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Studies on genetic diversity and variability for yield and quality traits in promising germplasm lines in rice (*Oryza sativa* L.)

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Abstract
An experiment was conducted with 71 rice genotypes to assess the genetic diversity and variability by using Mahalanobis D^2 Statistical and principal component analysis. All genotypes exhibited a wide and significant variation for 21 traits. The cluster analysis indicated that 71 genotypes were grouped into eleven clusters and cluster 1 followed by cluster 11 consisted with 33 and 29 genotypes respectively and rest of the nine clusters contain one genotype each. The maximum inter cluster distance was recorded between clusters VIII (906.17) with cluster V followed by cluster VII (682.74) and cluster I and also between cluster V (657.43) and cluster11. The lowest inter cluster distance (70.66) was observed between cluster III and cluster IV. The intra cluster D^2values ranged from zero (cluster XI, X, IX, VIII, VII, VI, V, IV, III) to 128.42 (cluster I). Cluster VIII recorded highest cluster mean for water uptake, alkali spreading value, while cluster IX showed highest cluster mean for grain yield/plant and effective tillers and second highest for kernel length, days to 50% flowering and panicle density. Milling percent head rice recovery Kernel length. length/breadth ratio, Kernel length after cooking and water uptake. Contribution of days to 50% flowering was highest towards genetic divergence (36.05) by taking 896 times ranked first followed by kernel length after cooking (23.9) by 593 times, water uptake (10.0)and kernel length(8.5).The PCA analysis showed that the first five principal components accounted for about 82.23% of the total variation and exhibited very high correlation among them. Phenotypic coefficient of variation was higher than genotypic coefficient of variation. The traits panicle density, filled seeds/panicle volume expansion ratio and yield per plant exhibited high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation. High heritability coupled with high genetic advance as percent of mean was recorded for the characters panicle density (83.5; 62.7), filled grains/panicle (82.6; 60.5), test weight (93; 52.9) and water uptake (90.9, 51.1). The genotypes RCPR32-HHZ-5-DT-20-DT-3 and RGL 7011 having maximum genetic divergence with high mean values for desirable yield contributing characters and quality traits could be utilized in the breeding programmes.

Keywords: Cluster mean, D^2 analysis, rice, PCA, variability, heritability, genetic advance

Introduction
Rice (*Oryza sativa* L.) being the staple food for more than 70 percent of our national population also source of livelihood for 120-150 million rural households and back bone to indian agriculture. Rice is cultivated in highly diverse situations that ranged from flooded wetland to rain fed dry land (Degenokolbe *et al.*, 2009) [4]. Irrigated rice which accounts for 55% of the global rice area provides 75% of the production and consumes about 90% of the fresh water resources used for agriculture in Asia. The development of high yielding, widely adapted pure line rice varieties coupled with advances in production technology in past four decades has enabled us to come up with the demand of rice to a satisfactory level. However rapidly increasing demand due to ever increasing Indian population has forced us to search for another quantum jump in rice production. The projection of India's rice production target for 2020 A.D is 120 million tones which can be achieved only by increasing the rice production by over 2.0 million tones /year in the coming decade (Viraktamath and Shobha Rani 2008) [8]. Genetic diversity is a prerequisite for any crop improvement program and it helps in the development of superior segregants. The importance of genetic diversity in selecting parents to recover transgressive segregants has been repeatedly emphasized by many workers (Archana Devi *et al.*, 2017) [5].The crosses between parents with maximum genetic divergence are responsive for genetic improvement. The multivariate analysis developed by Mahalanobis (1936) [10] has been found to be most suitable in quantify the degree of divergence in germplasm.

The presence of genetic variability for morphological, yield components and quality traits is of at most importance for identification and development of desirable genotypes as improvement in any trait is depend on the amount of genetic variability present in the experimental material for that trait. Besides genetic variability, heritability and genetic advance are useful parameters on which selection efficiency depends upon. Heritability is an index of transmissibility of the character from parents to offspring and has a predictive role in crop breeding programme. However estimates of heritability alone fails to indicate the response to selection. Therefore estimates of genetic advance along with heritability estimates takes into account for genetic improvement of the related genotypes over the parental population for various traits. Recognizing the importance of genetic diversity and variability in plant breeding experiments present research work was undertaken in rice.

Materials and Methods

The experiment was conducted during *Kharif*, 2017 at Regional Agricultural Research station, Warangal, Telangana State, India, The experimental material comprised of 71 rice genotypes (Belongs to different agro ecological regions of India) and it was laid out in randomized block design with two replications. Each plot consists of 3 rows of 4m length. Thirty days old seedlings were transplanted with a spacing of 20cm between rows and 15cm between plants at the rate of 20 plants per row grown with the application of fertilizers NPK at the rate of 120:60:40kg/ha respectively and the recommended package of practices were followed for raising a healthy crop. A composite sample of 10 plants from the middle row was used to record observations on the plants for yield components like plant height (cm) effective tillers, panicle length (cm), panicle density, panicle weight(g), filled seeds per panicle, test weight (g) and yield per plant (g) except days to 50% flowering which was computed on plot basis.

Data was recorded on physical and chemical quality characters *viz*., hulling percent (%) milling percent (%) head rice recovery (%) kernel length (mm), kernel width(mm), length/breadth ratio, Kernal length after cooking (mm), Kernal elongation ratio, alkali spreading value, water uptake (ml) and volume expansion ratio. Observations on hulling and milling were taken with the help of Satake Company make laboratory huller and polisher. Data on head rice recovery was recorded. Kernal length and kernel width of 20 whole milled rice were measured by means of dial caliper and length and breadth ratio was computed as per Murthy *et al.* (1967) [11]. Kernal elongation was determined by soaking 5g of whole milled rice in 12ml distilled water for 10minutes and later cooked for 15 minutes in water bath. Observations on the length and breadth of cooked Kernels and elongation ratio were recorded with the help of graph sheet to quantity cooking traits, while water uptake, volume expansion ratio and alkali spreading value by following the standard procedures. The treatment means for all the characters were subjected to analysis of variance techniques on the basis of model proposed by Panse end Sukhatme, 1967 [12]. The genotypic and phenotypic variances were calculated as per formulae proposed by Burton, 1952 [1]. Heritability in broad sense (h^2b) was calculated by the formula gives by Lush, 1940 [9]) as suggested by Johnson *et.al* 1955 [7]. From the heritability estimates the genetic advance (GA) was calculated by the following formula given by Johnson *et.al* (1955) [7].

Cluster analysis and principal component analysis were performed to detect the diversity of genotypes and the contribution of traits to total divergence respectively using the software Windostat Version 3.1

Results and Discussions.

The analysis of variance revealed highly significant differences for all the characters studied (Table.1) indicating the existence of considerable amount of variability among the genotypes. The perusal of results revealed that all the 71 genotypes were grouped into 11 clusters (Table 2: fig 1) on the basis of D^2 values. The distribution of genotypes indicated that the geographical and genetic diversities were not related to each other and thus forces other than geographical separation. Such as natural and artificial selection, exchange of breading material, genetic drift and environmental variation existed which were responsible for diversity. Cluster analysis using average linkage methods on the basis of their similarity through quantitative traits grouped 71 rice genotypes into 11 clusters. Maximum genotypes were included in Cluster 1 (33) followed by cluster 11 (29) with 48.47 and 40.81 proportion from the studied genotypes and rest of nine clusters had one genotype each. Clustering did not follow any particular pattern with respect to origin.

The discrimination of germplasm lines into so many clusters suggested presence of high degree of genetic diversity in the material studied. Earlier workers have also reported substantial genetic divergence in the rice material Presence of substantial genetic diversity among the germplasm lines screened in the present study indicated that this material many reserve as good source for selecting the diverse parents for hybridization programmes aimed at isolating desirable segregants for grain yield and other important characters. More over selection and choice of parents mainly depends upon contribution of characters. (Rukmini Devi *et al.* 2016) [13]. The choice of the suitable diverse parents based on genetic divergence analysis would be more fruitful than the choice made on the basis of geographical distances.

This finding is in conformity with the previous reports advocating lack of parallelism between genetic and geographical diversity in rice. Cheema *et al.* 2004 [3] advocated that the number of clusters formed, number of genotypes within the cluster indicated that possibility of genetic improvement for yield and yield component, in order to increase the possibility of isolating good segregants in segregating populations. The chances of obtaining good segregants by crossing the little diverse genotypes belonging to same cluster are very low.

The estimates of average intra and inter cluster distance for eleven clusters revealed that the genotypes present in a cluster had little genetic divergence from each other with respect to aggregate effect of 21 characters under study while much more genetic diversity was observed between the genotypes belonging to different clusters. The intra and inter cluster distances among the genotypes studied were of varying magnitude (Table 3). The maximum cluster distance was obtained between cluster VIII constituted by single entry (RCPR 32-HHZ-5-DT-20-DT-3) which showed highest inter cluster distance from cluster V (906.17) besides having very high inter cluster distance from cluster VII (682. 74). High inter-cluster distances were also shown by cluster VI from cluster V (657.43) followed by cluster XI and X cluster (629, 52), cluster V and cluster IV (551.9), cluster XI and VIII (524.94).

Greater the distance between two clusters wider the genetic diversity among the genotypes of those clusters and such highly divergent high performing genotypes would be of great use in recombination breeding programme in order to get high heterotic recombinants. The lowest inter cluster distance was observed between cluster III and cluster IV (70.66) followed by cluster VI and VIII (113.49) cluster X (157.77) and cluster III and between cluster V and VII cluster (180.34) indicating that the genotypes included in them were closely related. Avoidance of selection of parents from genetically homogeneous clusters should be preferred to maintain relatively broad genetic base. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. But for a plant breeder the objective is not only high heterosis but also quality characters.

Keeping in view it is indicated that hybridization between the genotypes of clusters VIII i.e. RCPR-32-HHZ-5-20-DT-3 and RGL7011 of cluster V and with NR1011 of cluster VII, PAU2K10-23-54-14-52-107-0-1 of cluster VI with RGL7011 of cluster V, RGL7011 of cluster V with twenty nine genotypes of cluster II and BPT5204 of cluster XI with WGL915 of cluster X are expected to produce highly heterotic hybrids. The genotypes of these clusters may be used as parents in the crossing programme to generate breeding material with high genetic diversity.

The intra cluster D^2 values ranged from Zero (Cluster XI, X, IX, VIII, VII, VI, V, IV, III to 128.42 (Cluster I). Maximum intra cluster distance was observed in cluster I (128.42) and Cluster II (128.40) indicating that some genetic diversity still exist among the genotypes within each of the clusters.

Cluster mean analysis revealed a wide range of variation for all the traits under study (Table 4). Most of the minimum and maximum cluster means were distributed in relatively distant clusters. Cluster VIII recorded highest cluster means for water uptake, alkali spreading value and second highest cluster means for kernel breadth, kernel length after cooking, days to 50% flowering, panicle density and third highest for filled grains/panicle. Cluster IX recorded higher cluster means for grain yield/plant (37.35), effective tillers and second highest cluster means for milling percent, head rice recovery, kernel length, length/breadth ratio, kernel length after cooking and water uptake, while cluster X for plant height, panicle length, panicle density, panicle weight, filled seeds/panicle, kernel length, kernel weight and kernel breadth after cooking. Cluster II desirable for early flowering, plant height, effective tillers, panicle length, panicle weight, filled seeds/panicle, grain yield/plant, hulling percent, head rice recovery, kernel length, kernel elongation ratio, alkali spreading value and water uptake.

Cluster XI (50.05%) and cluster IV (21.7) recorded highest and lowest cluster means for head rice recovery. The results indicate the selection of genotypes with high cluster mean values for particular trait could be used in the hybridization programme for improvement of the character. A critical appraisal of the observations indicated that none of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. Therefore hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits. Cluster V characterized by late flowering with less grain yield/plant but highest cluster means for hulling percent, milling percent followed by cluster VI for early flowering, dwarf plant height, high panicle length, kernel length after cooking with less cluster means for effective tillers, panicle density, grain yield/plant, head rice recovery and recorded moderate values for other characters. Cluster IX showed highest cluster means for head rice recovery, kernel elongation ratio, second highest value for filled grains/panicle, hulling percent, moderate value for panicle density, grain yield/plant, milling percent, alkali spreading value and low value for panicle length, panicle weight, test weight, kernel length, kernel weight, kernel length after cooking, kernel width after cooking, in desired direction water uptake and volume expression ratio Cluster II and Cluster VI recorded less grain yield/plant and showed lowest cluster means for days to 50%flowering, plant height and moderate mean values for rest of the characters

The utility of D^2 statistics is a potential tool to quantify the extent of divergence in biological populations at genetic level is further enhanced by its applicability to estimate the relative contribution of the various plant characters to total genetic divergence. The number of times that each of 21 characters appeared in first time and its respective present contribution towards genetic divergence is presented in Table 6. Contribution of days to 50 flowering was highest towards genetic divergence (36.05%) by taking 896 times ranked first followed by kernel length after cooking (23.9%) by 593 times, water uptake (10%) by 249 times, kernel length (8.5%) by 212 times, test weight (3.9%) by 97 times, alkali spreading value (3.0%) by 75 times, plant height (2.8%) by 69 times, filled seeds/panicle (2.6%) by 65 times. Length/breadth ratio and panicle length exhibited zero contribution while effective tillers (0.12), panicle weight, hulling percent, milling percent, kernel width, kernel elongation ratio exhibited low contribution.

The PCA analysis showed that the first five principal components accounted for about 82.23% of the total variation and exhibited very high correlation among them (Table 7) The first, second, third, fourth and fifth principal components explained about 40.09%, 64.88%, 72.75%, 77.77 and 82.29 of the variation obtained in the ei gen vector analysis. In the first PC, days to 50% flowering, kernel length after cooking, kernel width, test weight, water uptake were more important contributing traits. Similarly days to 50% flowering, kernel elongation ratio, panicle density, milling recovery were the important parameters for second PC, while third PC was characterized by test weight, kernel length, kernel elongation ratio were important parameters. Grain yield /plant, water uptake, volume expansion ratio were important contributing characters in PC4. In PC 5 alkali spreading value, milling percent, kernel length after cooking and panicle density were important traits. Similarly days to 50% flowering, length/breadth ratio, kernel elongation ratio had greater contribution in PC1, PC2, PC3, and PC4, PC5, Filled grains / panicle had high contribution in PC1.Similarly grain yield/plant partitioned positively in all components except PC1. Based on these principal components mean genotypic scores were computed. Principal factor scores for all the 71 genotypes were utilized to construct precise 3D plot (Fig.2) all the genotypes were plotted for PC1, PC2, PC3, PC4 and PC5 which completely explained 82.2% variability which accounts for all the characters. In component based genotypic scoring RGL 7011 in PC1, NVSR 2086 in PC3 showed maximum score while JGL 21820 in PC1 and MTU 1236 in PC3 recorded minimum score. The genotypes PCPR-32-HHZ-5-DT-20-DT-3 and RGL 7011 having maximum genetic divergence with high mean values for yield contributing

characters and quality traits could be utilized in the breeding programmes. However crossing of the genotypes with diverse local and popular cultivars may also give potential transgressive segregants with high yield.

The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2b) and expected genetic advance as percent of mean (GAM) are presented in Table. 8 The results on genetic variability revealed that phenotypic coefficient of variation was higher than genotypic coefficient of variation. The difference between PCV and GCV was minimum for all the characters studied except effective tillers (16.3: 9.78), kernel width (12.14:9.98) and volume expansion ratio (28.35:24.95). The apparent variation is not only due to influence of genotype but also due to environment. A close difference between phenotypic and genotypic coefficient of variation revealed that there was a little influence of environment on the expression of the character studied. The estimates of PCV and GCV were classified as high (>20%), moderate (10-20%) and low (<10%). The estimates of GCV were high for filled seeds/panicle (25.2), volume expansion ratio (24.95), grain yield/plant (24.4), panicle weight (20.8), test weight (20.7), water uptake (20.34), head rice recovery (20.04) indicating that all these characters are amenable for further improvement. Similar results were reported by Vinod kumar *et al.* 2018 [17] for grain yield /plant and filled seeds/panicle and Chandramohan *et al*, 2016 [2] for filled seeds/panicle and test weight. Moderate estimates of GCV were observed for length/breadth ratio, kernel length after cooking and kernel breadth after cooking.

Lower degree of PCV and GCV were recorded for the traits *viz*., hulling recovery (3.8), panicle length (5.3), plant height (7.17), kernel elongation ratio (7.24), days to 50% flowering (9.075), milling recovery (9.175), effective tillers (9.78) and Length/breadth ratio (10.58). These results are in conformity with findings of Srujana *et al.* 2017 [15] for days to 50% flowering, plant height, length/breadth ratio, panicle length, kernel length, kernel width and kernel elongation ratio and Rukmini Devi *et al.* 2017 [14] for hulling percent, panicle length, length/breadth ratio indicating that these characters are under genotypic control and improvement of such traits can be improved through hybridization.

High heritability (broad sense) estimates (>80%) were observed for almost all the traits *viz*., days to 50% flowering (97.9%), kernel length after cooking (95.0%), test weight (93.0%), kernel length (92.9%), water uptake (90.9%), kernel breadth after cooking (86.1%), head rice recovery (84.8%), plant height (83.2%) and panicle density. Present results were in accordance with the findings of Rukmini Devi *et al.* 2017 [14], Srujana *et al.* 2017 [15], Dhanwani *et al.*2013 [6] indicating that the variation observed was mainly under genetic control and less influenced by environment and hence selection will be effective for these traits. However, moderate heritability was observed volume expansion ratio (77.4), grain yield/plant (72.8), panicle weight (75.8), kernel elongation ratio (72.4), alkali spreading value (71.5) indicating that characters are influenced by environmental effects and selection for improvement can be misleading, where as effective tillers, panicle length, hulling percent showed low heritability indicated that selection could be difficult due to masking effect of environment on the expression of traits. Since the estimates of heritability alone is misleading hence estimates of genetic advance as percent of mean is used for better prediction of characters under study. The genetic advance indicates the progress that can be expected for a trait as a result of selection. The values of genetic advance as percent of mean were high for (>50%) for characters panicle density (62.8%), filled seeds/panicle (60.5), volume expansion ratio (57.9), yield /plant (54.9), test weight (52.8) and water uptake (51.2) while moderate (25-50%) for characters head rice recovery (48.7), panicle weight (47.9), alkali spreading value (35.7), kernel length after cooking (32.3), kernel length (26.9) and kernel breadth after cooking (25.9). Estimates of genetic advance were low (<25%) for days to 50% flowering (23.7), Length/breadth ratio (22.1), milling percent (20.2), plant height (17.3), kernel elongation ratio (16.9), panicle length (10.8) and hulling percent (6.9). Similar results were reported by Kole *et al*. 2008 [8].Vinod kumar *et al*. 2016 [17] also reported high genetic advance as percent of mean for filled grains/panicle. Estimates of genetic advance as percent of mean was (<25%) observed for rest of the characters *viz*., days to 50%flowering, plant height, effective tillers, panicle length, hulling recovery, milling recovery, kernel width, length/breadth ratio, kernel elongation ratio. Similar results were reported by kole *et al* 2008 [8] and Vinod kumar *et al* 2018 [17].

Heritability alone fails to indicate the response to selection and a character having high heritability may not necessary give high genetic advance. Therefore heritability should be always considered along with genetic advance as percent of mean to arrive at a more reliable conclusion. (Johnson *et al* 1955) [7].

High heritability coupled with high genetic advance as percent of mean was observed for panicle density, filled seeds/panicle, test weight and water uptake which indicates the additive gene action and thereby the traits could be considered as reliable indices for selection. These results are in agreement with the results obtained by Vanisree *et al*. 2013 [16], Rukmini Devi *et al.* 2017 [14], Vinod Kumar *et al* 2018 [17].

High heritability coupled with moderate genetic advance was observed for kernel length after cooking, kernel breadth after cooking and kernel length indicating characters are governed by additive genes though influenced by environment. High heritability coupled with low GA was observed for kernel length after cooking, kernel breadth after cooking and kernel length indicating non additive gene action. High heritability is due to favorable environment rather than genotype therefore selection of such traits may not be rewarding. In the present study low heritability and low genetic advance was observed for panicle length and hulling percent indicated role of non-additive gene action of these characters. Hence improvement of these traits through heterosis breeding rather than selection could be adopted.

Table 1: Analysis of variance (mean squares) for grain yield and quality traits in rice (*Oryza sativa* L.)

S. No	Characters	Replication(d.f=1)	Treatments(d.f=70)	Error (d.f=70)
1	Days to 50% flowering	0.852113	140.3728**	1.4806
2	Plant height(cm)	19.781690	151.6834**	13.9085
3	Effective tillers	18.605350	3.011541**	1.418495
4	Panicle length (cm)	10.547110	5.186660**	1.340398
5	Panicle density	2.816901	11.590268**	1.041616
6	Panicle weight(g)	0.193363	2.384041**	0.32780
7	Filled seeds /Panicle)	1104.33800	7427.899**	708.8666
8	Test weight(g)	0.718380	34.203674**	1.246237
9	Yield/Plant (g)	12.245700	74.5956**	11.73184
10	Hulling percent (%)	74.856410	28.131817**	10.318123
11	Milling percent (%)	135.476700	80.91506**	14.6615
12	Head rice recovery (%)	0.375282	163.00992**	13.4485
13	Kernel length(mm)	0.136959	0.633254**	0.023306
14	Kernel width (mm)	0.013606	0.066587**	0.01284
15	length/breadth ratio	0.176056	0.265531**	0.050771
16	Kernel length after cooking(mm)	0.090761	1.311440**	0.033913
17	Kernel breadth after cooking (mm)	0.019406	0.113316**	0.00843
18	Kernel elongation ratio	0.023327	0.020186**	0.00323
19	Alkali spreading value	0.693003	1.405978**	0.233380
20	Water uptake (ml)	494.542300	5161.7354**	247.3993
21	Volume expansion ratio	0.23.2835	0.574641**	0.073062

*Significant at 5% level
** Significant at 1% level

Table 2: Clustering composition with distribution of 71 genotypes in rice by Tocher method

Cluster no	No of genotypes / Entry no	Genotypes
1	(33) 2,68,5,66,34,61,7,10,1,15,6,45,24,43,39,52,35,17,36,37,14,8,41,27,16,32,42,19,40,23,20,21,54	RP5950-24-6-2-1-B,NLR344449,RTN28-1-5,WGL347,BPT2808,ADT-49,AD12161,MTU1207,MTU1190,MTU1237,AD13121,MTU1238,NVSR326,PNP9557,RP5865-30,PRNP38,OR2560-6,CR2906-25,MTU1239,MTU1219,OR2537-7,CB3808-13,OR2427-5,OR2512-5,HHZ-5-Y4-5,TTB404-2,DLRH-4,CR3783-3-1,VNR216,NLR3296,TRC2015-7,OR2573-7,CB8632
II	(29) 46,51,67,63,69,49,64,56,48,47,57,58,33,50,3,70,60,59,29,38,44,22,26,65,62,13,25,18,9	NLR3354,AAGP2079,NP9109,WGL9623,SIDDHI,JGL21820,TM09086,ORJ1311,WGL823,GNV14-05,B13966-39,RP6112-MS-M-114-3-1-7-1-3,YNP9183,RP6112-SM-M-93-9-2-3-4-3,NP9359-9,NR1011,MTU1061,PUSA1701-10-5-8,JGL24423,RP5599-312-63-5-1,Gontrabidhan,JR206,JGL21028,HHZ-26-SAL-12Y1-Y1,SVZ903R-GM-AS-40,CR3959-1-1-2-1-1,UPR3919-10-1-1-1,MTU1236
III	(1)12	OR2573-15
IV	(1)30	NVSR2086
V	(1)4	RGL7011
VI	(1)28	PAU2K10-23-54-14-52-107-0-1
V11	(1)53	NR1011
VIII	(1)31	RCPR32-HHZ-5-DT-20-DT-3
IX	(1)55	CR3985-1-1-3-1-1
X	(1)11	WGL915
XI	(1)71	BPT5204

Table 3: Intra-Inter cluster distances among eleven clusters in71 genotypes of rice (*Oryza sativa* L.)

	I cluster	II cluster	III cluster	IV cluster	V cluster	VI cluster	VII cluster	VIII cluster	IX cluster	X cluster	XI cluster
I cluster	128.42	248.94	197.95	209.59	282.43	243.27	212.99	336.72	211.59	285.14	309.24
II cluster		128.40	358.11	274.08	654.26	262.43	399.15	247.49	424.76	448.91	290.25
III cluster			0.00	70.66	463.30	122.52	299.21	314.51	127.69	157.77	518.28
IV cluster				0.00	551.92	77.28	317.68	218.95	160.96	225.46	452.77
V cluster					0.00	657.43	180.34	906.17	445.24	513.76	473.44
VI cluster						0.00	424.72	113.49	209.05	246.65	441.58
VII cluster							0.00	682.74	311.92	436.40	321.98
VIII cluster								0.00	319.80	374.74	524.94
IX cluster									0.00	337.26	504.62
X cluster										0.00	629.52
XI cluster											0.00

Bold values: Intra cluster distances

Table 4: Estimation of Mean values of eleven clusters by Tocher's method for 71 genotypes of rice for yield and yield components (*Oryza sativa* L.)

	Days to 50% flowering	Plant height(cm)	Effective tillers	Panicle length(cm)	Panicle density	Panicle weight (g)	Filled seeds/panicle	Test weight(g)	Yield/Plant (g)
I cluster	97.09	117.79	9.06	25.94	9.16	5.01	236.95	19.60	21.96
II cluster	84.66	113.54	9.19	25.72	9.01	230.52	230.52	18.09	23.03
III cluster	95.00	122.40	11.00	26.90	5.40	145.00	145.00	30.10	33.00
IV cluster	88.00	116.40	8.20	26.15	6.20	161.50	161.50	28.85	31.25
V cluster	115.50	112.60	9.30	27.70	8.30	230.00	230.00	15.90	9.00
VI cluster	88.50	102.50	6.90	27.05	5.30	154.50	154.50	27.00	21.00
VII cluster	108.00	111.10	9.90	26.45	5.65	150.00	150.00	22.30	30.75
VIII cluster	79.00	108.10	8.00	26.50	9.05	239.00	239.00	21.85	21.25
IX cluster	98.00	120.10	11.00	24.60	5.50	135.00	135.00	25.95	37.75
X cluster	92.00	134.30	7.00	31.50	9.90	312.50	312.50	28.50	31.50
XI cluster	96.50	102.90	11.00	22.95	7.85	286.00	286.00	15.25	25.35

Table 5: Estimation of Mean values of eleven clusters by Torcher's method for 71 genotypes of rice for quality traits (*Oryza sativa* L.)

	Hulling percent (%)	Milling percent (%)	Head rice recovery (%)	Kernel length (mm)	Kernel width (mm)	Length/ breadth ratio	Kernel length after cooking (mm)	Kernel breadth after cooking (mm)	Kernel elongation ratio	Alkali spreading value	Water uptake (ml)	Volume Expansion Ratio
I cluster	76.85	64.65	45.07	5.23	1.67	3.18	6.51	2.20	1.25	5.08	257.20	2.08
II cluster	76.33	61.38	42.78	4.99	1.59	3.17	6.02	2.10	1.20	4.33	228.53	1.93
III cluster	7410	57.70	40.20	6.12	1.86	3.30	7.68	2.30	1.21	4.60	190.00	1.80
IV cluster	80.70	63.75	21.70	5.79	1.73	3.35	7.55	2.05	1.31	4.95	230.00	1.66
V cluster	81.10	67.85	39.50	4.95	1.82	2.75	5.70	2.05	1.15	5.10	247.50	1.74
VI cluster	79.30	57.25	31.85	6.48	1.59	4.10	7.68	2.33	1.19	6.00	207.50	3.03
VII cluster	75.90	55.90	29.50	5.41	1.58	3.40	5.05	2.00	0.94	4.70	232.50	2.03
VIII cluster	76.10	65.10	37.40	6.19	1.63	3.85	7.84	2.60	1.27	6.40	322.50	2.50
IX cluster	76.00	67.65	49.85	6.32	1.59	4.00	7.78	2.00	1.24	5.95	270.00	2.10
X cluster	78.05	45.65	34.35	6.29	2.08	3.40	6.70	2.80	1.07	3.65	227.50	1.42
XI cluster	79.20	59.45	50.05	4.57	1.59	2.90	5.80	2.00	1.27	4.65	160.00	1.46

Table 6: Contribution of different characters towards genetic divergence in 71 genotypes of rice (*Oryza sativa* L)

S. No	Source	Times ranked 1st	Contribution (%)
1	Days to 50% flowering	896	3605.63
2	Plant height(cm)	69	277.67
3	Effective tillers	3	12.07
4	Panicle length (cm)	-	-
5	Panicle density	32	128.77
6	Panicle weight(g)	9	36.22
7	Filled seeds /Panicle	65	261.57
8	Test weight(g)	97	390.34
9	Yield/Plant (g)	25	100.6
10	Hulling percent (%)	3	12.07
11	Milling percent (%)	10	40.24
12	Head rice recovery	37	148.89
13	Kernel length(mm)	212	853.12
14	Kernel width (mm)	8	32.19
15	length/breadth ratio	-	-
16	Kernel length after cooking(mm)	593	2386.32
17	Kernel breadth after cooking (mm)	60	241.45
18	Kernel elongation ratio	2	8.05
19	Alkali spreading value	75	301.81
20	Water uptake (ml)	249	1002.01
21	Volume expansion ratio	40	160.97

Table 7: Eigen vectors and Eigen values of the first five principal components of 21 traits of in rice (*Oryza sativa* L)

	PC1	PC2	PC3	PC4	PC5
Eigene value	3073.6700	1900.52000	603.25640	384.89380	341.69040
% Var. Exp	40.09614	24.79231	7.86949	5.02094	4.45736
Cum. Var. Exp	40.09614	64.88843	72.75793	77.77887	82.23622
Days to 50% flowering	0.66248	0.36926	0.00504	0.12184	0.16878
Plant height(cm)	0.23844	0.05294	0.00996	-0.18043	-0.25758
Effective tillers	-0.249936	-0.08345	-0.1258	0.13117	0.09191
Panicle length (cm)	-0.00628	-0.04077	0.06325	-0.04142	-0.10637
Panicle density	0.3902	0.13898	-0.18233	-0.43309	0.186554
Panicle weight(g)	0.05842	-0.07678	0.05444	-0.30151	-0.13478
Filled seeds /Panicle	-0.00413	0.04488	0.05474	0.06637	0.12967
Test weight(g)	0.27356	-0.27910	0.34835	0.17363	-0.03241
Yield/Plant (g)	-0.13443	-0.10987	0. 0 3 70 7	0.27531	0.03597
Hulling percent (%)	-0.04572	0.01209	0.00674	-0.10871	0.15578
Milling percent (%)	0.19530	0.123352	-0.05605	0.07829	0.260573
Head rice recovery (%)	0.08368	0.08442	-0.35330	0.07802	-0.11352
Kernel length(mm)	0.05090	-0.53600	0.18172	0.10056	-0.077 22
Kernel width (mm)	0.22804	0.02445	-0.07116	0.16806	-0.14313
length/breadth ratio	0.1418	0.03295	0.10857	0.06908	0.08773
Kernel length after cooking(mm)	0.35757	-0.58740	-0.17555	-0.07570	0.22653
Kernel breadth after cooking (mm)	0.00103	-0.13820	-0.30029	-0.33514	-0.35922
Kernel elongation ratio	0.02024	0.14260	-0.14789	0.21184	0.10578
Alkali spreading value	-0.08054	-0.17707	-0.29791	-0.18492	0.63965
Water uptake (ml)	0.20640	-0.08016	-0.61772	0.45297	-0.24621
Volume expansion ratio	-0.20747	0.03629	-0.20673	0.274583	0.11300

Table 8: Components of genetic parameters for yield and quality traits in rice (*Oriza sativa* L.)

Character	Mean	Range	PV	GV	PCV	GCV	Heritability in broad sense (%)	Genetic advance as percent of mean
Days to 50% flowering	91.8	76.-116	7.0.927	69.446	9.172	9.075	9.79	23.708
Plant height(cm)	115.6	86-124.6	82.796	68.887	7.869	7.178	8.32	17.284
Effective tillers	9.1	66-12.8	2.215	0.797	16.314	9.783	3.60	15.488
Panicle length (cm)	25.9	21.6-31.5	3.264	1.923	6.964	5.346	5.89	10.834
Panicle density	8.825	5-14.5	6.316	5.274	28.477	26.023	8.35	62.780
Panicle weight(g)	4.862	2.92-9.95	1.356	1.028	23.949	20.854	7.58	47.941
Filled seeds /Panicle	229.831	128.5-356.5	4068.383	3359.516	27.753	25.219	8.26	60.501
Test weight(g)	19.537	12.8-30.1	17.725	16.479	21.549	20.778	9.30	52.890
Yield/Plant (g)	23.004	9.0-37.8	43.164	31.432	28.560	24.372	7.28	54.906
Hulling percent (%)	76.763	68.0-88.23	19.225	8.907	5.712	3.888	4.63	6.986
Milling percent (%)	62.730	40.6-73.5	47.788	33.127	11.020	9.172	6.93	20.167
Head rice recovery (%)	43.133	21.7-60.45	88.229	74.781	21.777	20.049	8.48	48.728
Kernel length(mm)	5.206	7.37-6.47	0.328	0.305	11.005	10.607	9.27	26.991
Kernel width (mm)	1.642	1.33-2.23	0.040	0.027	12.140	9.985	6.77	21.683
length/breadth ratio	3.213	2.35-4.10	0.158	0.107	12.379	10.200	6.79	22.188
Kernel length after cooking(mm)	6.352	5.05-7.87	0.673	0.639	12.911	12.581	9.50	32.367
Kernel breadth after cooking (mm)	2.165	1.85-2.92	0.061	0.052	11.399	10.580	8.61	25.923
Kernel elongation ratio	1.221	0.93-1.55	0.012	0.008	8.861	7.540	7.24	16.936
Alkali spreading value	4.778	3.25-6.50	0.820	0.586	18.950	16.026	7.15	35.783
Water uptake (ml)	243.697	127.5-370.0	2704.567	2457.168	21.340	20.341	9.09	51.185
Volume expansion ratio	2.007	1.13-3.50	0.324	0.251	2 8. 355	24.952	7.74	57.970

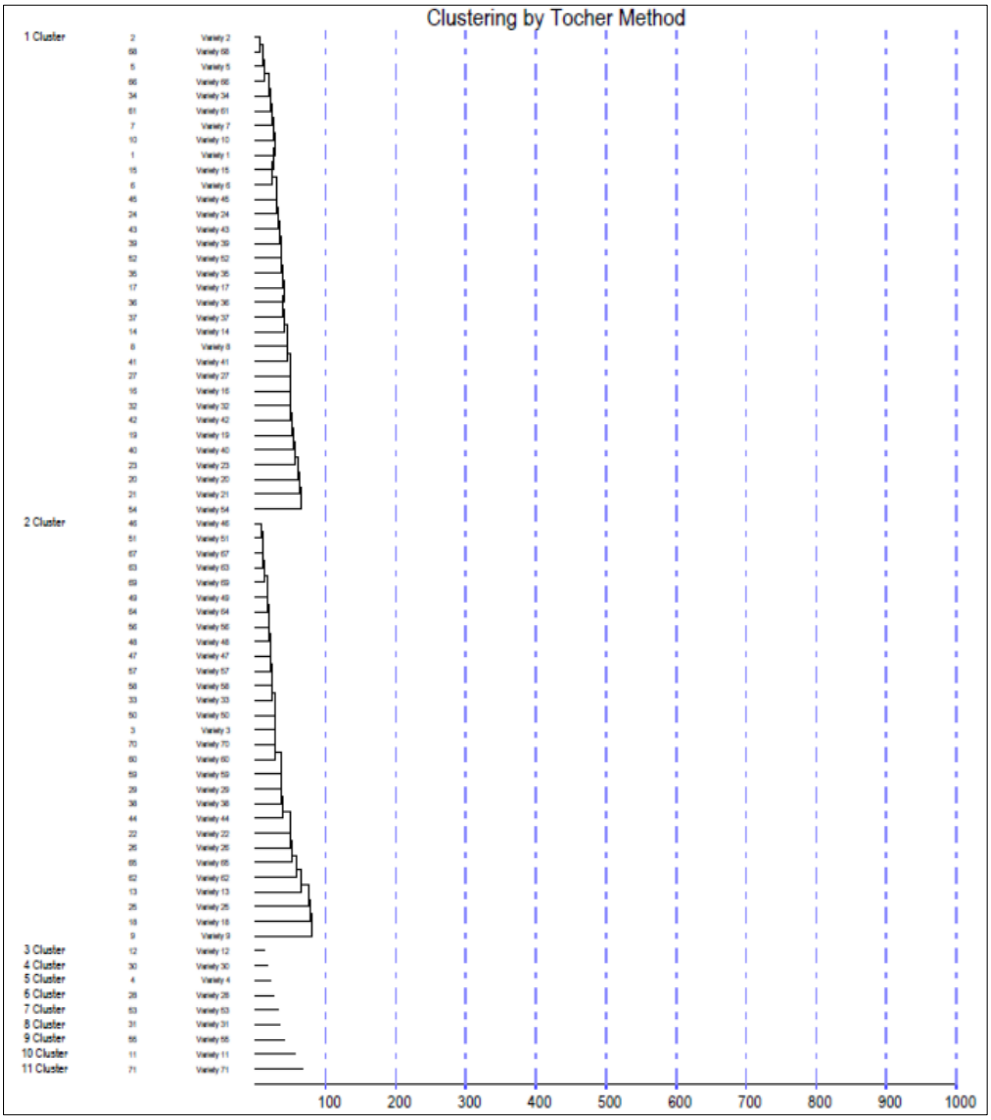

Fig 1: Clustering pattern of 71 Promising Germplasm lines in Rice according to Tocher method

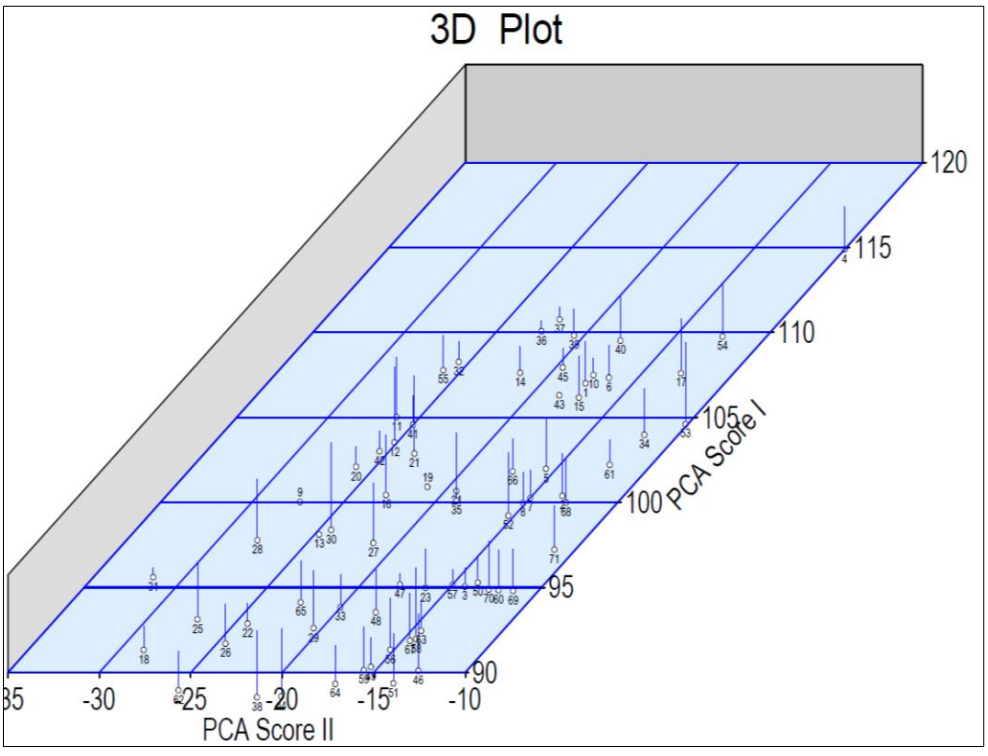

Fig 2: Three-dimensional graph of 71 promising Germplasm lines in Rice based on yield and quality traits (principal component analysis)

Conclusion

On the basis of results summerized above it is concluded that the parents for hybridization programme 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 programme for obtaining a wide spectrum of variation among the segregants. Current study reports that days to 50% flowering, kernel length after cooking, water uptake and kernel length are greater contribution of variability and due weightage should be given while formulating breeding schedule. Among the genotypes RCPR 32-HHZ-5-DT-20-DT-3 and RGL 7011 are considered as most diverse among population studied. High PCV and GCV were observed for filled seeds/panicle, volume expansion ratio, grain yield/plant, panicle weight, test weight, water uptake and head rice recovery, these characters are amenable for further improvement. High heritability coupled with high genetic advance was observed for panicle density, filled seeds/panicle, test weight, water uptake which indicates the additive gene action and there by the traits could be considered as reliable indices for selection.

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