

**RESEARCH ARTICLE :**

Study on genetic divergence in boro rice (*Oryza sativa* L.) germplasm

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SUMMARY : Genetic diversity among fifty genotypes of boro Rice from Directorate of Rice Research, India was evaluated using Mahalanobis D^2 statistic. The experimental materials were evaluated during *Rabi* 2013-14, Directorate of Rice Research Farm, ICRISAT Campus, Patancheru, Hyderabad. Situated at 17.53°N latitude, 78.27°E longitude and altitude of 545m above mean sea level. Based on 10 quantitative characters which includes days to 50% Flowering, Plant Height (cm), Number of tillers/ plant, Number of productive tillers/plant, Panicle length(cm), Number of filled grains/panicle, Number of unfilled grains/panicle, Days to maturity, Grain yield/plant(g) and 1000 grain weight(g). These genotypes were grouped into 10 clusters. Out of Ten clusters, cluster I was the largest comprising of 18 genotypes followed by clusters II with 15 genotypes, cluster IV with 10 genotypes, and cluster III, V, VI, VII, VIII, IX, X with one genotype each. The clusters III, V, VI, VII, VIII, IX, X were represented by single genotype indicating high degree of heterogeneity among the genotypes. Clusters VIII, IX, and X exhibited high values for most of the characters. The intra cluster distance was maximum ($D^2 = 38.68$) in cluster IV. The maximum inter cluster distance ($D^2 = 387.67$) was recorded between clusters VI and VIII. Cluster X recorded highest mean value for grain yield per plant and lowest mean value for panicle length(cm). Days to fifty per cent flowering (41.22%) followed by number of filled grains per panicle (30.61%) contributed maximum to total divergence. Based on the inter cluster distances, a hybridization between the genotypes (IC-70855) of cluster VI and cluster VIII (IC-145639), cluster VIII (IC-145639) and cluster X (IC-86143), cluster III (IC-67935) with cluster V (IC-145633), is suggested to generate promising segregants for grain yield would produce encouraging results.

KEY WORDS :Cluster analysis,
Genetic divergence,
Hybridization, Rice

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BACKGROUND AND OBJECTIVES

Boro rice (*Oryza sativa* L.) is widely grown during winter (November-April) in the flood prone areas in As- sam. Heavy rainfall in the rainy season (June-September) causes flood every year in the low lying rice growing

areas and makes rice cultivation a nightmare to the resource poor farmers. The farmers of this region prefer to grow boro rice in winter with assured irrigation for better yield. But the average productivity of boro rice (1.5 t/ha) in Assam is much lower than its potential (7t/ha). This calls for urgent attention of the

rice breeders to develop high yielding genotypes of boro rice catering to such conditions. The development of a high yielding genotype through breeding rice, an autogamic species, requires a thorough knowledge of the association of the yield components (Kishor *et al.*, 2008). Success of hybridization and subsequent selection of desirable segregants depends largely on the selection of parents with high genetic variability for different characters. The more diverse the parents, within overall limits of fitness, greater are the chances of obtaining higher amount of heterotic expression in F₁s and broad spectrum of variability in segregating generations (Singh and Bains, 1968). The use of Mahalanobis (1936) D² statistic for estimating genetic divergence has been emphasized by Shukla *et al.* (2006).

RESOURCES AND METHODS

The experimental material comprised of 50 genotypes evaluated during *Rabi* 2013-14, Directorate of Rice Research Farm, ICRISAT Campus, Patancheru, Hyderabad. Situated at 17.53°N latitude, 78.27°E longitude and altitude of 545m above mean sea level. The seedlings were transplanted to the main field at the rate of one seedling per hill, after 25 days, with a spacing of 20 cm x 30 cm. The experiment was arranged in a Randomized Block Design with three replications, in six-row plots of 6 m length. The recommended agronomical practices and plant protection measures were followed to ensure a normal crop. Observations were recorded on five randomly tagged plants of each genotype per replication. Ten quantitative characters *viz.*, Days to 50% Flowering, Plant Height (cm), Number of tillers/ plant, Number of productive tillers/plant, Panicle length (cm), Number of filled grains/panicle, Number of unfilled grains/panicle, Days to maturity, Grain yield/plant (g) and 1000 grain weight (g) were recorded. Mahalanobis D² analysis (Sarawgi and Bisne, 2007) was used to estimate genetic divergence among the 50 genotypes. Grouping of genotypes into clusters was carried out following Tocher's methods (Rao, 1952). Mean values of the variables, calculated based on measurements on plants for each genotype, were used in the cluster analysis.

OBSERVATIONS AND ANALYSIS

The analysis of variance revealed a significant difference among the 50 genotypes for all the ten

characters indicating the existence of high genetic variability among the genotypes for all the traits. The D² values of the genotypes ranged from 21.35 to 387.16 indicating that the material was quite diverse. In order to assess the genetic diversity among 50 genotypes, D² statistic was used following the procedure given by Rao (1952). Fifty genotypes were grouped into ten clusters based on D² values using Tocher's method. Such that the genotypes belonging to same cluster had an average smaller D² values than those belonging to different clusters. The distribution of genotypes into various clusters is shown in Table 1. Out of Ten clusters, cluster I was the largest comprising of 18 genotypes followed by clusters II with 15 genotypes, cluster IV with 10 genotypes, and clusters III, V, VI, VII, VIII, IX, X with one genotype each. The clusters III, V, VI, VII, VIII, IX, X were represented by single genotype indicating high degree of heterogeneity among the genotypes. The average intra and inter cluster D² values are presented in Table 2 and Fig. 1. Intra cluster D² values ranged from zero (cluster III, V, VI, VII, VIII, IX, X) to 38.68 (cluster IV). Maximum intra cluster distance was observed in cluster IV (38.68), followed by cluster II (30.90), cluster I (26.30), indicating that some genetic divergence still existed among the genotypes. This could be made use of in the yield improvement through recombination breeding. From the inter cluster D² values of the ten clusters, it can be seen that the highest divergence

Table 1 : Distribution of 50 rice genotypes in different clusters

Cluster no.	No. of genotypes	Names of the genotypes
I	18	IC-99132, IC-99520, IC-99527, IC-98974, IC-67626, IC-98997, IC-99487, IC-67729, IC-86142, IC-67589, IC-99143, IC-67638, IC-89143, IC-89138, IC-99510, IC-65889, IC-85969, IC-89125.
II	15	IC-145635, IC-203562, IC-99518, IC-145194, IC-145634, IC-145645, IC-145239, IC-145632, IC-145643, IC-145408, IC-99445, IC-98734, IC-145640, IC-86154, IC-89079
III	1	IC-67935
IV	10	IC-89115, IC-98938, IC-99512, IC-67586, IC-86011, IC-99288, IC-86123, IC-99513, IC-98731, IC-99437
V	1	IC-145633
VI	1	IC-70855
VII	1	IC-145651
VIII	1	IC-145639
IX	1	IC-137335
X	1	IC-86143

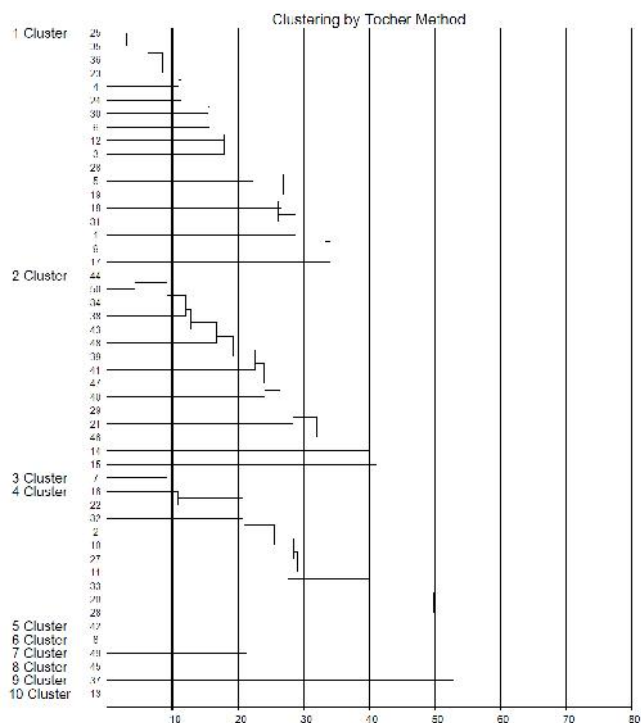


Fig. 1 : Clustering pattern of fifty genotypes in boro rice by Tocher Method

occurred between cluster VI and VIII (387.67) followed by cluster VIII and X (387.16), cluster III and VIII (321.26), cluster V and X (275.89) and cluster VII and X (267.84), cluster VIII and IX (256.80) suggesting that

the crosses involving varieties from these clusters would give wider and desirable recombination. While the lowest was noticed between cluster V and VII (21.35), followed by cluster III and VI (30.21), cluster II and III (39.62), cluster II and V (47.60), cluster II and VII (52.61) cluster V and IX (56.60). It is assumed that Parental lines selected from these clusters may be used in a hybridization programme, since hybridization between divergent parents is likely to produce wide variability and transgressive segregations with high heterotic effects. Such recommendations were also made by Murty and Arunachalam (1966); Qian and He (1991) and Rao and Gomanthinayagam (1997). Nevertheless, the genetic divergence for the maximum expression of the heterotic effect has a limit (Arunachalam and Bandyopadhyay, 1984). But for a plant breeder, the objective is not only high heterosis but other quality characters also. The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Keeping this in view, it is indicated that hybridization between the genotypes Based on the inter cluster distances, a hybridization between the genotypes (IC-70855) of cluster VI and cluster VIII (IC-145639), cluster VIII (IC-145639) and cluster X (IC-86143), cluster III (IC-67935) with cluster V (IC-145633), is suggested to generate promising segregants for grain yield, and would produce encouraging results. The genotypes of these clusters may be used as parents in the crossing

Table 2 : Intra (diagonal) and inter-cluster average of D^2 values of 50 rice genotypes

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	5.12 (26.30)	9.37 (87.80)	6.29 (39.62)	10.60 (112.46)	10.86 (117.84)	7.56 (57.08)	11.18 (124.92)	14.00 (195.88)	9.25 (85.58)	10.42 (108.62)
Cluster II		5.56 (30.90)	13.11 (171.98)	9.62 (92.56)	6.90 (47.60)	14.48 (209.68)	7.25 (52.61)	8.02 (64.28)	10.61 (112.60)	15.75 (247.91)
Cluster III			0.00	14.41 (207.59)	14.24 (202.86)	5.50 (30.21)	15.26 (232.81)	17.92 (321.26)	10.75 (115.56)	10.21 (104.31)
Cluster IV				6.22 (38.68)	12.05 (145.23)	13.50 (182.14)	10.26 (105.20)	11.46 (131.40)	13.71 (187.88)	12.48 (155.74)
Cluster V					0.00	15.50 (240.30)	4.62 (21.35)	10.80 (116.59)	7.52 (56.60)	16.61 (275.89)
Cluster VI						0.00	15.33 (234.87)	19.69 (387.67)	10.86 (117.89)	8.60 (73.93)
Cluster VII							0.00	11.17 (124.86)	8.71 (75.92)	16.37 (267.84)
Cluster VIII								0.00	16.02 (256.80)	19.68 (387.16)
Cluster IX									0.00	14.59 (212.91)
Cluster X										0.00

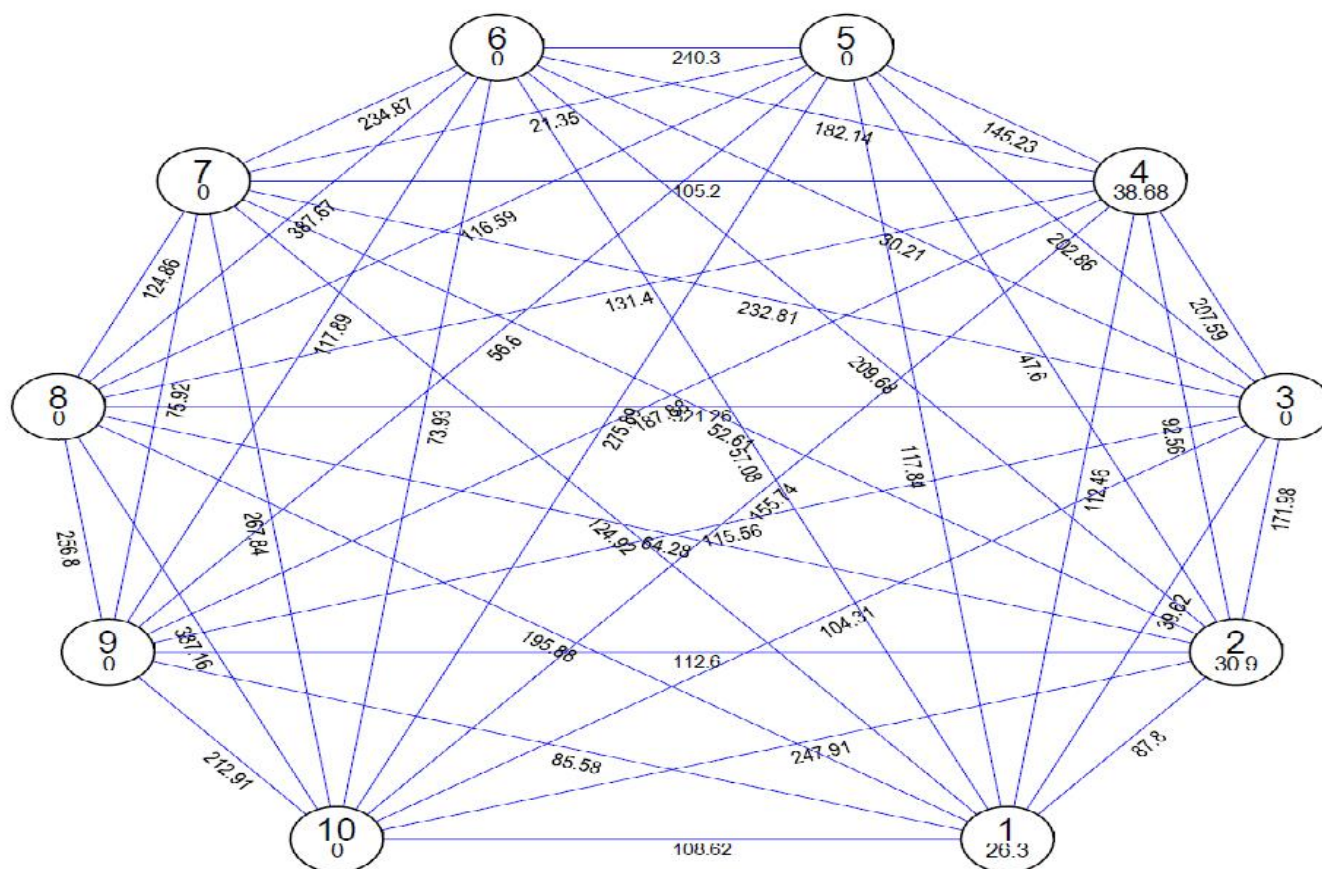


Fig. 2 : Mahalanobis Euclidean Distance among 50 genotypes of boro rice

programme to generate breeding material with high diversity.

The cluster means for each of fifteen characters are presented in Table 3. From the data it can be seen that considerable differences existed for all the characters under study. The data indicated that the cluster mean for days to 50 per cent flowering was highest in cluster VIII (123.67) and the lowest in cluster VI (88.00). Plant height was highest in cluster VIII (111.57cm) and lowest in cluster VII (74.20cm). Cluster X recorded the highest number of tillers per plant (16.7) and the lowest number of productive tillers per plant was in cluster IX (9.63). Cluster X recorded the highest number of productive tillers per plant (13.74) and the lowest number of productive tillers per plant was in cluster IX (6.86). Cluster VIII recorded the highest panicle length (25.81cm) and the lowest was recorded in cluster V (21.01cm). The number of filled grains per panicle was highest in cluster X (272.90) and the lowest in cluster III (128.97). The number of unfilled grains per

panicle was highest in cluster IX (45.33) and the lowest in cluster VIII (9.25). highest mean for days to maturity was highest in cluster VIII (154.00) and the lowest in cluster VI (119.33). Highest 1000 grain weight was recorded in cluster X (27.78 g) and the lowest in cluster VII (14.72 g). Cluster X recorded the highest grain yield per plant (18.10 g) while in cluster IX it was low (4.11g). the result indicates that selection of genotypes having high values for particular trait could be made and used in the hybridization programme for improvement of that character. It is observed that no cluster contained at least one genotype with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits. The cluster VIII is having highest mean value for days to fifty per cent flowering, plant height, panicle length, days to maturity. cluster IX number of unfilled grains per panicle and cluster X for number of tillers per plant, number of

Table 3 : Cluster means for 10 characters in 50 rice genotypes (cluster analysis)

Cluster no.	Days to 50% flowering	Plant height (cm)	No. of tillers/plant	No. of prod. Tillers/ Plant	Panicle length (cm)	No. of filled grains/Panicle	No. of unfilled grains/Panicle	Days to maturity	1000 grain weight (g)	Grain yield/Plant (g)
I	100.07	92.06	14.29	9.64	23.70	154.47	14.44	130.13	21.43	11.71
II	114.40	90.95	11.79	8.54	22.89	147.10	16.96	144.60	20.73	9.92
III	92.00	94.87	14.20	11.07	22.76	128.97	13.04	121.67	24.63	12.30
IV	109.13	106.90	13.45	9.63	24.65	244.79	13.53	139.83	16.43	13.10
V	116.00	79.63	10.87	8.58	21.01	143.33	36.20	147.33	22.72	5.71
VI	88.00	96.81	13.41	8.81	22.87	181.77	19.07	119.33	15.78	11.97
VII	117.00	74.20	13.30	9.32	24.03	175.73	33.90	146.33	14.72	5.96
VIII	123.67	111.57	12.90	8.73	25.81	133.90	9.25	154.00	25.62	15.44
IX	103.33	92.87	9.63	6.86	23.67	130.17	45.33	134.00	17.67	4.11
X	92.67	90.20	16.70	13.74	21.70	272.90	18.03	123.33	27.78	18.10

productive tillers per plant, number of filled grains per panicle, 1000 grain weight and grain yield per plant. The genotypes IC-145639, IC-137335, and IC-86143, from these clusters having high mean values may be directly used for adaptation or may be used as parents in future hybridization programme. The number of times that each of the ten characters appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 4. The results showed that the contribution of days to fifty per cent flowering was highest towards genetic divergence (41.22%) by taking 505 times ranking first, followed by Number of filled grains per panicle (30.61%) by 375 times, No. of unfilled grains/panicle (9.80%) by 120 times, Days to maturity (6.04%) by 74 times, 1000 Grainweight (4.65%) by 57 times, Plant Height (3.27%) by 40 times, Grain yield per plant (2.29%) by 28 times, Number of productive tillers per plant (1.22%) by 15 times, Number of tillers per plant (0.82%) by 10 times, panicle length (0.08%) by 1 time, respectively to the genetic divergence in decreasing order. The results were inconformity with Ramya and Senthil Kumar (2008) for number of filled grains per panicle, number of productive tillers per plant and grain yield per plant, Vennila *et al.* (2011) number of grains per panicle, plant height contributed maximum towards genetic diversity. The days to fifty per cent flowering and number of filled grains per panicle together contributed 71.83% towards total divergence. Therefore, these characters should be given importance during hybridization and selection of segregating populations. The conclusion drawn by the cluster analysis is that in the studied population high variability observed between the

genotypes in different clusters for different traits. Recombination breeding among genotypes belonging to cluster IV having maximum intra-cluster distance can improve the yield potential. As maximum inter-cluster distance was noticed between cluster VI and VIII, cluster VIII and X, crosses involving genotypes from these clusters would give wider and desirable recombination's.

Table 4 : Relative contribution of different characters to genetic diversity in rice genotypes

Sr. No.	Characters	Contribution (%)
1.	Days to 50% flowering	41.22
2.	Plant height (cm)	3.27
3.	No. of tillers/ plant	0.82
4.	No. of productive tillers/plant	1.22
5.	Panicle length(cm)	0.08
6.	No. of filled grains/panicle	30.61
7.	No. of unfilled grains/panicle	9.80
8.	Days to maturity	6.04
9.	Grain yield/plant(g)	2.29
10.	1000 grain weight(g)	4.65

Conclusion :

The genotypes IC-145639, IC-137335, IC-86143 from these clusters having high mean values may be directly used for adaptation or may be used as parents in future hybridization programme. Two characters *viz.*, days to fifty per cent flowering, number of filled grains per panicle and accounts for more than 70% towards genetic divergence. Hence these two characters are very important for selection indices.

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