



Screening of Indica Rice (*oryza sativa* L) Genotypes against Low Temperature Stress Using Diversity Analysis

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Abstract:

The nature and the magnitude of genetic divergence were estimated in 52 rice genotypes using Mahalanobis's D^2 – statistics. The genotypes were grouped into 8 clusters showing fair degree of relationship between geographic distribution and genetic divergence. Cluster VIII showed maximum intra cluster divergence while inter cluster divergence was maximum between clusters IV and VIII. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. Traits like plant height followed by days to maturity, panicle exertion, days to 50% flowering and panicle length were the major contributors to genetic divergence.

Key words: Genetic divergence, cold tolerance, rice, inter cluster distance

Introduction:

Rice occupies 44.80 million ha area with 99.180 million tones production which is 42.4% of total food grains and productivity of 2214 kg/ha, respectively in India. In Andhra Pradesh it is grown in an area of 43.75 lakh ha with a production of 14.21 lakh tones and productivity of 3248 kg/ha. Rice yields are low in Telangana region during Rabi season. In Telangana region the low temperature vary from 8°C to 16°C starting from December to first fortnight of February. The optimum day temperature before heading is 31°-32°C and optimum night temperature is 21°-22°C and in the period for 15 days after heading vary from 8° to 16°C [1]. These critical temperatures vary with genotype, duration of critical temperature, diurnal changes and physiological status of the plant. Rice might suffer from low temperature at the seedling stage of the crop [2] Even low temperature at the crop establishment and tiller development stage (vegetative phase) of the crop might affect the growth and development of the crop. Conventional high yielding varieties have little tolerance to low temperature. The major constraint is lack of suitable varieties for this ecosystem. The development of stable rice varieties for this fragile ecosystem should be the major thrust in present situation. The estimate of genetic divergence in the available germ plasm is important for the selection of

desirable donors for breeding programme. Hence the present study was conducted to achieve objectives to screen genotypes with good phenotypic acceptability and good emergence index with better tolerance to low or minimum temperature and to have a preliminary understanding about the nature of tolerance of genotypes with respect to low or minimum temperature. Several workers have emphasized the importance of genetic divergence for the selection of desirable parents [3, 4] Therefore, the magnitude of genetic divergence and characters contributing to the genetic divergence were studied for cold tolerance.

Materials and Methods:

The materials for the present investigation consisted of 52 rice genotypes collected from different parts of the country. These were grown in randomized complete block design with three replications during wet season 2010 in low land with water depth varying from 50-100 cm at the time of growth period of the crop. Thirty-day old seedlings were transplanted in six rows/entry, each row having 30 hills with single seedling/ hill and 20 x 15 cm spacing. observations for quantitative traits viz. plant height, panicle length, EBT/m² and seed test weight were recorded on five randomly selected plants excluding the border rows from each entry. Days to 50% flowering was recorded on plot basis. The data was analyzed utilizing Mahalanobis's generalized distance (D^2) to measure the genetic divergence among the test varieties and their grouping into different clusters.

Results and Discussion:

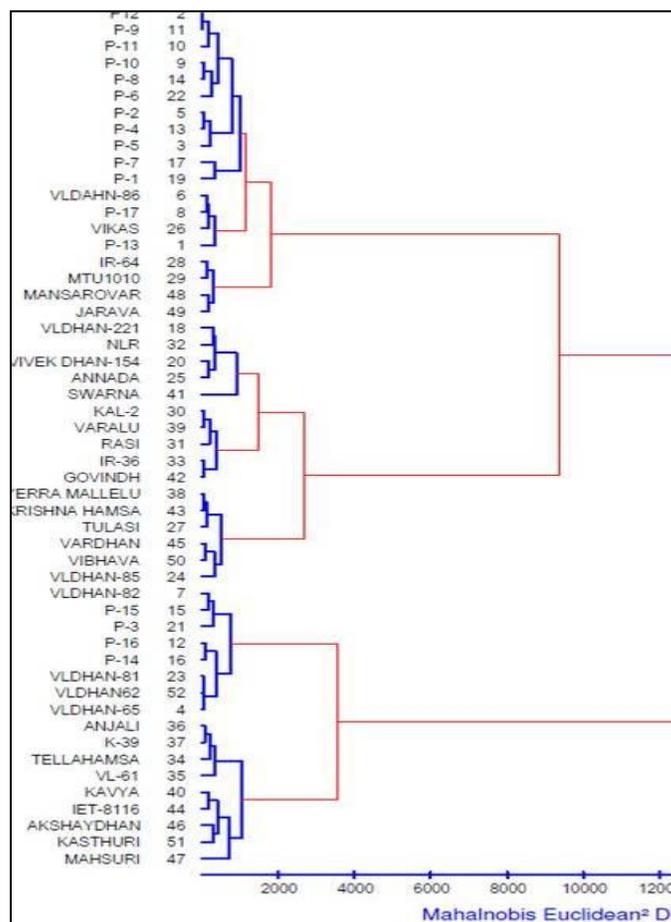
The analysis of variance revealed significant differences among the 52 genotypes for all the sixteen characters studied (Table 1). The results indicated high variances for most of the characters, which may favor the selection and its further utilization in recombination-breeding programmes in the mere future. The quantum of genetic divergence was also assessed by cluster analysis using Mahalanobis's Euclidean squared distances which grouped the entire material into more precised clusters and estimates the average distance between

them. The Euclidean squared distance grouped the material into 8 clusters.

Table 1: Analysis of variance for sixteen characters of 52 rice genotypes

S. No	Character	Replication (d.f=2)	Treatments (d.f=51)	Error (d.f=102)
1.	Panicle length	0.914	36.088	0.506
2.	Panicle exertion	0.00	0.88	0.0039
3.	Days to maturity	5.044	952.597	1.554
4.	Spikelet sterility	16.59	98.119	2.052
5.	Test weight	0.013	0.334	0.015
6.	Seed yield/plant	10.399	16.64	2.039
7.	Early seedling vigor	0.0833	0.520	0.070
8.	Plant height	1.073	432.586	0.324
9.	Tillers/plant	0.653	35.789	0.692
10.	Days to 50% flowering	0.519	288.939	1.473
11.	Productive tillers	0.208	44.144	0.942
12.	Germination%	0.391	0.426	0.351
13.	Coleoptile length	34.787	67.085	11.468
14.	Seedling growth	13.842	67.626	9.0064
15.	Radical length	1.526	3.28	0.522
16.	Seed vigor	17769.40	675918.80	89914.85

Fig 1: The 52 rice genotypes were grouped into 8 clusters



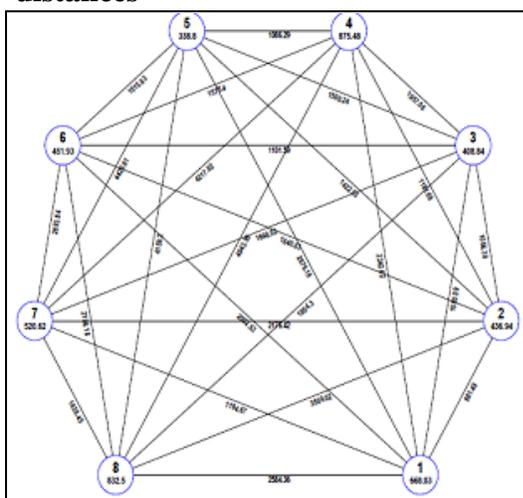
The 52 rice genotypes were grouped into 8 clusters (Fig. 1). Among the clusters, cluster VIII, I, VII, VI, II, III and V respectively. comprising of 13 genotypes followed by cluster IV (10), cluster III (9), cluster II (6) cluster VI (7) and cluster VII having one genotype. Cluster I is the largest cluster comprising of eleven genotypes followed by Cluster V containing nine genotypes. Eight genotypes were grouped in Cluster seven; six in ClusteVI five genotypes in Cluster IV, V and four genotypes in Cluster III, II. It is interesting to observe that most of the genotypes of one cluster were adapted to only one region. The clustering pattern reflects the closeness between the clusters and the geographical adaptation of the genotypes [5].

Table 2. Average intra (bold) and inter cluster D² values

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8
cluster1	668	861.4	1080.0	2242.6	2676.1	2092.5	1194.6	2584.3
cluste2		436.9	1056.3	1181.6	1422.5	1640.8	2176.4	3509
cluster3			408.8	1957	1500.2	1101.5	1648.8	1804.3
cluster4				875.4	1086.2	1575.4	4217.8	4943.9
cluster5					338.7	1015.8	4420.8	4159.2
cluster6						451.9	2693.8	2196.1
cluster7							520.6	1439.4
cluster8								832.5

The average intra and inter cluster D² values are presented in Table 2. Most of the intra clusters were closely related and cluster D² values ranged from 338 (cluster V) to 832.502 (cluster VIII). The intra cluster distance analysis revealed that the maximum divergence was observed in cluster VIII (875.477). It is reported that genotypes within the cluster with high degree of divergence would produce more desirable breeding materials for achieving maximum genetic advance. The other clusters showing high intra cluster values

Fig.2: Intra (bold) and Inter cluster distances



Inter cluster cluster D² values ranged from 4943.945(VIII) to 861.489(II). From the inter cluster D² values of the eight clusters, it can be observed that the highest divergence was between cluster IV and VIII (4943.945) while, lowest divergence was noticed between cluster I and II (861.489). The 282

clusters II and III and VI were closely related, while rests of the clusters were moderately divergent. Highly divergent genotypes would produce a broad spectrum of variability in the subsequent generation enabling further selection and improvement, which would facilitate successful breeding of rice. Thus hybrids developed from the distant cross may produce high magnitude of heterosis or desirable transgressive segregants, which would facilitate successful breeding of rice. The selection of parents for hybridization should be from two clusters having wider inter cluster distance to get maximum variability in the segregating generations [6]. The number of times that each yield component appeared in first rank and its respective percent contribution towards genetic divergence is presented in Table 3. The results showed that the contribution of plant height towards genetic divergence was highest (53.85%) by taking 714 times ranking first, followed by days to maturity (28.96%) by 384 times, panicle exsertion (8.6%) by 114 times, days to 50% flowering (4.63%) by 61 times. Panicle length (1.73%) by 23 times, tillers per plant, productive tillers (0.75%) by 10 times. Seed yield/plant, early seedling vigor, seedling maturity after transplanting, coleoptile length, seed vigor, radical length, and seedling growth did not contribute towards genetic divergence among the genotypes under investigation.

Table 3: Relative contribution of different traits to genetic diversity in rice

Source	Times Ranked 1st	Contribution %
1 Panicle exsertion	114	8.60
2 Panicle length cm	23	1.73
3 Days to maturity	384	28.96
4 Spikelet sterility	6	0.45
5 Test Weight (g)	4	0.30
6 Seed yield/plant (g)	0	0.00
7 Early seedling vigor	0	0.00
8 Plant height.	714	53.85
9 Tillers/ Plant	10	0.75
10 Days to 50% flowering	61	4.60
11 Productive Tillers	10	0.75
12 Germination %	0	0.00
13 Coleoptile Length (cm)	0	0.00
14 Seedling growth (cm)	0	0.00
15 Radical length (cm)	0	0.00
16 Seed vigor.	0	0.00

Mean values of clusters for yield contributing characters are presented in Table 4. Mean values for panicle exertion (2.273cm) and high values for days to maturity (135.758), related to Panicle exertion were high in cluster VI (3.00). Panicle length was found to be high in cluster VIII (25.841cm). Days to maturity was found to have highest value in cluster I (135.89). Spikelet sterility was found to be highest in cluster IV (22.694). Test weight was recorded with highest value in cluster III (2.500 g). Seed yield per plant was highest in cluster III (12.413g). Early seedling vigor was highest in cluster VI (2.278). Seedling maturity after transplanting is highest in cluster II (5.003days). Plan height is high in cluster VIII (115.378cm). Tillers per plant are highest in cluster VIII (16.496). Days to 50% flowering was highest in cluster III (11.37 days). Productive tillers recorded highest in cluster V (14.027). Germination percentage recorded highest in cluster IV (99.867). Coleoptile length was highest in cluster I (23.801cm). Seedling growth was highest in cluster I (39.062 cm). Radical length highest in cluster III (16.490cm). Hybridization between genotypes of different clusters is necessary for the development of desirable genotypes^[7, 8]

Conclusion:

In the present investigation, it is suggested that hybridization programme within the divergent cluster V and VIII are expected to give promising and desirable recombinants in the segregating generations. Also, traits contributing to the maximum genetic divergence viz. plant height followed by days to maturity, panicle exertion, days to 50% flowering and panicle length may be utilized in selecting genetically diverse parent.

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