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Genetic Divergence Study in Rice (*Oryza sativa* L.) Genotypes under Drought Condition

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ABSTRACT

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A field screening of thirty four drought tolerant rice genotypes was conducted during *Kharif* 2017 and *Kharif* 2018 with the objective to identify different genotypes under drought stress condition. Significant variation was observed among genotypes for all studied traits including leaf rolling, leaf drying and relative water content. The tolerant lines maintained high leaf water status, membrane stability and plant biomass under reproductive stage drought condition. All thirty four genotypes were distributed in nine clusters. Out of thirty four genotypes seventeen were placed in cluster I, eight in cluster II, three genotypes in cluster III while in rest of the clusters are mono genotype. The findings of this study indicate that the cluster III, IV, VI, VII and IX showed the higher distance under drought stress condition.

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). 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 self sufficiency 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 cultivation 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). Drought is the second most severe 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). Genetic divergence among the genotypes plays an important role in selection of parents having wider variability for different traits (Naik *et al.*, 2004) and it also helps in the development of superior recombinants (Manonmani and Khan, 2003b). Therefore, the present study was undertaken to determine the genetic diversity of thirty four rice genotypes under drought condition.

Materials and Methods

Field experiments were carried out during *Kharif* 2017 and *Kharif* 2018 at Research Farm of Rajendra Central 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. Thirty four rice genotypes including check variety Sahbhagi dhan were evaluated for different morpho-physiological traits under drought stress condition. The rice genotypes used under present study were collected from RPCAU, PUSA (Bihar) and IRRI. Thirty four rice genotypes were grown under drought condition opting the direct seeded method under rainout shelter. The experiment was laid out in Completely Randomized Block Design with three replications. In each replication each genotype was grown in a plot of 5 rows of 1.5 meter length each with a spacing of 20 cm between rows under direct seeded condition using the fertilizer @ 80:40:40 kg (N: P: K) per ha. Nitrogen was

applied on three stages (1/3rd each at basal, maximum tillering and panicle initiation stage), while the P₂O₅ and K₂O were applied as a basal application. 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 twenty one characters viz, Days to fifty per cent flowering, days to physiological maturity, plant height, number of tillers per plant, panicle length, panicle number per plant, number of grains per panicle, spikelet fertility, 1000 grain weight, leaf rolling at vegetative stage, leaf drying at vegetative stage, canopy temperature, chlorophyll content, relative water content, root length, root volume, fresh root weight, dry root weight, grain yield per plant, straw yield per plant and harvest index.

The drought scores leaf rolling and leaf drying observations were taken as per SES method, 1 to 9 scales (IRRI, 1996). 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) / (turgid weight- Oven dry weight) x 100]. 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) under full sunshine conditions. Yield attributes i.e. seed yield, straw yield, harvest index and dry matter was measured at maturity.

Data Analysis

The morpho-physiological data were analyzed by appropriate statistical analysis (Gomez and Gomez, 1984) using WinStat 9.3 programme.

Results and Discussion

Analysis of variance (Table 1) revealed that significant differences among the genotypes for all the studied characters. The analysis from distance matrix gave nonhierarchical clustering among thirty four rice genotypes. All genotypes were grouped into nine clusters (Table 2). Cluster I had seventeen genotypes viz., IR 83140-B-11-B, IR 93856-10-2-3-2, IR10M243, IR 95793-5-2-2-3, IR 93827-29-1-1-2, IR 95785-15-2-1-2, IR14D197, Rajendra Bhagwati, IR 95785-31-2-1-2, GSR IR1-DQ62-D6-D1, Abhishek, IR 93849-22-3-1-1, IR 95817-14-1-1-2, GSR IR1-DQ150-R5-Y1, IR 83142-B-19-B, IR 10G104 and IR 89889-34-2-1-1. Cluster I had maximum number of genotypes (17) followed by cluster II (8), cluster III (3) and one each in rest of the clusters. The thirty four rice genotypes taken for genetic divergence analysis differed significantly with regard to the characters studied and displayed marked divergence and grouped into nine clusters following Tocher's method (table 2). The clustering pattern showed that genotypes of same geographical areas were grouped in different clusters indicating that there was no formal relationship between geographical diversity and genetic diversity. The highest contribution in the manifestation of genetic divergence was exhibited by grain yield per plant (35.12) followed by straw yield per plant (24.6), fresh root weight (16.22), root volume (4.28) and panicle length (3.74) under drought condition (table 3). De and Rao (1987) and Singh *et al.*, (1987) also revealed that geographical diversity is not necessarily related to genetic diversity. Intra and inter cluster distances are presented in (Table 4).

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 distant groups. Maximum intra cluster distance was obtained in cluster II followed by cluster I and cluster III and rest clusters did not impress intra cluster distance. These results are in agreement with those reported by Iftekharruddaula *et al.*, (2002) and Kulsum *et al.*, (2011) in rice. Maximum inter cluster distance was recorded between cluster III and Cluster IX followed by cluster V and Cluster IX, cluster VII and cluster IX, cluster IV and cluster IX cluster VII and IX as well as cluster I and Cluster IX and cluster III and cluster VIII while minimum inter cluster distance was recorded between cluster IV and cluster VI followed by cluster V, cluster VII and cluster I and cluster V suggesting that the genotypes belongs to cluster III and IX are more divergent among themselves. By using these genotypes heterotic recombinant may be developed. The results reported by Roy *et al.*, (2002) and Naik *et al.*, (2004) were agreement with these findings. The D^2 value ranged from 0.32 to 2.49 under drought stress condition indicated a high degree of genetic diversity among the genotypes. Chaturvedi *et al.*, (2011) 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. Cluster mean values for 21 characters are presented in Table 5. Difference in cluster means existed for almost all the characters studied. Among 21 characters, cluster III was maximum mean value for number of tillers per plant, panicle number per plant, number of grains per panicle, 1000 grain weight, grain yield per plant and straw yield per plant while minimum mean value for leaf rolling at vegetative stage and leaf drying at vegetative stage. Cluster IV was found maximum mean value for spikelet fertility, chlorophyll content

and minimum mean value for canopy temperature. Cluster VI was rich for plant height may be selected as a donor for dwarfness, maximum mean value for panicle length and relative water content. Cluster VII was suitable for early days to fifty percent flowering and physiological maturity and maximum for harvest index. Cluster IX was

suitable for maximum mean value for root length, root volume, fresh root weight and dry root weight. For the purpose of earliness, cluster VII is suitable genotypes to have the heterotic recombinant for yield and yield attributing traits under drought stress condition. Parents may be selected from cluster III and cluster IX.

Table.1 Analysis of variance for twenty one morpho-physiological traits in rice genotype under drought stress condition

S. No.	Characters	Mean sum of squares		
		Replication (d.f.=2)	Treatments (d.f.=33)	Error
1	DFF	16.51	19.68**	2.92
2	DPM	10.16	23.55**	5.49
3	PH	5.18	120.14**	40.72
4	NOTP ⁻¹	48.73	23.21**	6.18
5	PL	27.85	15.63**	2.31
6	PNP ⁻¹	43.42	7.81*	4.45
7	NOGP ⁻¹	187.71	3011.86**	390.24
8	SF	228.53	125.90**	34.02
9	TGWT	2.11	11.86**	2.21
10	LR	0.31	13.96**	0.47
11	LD	0.31	11.92**	0.45
12	CT	3.30	5.35**	1.03
13	CC	24.11	8.92 *	4.63
14	RWC	1475.62	198.17**	82.96
15	RL	7.11	5.12**	1.33
16	RV	2.51	652.74**	22.65
17	FRW	31.68	1238.35**	22.36
18	DRW	16.55	586.66**	9.70
19	GYP ⁻¹	50.58	809.78**	36.02
20	SYP ⁻¹	23.39	1157.60*	70.15
21	HI	6.18	12.75**	6.44
** Significance at 1 % level				
* Significance at 5 % level				

Table.2 Clustering pattern of 34 drought tolerant genotypes of rice on the basis of D² statistic

Cluster No.	No. of Genotypes within cluster	Genotypes in cluster
I	17	IR 83140-B-11-B, IR 93856-10-2-3-2, IR10M243, IR 95793-5-2-2-3, IR 93827-29-1-1-2, IR 95785-15-2-1-2, IR14D197, Rajendra Bhagwati, IR 95785-31-2-1-2, GSR IR1-DQ62-D6-D1, Abhishek, IR 93849-22-3-1-1, IR 95817-14-1-1-2, GSR IR1-DQ150-R5-Y1, IR 83142-B-19-B, IR 10G104, IR 89889-34-2-1-1
II	8	IR 10A114, IRRI-123, IR 95817-5-1-1-2, Rajendra Nilam, IR 93827-29-2-1-3, GSR IR1-DQ187-Y3-D1, IR 93810-17-1-2-3, GSR IR1-DQ125-L2-D2
III	3	IR 91648-B-89-B-81-B, IR 95781-15-1-1-4, IR 95122:13-B-7-4-7-3
IV	1	IR 96279-33-3-1-2
V	1	IR 95795-53-1-1-2
VI	1	IR 91648-B-89-B-12-1-B
VII	1	Sahbhagi Dhan (C)
VIII	1	IR14D180
IX	1	GSR IR1-DQ139-R1-L2

Table.3 Percent Contribution of twenty one morpho-physiological traits towards genetic divergence

S. No.	Source	Times Ranked 1st	Contribution %
1	Days to fifty percent flowering	17	3.03
2	DPM Days to physiological maturity	8	1.43
3	Plant height (cm)	2	0.36
4	Number of tillers plant ⁻¹	0	0
5	Panicle length (cm)	21	3.74
6	Number of panicle plant ⁻¹	2	0.36
7	Number of grains panicle ⁻¹	6	1.07
8	Spikelet fertility (%)	10	1.78
9	1000 grain weight (g)	9	1.6
10	Leaf rolling (0-9 Scale)	3	0.53
11	Leaf drying (1-9 Scale)	3	0.53
12	Chlorophyll content	14	2.5
13	Canopy temperature	1	0.18
14	Relative water content (%)	3	0.53
15	Root length (cm)	6	1.07
16	Root volume (cm ³)	24	4.28
17	Root fresh wt. (g.)	91	16.22
18	Dry fresh wt. (g.)	5	0.89
19	GYP ⁻¹ Grain yield plant ⁻¹ (g)	197	35.12
20	Straw yield plant ⁻¹ (g)	138	24.60
21	Harvest-index (%)	1	0.18

Table.4 Mean intra and inter cluster distance (D^2) among nine clusters in rice genotypes under drought stress condition

Inter & Intra Cluster Distances : Tocher Method									
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	0.28	0.76	0.8	0.45	0.39	0.51	0.45	0.61	1.41
Cluster II		0.39	1.5	1.17	1.21	0.76	1.15	0.5	0.51
Cluster III			0.24	1.3	0.81	1.39	1.11	1.41	2.49
Cluster IV				0	0.52	0.32	0.47	0.88	1.82
Cluster V					0	0.65	0.37	0.76	2.16
Cluster VI						0	0.6	0.65	1.28
Cluster VII							0	0.94	1.84
Cluster VIII								0	0.72
Cluster IX									0

Table.5 Cluster mean values of nine clusters for twenty one morpho-physiological traits in rice genotypes under drought stress condition

Cluster Means :Tocher Method											
	DFP	DPM	PH	NOTP ⁻¹	PL	PNP ⁻¹	NOGP ⁻¹	SF	TGWT	LR	LD
Cluster I	94.68	121.51	111.31	21.02	29.38	13.32	150.2	19.72	23.69	2.89	3.15
Cluster II	95.25	121.78	111.66	21.36	29.52	13.58	153.23	19.97	23.70	2.79	3.04
Cluster III	95.82	122.78	112.99	23.53	30.35	14.66	179.3	19.77	25.16	1.13	1.51
Cluster IV	93.71	120.58	111.20	22.35	30.15	13.71	131.48	25.01	23.84	4.05	4.11
Cluster V	94.12	121.08	112.35	22.41	30.31	12.77	141.75	18.13	23.14	2.93	3.22
Cluster VI	94.38	121.33	109.15	21.86	31.93	13.69	149.93	19.29	23.13	4.04	4.19
Cluster VII	92.00	117.42	113.56	21.46	29.62	13.17	154.78	14.3	24.37	3.30	3.76
Cluster VIII	95.33	121.79	113.06	22.95	29.37	13.37	152.83	23.58	23.09	3.33	3.61
Cluster IX	94.33	121.63	111.85	20.11	28.49	13.13	144.52	18.44	23.98	3.15	3.38

Cluster Means :Tocher Method										
	CT	CC	RWC	RL	RV	FRW	DRW	GYP ⁻¹	SYP ⁻¹	HI
Cluster I	35.18	42.99	50.96	10.31	17.88	22.74	13.39	40.18	56.34	41.2
Cluster II	35.32	43.2	51.44	10.3	24.58	35.78	22.63	39.78	56.94	41.32
Cluster III	35.47	43.21	54.45	9.55	16.86	18.99	11.33	53.97	76.81	41.5
Cluster IV	34.54	44.5	54.69	10.85	15.86	19.7	11.2	36.54	54.4	41.19
Cluster V	36.4	42.29	51.35	9.69	15.4	18.49	10.32	41.98	55.9	40.21
Cluster VI	34.56	43.01	58.01	9.74	18.92	26.11	16.02	34.62	54.24	40.56
Cluster VII	35.35	42.58	50.79	10.27	14.43	20.46	11.91	40.91	56.16	41.87
Cluster VIII	35.63	41.9	50.02	10.49	29.95	30.2	18.13	40.29	54.67	40.64
Cluster IX	35.31	43.04	55.73	11.05	33.18	41.55	25.93	36.2	58.27	41.19

Selection of genotypes based on cluster mean for the better exploitation of genetic potential also reported by Abarshahr, et al.(2011), Chaturvedi, *et al.*, (2011), Raut *et al.*, (2009), Ramya and Senthil kumar (2008), Arivoli et. al.(2009), Gahalain *et al.*, (2010). Total divergence estimation based on D² distances were also carried out by Hegde and patil (2000). 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 5 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, 34 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 Sahbhagi Dhan grouped in cluster VII exhibited earliness in days to fifty percent flowering and days to physiological maturity based on cluster mean (lowest) and harvest index with highest cluster mean showed the significantly superior per se performance. The genotypes namely IR 91648-B-89-B-12-1-B was selected from cluster VI for plant height for dwarfness based on cluster mean and superior per se performance and also selected for high cluster mean for panicle length and relative water content. Cluster IV having genotype IR 96279-33-3-1-2 was selected for maintaining lower canopy temperature with least cluster mean and per se performance and

also having highest cluster mean for spikelet fertility and chlorophyll content. Genotypes IR 91648-B-89-B-81-B, IR 95781-15-1-1-4 and IR 95122:13-B-7-4-7-3 from cluster III were selected for highest number of tillers per plant, panicle number per plant, number of grain per panicle, 1000 grain weight, grain yield per plant, straw yield per plant based on highest cluster mean with superior per se performance and also selected for minimum leaf rolling at vegetative stage and leaf drying at vegetative stage. Cluster IX having genotype GSR IR1-DQ139-R1-L2 was selected for root length, root volume, fresh root weight and dry root weight and superior per se performance. Similar results were reported by Rashidi *et al.*, (2011). 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, VI, VII and IX showed the higher distance under drought 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.

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