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STUDIES ON GENETIC DIVERSITY OF RICE (*ORYZA SATIVA*) UNDER SUBMERGENCE

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Abstract

The present investigation was conducted to study the submergence tolerance of 26 rice genotypes with submergence tolerant check variety Swarna Sub 1 during Samba, 2011. In the present study, 26 genotypes were chosen and evaluated under normal and submergence conditions. The experiment was conducted in cement concrete tanks in pot culture yard. Based on eleven characters namely, days to first flowering, plant height, number of tillers per plant, number of panicles per plant, panicle length, 1000 grain weight, photosynthetic rate, stomatal conductance, intercellular CO_2 conc., transpiration rate and grain yield per plant, diversity analysis was made. Genetic divergence was studied based on Mahalanobis D^2 statistics and grouping of cluster was done by Toucher's method. The analysis of variance revealed the presence of variability among the genotypes for all the eleven characters taken under studies both in normal and submergence conditions. In D^2 analysis, the 26 rice genotypes were grouped into three different clusters in normal and five clusters in submergence. Genotypes Swarna Sub 1, AURL41051, AURL4135, AURL4139, AURL4125 was predicted as the best to their superior per se performance in normal and submergence. The maximum intra cluster distance was observed in cluster IV in submergence. The maximum inter cluster distance was observed between clusters III and I in normal and clusters III and V in submergence. The genotypes from the above mentioned clusters when taken as parents would produce superior progenies and hybrids for submergence tolerance.

Key words : Genetic diversity, submergence tolerance, grain yield, *Oryza sativa*.

Introduction

Rice (*Oryza sativa* L. 2n : 2X : 24) is the most important cereal crop cultivated widely in many parts of the world. Genus Oryza belongs to the tribe Oryzeae in the family Poaceae. Out of the 24 species of rice, 22 species are wild and only 2 species are cultivated *i.e.*, *O. sativa* and *O. glaberima*.

It is one of the main sources of carbohydrate for nearly one half of the world population. In 2015, the world rice production was 478.8 m tons. In India about 44.6 million ha area is under rice cultivation and produced 90 million tonnes.

Genetic variability is the basic requirement for making progress in crop breeding. 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. Submergence stress is the third most importance one among the 42 biotic and abiotic stresses (Widawsky and O'Toole, 1995). Hence, the present study helps in identifying new genes or alleles for higher levels of tolerance (Sarkar *et al.*, 2006).

Materials and Methods

The present experiment was carried out to study about the submergence tolerance of 26 genotypes as well as the check variety Swarna Sub 1 during Samba 2011. The experiment was carried out in pot culture yard of Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamil Nadu, India. The experimental material for the study of genetic divergence, variability and character associated of the selected genotypes comprised of 26 genotypes *viz*., AURL 4101, AURL 4102, AURL 4103, AURL 4104, AURL 4105, AURL 4106, AURL 4107, AURL 4108, AURL 4109, AURL 4110, AURL 4111, AURL 4112, AURL 4113, AURL 4114, AURL 4115, AURL 4116, AURL 4117, AURL 4118, AURL 4122, AURL 4125, AURL 4127, AURL 4138, AURL 4135, AURL 4138, AURL 4139 collected International Rice Research Institute (IRRI), Philippines.

The seeds of each genotypes of rice were directly sown in pots during Samba 2011 (Aug-Dec) and thinning was employed on tenth day such that only three healthy sturdy seedlings were left per plot. During tillering stage, the plants were submerged in an outdoor cement concrete tank to a depth of 1.5 m and subsequently the same rice genotypes in pots are kept without submergence as control.

The experimental design followed was RBD with three replications. On single plant basis of the three randomly selected plants of each genotype per replication eleven traits were recorded (Statistical Analysis Panse and Sukhatme, 1978). The traits taken under study were days to flowering, plant height, number of tillers per plant, number of panicles per plant, panicle length, 1000 grain weight, photosynthetic rate, stomatal conductance, intercellular CO_2 conc., transpiration rate and grain yield per plant. The mean values were used for statistical analysis.

Results and Discussion

The genetic divergence of 26 genotypes of rice was studied by using Mahalanobis D^2 analysis. Based on D^2 analysis, the 26 genotypes were grouped into three clusters in normal condition and five clusters in submergence condition. In normal, the number of genotypes in cluster I comprised the maximum number of genotypes 17 whereas cluster II comprised of 8 genotypes, hence cluster III comprised of 1 genotype (Hilal Ahemed *et al*., 2010). In submergence, cluster I comprised of 7 maximum numbers of genotypes, cluster II comprised of 2 genotypes, cluster III and IV comprised of 8 genotypes each and cluster V comprised of 1 genotype. These results were in accordance with those reported by Subudhi *et al*. (2008). The intra and inter cluster distance among three clusters in normal and five clusters in submergence were computed and presented in the tables 1, 2, 3 & 4. The maximum intra cluster distance among both normal and submergence conditions were obtained in cluster I (13.52) in normal, followed by cluster IV (7.35), cluster III (5.84) and cluster I (5.40) in submergence condition.

Table 1 : Average inter and intra cluster D^2 values for 26 rice genotypes in normal condition.

Cluster number	I	II	III
I	**182.90**	448.58	635.89
II		**88.09**	600.05
III			**0.00**

Intra cluster Diagonal values.
Inter cluster off diagonal values.

Table 2 : Average inter and intra cluster D values for 26 rice genotypes in normal condition.

Cluster number	I	II	III
I	**13.52**	21.17	25.21
II		**938**	24.49
III			**0.00**

Intra cluster Diagonal values.
Inter cluster off diagonal values.

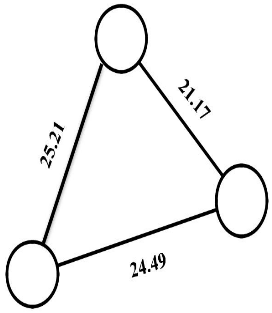
The maximum and minimum inter cluster distance among clusters in normal and submergence conditions was between cluster I and cluster III (25.21) of normal condition and cluster I and cluster II (5.82) in submergence condition. The minimum inter cluster distance in normal was found to be between cluster I and cluster II (21.17). The maximum inter cluster distance in submergence was to be between cluster III and cluster V (12.84).

Table 3 : Average inter and intra cluster D^2 values for 26 rice genotypes in submergence condition.

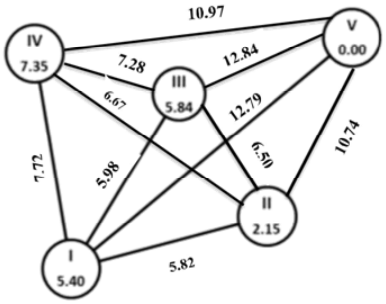
Cluster Number	I	II	III	IV	V
I	**29.16**	33.87	35.75	59.68	163.63
II		**4.65**	42.34	44.53	115.43
III			**34.16**	53.10	164.98
IV				**54.13**	120.35
V					**0.00**

Table 4 : Average inter and intra cluster D values for 26 rice genotypes in submergence condition.

Cluster Number	I	II	III	IV	V
I	**5.40**	5.82	5.98	7.72	12.79
II		**2.15**	6.50	6.67	10.74
III			**5.84**	7.28	12.84
IV				**7.35**	10.97
V					**0.00**



Cluster diagram for 26 rice genotypes in normal condition**.



Cluster diagram for 26 rice genotypes in submergence condition**

(**not to scale)

Table 5 : Cluster mean of 26 rice genotypes for various characters in normal condition.

S. no.	Characters	Clusters			General mean
		I	II	III	
1.	Days to first flowering (days)	65.61	55.32	54.65	60.72
2.	Plant height (cm)	96.54	98.34	105.23	97.43
3.	Number of tillers per plant	16.44	15.66	17.76	16.25
4.	Number of panicles per plant	11.34	11.02	12.84	11.30
5.	Panicle length (cm)	18.95	17.32	20.33	18.50
6.	1000 grain weight (g)	24.12	23.65	26.49	24.07
7.	Photosynthetic rate	49.11	43.30	67.81	48.04
8.	Stomatal conductance	0.50	0.24	0.18	0.40
9.	Intercellular CO_2 conc.	148.3	192.9	448.8	173.61
10.	Transpiration rate	8.70	6.35	2.61	7.74
11.	Grain yield per plant (g)	17.56	18.02	23.11	17.91

Table 6 : Cluster mean of 26 rice genotypes for various characters in submergence condition.

S. no.	Characters	Clusters					General mean
		I	II	III	IV	V	
1.	Days to first flowering (days)	74.72	73.85	72.67	75.40	75.68	74.25
2.	Plant height (cm)		116.28		113.96	115.81	114.04
3.	Number of tillers per plant	12.72	15.37	13.28	14.41	18.08	13.82
4.	Number of panicles per plant	7.90	11.033	8.30	9.46	13.85	8.97
5.	Panicle length (cm)	15.52	19.30	16.89	17.97	19.45	17.13
6.	1000 grain weight (g)	20.02	21.28	20.91	23.15	27.08	21.63
7.	Photosynthetic rate	57.93	59.35	49.80	50.38	76.92	53.95
8.	Stomatal conductance	0.62	0.60	0.37	0.49	0.20	0.49
9.	Intercellular CO_2 conc.		128.80		203.42	542.33	163.96
10.	Transpiration rate	6.43	9.22	5042	6.15	4.86	6.19
11.	Grain yield per plant (g)	13.24	19.86	12.57	16.34	21.12	14.80

The cluster mean values for various economic and physiological characters in normal and submergence conditions were studied and presented in the tables 5 & 6.

In normal condition, cluster I recorded the minimum plant height, cluster III recorded the minimum for characters days to first flowering, stomatal conductance, transpiration rate and the maximum for characters number of tillers per plant, number of panicles per plant, panicle length, 1000 grain weight, photosynthetic rate, intercellular CO_2 conc. and grain yield per plant.

In submergence condition, cluster III recorded the minimum for characters days to first flowering and plant height, cluster V recorded the minimum for characters stomatal conductance and transpiration rate and the maximum for characters number of tillers per plant, number of panicles per plant, panicle length, 1000 grain weight, photosynthetic rate, intercellular CO_2 conc. and grain yield per plant.

From the above observations, two conclusions were drawn. First one, the selection of cluster III and I in normal and cluster III and V in submergence, genotypes for hybridization programme would be suitable for production of superior progenies and hybrids of submergence tolerance. The other was the characters like days to first flowering and transpiration rate recorded to contribute towards the genetic divergence. The most important characters which contribute to the genetic divergence were found to be number of panicles per plant, panicle length and 1000 grain weight. All the above characters would give greater divergence in the grain yield per plant character.

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