SHORT COMMUNICATION

Genetic Divergence Studies in Puddle Wetland *Boro Rice*

LK Bose, MK Kar, ON Singh and K Pande
Central Rice Research Institute, Cuttack-753006, Odisha

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The nature and magnitude of genetic divergence was estimated in forty nine early maturing rice varieties suitable for *boro* ecosystem using Mahalanobis D^2 statistics. All the genotypes were grouped into five distinct non overlapping clusters. Cluster II was largest group which accommodated 21 genotypes. Cluster IV exhibited maximum intra cluster distance (D^2= 85.01) followed by cluster V (74.48) and cluster I (55.80). Cluster II and cluster IV were found to be the most divergent clusters as indicated by maximum D^2 value (453.69).

Key Words: Genetic divergence, *Boro* rice, Direct seeded rice

The present study was taken up to assess the genetic diversity in early maturing varieties of rice suitable for *boro* ecosystem. For this purpose forty nine early duration genotypes were evaluated in Simple Lattice Design during 2008 and 2009 Dry seasons. The field was puddled and pre-germinated seeds were sown in 5 x 3 m^2 plots. In each plot, 150 g seed was sown @ 100 kg/ha with fertilizer doses of 80:40:40 kg ha^{-1} N:P:K. Standard cultural practices and need based plant protection measures were adopted. Observations on plant height (cm), panicle bearing tiller/m, panicle weight (g), test weight (g) and grain yield/ plant (g) were recorded. Multivariate analysis of genetic divergence among the genotypes was done using Mahalanobis (1936) D^2 statistics and grouping of genotypes into clusters was done by Tocher's method (Rao, 1952).

It has been recorded that direct seeded *boro* rice matures earlier than the transplanted rice by 7-10 days. Therefore, it is important to characterize *boro* rice varieties and their genetic divergence adaptive to this growing condition of eastern India, which is gaining popularity in India and Bangladesh (Pande and Singh, 2004). Data presented in Table 1 revealed that phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters studied. It was highest for grain yield/plant(g) followed by panicle weight and panicle bearing tiller/m^2, while GCV was highest for grain yield. Similar results were also reported by Singh *et al.* (2007). Test weight (g) showed lowest values for GCV and PCV. Genotypic coefficient of variation was slightly lower than corresponding PCV for all the characters because of more influence of environment in the expression of these characters.

Present study revealed high heritability coupled with high genetic advance for plant height. Days to 50 per cent flowering, test weight and grain yield showed high heritability, this observation confirmed the earlier findings of Singh *et al.* (2007). Panicle weight, grain yield and test weight exhibited low genetic advance indicating the major role of non fixable gene action.

Based on the D^2 analysis, all genotypes were grouped into five distinct non overlapping clusters (Table 2). Cluster II was largest which accommodated 21 genotypes followed by cluster I which accommodated 11 genotypes. Cluster

Table 1. Mean, Range, Genotypic and Phenotypic Coefficient of Variation, Heritability and Genetic Advance for six characters in 49 Rice Genotypes

Characters	Days to 50% flowering	Plant height (cm)	Panicle bearing tiller/m^2	Panicle weight (g)	Test weight (g)	Grain yield/ plant (g)
General Mean	102.94SE ±0.99	92.86SE ±1.11	401.08SE ±26.17	2.33SE ±0.20	23.48SE ±0.37	6.78SE ±0.42
Range	80.00-115.50	70.00-113.00	276.00-500.00	1.31-2.85	17.10-28.20	3.60-11.90
h^2 (Broad sense)	98.00	98.22	58.30	51.68	94.71	88.46
Genetic Advance	21.24	22.44	68.83	0.43	4.45	3.19
Genetic Advance as per cent of mean	20.63	24.17	17.16	18.55	18.95	47.01
Genotypic Coefficient of Variation (GCV)	10.11	11.85	10.91	12.52	9.45	24.26
Phenotypic Coefficient of Variation (PCV)	10.20	11.97	14.29	17.42	9.71	25.80

Table 2. Distribution of 49 rice genotypes in different clusters

Cluster No.	No. of genotypes	Name of the genotypes
I	11	Pusa Basmati 1, Sugandha, Lalat, CRK12, Shatabdi, Lachit, IRRBB 44, Gautam, CRK18, Khitish, CRK 15
II	21	CRAC2222-255, WITA1, IR 64, CRAC2222-537, CRK27, CRAC2224-1048, CRAC2224-969, CRAC2224-913, CRAC2224-916, CRAC2224-914, CRK14, CRK21, CRK22, CRK26, CRAC2224-910, Naveen, CRK28, PUSA 44, CRAC2222-533, Bishmprasad, WITA12
III	8	CRK16, Gitanjali, Ratna, CRK7, CRK10, CRAC2222-257, IR 36, CRK13
IV	4	Annada, Heera, Parijat, Khandagiri
V	5	WARDA33, WARDA39, WARDA44, Kalaboro, Vandana

Table 3. Intra and inter-cluster D^2 and D values (parenthesis) among five clusters

Cluster	I	II	III	IV	V
I	55.80 (7.47)	135.96 (11.66)	100.80 (10.04)	175.30 (13.24)	130.65 (11.43)
II		43.69 (6.61)	136.19 (11.67)	453.69 (21.30)	175.30 (13.24)
III			43.17 (6.57)	240.25 (15.50)	283.92 (16.85)
IV				85.01 (9.22)	348.57 (18.67)
V					74.48 (8.63)

Note: Diagonal values for intra cluster and rest inter-cluster

Table 4. Cluster mean for six agro-morphological traits in 49 rice genotypes

Clusters	Days to 50 % flowering	Plant height (cm)	Panicle bearing tillers m^{-2}	Panicle weight (g)	Test weight (g)	Grain yield/ plant (g)
I	96.45	90.77	404.36	2.20#	23.13	5.87
II	111.05+	98.43	414.00+	2.37	24.17	7.86+
III	107.50	79.38	400.94	2.23	22.33	6.18
IV	83.00#	77.63#	390.00	2.25	20.26#	5.15#
V	91.80	107.80+	348.70#	2.66+	25.75+	6.50

Note: #, + Indicates lowest and highest values, respectively.

III and V consisted of eight and five genotypes, respectively, while cluster IV contained four genotypes. This indicates that a wide diversity existed among the genotypes for different traits studied.

Intra- and inter-cluster distance were presented in Table 3. Cluster IV exhibited maximum intra-cluster distance ($D^2 = 85.01$) followed by cluster V (74.48) and cluster I (55.80). So far as the inter cluster divergence is concerned, cluster II and cluster IV were found to be highly divergent as indicated by maximum D^2 value (453.69). This was followed by cluster IV and V (348.57), cluster III and V (283.92) and cluster III and IV (240.25). High inter-cluster distance are likely to produce maximum heterobeltiosis and variability in hybridization programme (Pradhan and Roy, 1990). The minimum inter-cluster distance was observed between cluster I and III which indicated that genotypes in those clusters have maximum number of common gene complexes. All the anther culture derived materials (CRAC lines) except CRAC 2222-257 were clubbed into one cluster. The short duration upland varieties Annada, Heera, Parijat and Khandagiri were in cluster IV showing their genetic similarity. Similarly all the three cultures from Africa (WARDA33, WARDA39 and WARDA44) were present in one cluster (cluster V).

The genetic differences between the clusters are reflected in cluster means (Table 4). Cluster II is characterized by highest value for days to 50% flowering, ear bearing tillers/m^2 and grain yield/plant. Cluster IV had genotypes with shortest duration, lowest plant height, lowest test weight and lowest grain yield/plant. Cluster V is characterized by tallest genotypes, highest panicle weight, highest test weight and lowest panicle bearing tillers/m^2.

Cluster II and IV are not only the most divergent clusters, but also the store house of many desirable traits. Cluster II is characterized by two most important traits such as ear bearing tillers/m^2 and grain yield/plant, while cluster IV is characterized by lowest duration and plant height. Hence, hybridization among the genotypes of these two clusters will help in developing early maturing, short statured, high yielding varieties suitable for various cropping systems under *Boro* ecosystem.

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