Original Research Article

Genetic divergence study in different rice (*Oryza sativa* L.) genotypes under irrigated and drought stress condition

Abstract:

Thirty rice genotypes were evaluated to study genetic divergence under irrigated and drought stress conditions in randomized block design at Bagusala farm, M. S. Swaminathan School of Agriculture, CUTM, Odisha, during summer 2019. The main objective of this experiment was to identify reproductive phase drought tolerant genotypes through study the effect of drought stress on yield, yield attributing and biochemical traits performance of selected genotypes using Mahalanobis D^2 statistics. Set of 30 genotypes were grouped in to five and nine clusters under irrigated and drought situation. Under irrigated conditions cluster-□ was largest cluster with 22 genotypes followed by cluster-□ includes 5 genotypes cluster-□, IV and V each consisted with only one genotype. Under drought condition, genotypes were grouped into nine different clusters, cluster-□ was the largest cluster involving 20 genotypes followed by cluster-□ having 3 genotypes whereas, cluster-□, IV, □, □, □, □ and □ were recorded with single genotype. The maximum intra cluster distances under irrigated conditions were found in cluster- □ (27111.9) followed by cluster-□ (17587.7). Whereas, in case of stress cluster-□ had maximum distance (21110.9) fallowed by cluster-□ (17957.8). Under irrigated maximum inter-cluster distances recorded between cluster-□ and □ (62310.8) followed by cluster-□ and □ (57656.0). In case of stress maximum inter cluster distances recorded between cluster -□ and □ (69865.5) fallowed by cluster- □ and □ (67848.9), cluster-□ and □ (65239.2). Under irrigate conditions highest manifestation towards genetic divergence was exhibited by chlorophyll followed by plant yield, 1000 grain weight, proline, number of spikelets, carbohydrates, grain weight, phenols, panicle length, panicle weight, flavonoids, number of filled grains, plant height and number of tillers. In case of drought stress, maximum percentage contribution towards to the genetic divergence was observed for Proline followed by carbohydrates, plant height, plant yield, grain weight, chlorophyll, number of spikelets, flavonoids, 1000grain weight, filled grains, phenols, panicle weight, panicle length and number of tillers, while other trait like root length did not contribute to the total divergence. The genotypes grouped under cluster □, □, □, □ namely MTU1010, MTU1075, MTU1224, RNR2465 and Manipur black rice exhibited maximum drought tolerance under stress conditions. These genotypes can be used as the donor parents for development of drought tolerant lines in crop improvement programme.

Key words: genetic divergence, inter cluster, intra cluster, crop improvement and drought

Introduction

Rice (Oryza sativa L.) is the most important food crop and a primary food source for more than one third of the world's population. It is a self-pollinated crop belonging to family Poaceae with a genome size of 430 mb. Globally, rice production is more than 470 million metric tons where India is contributing 112.91 million tons production occupying 60.09 million hectares area with the productivity of 2578kg/ha (Agricultural statistics briefly 2018). Due to its wide distribution and adaptability, serves as an excellent model system for studying plant evolutionary with a broad range of morphological, physiological, and developmental diversity found in both *Oryza sativa* and its widely distributed wild ancestors, *Oryza rufipogon* and *Oryza nivara* (Zhao *et al.,* 2010). Rice, being a water dependent crop, it severely affected by drought stress that depresses yield by 15 – 50% depending on the vigour and period of stress (Kumar *et al.,* 2008). Rainfed area includes 13% upland ecosystem, 11% deep water ecosystem and 25% rainfed lowland ecosystem of the total rice area (Fukai and Cooper, 1995). Drought is the second most sever limiting factor (Caldo *et al.,* 1996). In upland rice, depth of rooting, root thickness and root-shoot dry weight ratio are related to drought resistance (Fukai and Cooper, 1995). In general, responses to drought are numerous and interconnected. It is well established that drought stress impairs numerous metabolic and physiological processes in plant which ultimately resulted in reduce plant growth, loss of chlorophyll pigments, accumulation of osmolytes, etc. (Lima *et al.,* 2002; Colom and Vazzana, 2003; Souza *et al*., 2004; Ekmekci *et al.,* 2005; Li *et al.,* 2006; Nayyar and Gupta, 2006; Yang *et al.,* 2006; Efeoglu *et al.,* 2009). Improving drought tolerance and productivity is the most difficult task for cereal breeders because of the diverse strategies adopted by plants at various stages of development among the species and cultivars to cope with water stress. To develop the tolerant cultivars based on genetic divergence studies fallowed with the D^2 technique developed by Mahalanobis had been found to be a potent tool in quantifying the degree of divergence in germplasm. This analysis provides a measurement of relative contribution of different components on diversity both at inter-cluster and intra-cluster level and genotypes. it also helps in the development of superior recombinants (Manonmani and Khan, 2003.Therefore, the present study was undertaken to determine the genetic diversity of thirty rice genotypes under drought condition.

Material and methods

The experiment was carried out by using 30 rice genotypes (table 1) in randomized block design (RBD) with three replications under optimum irrigation and drought stress conditions at the instructional farm of Bagusala. Centurion university of technology and management (CUTM) Odisha Paralakhemundi. Plot size for each genotype was 3m x 2m with spacing of 15 x 15 cm. The recommended agronomic practices were followed up to tillering stage. After tillering stage irrigation was withheld for 10 days in one set of experiment to impose artificial drought. Recorded the data on fifteen morphological characters under both conditions. Such morphological traits include Root length at 35 DAS (cm), Plant height at maturity stage (cm), Number of tillers per plant, Panicle length (cm), Panicle weight (g), Number of spikelets per panicle, filled grains per panicle, grain weight per panicle (g), 1000 grain weight (g) and Yield per plant (g). Various chemical analysis was also conducted for leaf sample of 90days old were used for chlorophyll (Aronon 1949), phenols (Mlick and Singh, 1980), flavonoids (Zhishen *et al.* (1999) and proline (Bates *et al.*, 1973) estimation. While harvested rice grains were used for estimation of carbohydrate content from both well irrigated and drought field by fallowing Anthron method (Hedge et al., 1962). The recorded data of individual plant basis was subjected to the version 9.2. by using software window-stat.

Table :1 List of genotypes

SI. NO	Genotype	Source of Genotype
1	BPT2231	Srikakulam (A.P)
2	BPT3291	Local area of Kotturu (A.P)
3	MTU7029	Maruteru Rice Research Station (A.P)
4	MTU1010	West Godavari (A.P)
5	RNR2465	Parlakhemundi (OR)
6	MTU1224	Maruteru Rice Research Station (A.P)
7	PLA1100	Srikakulam (A.P)
8	CR DHAN	Srikakulam (A.P)
9	SAMPATH	Parlakhemundi (OR)
10	MTU1061	Maruteru Rice Research Station (A.P)
11	MTU3626	Local area of Kotturu (A.P)
12	POOJA	Local area of Kotturu (A.P)
13	MTU1075	Local area of west Godavari (A.P)
14	RGL2537	Srikakulam (A.P)
15	MTU2716	Maruteru Rice Research Station (A.P)
16	SARALA	Parlakhemundi (OR)
17	BPT5204	Srikakulam (A.P)
18	MTU1064	West Godavari (A.P)
19	MTU4001	Maruteru Rice Research Station (A.P)
20	MTU1156	Maruteru Rice Research Station (A.P)
21	MTU1121	West Godavari (A.P)
22	MTU1001	Maruteru Rice Research Station (A.P)
23	MTU1201	Maruteru Rice Research Station (A.P)
24	TELANGANA SANNALU	Hyderabad (Telangana)
25	RJL	Srikakulam (A.P)
26	KUDRUTH-5	Odisha
27	MANIPURIBLACK RICE	Manipur (Imphal)
28	BASMATI	Srikakulam (A.P)
29	SMALL-CR	Parlakhemundi (OR)
30	BALIMA	Odisha

Results

The analysis of variance bare significant differences among the genotypes for all the attributes indicating presence of variability between the genotypes for the characters studied. The D^2 values between genotypes were calculated as sum of squares of the differences between the mean values of all the characters studied and were used for clustering of the genotypes. The Tocher method (Rao, 1952) used to grouped the 30 genotypes into five and nine clusters under control and drought situation respectively. The clustering pattern presented in table (2,3)

Table 2: Clustering patterns of thirty genotypes of rice on basis of D^2 statistics under control condition.

Cluster Number	**Number of Genotypes**	**Genotypes**
□	22	BPT3291, MTU 3626, MTU 7029, RGL2537, CR-Dhan1009, MTU1064, MTU1010, Basmati, MTU1001, BPT 2231, Sarala, PLA1100, RJL, Sampath, MTU1061, MTU1121, MTU1201, Kudruth-5, Telangana, Balima, MTU2716, BPT5204
□	5	MTU1156, Smaller CR, MTU4001, MTU1224, RNR2465
□	1	MTU1075
□	1	Manipur black rice
□	1	Pooja

Table 3: Clustering pattern of thirty genotypes of rice on basis of D^2 statistics under stress condition.

Cluster Number	**Number of Genotypes**	**Genotypes**
□	20	CR-Dhan1009, MTU1061, MTU1001 MTU1064, Basmati, MTU1010, Sampth, MTU1121, BPT2231, Sarala, RJL, MTU3626, BPT3291, PLA1100, MTU1201, Telangana, Pooja, Kudruth-5, Balima and Small CR
□	3	MTU4001, MTU1156, BPT5204
□	1	MTU1224
□	1	MTU7029
□	1	Manipur Black rice
□	1	RNR 2465
□	1	RGL 2537
□	1	MTU1075
□	1	MTU2716

Cluster classification under control and drought

The genetic divergence results reviled by from the genotypes in to various clusters, under irrigated conditions cluster-□ was largest cluster with 22 genotypes (BPT3291, MTU 3626, MTU 7029, RGL2537, CR-Dhan1009, MTU1064, MTU1010, Basmati, MTU1001, BPT 2231, Sarala, PLA1100, RJL, Sampath, MTU1061, MTU1121, MTU1201, Kudruth-5, Telangana, Balima, MTU2716 and BPT5204 followed by cluster-□ includes 5 genotypes (MTU1156, Smaller CR, MTU4001, MTU1224, and RNR2465). Cluster-□ (MTU1075), IV (Manipur black rice) and V (Pooja) each consisted with only one genotype.

Under drought condition, genotypes were grouped into nine different clusters, cluster-□ was the largest cluster involving 20 genotypes (CR-Dhan1009, MTU1061, MTU1001 MTU1064, Basmati, MTU1010, Sampath, MTU1121, BPT2231, Sarala, RJL, MTU3626, BPT3291, PLA1100, MTU1201, Telangana, Pooja, Kudruth-5, Balima and Small CR) followed by cluster-□ having 3 genotypes (MTU4001, MTU1156 and BPT5204). Whereas, cluster-□ (MTU1224), IV (MTU7029), □ (Manipur Black rice) □ (RNR 2465), □ (RGL 2537), □(MTU1075) and □ (MTU2716) were recorded with single genotype.

Mean intra and inter cluster distance under control and drought

The maximum intra cluster distances under irrigated conditions were found in cluster- □ (27111.9) followed by cluster-□ (17587.7). Whereas, in case of stress cluster -□ had maximum distance (21110.9) fallowed by cluster-□ (17957.8). The mean intra and inter cluster distance under control and drought were presented in Table (4,5)

Maximum inter-cluster distances recorded between cluster-□ and □ (62310.8) followed by cluster-□ and □ (57656.0). While, lowest inter cluster distance observed between cluster-□ and □ (29847.8) under normal conditions. In case of stress maximum inter cluster distances recorded between cluster -□ and □ (69865.5) fallowed by cluster- □ and □ (67848.9), cluster-□ and □ (65239.2) whereas, lowest distance was found between the cluster -□ and □II (14737.9).

Table 4: Average intra (diagonal) and inter cluster (off diagonal) distance (D^2) of five clusters from thirty rice genotypes under control condition.

Cluster Distances	**Cluster-□**	**Cluster-□**	**Cluster-□**	**Cluster-□**	**Cluster-□**
Cluster-□	17587.7 (**132.6**)	36636.6 (191.4)	29847.8 (172.7)	31705.8 (178.0)	41134.4 (202.8)
Cluster -□		27111.9 (**164.6**)	38474.6 (196.1)	50382 (224.4)	62310.8 (249.6)
Cluster-□			0 (00.0)	47309.6 (217.5)	36698.7 (191.5)
Cluster-□				0 (00.0)	57656 (240.1)
Cluster-□					0 (00.0)

Table 5: Average intra (diagonal) and inter cluster (off diagonal) distance (D^2) of nine clusters from thirty rice genotypes under stress condition.

Cluster	□	□	□	□	□	□	□	□	□
□	17957.8 (**134.0**)	36374 (190.7)	26858.4 (163.8)	26448.8 (162.6)	27566.3 (166.0)	38487.8 (196.1)	32078.8 (179.1)	31675.2 (177.9)	36131.8 (190.0)
□		21110.9 (**145.2**)	51446.5 (226.8)	39272.3 (198.1)	44752 (211.5)	49057.5 (221.4)	69865.5 (264.3)	60197.3 (245.3)	65239.2 (255.4)

□			0 (00.0)	20999.8 (144.9)	27214.9 (164.9)	27871.2 (166.9)	42407.3 (205.9)	32806.1 (181.1)	35523.8 (188.4)
□				0 (00.0)	43773.2 (209.2)	33405 (182.7)	32361.8 (179.8)	34043.7 (184.5)	42389.3 (205.8)
□					0 (00.0)	20581.6 (143.4)	42857.1 (207.0)	45142.7 (121.4)	38480 (196.1)
□						0 (00.0)	43246.7 (207.95)	58882.3 (242.6)	29996.8 (173.1)
□							0 (00.0)	24836 (157.5)	35406.7 (188.1)
□								0 (00.0)	67848.9 (260.4)
□									0 (00.0)

Nearest and closest clusters distance under irrigated and drought

Under irrigated condition, cluster-□ was nearest to cluster - □ (172.7) and distant from cluster-□ (202.8). Cluster-□ exhibited close propinquity with cluster- □ (191.4) and far away from cluster- □ (249.6). Similarly, Cluster-□ was in proximity with cluster- □ (172.7)and distant from cluster -□ (127.5). Cluster-□ was nearest to cluster- □ (178.0) and far away from cluster- □ (240.1). Cluster- □ was very closer to cluster-□ (191.5) and distant from cluster- □ (249.6). Under stress condition, the cluster-□ was nearest to cluster- □ (162.6) and far away from cluster - □ (196.1). Cluster-□ exhibited close propinquity with cluster- □ (190.7) and far away from cluster- □ (264.3). Cluster-□ was closed to cluster- □ (144.9)and distant from cluster- □ (205.9). Cluster-□ was closed to cluster- □ (144.9) and distant from cluster- □ (205.8). Cluster-□ was nearest to cluster - □ (121.4) and far away from cluster-□ (209.2). Cluster-□ was in proximity with cluster-□ (143.4) and distant from cluster -□ (242.6). Cluster-□ was nearest to cluster-□ (157.5) and far away from cluster - □ (264.3). Cluster- □ near to cluster-□ (121.4) and far away from cluster -□ (260.4). Cluster-□ exhibited close propinquity with cluster- □ (173.1) and far away from cluster-□ (260.4) table (6,7)

Table 6: The nearest and farthest clusters from each cluster based on D values in rice genotypes under control conditions.

Cluster No.	Nearest cluster with D values	Farthest cluster with D value
□	□ (172.7)	□ (202.8)
□	□ (196.1)	□ (249.6)
□	□ (191.5)	□ (121.5)
□	□ (178.0)	□ (240.1)
□	□ (191.5)	□ (249.6)

Table 7: The nearest and farthest clusters from each cluster based on D values in rice genotypes under stress conditions.

Cluster No.	Nearest cluster with D values	Farthest cluster with D value
□	□ (162.6)	□ (190.9)
□	□ (198.1)	□ (264.3)

□	□ (144.9)	□ (205.9)
□	□ (179.8)	□ (209.2)
□	□ (143.4)	□ (196.1)
□	□ (173.1)	□ (242.6)
□	□ (157.5)	□ (188.1)
□	□ (121.4)	□ (260.4)
□	□ (173.1)	□ (260.4)

Contribution of different traits towards genetic divergence under control and drought condition

The percent contribution of each character towards divergence under irrigated and drought situation were presented in table (8,9)

Under irrigate conditions highest manifestation towards genetic divergence was exhibited by chlorophyll (16.09%) followed by plant yield (15.63%), 1000 grain weight (11.03%), proline (11.03%), number of spikelets (7.59%), carbohydrates (7.36%), grain weight (5.52%), phenols (5.29%), panicle length (5.06%), panicle weight (4.60%), flavonoids (3.68%), number of filled grains (3.22%), plant height (2.30%) and number of tillers (1.61%). The trait root length did not show any contribution to the total divergence. Under drought stress, maximum percentage contribution towards to the genetic divergence was observed for Proline (17.01%) followed by carbohydrates (11.03%), plant height (9.98%), plant yield (9.20%), grain weight (9.20%), chlorophyll (8.97%), number of spikelets (7.13%), flavonoids (6.67%), 1000grain weight (5.06%), filled grains (4.37%), phenols (3.91%), panicle weight (3.91%), panicle length (2.07%) and number of tillers (1.61%), while other trait like root length did not contribute to the total divergence.

Table 8: Contribution of individual characters towards genetic divergence undercontrol conditions.

Source	**Times Ranked 1st**	**Contribution %**
Root length (cm)	0	0.00%
Plant height (cm)	10	2.30%
Number of tillers per plant	7	1.61%
Panicle length (cm)	22	5.06%
Panicle weight (g)	20	4.60%
No of spikelet per panicle	33	7.59%
Filled grain per panicle	14	3.22%
Grain wt per panicle (g)	24	5.52%
1000 grain wt. (g)	48	11.03%
Yield per plants (g)	68	15.63%
Flavonoids (mg/g)	16	3.68%
Phenols (mg/g)	23	5.29%
Proline (µ moles/g)	48	11.03%
Carbohydrates (mg/g)	32	7.36%
Chlorophyll (mg/g tissue)	70	16.09%

Table 9: Contribution of individual characters towards genetic divergence under stress conditions.

Source	Times Ranked 1st	Contribution %
Root length (cm)	0	0.00%
Plant height (cm)	43	9.89%
Number of tillers/ plants	7	1.61%
Panicle length (cm)	9	2.07%
Panicle weight (g)	17	3.91%
No of spikelet per panicle	31	7.13%
Filled grain per panicle	19	4.37%
Grain wt per panicle (g)	40	9.20%
1000 grain wt. (g)	22	5.06%
Yield per plants (g)	40	9.20%
Flavanoides (mg/g)	29	6.67%
Phenols (mg/g)	17	3.91%
Proline (µ moles/g)	74	17.01%
Carbohydrates (mg/g)	48	11.03%
Chlorophyll (mg/g tissue)	39	8.97%

Mean performances of characters in clusters

Under control, the genotypes present in cluster –II resulted with maximum mean value of root length (25.43 cm) whereas, its minimum value observed in cluster- □ (22.17 cm). The mean performance of plant height found maximum in genotypes of cluster- I□ (120 cm) and minimum was noticed in cluster-V (85.55 cm). The cluster-□ includes the greater number of tillers (14.33) whereas, genotypes of cluster -□ noticed with a smaller number of tillers (9.47). Genotypes grouped in cluster-□ exhibited maximum panicle length (24.67cm) while it was minimum in cluster -□ (18.13 cm). Panicle weight was found maximum in cluster-□ (5.27g) and minimum in cluster -□ (3.02 g).

Maximum number of spikelets per panicle (160.33) were recorded in the genotypes of cluster -□ while, it was minimum in cluster-□ (115.0) genotypes grouped in cluster -□ noticed with maximum number of filled grains (144.8) whereas, genotypes confined to cluster -□ had a smaller number of filled grain (109.23) also grain weight per panicle were found maximum in cluster -□ (5.08) and less weight in cluster -□ (2.83), 1000 grain weight were more in cluster -□ (33.33) and less in cluster -□ (22.71), pant yield were found high in cluster -□ (24.13) and low in cluster -□ (11.18).

Genotypes grouped in Cluster-□ noticed maximum number of flavonoids (18.78), minimum was found in cluster-□ (12.05), the amount of phenol compounds high in cluster- □ (18.8) and low in cluster-□ (15.61) whereas, the proline content was found high in cluster □ (64.33), low proline content was found in genotypes confined to cluster -II (46.13). Maximum carbohydrates were noticed in cluster-□ (16.33) while, its lowest value recorded for genotypes grouped under cluster-V (9.05) and chlorophyll content in cluster -IV was found to be high (12.55) but low in cluster-□ (8.69).

Under drought, maximum mean values for traits root length were found for cluster-□ (27.53) while, minimum in cluster -□ (19.2), maximum plant height was found for genotypes present in cluster -□ (111.67) and minimum in cluster-□ (77.67), also maximum number of tillers was found in cluster -□ (11.67) whereas, genotypes grouped in cluster □ (5.33) appeared with low number of tillers. Maximum panicle lengths were found in cluster - □ (24.67) while minimum lengths in cluster -VII (16.33), maximum panicle weight was found in cluster -□ (4.41) and minimum in genotypes confined to cluster-□ (2.06).

Cluster mean for number of spikelets per panicle was highest in cluster -□ (141.15) and lowest in cluster -□ (113.44). Number of filled grains were found maximum for the genotypes in cluster -□ (126.67) and minimum were recorded in cluster -□ (99.27), also grain weight per panicle were found maximum in cluster-□ (4.21) and lowest in cluster -□ (1.93), 1000 grain weight were found maximum in cluster -□ (32.33) and minimum in cluster -□ (15.07). Maximum plant yield was found in genotypes grouped in cluster -□ (22.64) and it was minimum in cluster-□ (9.87).

Genotypes grouped under Cluster -V was found with maximum flavonoids (26.80) and it was found minimum in cluster- □ (13.3). The amount of phenol compounds recorded high in cluster-□ (31.73) and low in cluster-□ (20.9) whereas the highest value of proline content was noticed in cluster -□ (144.68) and its lowest value was found in genotypes confined to cluster - □ (72.63). Maximum amount of carbohydrates was noticed in cluster-□ (16.8) while, it was lowest for genotypes grouped under cluster-□ (7.56). The chlorophyll contentin cluster -□ was found to be highest (8.55) and lowest in cluster-□ (3.21). Table (10,11)

Table 10: Cluster means performances of fifteen characters of thirty rice genotypes under control conditions.

Characters	**Cluster □**	**Cluster □**	**Cluster □**	**Cluster □**	**Cluster □**
Root length (cm)	22.17	25.43	22.23	24.53	24.07
Plant height (cm)	86.61	90.41	88.73	120	83.55
Number of tillers/ plants	9.47	9.87	14.33	12.67	13.33
Panicle length (cm)	19.43	22	24.67	24.27	18.13
Panicle weight (g)	3.02	3.9	4.46	5.27	3.14
No of spikelet/ panicle	123.66	134.67	150	160.33	115
Filled grain/panicle	112.97	127.35	140.27	144.8	109.23
Grain wt. /panicle (g)	2.83	3.67	4.21	5.08	2.91
1000 grain wt. (g)	22.71	26.58	28.2	33.33	24.33

Yield/ plants (g)	11.18	16.5	24.13	22.15	17.38
Flavanoides (mg/g)	12.65	14.67	18.63	18.78	12.05
Phenols (mg/g)	15.73	15.61	18.7	18.8	17.87
Proline (µ moles/g)	49.57	46.13	62.33	64.33	55.27
Carbohydrates (mg/g)	9.74	12.84	12.57	16.33	9.05
Chlorophyll (mg/g tissue)	8.69	9.47	12.04	12.55	10.65

Table 11: Clusters mean performances of fifteen characters of thirty rice genotypes under stress conditions.

Characters	□	□	□	□	□	□	□	□	□
Root length (cm)	22.07	23.44	20.27	20.93	22.73	22.17	25.5	27.53	19.27
Plant height (cm)	85.56	87.55	90.09	77.67	111.67	100.25	86.58	91.12	84.21
Number of tillers/ plants	7.26	6	8	5.67	9.67	9	7.7	11.67	5.33
Panicle length (cm)	17.68	16.89	21.67	17.63	24.67	22	16.33	24.17	16.9
Panicle weight (g)	2.76	2.76	3.42	2.06	4.41	4.33	2.74	3.79	3.25
No of spikelet/ panicle	114.38	113.44	138	129.33	141.15	139.33	122.33	135.6	137.78
Filled grain/panicle	99.27	100.42	125	106.2	120.07	126.67	100.47	121	120.3
Grain wt /panicle (g)	2.56	2.57	3.06	1.93	4.21	4.09	2.55	3.54	3.08
1000 grain wt. (g)	22.35	22.33	21.8	15.07	32.33	29.67	22.13	26.5	22.9
Yield/ plants (g)	11.36	10.04	15.92	9.87	19.36	20.4	11.83	22.64	10.23
Flavanoides (mg/g)	17.11	17.69	25.67	13.3	26.8	26.23	13.78	20.5	18.9
Phenols (mg/g)	24.11	25.55	31	20.9	31	27.5	21.11	31.73	21.1
Proline (µ moles/g)	97.2	104.14	107.09	85	144.68	105.27	72.63	101.84	94.75
Carbohydrates (mg/g)	9.08	11.09	13.47	7.57	16.8	15.37	8.3	10.23	8.5
Chlorophyll (mg/g tissue)	5.13	3.21	8.22	5.25	8.54	8.55	3.47	7.47	4.24

Discussion

The genetic divergence between the genotypes was estimated by using Mahalanobis D2 statistical analysis. In present investigation 30 rice genotypes were grouped in to five clusters under control and nine clusters under drought stress conditions suggesting that there was a considerable amount of diversity existed in experimental material used under study. 84 Distances within clusters represent the genetic diversity among each cluster. The inter cluster distance were found minimum between cluster □ and □ under control and in case of drought between □ and VIII indicating close relationship and similarity for most of the traits with the genotypes belongs to this cluster. Thus, selection of these genotypes will be resulted with less divergent genotypes as the out of these crosses. The maximum inter cluster distance was found between cluster □ and □ under control and between cluster in □ and □ case of drought stress condition. This represents that there was a wide genetic diversity between the genotypes of these clusters. Selection of parents from these diverse clusters for hybridization programme would help in achieving novel recombinants. In order to select the genetically diverse genotypes for hybridization, the genotypes should be screened with important traits having high percent of contribution towards genetic divergence. The traits with high contribution towards genetic divergence under control conditions include chlorophyll, plant yield and 1000 grain weight. In case of drought stress proline, carbohydrates, and plant yield were resulted. Present findings are also like the findings of Garg et al., (2017), Pervin et al., (2017) and Gaurav et al., (2017). The highest mean values for most of the yield attributing and biochemical traits under control were found in cluster- IV and in case of stress it was noticed in cluster-V. To obtain a best diverge genotype it always depends on theselection of superior parents with high mean value within the cluster will be a rewarding in getting diverge genotypes with best performing traits. The traits with maximum contribution towards genetic divergence and high cluster mean with maximum inter cluster distance along with the genotypes present in clusters can be selected for hybridization programme. The confirmatory results were like findings of Perween et al., (2020), Garget al., (2017) and Pervinet al., (2017).

Conclusion

The study concluded that genotypes MTU1010, MTU1075, MTU1224, RNR2465 and Manipur black rice exhibited maximum drought tolerance under stress conditions. Might be useful as donors in future breeding programmers for development of drought tolerant varieties.

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