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## Differential stage specific diversity assessment under drought stress

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#### Abstract

A field experiment consisting of 25 rice genotypes was laid out in a Randomized Block Design (RBD) with two replications in two sets at Tillering and Flowering stages during kharif, 2016. The data were recorded on fourteen characters namely, days to flowering, days to maturity, plant height, panicle length, spikelet fertility, number of tillers per plant, 1000-grain weight, relative water content in flag leaf, recovery percent after stress, flag leaf area, chlorophyll content, canopy temperature, harvest index grain yield per plant. All the recommended agronomical practices were performed during the crop period and the differential response at tillering and flowering stage were studied.

**Keywords:** Genetic divergence, cluster,  $D^2$  statistics

#### Introduction

Rice (*Oryza sativa* L.) is one of the staple cereal crops of the world and it is one of the main sources of carbohydrate for nearly one half of the world population. Inclusion of genetically divergent parents in any breeding programme is essential to create new genetic stocks. Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization programme. The divergence can be studied by technique using  $D^2$  statistics developed by Mahalanobis (1936). It is based on multivariate analysis and grouped into various cluster as given by Spark (1973). This is considered as the most effective method for qualifying the degree of genetic diversity among the genotypes included in the study. The present investigation aimed to estimate the magnitude of genetic divergence present in the 25 rice genotypes and to identify the diverse genotypes for future breeding programme.

#### Materials and methods

The analysis of variance for all the characters were carried out to partition the total variance into variance due to genotype and other sources for all characters. Mean sum of square due to treatment were found highly significant for all the morpho-physiological characters under study indicating presence of ample amount of variability present among the treatments.

To have an idea about the extent of similarity and differences among the studied rice cultivars under stress at tillering and flowering stages, cluster analysis of genotypes was performed based on all the traits associated with tolerance to drought using Ward minimum variance method. All the early maturing rice genotypes were grouped into six clusters on the basis of genetic distance among the genotypes. The distribution of genotypes, intra and inter-cluster divergence ( $D^2$ ) value and cluster means for different clusters are presented in table 1, 2 and 3, respectively.

#### Results and Discussion

The twenty five genotypes under study were grouped into six clusters using Mahalanobis  $D^2$  analysis (Table 6 & 7). The genotypes within each cluster were closer to each other than the genotypes in different clusters. Cluster I had eight genotypes namely BRR0066, RCPR8, RCPR21, Sahbhagi, BRR0048, CR Dhan1, TRC2015-14, UPR3837-2-2-1-3. Cluster II included single genotype i.e CR3721-11. Cluster III included three genotypes namely KMP223, Rajendra bhagwati, Rajendra Nilam. Cluster IV also had three genotypes like RYT3379, RP5587-13-13- 305-13 and RP5940-15-13-2-1-1 and V comprised of six genotype R1973-206-2-86-1, KMP175, MC-13, TRC 2015-12, CR3948-2-1-2-2-1 and RP5177-322--8-5-3-2. Cluster VI comprised of four genotypes i.e. RP5938-243-8-6-2-2-1, RCPR20, UPR-3929-8-1-1 and TRC2015-20 under stress at tillering stage. Under flowering stage stress Cluster I had seven genotypes namely BRR0066, CR3948- 2-1-2-2-1,TRC 2015-12,TRC2015-14,RP5587-13-13-305-13,RCPR21 and CR Dhan1. Cluster II and Cluster IV included two

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genotype i.e. UPR-3929-8-1-1 and RCPR20 and RP5940-15-13-2-1-1 and RYT3379 respectively. Cluster III included three genotypes namely RCPR8, Sahbhagi, UPR3837-2-2-1-3 and CR3721-11. Cluster V comprised of seven genotypes R1973-206-2-86-1, MC-13, KMP175, BRR0048, RP5938-243-8-6-2-2-1, RP5177-322--8-5-3-2 and TRC2015-20. Cluster VI comprised of three genotypes i.e. Rajendra bhagwati, Rajendra Nilam, and KMP223.

A comparison of cluster means for different clusters showed considerable differences among them (Table 3&4) the cluster mean values showed a wide range of variations for all the characters undertaken in the study. Cluster I exhibited highest mean value for plant height, spikelet fertility, number of tillers per plant. Cluster II exhibited highest mean value for days to flowering., days to maturity, flag leaf area, grain yield per plant and lowest mean value for plant height, harvest index Cluster III exhibited highest mean value for panicle length, relative water content in flag leaf, recovery percent after stress, chlorophyll content and lowest mean value for canopy temperature. Cluster IV recorded highest mean value for 1000 grain weight, canopy temperature and lowest mean value for recovery percent after stress, chlorophyll content Cluster V recorded highest mean value for harvest index and lowest mean value for panicle length, spikelet fertility, grain yield per plant. Cluster VI recorded lowest mean value for days to flowering, days to maturity, number of tillers per plant, 1000 grain weight, relative water content in flag leaf, flag leaf area when stressed at tillering stage whereas when under flowering stage stress Cluster I exhibited highest mean value for days to maturity. Cluster II exhibited highest mean value for plant height and canopy temperature and lowest mean value for days to flowering, days to maturity, number of tillers per plant and harvest index Cluster III exhibited highest mean value for days to flowering and lowest mean value for plant height. Cluster IV recorded highest mean value for days to maturity, flag leaf area and lowest mean value for recovery percent after stress, chlorophyll content. Cluster V recorded and lowest mean value for panicle length, spikelet fertility, 1000 grain weight, relative water content in flag leaf, flag leaf area and grain yield per plant. Cluster VI recorded highest mean value for panicle length, spikelet fertility, number of tillers per plant, 1000 grain weight, relative water content in flag leaf, recovery percent after stress, chlorophyll content, harvest index and grain yield per plant and lowest mean value for canopy temperature. Similar findings were reported by

Praveen and Anurag (2010) and Singh *et al.* (2013). Clusters with desired mean value may be used in hybridization programme to achieve desired high yielding segregants (Saraswathi *et al.* 1996).

The average intra and inter distances among six clusters were computed and have been given (table 6&7). The intra cluster distance ranged from 00.00 (cluster II) to 273.72 (cluster IV). The inter cluster distance was maximum between cluster III and VI (1037.964) suggesting maximum diversity among them and minimum inter cluster distance was observed between cluster I and cluster II (338.308 ) under stress at tillering whereas under flowering stage stress The intra cluster distance ranged from 108.412 (cluster VI) to 348.936 (cluster IV). The inter cluster distance was maximum between cluster IV and VI (2185.339) suggesting maximum diversity among them and minimum inter cluster distance was observed between cluster I and cluster III (332.899). Parikh *et al.* (2011) reported clusters showed maximum inter-cluster distance hence, genotypes belonging to this cluster can be used as parents for hybridization programme for the development of high yielding rice genotypes. This would be useful in rice breeding programme to evolve miracle varieties with high yield potential and a similar finding was of Sarawgi and Rastogi (2000), Nayak *et al.* (2004) and Parikh *et al.* (2011).

The selection and choice of parents mainly depends upon contribution of characters towards divergence (Bose *et al.* 2011). Under tillering stage stress, the highest contribution in manifestation of genetic divergence was exhibited by harvest index (24.33) followed by recovery percent after stress (23.33), 1000 grain weight (13.67) and spikelet fertility (13). Such results indicated that those four characters contributed maximum towards diversity. Under stress at flowering stage highest contribution in manifestation of genetic divergence was exhibited by harvest index (41.33) followed by grain yield per plant (31.67), recovery percent after stress (11.00) and chlorophyll content (8.00). The greater diversity in the present materials is due to these four characters which will offer a good scope for improvement of yield through rational selection of parental genotypes These characters can be used for choice of parent in the hybridization programme. Waghmare *et al.* (2008) also reflected high relative genetic contribution of specific traits such as relative water content and chlorophyll content towards the total divergence under moisture stress in early rice genotypes.

**Table 1:** Genetic divergence analysis for drought stress at tillering stage

Cluster No	No of genotypes within cluster	Genotypes
I	8	BRR0066, RCPR8, RCPR21, Sahbhagi, BRR0048, CR Dhan1, TRC2015-14, UPR3837-2-2-1-3
II	1	CR3721-11
III	3	KMP223, Rajendra bhagwati, Rajendra Nilam
IV	3	RYT3379, RP5587-13-13-305-13 and RP5940-15-13-2-1-1
V	6	R1973-206-2-86-1, KMP175, MC-13, TRC 2015-12, CR3948-2-1-2-2-1 and RP5177-322--8-5-3-2
VI	4	RP5938-243-8-6-2-2-1, RCPR20, UPR-3929-8-1-1 and TRC2015-20

**Table 2:** Genetic divergence analysis for drought stress at flowering stage

Cluster No	No of genotypes within cluster	Genotypes
I	7	BRR0066, CR3948-2-1-2-2-1, TRC 2015-12, TRC2015-14, RP5587-13-13-305-13, RCPR21 and CR Dhan1
II	2	UPR-3929-8-1-1 and RCPR20
III	4	RCPR8, Sahbhagi, UPR3837-2-2-1-3 and CR3721-11
IV	2	RP5940-15-13-2-1-1 and RYT3379
V	7	R1973-206-2-86-1, MC-13, KMP175, BRR0048, RP5938-243-8-6-2-2-1, RP5177-322--8-5-3-2 and TRC2015-20
VI	3	Rajendra bhagwati, Rajendra Nilam, KMP223

**Table 3:** Cluster mean values for different quantitative characters in 25 rice genotypes under drought stress at tillering stage

	DF	DM	PH	PL	SF	TPP	TGW	RWC	RAS	FLA	CC	CT	HI	YPP
1 Cluster	79.625	96.813	92.875	20.375	78.000	14.313	22.806	79.603	72.143	20.062	40.880	28.479	52.125	13.750
2 Cluster	91.000	109.500	73.500	20.000	77.000	12.500	21.850	77.470	76.650	25.410	40.500	29.310	47.000	15.600
3 Cluster	80.667	98.000	84.000	23.333	81.667	17.000	25.300	81.983	79.562	21.088	45.610	26.577	63.333	15.333
4 Cluster	78.000	94.333	84.667	19.167	74.000	14.500	23.850	77.063	55.507	20.652	34.998	29.522	50.667	12.800
5 Cluster	79.417	96.500	84.833	18.417	66.000	13.250	22.983	79.767	71.191	22.466	40.190	28.152	58.417	11.358
6 Cluster	76.500	92.875	90.500	19.750	72.875	12.250	21.188	76.270	75.021	18.904	40.620	29.075	48.250	13.363

**Table 4:** Cluster mean values for different quantitative characters in 25 rice genotypes under drought stress at flowering stage

	DF	DM	PH	PL	SF	TPP	TGW	RWC	RAS	FLA	CC	CT	HI	YPP
1 Cluster	82.929	100.500	84.143	18.357	71.286	11.714	22.907	74.312	66.952	19.701	36.521	29.056	52.929	12.607
2 Cluster	80.000	96.500	101.250	19.000	70.000	9.750	21.675	74.732	73.925	19.460	40.842	29.235	43.500	13.075
3 Cluster	87.750	104.875	82.375	18.875	77.125	14.000	22.213	71.351	72.113	19.825	39.484	28.726	46.750	13.987
4 Cluster	82.750	100.500	86.750	20.000	71.750	12.750	22.775	72.690	48.575	20.015	33.750	28.563	46.000	12.300
5 Cluster	82.429	100.143	85.286	16.786	65.714	11.214	20.943	67.466	71.500	19.178	37.936	28.512	55.429	11.136
6 Cluster	83.667	101.333	84.333	22.833	80.667	16.000	24.283	80.317	77.343	21.233	42.317	25.682	62.333	14.783

**Table 5:** Character contribution (%) towards divergence

S. No	Source	Tillering stage stress		Flowering stage stress	
		Times ranked 1st	Contribution %	Times ranked 1st	Contribution %
1.	DF	0	0.00	0	0.00
2.	DM	0	0.00	0	0.00
3.	PH	5	1.67	1	0.33
4.	PL	0	0.00	0	0.00
5.	SF	39	13.00	3	1.00
6.	TPP	5	1.67	1	0.33
7.	TGW	41	13.67	9	3.00
8.	RWC	19	6.33	8	2.67
9.	RAS	70	23.33	33	11.00
10.	FLA	3	1.00	1	0.33
11.	CC	14	4.67	24	8.00
12.	CT	0	0.00	1	0.33
13.	HI	73	24.33	124	41.33
14.	GYPP	31	10.33	95	31.67

**Table 6:** Mean intra and inter cluster distances ( $D^2$ ) among 6 clusters in rice under tillering stage

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	174.031	338.308	390.069	462.687	343.02	395.664
2 Cluster		0	531.814	939.478	690.295	494.936
3 Cluster			89.492	852.061	637.053	1037.964
4 Cluster				273.72	556.995	820.627
5 Cluster					162.278	417.123
6 Cluster						183.134

**Table 7:** Mean intra and inter cluster distances ( $D^2$ ) among 6 clusters in rice under flowering stage

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	206.643	409.248	332.899	597.161	389.96	1048.961
2 Cluster		271.646	537.435	629.611	530.915	1799.233
3 Cluster			209.525	756.2	634.141	1085.995
4 Cluster				348.936	1042.649	2185.339
5 Cluster					188.392	1653.986
6 Cluster						108.412

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