 1: List of rice genotypes used for diversity analysis.

Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype
1.	CRDhan801	17.	CGZR-1	33.	IR106516-1-2-2-2
2.	Aus314	18.	NDR359	34.	Swarna
3.	HUR105	19.	HUR4-3	35.	IR90257-B-577-2-1-3-B
4.	JagliBoro	20.	HUR5-2	36.	IR93827-29-1-1-4
5.	Puttige	21.	Pantdhan12	37.	IR95817-5-1-1-2
6.	IR64	22.	PusaBasmati	38.	MTU1010
7.	Genit	23.	Kalanamak	39.	IR13L378
8.	Chiayiwei-Ko	24.	Pusa11-21	40.	IR108199-24-32-1-1-B
9.	DRRDhan44	25.	SambaMahsuri	41.	IRRI123
10.	IR62266-42-6-2	26.	IR103587-22-5-5-B	42.	IR80310-12-B-1-3-B
11.	E2040	27.	TRP-20-7-1-B-2-B	43.	Sahabagidhan
12.	HUBR2-1	28.	IR95785-31-2-1-2	44.	Aus301
13.	N22	29.	IR107891-B-B-90-3-1	45.	BakTulsi
14.	Vandana	30.	IR127363-76-1	46.	Perunel
15.	HUR3022	31.	IR114155		
16.	Sarjoo-52	32.	IR106312-50-1-1-1		

Observations recorded: The data was collected for a total of 17 traits consisting of 13 yield traits *viz.*, days to 50% flowering, days to maturity, plant height, effective tillers per plant, panicle length, spikelets per panicle, grains per panicle, spikelet fertility %, 1000-Grain weight, kernel L/B ratio, grain yield per plant, biomass, harvest Index and 4 drought related traits *viz.*, SPAD value, canopy temperature, stomatal conductance and proline content for all the 46 rice genotypes under severe drought stress condition. For most of the traits, the data was collected on five randomly selected plants in each replication, whereas, days to 50% flowering, days to maturity and canopy temperature were recorded on plot basis.

Statistical Analysis: The quantitative trait mean values computed based on data of five randomly tagged plants in each genotype were used for statistical analysis. Analysis of variance (ANOVA) was performed to partition the total variation into its sources following Alpha lattice design as given by Williams and Patterson, 1976 using R software. Genetic diversity analysis was done using Mahalanobis's D^2 statistic (1936). The grouping of genotypes into different clusters was done using Tocher's method as described by Rao, 1952. Genetic divergence analysis was done using INDOSTAT version 8.1. PCA reduces the dimensions of a multivariate data to a few principal axes, generates an Eigen vector for each axis and produces component scores for the characters. PCA for the 46 genotypes for 17 traits was done using factroextra package of R software.

RESULTS AND DISCUSSION

ANOVA: The ANOVA revealed that the genotypes differed significantly for all the 17 traits included in the study, indicating the existence of sufficient amount of variability among the genotypes taken for the study (Table 2). However, the variation among blocks within the replication was insignificant. Significant differences among the genotypes were earlier reported by Ranjith *et al*., (2018), Kumari *et al*., (2019) and Singh *et al*., (2020).

Mahalanobis's D^2 analysis: Assessment of genetic diversity is an essential prerequisite for any crop improvement program (Mehmood *et al*., 2021). The models of multivariate analysis like Mahalanobis' D^2 statistic provides as a useful statistical tool for measuring the genetic diversity in a given population with respect to characters that were considered together. It also gives a quantitative measurement of divergence among genotypes and also define the relative contribution of different characters towards total divergence (Khadakabhavi *et al*., 2014; Kumar *et al.*, 2017; Mounika and Lal, 2018). Many researchers have utilized Mahalanobis's D^2 statistic for multivariate analysis, such as degree of divergence studies in crop germplasm collections (Akhtar *et al.*, 2012, Kumar *et al*., 2014, Bhati *et al*., 2015; Dey *et al.*, 2018).

Table 2: Analysis of variance of 46 rice genotypes for 17 traits.

Source of Variation **Traits**	**Replication** (df=2)	**Genotype** (df=45)	**Block(rep)** (df=3)	**Residuals (df=87)**
Days to 50 flowering	0.79	240.56***	0.55	1.51
Days to maturity	1.37	260.46***	3.35	1.55
Plant height	25.89	968.82***	42.64	19.78
Effective tillers per plant	2.43*	4.79***	1.27	0.43
Panicle length	1.64	18.55***	0.65	1.95
Spikelets per panicle	534.9	4490.0***	135.2	274.3
Grains per panicle	337.6	3619.8***	119.9	276.6
Spikelet fertility %	3.81	308.87***	5.51	23.74
Test weight	0.10	27.22***	0.17	0.12
Kernel L/B ratio	0.02	1.08***	0.02	0.03
Grain yield per plant	1.57	78.98***	3.58	2.92
Biomass	45.14	383.25***	18.51	19.00
Harvest Index	123.21*	469.19***	21.31	34.49
SPAD value	4.03	41.99***	11.88	5.88
Canopy Temperature	1.30*	4.22***	0.59	0.41
Proline content	0.12	17.35***	0.03	0.11
Stomatal conductance	5316.0***	47681.00***	72.00	59.00

*, ** , *** Significant at 0.05, 0.01 and 0.001 percent probability levels respectively

Grouping of the genotypes: The magnitude of values suggested that there is considerable variability in the material studied, which led to genetic diversity and grouped the 46 genotypes into five clusters based on D^2 values using Tocher's method. A trait based classification can be observed in the pattern of grouping. Cluster I is the largest with 26 genotypes comprising mostly of high yielding varieties of rice *viz*., MTU 1010, IR 64, Sarjoo-52, Pantdhan 12 *etc* and advanced varietal lines for drought tolerance which performed moderately under drought stress followed by cluster II with 10 genotypes which are mostly drought tolerant varieties of rice like DRR Dhan 44, Sahabagidhan *etc*. and other advanced varietal lines for drought tolerance and cluster III with 8 genotypes comprising of high yielding varieties with very poor performance under drought stress. Clusters IV and V are solitary clusters with single genotype *viz*., IR62266-42-6-2 and Swarna respectively (Table 3).

Table 3: Distribution of 46 rice genotypes into 5 clusters.

Clusters	**No. of genotypes**	**Name of the genotypes**
Cluster I	26	MTU1010, IR13L378, IR64, IR114155, IR106312-50-1-1-1, IRRI123, IR127363-76-1, HUR4-3, IR103587-22-5-5-B, Aus301, BakTulsi, Chiayiwei-Ko, NDR359, IR95817-5-1-1-2, Sarjoo-52, Pantdhan12, TRP-20-7-1-B-2-B, HUBR2-1, HUR5-2, IR107891-B-B-90-3-1, Pusa11-21, JagliBoro, Vandana, Aus314, IR95785-31-2-1-2, IR93827-29-1-1-4
Cluster I I	10	DRRDhan44, IR108199-24-32-1-1-B, IR90257-B-577-2-1-3-B, IR80310-12-B-1-3-B, CGZR-1, IR106516-1-2-2-2, Sahabagidhan, HUR3022, CRDhan801, N22
Cluster III	8	Puttige, Perunel, Genit, Kalanamak, PusaBasmati, SambaMahsuri, HUR105, E2040
Cluster IV	1	IR62266-42-6-2
Cluster V	1	Swarna

The local drought donors were distributed in the first three clusters based on their performance. Similar pattern of grouping of genotypes into different clusters based on D^2 values using tochers method were reported by Kamlesh *et al*., (2015), Dey *et al.,* (2018), Singh *et al*., (2019), Singh *et al.,* (2020), where they classified 40, 12, 50, 29 genotypes into 8, 4, 8 and 6 clusters respectively. A dendrogram representing the relationship among the 46 rice genotypes is presented in Fig. 1.

Intra and Inter-cluster genetic distances (D^2 values): The intra cluster distances in the 5 clusters varied from 0 in clusters IV and V to a maximum distance of 38.30 in cluster III followed by 30.43 in cluster II and 24.09 in cluster I, indicating the presence of diverse genotypes within these clusters and hybridization between the genotypes within this cluster would yield considerable heterosis. The highest inter-cluster distance was found between clusters II and III (54.52), followed by clusters I and V (52.26), clusters IV and V (50.83) and clusters III and IV (50.77). The average genetic distances between the five clusters are well presented in Table 4.

Table 4: Intra and Inter cluster D^2 values among the five clusters.

	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**
Cluster I	**24.09**	44.10	35.03	37.82	52.26
Cluster II		**30.43**	54.52	47.75	41.13
Cluster III			**38.30**	50.77	54.07
Cluster IV				**0.00**	50.83
Cluster V					**0.00**

General notion exists that the larger is the divergence between the parental genotypes, the higher will be the heterosis in crosses (Falconer, 1964). Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses which are likely to yield a wide range of segregants on which selection can be practiced. Cluster II with 10 genotypes having drought tolerant high yielding varieties of rice and cluster III with 8 genotypes comprising of high yielding but susceptible to drought showed maximum inter cluster distance and are the most divergent groups and thus it is desirable to select genotypes from these clusters as parents in recombination breeding programs. Hybridization between the genotypes of these clusters would yield in recombinants with higher yield along with drought tolerance.

However, lowest inter-cluster distance was observed between clusters I and III followed by clusters I and IV suggesting similarities among the genotypes in these clusters for most of the traits. Similar findings were reported by Priyanka *et al*., (2015), Ashok *et al.,* (2017), Behera *et al*., (2018), Srinivas, (2018) and Pathak *et al.,* (2020). Mukul *et al.,* (2019), have classified 100 rice genotypes into 11 clusters and the highest inter-cluster distance was recorded between clusters X and XI (458.41), whereas, maximum intra-cluster distance was observed in cluster IX (63.20) and cluster 1 recorded the lowest intra-cluster distance (13.46) suggesting a closer relationship and low degree of diversity among the genotypes of this cluster.

Cluster means: The average performance of all genotypes in a cluster is represented by the cluster means and shows the mean values for different traits for different clusters (Table 5).

Table 5: Cluster mean values estimated by Tocher's method from 46 rice genotypes and percent contribution of each character towards total divergence.

Cluster **Characters**	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Times ranked 1^{st}**	**% Contribution**
Days 50% flowering	91.67	93.33	99.17	92.67	122.67	45	3.35
Days to maturity	119.31	123.37	128.42	123.67	147.33	103	5.95
Plant height	102.38	100.66	121.24	105.73	91.4	28	2.71
Effective tillers per plant	6.99	6.93	6.5	4.33	7.67	4	7.00
Panicle length	24.46	24.4	23.22	24.41	24.61	3	3.10
Spikelets per panicle	133.62	166.33	131.75	85.67	220.33	2	0.19
Grains per panicle	111.87	146.2	97.21	77.33	171	7	0.68
Spikelet fertility %	83.86	87.7	76.3	89.99	77.67	0	0.00
Test weight	24.09	23.36	20.96	34.13	24.08	168	16.23
Kernel L/B ratio	3.25	3.19	2.97	2.85	2.88	6	1.48
Grain yield per plant	15.21	20.07	11.55	13.67	22.78	8	4.58
Biomass	36.96	41.95	36.45	25.23	43.17	4	0.39
Harvest Index	43.67	48.95	32.28	54.37	53.28	2	0.19
SPAD value	37.81	37.24	34.25	37.97	38.3	0	0.00
Canopy Temperature	32.01	31.74	33.08	32.57	32.43	0	0.00
Proline content	10.89	13.16	11.76	9.64	13.88	145	14.01
Stomatal conductance	473.54	713.37	425.95	522.21	655.32	499	40.14

The highest mean value for 10 traits *viz.*, days to 50% flowering, days to maturity, effective tillers per plant, panicle length, spikelets per panicle, grains per panicle, grain yield per plant, harvest index, SPAD value, proline content were seen in cluster V, meaning the performance for most of the traits in this cluster is good. Cluster III had the highest average values for plant height and canopy temperature which is a negative aspect in context of rice and cannot be considered for selection at least for these traits, whereas, cluster IV displayed the highest mean values for spikelet fertility %, test weight and biomass which is a positive aspect in relation to yield and can be considered during selection. In the case of kernel L/B ratio, the highest mean value was seen in cluster I and cluster II had the highest mean for stomatal conductance and can be considered for selection of these traits in the mentioned clusters. Similar reports of cluster mean for various traits and use of genotypes of that particular cluster for specific traits improvement was earlier reported in rice by Singh *et al.,* (2019); Singh *et al.,* (2020) and Pathak *et al*., (2020) where they grouped 50, 29 and 29 genotypes into 8, 6 and 6 clusters respectively.

Percent contribution of each character towards total divergence: The more is the variation present in a particular trait, the more it contributes to total divergence among the genotypes. Among the 17 characters included in the study, stomatal conductance (40.14%) contributed the most to total divergence, followed by test weight (16.23%), proline content (14.01%), effective tillers per plant (7.00%), days to maturity (5.95%), grain yield per plant (4.58%), days to 50% flowering (3.35%), panicle length (3.10%), Plant height (2.71%), grains per panicle (0.68%), biomass (0.39%), harvest index (0.19%) and spikelets per panicle (0.19%). The remaining three traits *viz.*, spikelet fertility %, SPAD value and canopy temperature do not have any contribution towards total divergence. The contribution of each character towards total divergence is presented in Table 5. The characters showing major contributions towards genetic divergence should be given more consideration in crop improvement programs. The results were in agreement with the findings of Subudhi *et al.,* (2008) for plant height, days to 50% flowering and test weight. Kumari *et al.,* (2019) for effective tillers per plant and test weight. Priyanka (2015); Ranjith *et al*., (2018) and Manohara *et al.,* (2019) reported similar results in explaining the contribution of each trait towards total divergence.

Principal Component analysis (PCA): To find out independent impact of all the traits under study, PCA was conducted. Principal Components (PCs) are orthogonal, independent and explain the variation that is not explained by others (Mohammadi and Prasanna, 2003; Woredo *et al*., 2014). In the current study, the first six PCs with Eigen values > 1 contributed 75.30 % variability existing in the rice varieties for the 17 characters indicates that the identified traits within the axes exhibited great influence on the phenotype of germplasm lines. PCA provided eigenvalues and percent variation for 17 principal component axes in 46 rice genotypes (Table 6). Remaining components with Eigen values < 1 contributed 24.97 % variability. PC 1 with Eigen value 3.99 contributed 23.49 % of total variability. PC 2 and PC 3 with Eigen values of 3.41 and 1.65 contributed 20.09 % and 9.75% of total variability respectively. A Scree plot illustrating the variance explained by the 17 PCs was shown in Fig. 2. It can be observed that maximum variation was present in first 2 PCs and hence, selection of genotypes from these PCs will be useful. Similarly, Kasyap and Yadav, 2020 have done PCA and revealed that first five principal components addressed 80.03 (%) of the total variability with PC1, PC2 and PC3 explaining 33.48 %, 13.75% and 11.75% respectively.

Table 6: Eigenvalue, Percent variance and Cumulative percent variance explained by 17 principal components.

PC	Eigenvalue	Percent Variance	Cumulative percent variance
PCI	3.993528657	23.49134504	23.49134504
PCII	3.416918448	20.09952028	43.59086532
PCIII	1.658508026	9.755929567	53.34679489
PCIV	1.510997622	8.888221307	62.2350162
PCV	1.153410342	6.78476672	69.01978292
PCVI	1.068507009	6.285335344	75.30511826
PCVII	0.885614032	5.209494308	80.51461257
PCVIII	0.789475642	4.643974366	85.15858694
PCIX	0.598433801	3.52019883	88.67878577
PCX	0.558659448	3.286232046	91.96501781
PCXI	0.447388243	2.631695549	94.59671336
PCXII	0.432773148	2.545724402	97.14243776
PCXIII	0.231713738	1.363021988	98.50545975
PCXIV	0.202274599	1.189850582	99.69531033
PCXV	0.03536022	0.208001296	99.90331163
PCXVI	0.01446614	0.085094939	99.98840657
PCXVII	0.001970883	0.011593432	100

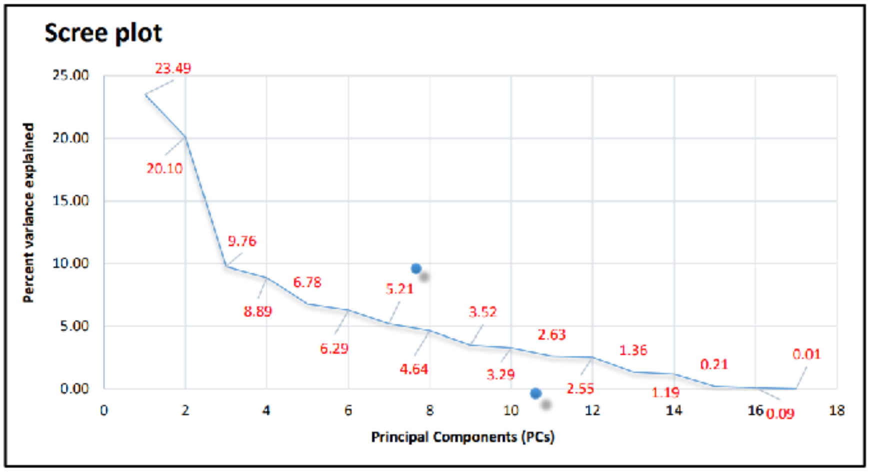


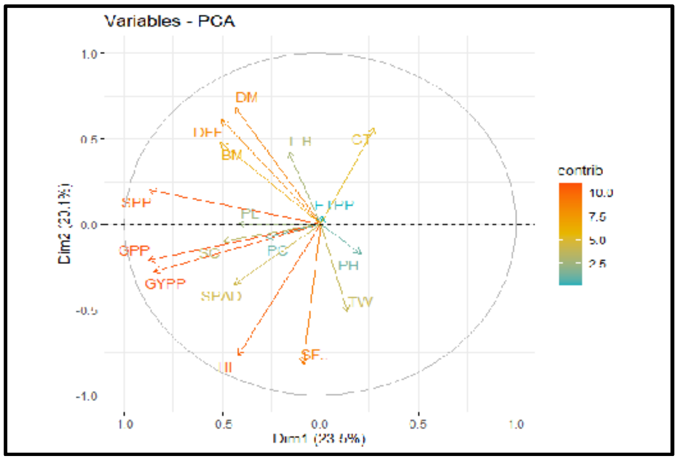
Fig. 2. Scree plot representing the percent variance explained by each Principal Component (PC).

Factor loading of different characters: The contribution of all the characters in the first six PCs to the total variability was shown in Table 7. PC1 has high component loading for grains per panicle (19.30), spikelets per panicle (19.02), grain yield per plant (18.14), biomass (6.44), days to 50% flowering (6.32), stomatal conductance (6.12) and others that accounted for 23.49% of total variation. PC2 had high component loadings for spikelet fertility % (19.65), harvest index (17.21), days to maturity (13.60), canopy temperature (9.24), test weight (7.27) etc. that accounted 20.09% of total variation. The contribution of variables to PC1 and PC2 was represented in Fig. 3. It indicates that a proper hybridization program can be formulated by selecting the genotypes from the first 2 Principal Components as they have variables contributing to higher yields and contributed maximum toward diversity with maximum eigenvalues. Similar results of factor loading in various PCs were reposted by Nachimuthu *et al,.* (2014); Sharma *et al.*, (2014); Mahendran *et al.*, (2015); Sanyal *et al.*, (2016) and Gour *et al*., (2017).

The PCA scores for 80 genotypes in the first 2 principal components were estimated and were considered from which the squared distances of each genotype were derived and are plotted on a biplot. The distribution of genotypes based on their diversity can be observed in the 4 quadrants in various colours (Fig. 4).

Table 7: Factor loading of different characters (unrotated) for the first 6 PCs (Eigen value > 1).

	PC1	PCII	PCIII	PCIV	PCV	PCVI
Eigenvalue	3.994	3.417	1.659	1.511	1.153	1.069
Percent variance	23.491	20.100	9.756	8.888	6.785	6.285
Cumulative percent variance	23.491	43.591	53.347	62.235	69.020	75.305
Days to 50% flowering	6.328	1.085	8.613	3.247	7.785	10.222
Days to maturity	4.778	13.609	3.792	3.500	0.304	13.312
Plant height	1.105	0.871	27.174	7.281	6.255	4.894
Effective tillers per plant	0.003	0.071	2.029	10.210	28.498	18.702
Panicle length	4.399	0.000	8.940	19.263	12.207	0.530
Spikelets per panicle	19.029	1.150	0.022	0.210	4.228	0.660
Grains per panicle	19.302	1.320	0.165	0.009	4.134	2.135
Spikelet fertility %	0.188	19.654	0.537	0.654	0.090	0.706
Test weight	0.503	7.727	0.223	7.368	0.057	27.052
Kernel L/B ratio	0.642	5.233	30.755	0.348	0.348	0.096
Grain yield per plant	18.141	2.259	2.600	0.008	1.305	0.188
Biomass	6.440	6.672	0.658	0.153	11.049	9.154
Harvest Index	4.385	17.215	0.801	1.564	2.866	3.474
SPAD value	4.802	3.649	6.128	0.955	6.687	2.620
Canopy Temperature	1.920	9.246	2.710	2.873	12.802	3.119
Proline content	1.909	0.187	2.135	36.645	0.533	0.090
Stomatal conductance	6.125	0.287	2.716	5.712	8.636	3.046



DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; ETPP: Effective tillers per plant; PL: Panicle length; SPP: Spikelets per panicle; GPP: Grains per panicle, SF: Spikelet fertility %; TW: 1000-Grain weight; L:B: Kernel L/B ratio; GYPP: Grain yield per plant; BM: Biomass; HI: Harvest Index; SPAD: SPAD value; CT: Canopy temperature; SC: Stomatal conductance; PC: Proline content.

Fig. 3. PCA graph of the 17 traits for first two principal components.

The genotypes *viz*., Samba Mahsuri, Pusa Basmati, Swarna, E2040, CR Dhan 801, DRR Dhan 44, Sahabagidhan etc. which are placed away from the centre are more diverse than the genotypes that are located around the origin and the crossing between them is expected to produce desirable transgressive segregants. As we can see from Fig. 4, the drought tolerant varieties of rice *viz*., CR Dhan 801, DRR Dhan 44, Sahabagidhan and donors like Jagli Boro, Bak Tulsi, Aus 314, E2040 *etc* are placed far from the drought susceptible varieties *viz*., Samba Mahsuri, Pusa Basmati, HUBR 2-1 *etc*. According to Raji (2002), a criterion was chosen to govern the limit for the coefficients of the proper vectors. Based on this, vector coefficient > 0.3 are having large effect and can be considered important, while vector coefficients < 0.3 were considered not to have important effect on the overall variation. Based on this concept, the genotypes distributed away from the origin and having values greater than 0.3 can be considered diverse and can be used in hybridization programs to obtain recombinants that can perform well under drought stress. Woredo *et al*., (2014) reported that, based on the PCA scores, the distribution pattern of 24 rice genotypes with 17 agro-morphological characters and suggested genotypes based on their diversity and genetic distance for further crossing programs. Similar use of PCA for data compression and interpretation was made by Hossain *et al*., (2016); Pathak *et al*., (2018) and Ranjith *et al*., (2019).

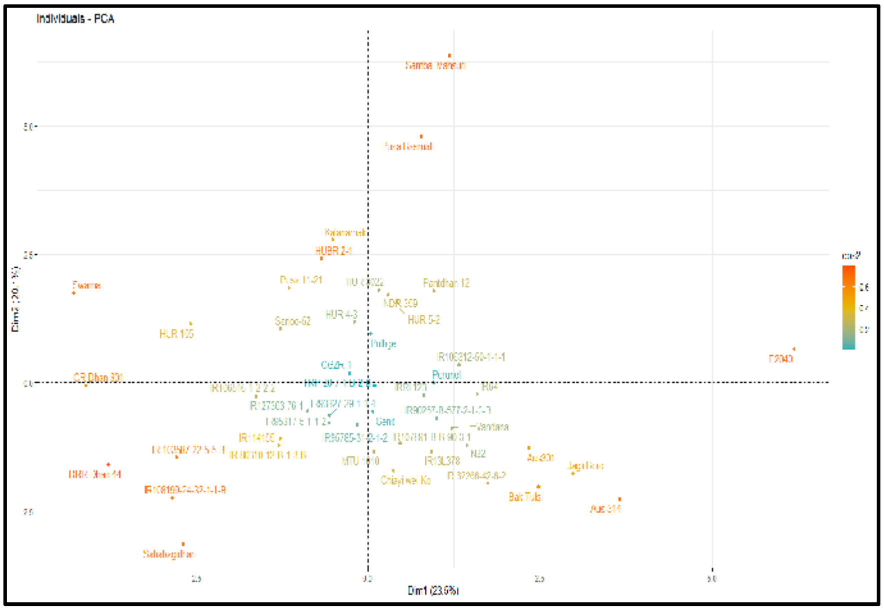


Fig. 4. PCA Biplot representing the distribution of 46 rice genotypes on the first 2 Principal Component axes.

The distribution pattern of the genotypes on the biplot can be correlated with the grouping obtained by Tochers method using Mahalanobis D^2 values. The distribution based on drought tolerance ability and their genetic distances can be observed in both the methods.

CONCLUSION

Diverse parents are expected to yield higher frequency of heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations. Multivariate analysis like D^2 and PCA based grouping would help in identification of diverse parents that can be used for future breeding programs. Based on these analyses, in the present study, genotypes *viz*., CR Dhan 801, DRR Dhan 44, Sahabagidhan which are high yielders and drought tolerant can be crossed with drought susceptible varieties like Samba Mahsuri, Swarna, Pusa Basmati etc. which would help in development of heterotic hybrids for drought prone areas and selections can be made for recombinants that perform well in advanced segregating generations under drought stress.

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