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Genetic diversity of drought tolerant rice (*Oryza sativa* L.) genotypes under drought stress condition

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Abstract
A field screening of thirty three rice genotypes under drought stress and irrigated non-stress condition was conducted during kharif 12 with the objective to study the effect of drought stress on yield and yield attributes performance of advanced breeding lines and current high yielding varieties. The effects of water deficit on various physiological traits associated with drought tolerance were also studied. Result revealed that significant yield decline was observed almost in all rice genotypes grown under water stress condition compared to irrigated situation. Significant variation was also observed among genotypes for leaf rolling, leaf drying, stress recovery and relative water content under drought stress conditions. The tolerant lines maintained high leaf water status, membrane stability and plant biomass under reproductive stage drought condition. The present study also indicates the agro-morphological and physiological traits that have direct and indirect effect on yield performance of rice genotypes under drought stress condition.

Keywords: Genetic diversity, drought tolerant, rice genotypes, cluster analysis and D^2 analysis

Introduction
Rice (*Oryza sativa* L.) is one of the world's most widely cultivated crop species and is staple food for more than half of the human population in the world and about two third in India. About 785 million tonnes of paddy which is 70 per cent more than the current production will be required to growing demand by 2025 (Manonmani and Khan, 2003a) [19]. Being staple food for majority of the population in India, improvement in its productivity has become crucial. The pace and magnitude of genetic improvement generally depend on the amount of genetic diversity present in a population and it is estimated that not even 15% of the potential diversity has utilized till date. We need to produce more rice per unit area. Achieving selfsufficiency in rice production and maintaining price stability are important in countries where rice provides food security and generates employment and income for people (Hossain, 1995). About half of the world's rice area is under rainfed culture where drought is the major limiting factor to rice production globally. Rainfed area includes 13% upland ecosystem, 11% deepwater ecosystem and 25% rainfed lowland ecosystem of the total rice area (Fukai and Cooper, 1995) [9]. Drought is the second most sever limiting factor (Caldo *et al*., 1996) [4]. In upland rice, depth of rooting, root thickness and root-shoot dry weight ratio are related to drought resistance (Fukai and Cooper, 1995) [9]. An understanding of association between yield and yield contribution traits has a great importance in Plant Breeding. For any crop, to setup a suitable breeding program, information about interrelationship among and between yield contributing characters is necessary. The genetic variations constitute a high proportion of the total variation for these traits. Thus, selection for these characters is expected to be highly effective (Abdel-Ghani *et al*., 2005) [2]. In any crop improvement programme, study of genetic diversity is an essential prerequisite for hybridization. Inclusion of genetically diverse parents in hybridization programme helps in isolation of superior recombinants. Genetic divergence among the genotypes plays an important role in selection of parents having wider variability for different traits (Naik *et al*., 2004) [21] and it also helps in the development of superior recombinants (Manonmani and Khan, 2003b) [19]. The use of D2 statistics has been emphasized by many workers (Roy *et al*. 2002, Datt and Mani, 2003 and Kumar *et al*., 2014) [25, 7, 18]. Estimation of genetic diversity is an important factor to know the source of genes for a particular trait within the available genotypes. Genetic diversity among the segregating population also helps to select suitable types as parents and also for commercial cultivation.

Therefore, the present study was undertaken to determine the genetic diversity of thirty three drought tolerant upland rice genotypes.

Materials and Methods

Field experiments were carried out during Kharif 2012 at Research Farm of Rajendra Agricultural University, Pusa, Samastipur, Bihar. Geographically, University Farm is situated between 25.980 N latitude and 85.670 longitudes at 51.8m above mean sea level. The experimental site was typical rainfed having clay loam soil with pH 7.5. 33 rice genotypes comprising of breeding lines and check varieties including viz., Sahbhagidhan, Vandana, Rasi and APO were evaluated for vegetative and reproductive stage were used for testing under irrigated (normal) and stress condition. The rice genotypes used under present study were collected under Stress-Tolerant Rice from RAU, PUSA, (Bihar), IRRI, INDIA, IGKV, Raipur and BAU, Ranchi-Jharkhand. The field experiments were conducted under reproductive stage water stress and irrigated non-stress (control) condition. 33 genotypes were grown under two environments *viz*, Rainout shelter (stress condition) and Normal (irrigated**)**. The experiment in each environment was laid out in Completely Randomized Block Design with three replications. In each replication each genotype was grown in a plot of 4 rows of 1 meter length each with a spacing of 20 cm between rows under both stress and under irrigated condition. Both water stress and non-stress control field were fertilized @ 60:40:30 kg (N: P: K) per ha. respectively. Nitrogen was applied on three occasion (1/3rd each at basal, maximum tillering and panicle initiation stage), while the P_2O_5 and K_2O were applied as a basal application. The stress condition was created by the technique involved irrigation until 45 days from sowing of rice seed, withholding water for about 15 days till the susceptible checks showed permanent wilting, drought scoring of test entries, rewatering, and then screening for recovery ability. Water tension by tension-meter was also monitored during the stress period. The relative yield (yield potential) under drought stress was calculated as the yield of specific genotypes under drought divided by that of the highest yielding genotype in the population. The data were recorded on five randomly selected plants from each genotype in each replication leaving the first two border rows from all the four sides, in order to avoid the sampling error. The observations were recorded as per the following procedure. Readings from five plants were averaged replication wise and the mean data was used for statistical analysis for 17 characters *viz*, Days to fifty per cent flowering, days to physiological maturity, plant height, flag leaf area, chlorophyll content, number of tillers per plant, leaf rolling at vegetative stage, leaf drying at vegetative stage, relative water content, panicle length, canopy temperature, recovery percentage after stress, drought susceptibility index, number of grains per panicle, 1000 grain weight, harvest index and seed yield per plant. was calculated as the yield of specific genotypes under drought divided by that of the highest yielding genotype in the population. The drought scores, leaf rolling, leaf drying and stress recovery observations were taken as per SES method, 1 to 9 scales (IRRI, 1996) [15]. Leaf relative water content (RWC) was estimated by recording the turgid weight of 0.5 g fresh leaf sample by keeping in water for 4h, followed by drying in hot air oven till constant weight is achieved (Weatherly, 1950). It is given as Relative water content (%) = [(Fresh weight- Oven dry weight) x 100 / (turgid weight- Oven dry weight)]. Leaf chlorophyll content was recorded by measuring leaf greenness using a portal chlorophyll meter (Monilta Camera Co. Ltd., Japan). Canopy temperature was measured using a hand-held infrared thermometer. Measurements were taken in the afternoon (1:00 to 2:00) of full sunshine conditions. Yield attributes i.e. seed yield, straw yield, harvest index and dry matter was measured at maturity. Flag leaf area was measured with the following function by Muller (1991) [20].

Flag leaf area = Flag leaf length × Flag leaf width × 0.74

Data Analysis

The agro-morphological data were analyzed by appropriate statistical analysis (Gomez and Gomez, 1984) [11] using CropStat 7.2 (IRRI, 2009) [16] programme. Physiological data was analyzed using OPSTAT software of Hisar Agricultural University, Hisar.

Results and Discussion

The analysis from distance matrix gave nonhierarchical clustering among 33 drought tolerant genotypes and varieties. All genotypes were grouped into six clusters (Table 1 & 2). Cluster I had three genotypes viz., RAU-1421-12-1-7-4-3, RAU-1415-35-76-9-5-3 and RAU-1428-6-7-3-6. Cluster IV had maximum number of genotypes (14) followed by cluster II (7), cluster III (5) and cluster V (3). However, the cluster VI contain only one genotype i.e., monogenotypic, comprising single genotype, namely 21284-BAU445-06 under stress condition. Under normal condition, the thirty three rice genotypes taken for genetic divergence analysis differed significantly with regard to the characters studied and displayed marked divergence and grouped into six clusters following Tocher's method (table 1 & 2). Cluster I had ten genotypes viz., RAU-1421-12-1-7-4-3, RAU-1415-35-76-9-5-3, Richharia, RAU-1428-31-5-4-3-2-2-2, RAU-1417-11-1-74-3-2, RAU-1428-31-5-4, RAU-1428-54-35-5-5, 21284-BAU445-06, Rasi(c.), RAU-1421-12-1-7-4-3.Cluster II hadmaximum number of genotypes (12) followed by cluster III (8). However, the clusters VI, V, VI contained only one genotype i.e., monogenotypic, comprising single genotype, namely RAU-1428-6-7-3-6, RAU-1463-16 and RAU-1426-43-2-5-7-2 and the cluster VI contain only one genotype namely 21284-BAU445-06 under stress condition, which was the smallest among the six clusters under both conditions. The clustering pattern showed that genotypes of different geographical areas were clubbed in one group and also the genotypes of same geographical area were grouped into same cluster as well as in different cluster indicating that there was no formal relationship between geographical diversity and genetic diversity. Based on the percentage, the distribution of genotypes into different clusters under stress and non-stress condition, each of the highest contribution in the manifestation of genetic divergence was exhibited by chlorophyll content (45.08) followed by number of grains per panicle (39.58), plant height (6.25), harvest index (3.60) and 1000 grain weight (3.03) under stress condition (table 3). Under normal condition, the contribution percentages of seventeen quantitative traits under studied towards total divergence is presented in table 4. The highest contribution in the manifestation of genetic divergence was exhibited by flag leaf area (40.53) followed by chlorophyll content (23.11), plant height (19.89), harvest index (13.45) and days to fifty per cent flowering (1.70). Chlorophyll content exhibited maximum contribution percentage to total divergence in both stress and normal condition. This indicated that selection of genotypes for based on this trait may be rewarding for future

utilization in breeding programme. Some varieties were locally developed and local cultivar for upland. Grouping of all genotypes from different sources indicated that there was no association between clustering pattern and eco-geographical distribution of the genotypes. De and Rao (1987) [8] and Singh *et al.* (1987) [27] also revealed that geographical diversity is not necessarily related to genetic diversity. Intra and inter cluster distances are presented in Table 5 and 6. The inter cluster distances in almost all of the cases were larger than the intra cluster distances indicating that wider diversity was present among the genotypes of distance groups.

The intra-cluster distances was low found in cluster I under both stress and non-stess conditions indicating that close resemblance between the genotypes presented in this cluster which indicate homogeneous nature of the genotypes within the clusters (Table 4 and 5). These results are in agreement with those reported by Iftekharuddaula *et al*. (2002) [14] and Kulsum *et al*. (2011) [17] in rice. The D 2 value ranged from 215.10 to 1924.70 and 469.24 to 2209.18 under stress and non-stress condition indicated a high degree of genetic diversity among the genotypes. Regarding the cluster distance, The genotypes in cluster V and cluster VI, due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme (transgressive breeding) for getting high yielding recombinants. Similar inter varietal crosses may be attempted between genotypes in cluster IV and V, cluster III and IV. The lowest inter cluster distance was observed between cluster I and II showing this cluster was relatively less divergent and crossing between them cannot produce vigorous offspring (F_1 progenies) under stress condition (control). Similar studied based on D^2 statistic was also performed by that of Chandra *et al*. (2007). Under normal condition, the maximum inter cluster distance was observed between cluster III and VIfollowed by cluster IV and V, cluster III and IV and cluster I and VI indicating the chances of getting high yielding recombinants would be better if the crosses are made among the genotypes of these groups. The lowest inter cluster distance was recorded between cluster I and IVshowing this cluster was relatively less divergent. Chaturvedi *et al*. (2011) [6] and Chandra *et al*. (2007) also identified most diverse cluster based on intra and inter cluster distance and suggested their use in hybridization programme for achieving high yielding varieties. It was observed that in all cases, the Cluster VI produced the highest D 2 values (368.64) and (2209.18) among the all clusters under both stress and non-stress condition. It revealed that wider diversity among them and crossing among the genotypes would yield the maximum heterosis. These results are supported by Saini and Kaicke (1987) [26]. The minimum inter cluster divergence was observed between cluster I and II (215.10) under stress whereas, cluster I and IV (469.24) indicating that the genotypes of these cluster were genetically closed. However, genotypes within the other pair of clusters indicate that they were less diverged. The selection of diverge parents from cluster would produce a broad spectrum of variability for morpho-physiological and quality traits studied which may enable further selection and improvement. The hybrid developed from the selected parental genotypes within the limit of compatibility of these clusters may produce high magnitude of heterosis. This would be rewarded in hybrid rice breeding program. The results reported by Roy *et al*. (2002) [25] and Naik *et al*. (2004) [21] were agreement with these findings.

Cluster mean values for 17 characters are presented in Table 7 and 8. Difference in cluster means existed for almost all the characters studied. Among 17 characters, cluster I was found rich for early days to fifty per cent flowering and plant height, maximum flag leaf area, chlorophyll content and harvest index. Cluster II also minimum mean value for leaf rolling at vegetative stage and leaf drying at vegetative stage, maximum value for number of tillers per plant and relative water content. Cluster III may be selected as a donor for dwarfness. Cluster III was suitable for panicle length and 1000 grain weight. Cluster V was suitable for early days to maturity and number of grain per panicle. Cluster VI had the genotype with the minimum mean value for canopy temperature, drought susceptibility index and maximum mean value foe seed yield per plant. For the purpose of earliness, cluster I and cluster V under stress condition. Therefore, this cluster may be selected for transferring the traits with high mean values through hybridization programme. Selection of genotypes based on cluster mean for the better exploitation of genetic potential also reported by Abarshahr, *et al*.(2011) [1], Chaturvedi, *et al.* (2011) [6], Raut *et al.* (2009) [24], Ramya and Senthil kumar (2008) [22], Arivoli *et. al*.(2009) [3], Gahalain *et. al.* (2010) [10]. Under normal condition, on the basis of cluster mean values, cluster II suitable for number of tillers per plant. Cluster I had maximum mean value for relative water content, number of grains per panicle and seed yield per plant. Cluster III minimum mean value for leaf rolling at vegetative stage, leaf drying at vegetative stage and canopy temperature, maximum mean value for flag leaf area, panicle length and number of grains per panicle. Cluster IV was suitable for early days to fifty per cent flowering, plant height, chlorophyll content and harvest index. Cluster VI showed minimum mean value for the traits like days to physiological maturity, leaf rolling at vegetative stage and leaf drying at vegetative stage and maximum value for 1000 grain weight. Cluster III and cluster VI had minimum mean value for leaf rolling at vegetative stage, leaf drying at vegetative stage and canopy temperature. Cluster IV has early days to fifty per cent flowering and cluster VI for early days to physiological maturity. Total divergence estimation based on D^2 distances werealso carried out by Hegde and patil (2000) [12]. Therefore, this cluster may be chosen for transferring the traits having high mean values through hybridization programme, that means the lines or varieties falling in cluster with maximum mean value having the potentialities to contribute better for maximizing yield of drought tolerant rice genotypes.

It was clear from Table 7 and 8 that the highest intra cluster means for yield were obtained from clusters having maximum cluster mean resulting, giving more emphasis on these cluster for selecting genotypes as a variety and as well as parents in crossing with other genotypes. The character contributing the maximum to the divergence are given greater emphasis for deciding on the cluster for the purpose of further selection and the choice of parents for hybridization. In the present study, 33 diverse genotypes were grouped into various cluster and suitable diverse genotypes were selected based on their cluster mean superiority and per se performance for different characters resulting RAU-1421-12-1-7-4-3 grouped in cluster I exhibited earliness in days to fifty percent flowering and RAU-1477-9-7-22-5-7-3 in cluster V for days to physiological maturity based on cluster mean (lowest) showed the significantly superior *per se* performance. The genotypes RAU-1421-12-1-7-4-3 also exhibited superiority for flag leaf area with highest cluster mean and superior *per se* performance. The genotype RAU-1415-35-76-9-5-3 from

Cluster I was selected for harvest index with highest cluster mean and superior *per se* performance. The genotypes namely RAU-1428-6-7-3-6 was selected from cluster I for plant height for dwarfness based on cluster mean and superior *per se* performance. Cluster VI was selected for least drought susceptibility index (DSI) and maintain lower canopy temperature with least cluster mean and *per se* performance and has 21284-BAU445-06 genotype. The 21284-BAU445-06 genotype from cluster VI was selected for highest seed yield per plant based on highest cluster mean and superior *per se* performance. Cluster II was selected for highest chlorophyll content, relative water content and number of tillers per plant whereas, it selected for minimum leaf rolling at vegetative stage and leaf drying at vegetative stage. Only RAU-1417-11-1-74-3-2, RAU-1428-31-5-4, RAU-1428-54-35-5-5from cluster II were exhibited significantly superior *per se* performance for that traits. RAU-1451-66-1-1-5-2 from cluster V has high cluster mean for number of grains per panicle with superior *per se* performance. RAU-1463-15 from cluster III has high cluster mean for panicle length and RAU-1428-31-5-4-3-2-2-2 has high cluster mean for 1000 grain weight with superior *per se* performance.RAU-1397-25-8-1-2-5-4 and RAU-1451-35-7-6-9-5-1 from cluster IVhas high cluster mean for recoverypercentage after stress with superior *per se* performance under stress condition. Similar results was reported by Rashidi *et al.* (2011) [23]. Under normal condition for the purpose of earliness in days to fifty percent flowering genotype RAU-1428-6-7-3-6 from cluster IVand cluster VI for days to maturity RAU-1426-43-2-5-7-2 was chosen as suitable parents based on highest cluster mean and significantly superior *per se* performance. RAU-1428-6-7-3-6 from cluster IVwas also chosen for dwarfness and higher Chlorophyll content, harvest index based on cluster mean and superior *perse* performance. The genotypes viz., RAU-1471-10, 22823 Rewa780-8, RAU-1463-15, Sahbhagidhan, RAU-1451-66-1-1-5-2, APO, RAU-1415-8-6-4-3-3, Vandana from cluster cluster IIIwas chosen for minimum leaf rolling at vegetative stage and leaf drying at vegetative stage based on highest cluster mean and superior *per se* performance. The genotypes viz., 22823Rewa780-8 and Vandana from cluster III exhibited minimum value for canopy temperature based on highest cluster mean and superior *per se* performance. Cluster III were selected as suitable parents for traits like flag leaf Area and panicle length for genotype RAU-1463-15 and RAU-1451-66-1-1-5-2 for panicle length based on superior *per se* performance. RAU-1417-2-1-5-7-7 and RAU-1397-25-8-1-2-5-4 (cluster II) depicted highest number of tillers per plant and 21284-BAU445-06 from cluster I exhibited maximum relative water content with highest cluster mean and superior *perse* performance. The genotypes viz. RAU-1451-66-1-1-5-2 and RAU-1428-54-35-5-5 from cluster III & I exhibited maximum number of grains per panicle based on highest cluster mean and superior *per se* performance. Cluster VI was selected for 1000 grain weight having RAU-1426-43-2-5-7-2genotype based on highest cluster mean and superior *per se* performance. The genotypes viz., RAU-1428-31-5-4-3-2-2-2 and RAU-1428-31-5-4 from cluster I exhibited maximum seed yield per plant based on highest cluster mean and superior *per se* performance. These results were in accordance of Chandra *et al.* (2007). Under stress condition, the genotypes viz., 21284-BAU445-06 was found to be promising as indicated by low drought susceptibility index, canopy temperature & high seed yield and can be used in future breeding programmes for drought tolerance. Thegenotypes viz., RAU-1421-12-1-7-4-3 from cluster I & RAU-1477-9-7-22-5-7-3 from cluster V were selected for earliness, 21284-BAU445-06 from VI were identified as promising parents for their further utilization in hybridization programme in order to develop genotypes suitable for drought condition. The genotypes viz., RAU-1428-6-7-3-6 from cluster IV were selected for traits like earliness, chlorophyll content, plant height and Harvest index and RAU-1426-43-2-5-7-2 for earliness, leaf rolling at vegetative stage, leaf drying at vegetative stage & 1000 grain weight, were identified as promising parents in normal condition.

Genetically distant parents are usually able to produce higher heterosis and the clustering pattern could be utilized in choosing parents for cross combinations which are likely to generate the highest possible variability for effective selection of various economic traits. The findings of this study indicate that the cluster III, IV,V and VI showed the higher distance under both stress and non-stress condition. Parental materials selection from these clusters would give the manifestation of heterosis as well as wide spectrum of variation when they are hybridized.

Table 1: Clustering pattern of 33 genotypes of rice on the basis of D^2 statistic under stress and normal condition

Cluster No.	No. of Genotypes within cluster	Genotypes in cluster
I	3	RAU-1421-12-1-7-4-3, RAU-1415-35-76-9-5-3, RAU-1428-6-7-3-6
II	7	RAU-1428-54-35-5-5, RAU-1428-31-5-4, RAU-1417-11-1-74-3-2, Sahbhagidhan (check), APO(C.), Richharia, Rasi(c.)
III	5	RAU-1471-10, 22823Rewa780-8, RAU-1463-15, Vandana(check), RAU-1428-31-5-4-3-2-2-2
IV	14	RAU-1463-16, RAU-1453-12, RAU-1401-18-1-5, RAU-1415-8-6-4-3-3, RAU-1421-15-3-2-5-3-7, RAU-1416-4-2-5-2-2, RAU-1401-18-1-4, RAU-1426-43-2-5-7-2, RAU-1397-25-8-1-2-5-4, RAU-1421-12-1-7-4-3, RAU-1421-15-3-2-5-7-3, RAU-1451-35-7-6-9-5-1, RAU-1478-52-2-4-6, RAU-1428-43-2-7-26
V	3	RAU-1417-2-1-5-7-7, RAU-1477-9-7-22-5-7-3, RAU-1451-66-1-1-5-2
VI	1	21284-BAU445-06

Table 2: Clustering pattern of 33 genotypes of rice on the basis of D^2 statistic under normal condition (non-stress)

Cluster No.	No. of Genotypes within cluster	Genotypes in cluster
I	10	RAU-1421-12-1-7-4-3, RAU-1415-35-76-9-5-3, Richharia, RAU-1428-31-5-4-3-2-2-2, RAU-1417-11-1-74-3-2, RAU-1428-31-5-4, RAU-1428-54-35-5-5, 21284-BAU445-06, Rasi(c.), RAU-1421-12-1-7-4-3
II	12	RAU-1477-9-7-22-5-7-3, RAU-1397-25-8-1-2-5-4, RAU-1417-2-1-5-7-7, RAU-1401-18-1-4, RAU-1421-15-3-2-5-3-7, RAU-1401-18-1-5, RAU-1478-52-2-4-6, RAU-1421-15-3-2-5-7-3, RAU-1416-4-2-5-2-2, RAU-1451-35-7-6-9-5-1, RAU-1453-12, RAU-1428-43-2-7-26

III	8	RAU-1471-10, 22823Rewa780-8, RAU-1463-15, Sahbhagidhan(check), RAU-1451-66-1-1-5-2, APO(C.), RAU-1415-8-6-4-3-3, Vandana(check)
IV	1	RAU-1428-6-7-3-6
V	1	RAU-1463-16
VI	1	RAU-1426-43-2-5-7-2

Table 3: Contribution % towards divergence under Stress condition

S. No	Source	Times Ranked 1st	Contribution %
1	Days to 50% Flowering	0	0.00
2	Days to Physiological Maturity	0	0.00
3	Plant Height (cm)	33	6.25
4	Flag Leaf Area (cm²)	2	0.38
5	Chlorophyll Content	238	45.08
6	Number of tillers per plant	0	0.00
7	Leaf Rolling at Vegetative Stage	0	0.00
8	Leaf Drying at Vegetative Stage	5	0.95
9	Relative Water Content	3	0.57
10	Panicle Length (cm)	0	0.00
11	Canopy Temperature	1	0.19
12	Recovery Percentage After Stress	0	0.00
13	Drought susceptibility index	2	0.38
14	Number of grains per panicle	209	39.58
15	1000 Grains Weight (g)	16	3.03
16	harvest Index	19	3.60
17	Seed Yield/ Plant (g)	0	0.00

Table 4: Contribution percentage towards genetic divergence under non-Stress condition

S. No	Source	Times Ranked 1st	Contribution %
1	Days to 50% Flowering	9	1.70
2	Days to Physiological Ma	0	0.00
3	Plant Height (cm)	105	19.89
4	Flag Leaf Area(cm²)	214	40.53
5	Chlorophyll Content	122	23.11
6	Number of tillers per plant	0	0.00
7	Leaf Rolling At Vegetative stage	0	0.00
8	Leaf Drying At Vegetative stage	0	0.00
9	Relative Water Content	2	0.38
10	Panicle Length(cm)	3	0.57
11	Canopy Temperature	0	0.00
12	Number of grains per panicle	1	0.19
13	1000 Grains Weight (g)	0	0.00
14	harvest Index	71	13.45
15	Seed yield per plant (g)	1	0.19

Table 5: Mean intra and inter cluster distance (D^2) among six clusters in rice under stress condition

Inter & Intra Cluster Distances: Tocher Method (Stress)						
	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**
Cluster I	76.57	215.10	559.79	1123.65	888.99	488.52
Cluster II		117.48	339.08	938.07	827.53	459.79
Cluster III			205.26	1334.94	511.12	1216.19
Cluster IV				220.47	1652.97	703.66
Cluster V					665.53	1924.70
Cluster VI						0.00

Table 6: Mean intra and inter cluster distance (D^2) among six clusters in rice under non-stress condition**.**

Inter & Intra Cluster Distances: Tocher Method (Non-Stress)						
	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**
Cluster I	195.91	575.35	589.25	469.24	1035.42	1348.10
Cluster II		254.11	1151.27	629.03	726.06	666.79
Cluster III			309.63	1594.27	1004.01	2209.18
Cluster IV				0.00	1768.35	1204.13
Cluster V					0.00	632.28
Cluster VI						0.00

Table 7: Cluster mean values of six clusters for different quantitative characters in 33 rice genotypes under stress condition

Cluster Means: Tocher Method (Stress)																	
	DFF	**DM**	**PH**	**FLA**	**CHL**	**TPP**	**LR**	**LD**	**RWC**	**PL**	**CT**	**RAS**	**DSI**	**GPP**	**TGW**	**HI**	**SYP**
Cluster I	64	94.55	71.37	32.48	37.60	5.11	2.11	0.66	77.72	21.97	31.57	52.22	0.86	80.22	34.40	46.75	5.90
Cluster II	71.29	98.52	84.30	30.96	37.32	6.38	1.05	0.57	84.64	22.91	31.77	42.38	0.83	81.19	33.55	38.09	7.00
Cluster III	70.27	99.53	96.61	31.57	36.10	6.33	1.47	0.80	82.76	24.49	31.26	45.33	0.89	92.80	34.69	40.00	6.63
Cluster IV	70.46	95.12	81.47	27.08	27.95	4.26	3.33	2.64	72.47	22.03	32.88	66.66	0.98	69.71	31.67	33.69	4.44
Cluster V	69.78	93.00	82.47	31.99	32.73	5.11	2.11	1.67	76.22	23.33	32.55	61.11	0.94	99.44	33.81	39.49	4.95
Cluster VI	66.67	99.00	75.93	30.17	36.60	6.33	2.33	1.00	82.17	23.819	30.38	33.33	0.51	63.67	29.5	36.61	7.66

Table 8: Cluster mean values of six clusters for different quantitative characters in 33 rice genotypes under non-stress condition

Cluster Means: Tocher Method (Non-stress)															
	DFF	**DM**	**PH**	**FLA**	**CHL**	**TPP**	**LR**	**LD**	**RWC**	**PL**	**CT**	**GPP**	**TGW**	**HI**	**SYP**
Cluster I	74.39	102.80	82.85	35.46	39.65	9.60	0.16	0.13	87.57	23.87	29.92	202.56	21.37	55.59	12.20
Cluster II	74.86	103.25	80.85	27.61	30.54	9.91	0.41	0.77	82.71	22.79	31.17	173.91	19.58	54.38	8.62
Cluster III	77.87	105.00	96.83	43.71	37.83	9.12	0.00	0.000	86.74	25.15	29.59	202.75	21.70	54.56	11.75
Cluster IV	68.00	97.33	69.20	26.520	40.03	9.33	1.00	0.66	85.59	21.13	30.73	108.73	18.66	59.20	6.31
Cluster V	78.66	107.00	93.00	34.29	30.48	8.00	1.00	0.66	84.15	22.41	30.35	157.00	19.73	38.72	7.52
Cluster VI	72.33	95.33	80.90	19.57	32.56	9.66	0.00	0.00	82.33	20.99	30.69	164.00	22.87	39.26	9.37

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References

1. Abarshahr, Mina, Rabiei B, Habibollah, Lahigi S. Assessing genetic diversity of rice varieties under drought stress conditions. Notulae Scientia Biologicae. 2011; 3(1):114-123.
2. Abdel-Ghani AK, Parzies SK, Ceccarelli Grando SS, Geiger HH. Estimation of Quantitative Genetic Parameters for outcrossing related traits in Barley. Crop Science. 2005; 45(1):98-105.
3. Arivoli V, Saravanan K, Prakash M. A study on D2 analysis in rice. International Journal of Plant Sciences Muzaffarnagar. 2009; 4(1):157-160
4. Caldo RA, Sabastian LS, Hernandez JE. Morphology-based genetic diversity analysis of Ancestral lines of rice in Philippine rice cultivars. Philippines Journal of Crop Sciences. 1996; 21(3):86-92.
5. Chandra R, Pradhan SK, Singh S, Bose LK, Singh ON. Multivariate analysis in upland rice genotypes. *World* Journal of Agricultural Science. 2007; 3(3):295-300.
6. Chaturvedi HP, Talukdar P, Sapu C. Genetic divergence in lowland rice (*Oryza sativa* L.) genotypes of Nagaland. Environment and Ecology. 2011; 29(1):27-29.
7. Datt S, Mani SC. Genetic divergence in elite genotypes of basmati rice (*Oryza sativa* L.). Indian J. Genet. Pl. Breed. 2003; 63:73-74.
8. De RN, Rao AVS. Genetic divergence in rice under low land situation. Crop improvement. 1987; 14(2):128-131.
9. Fukai S, Cooper M. Developments of drought resistant cultivars using physio-morphological traits in Rice. Field crops and research. 1995; 40:67-86.
10. Gahalain SS, Deepti B, Anita G. Genetic divergence in rice (*Oryza sativa* L.) cultivars grown in Kumaun Hills. *Vegetos*-. 2010; 23(1):83-88
11. Gomez KA, Gomez AA. Statistical Procedures for Agricultural Research. John Wiley & Sons Inc., Singapore, 2nd Edn, 1984.
12. Hegde SG, Patil CS. Genetic divergence in rainfed rice. Karnataka Journal of Agricultural Sciences. 2000; 13(3):549-553.
13. Hossain M. Sustaining the food security for fragile environments in Asia: achievement, challenges and implications for rice research, In: fragile lives in fragile ecosystems. Proceeding International Rice research Conference, 13-17 FEB 1995, Manila, Philippines. International Rice Research Institute. 1995, 3-23.
14. Iftekharuddaula KM, Akter K, Bashar MK, Islam MR. Genetic parameters and cluster analysis of panicle traits in irrigated rice. Bangladesh Journal of Plant Breeding and Genetics. 2002; 15(1):49-55.
15. IRRI. Standard evaluation system for rice. International Rice Research Institute, Los Banos, Philippines, 1996.
16. IRRI (International Rice Research Institute). Rough rice production by country and geographical region-USDA. Trend in the rice economy. In: world rice statistics, 2009. www. irri.org/science/ricestat
17. Kulsum MU, Hasan M, Begum JH, Billah MM, Rahman H. Genetic diversity of some restorer lines for hybrid rice development. Bangladesh Journal of Agricultural research. 2011; 36(1):21-28.
18. Kumar B, Gupta BB, Singh B. Genetic diversity for morphological and quality traits in rice (Oryza sativa L.). The Bioscan. 2014; 9(4):1759-1762.
19. Manonmani S, Fazlullah Khan AK. studies on combing ability and heterosis in rice. Madras Agric. J. 2003a; 90:228-231.
20. Muller J. Determining leaf surface area by means of linear measurement in wheat and triticale (brief report). Archiv Fuchtungsforsch. 1991; 21:121-123.
21. Naik AR, Chaudhury D, Reddy JN. Genetic Divergence studies in scented rice. Oryza. 2004; 40:79-82.
22. Ramya K, Senthilkumar. Genetic divergence in rice. Crop Improvement. 2008; 35(2):119-121.
23. Rashidi V, Yani SC, Tarinejad AR. Evaluation of drought tolerance in promising lines and cultivars of bread wheat (Triticum aestivum L.). Journal of Food Agriculture and Environment. 2011; 9(1):423-427.
24. Raut KR, Harer PN, Yadav PS. Genetic divergence in rice. Journal of Maharashtra Agricultural Universities. 2009; 34(2):172-174.
25. Roy B, Basu AK, Mandal AB. Genetic diversity in rice genotypes under humid tropics of Andaman based on grain yield and seed characters. India J Agril. Sci. 2002; 72:84-87.

26. Saini HC, Kaicke US. Genetic diversity in Opium. Poppy. India Journal of Genetics, 1987, 292-296.
27. Singh SK, Singh RS, Maurya DM, Verma OP. Genetic divergence among the low land rice cultivars. India Journal of Genetics. 1987; 39:315-322.