GENETIC DIVERSITY ANALYSIS OF RICE (*ORYZA SATIVA* L.) GERMPLASM UNDER AEROBIC CONDITION

Mamta Kumari*, G Suresh Babu and Nithin B Patil

Sam Higginbottom Institute of Agriculture, Technology and Sciences, Formerly Allahabad Agriculture Institute, Deemed- to- be-University, Allahabad, U.P. -211007

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Abstract

Analysis of variance revealed that genotypes were significantly different for all 13 characters under study. For diversity analysis, 24 rice germplasm were grouped into 5 clusters based on similarities in performances. Inter cluster distances were higher than the intra cluster distance reflecting wider genetic diversity among the genotypes of different groups. Highest inter cluster distance was observed between cluster II and V (9115.99), followed by cluster I and V (8173.51), whereas the highest intra cluster distance was found in the cluster III (854.58), and followed by cluster II (511.13) indicated that the highly divergent types existed within these clusters. Cluster III recorded desirable mean value for maximum number of productive traits *viz.*, plant height (106.35), flag leaf length (31.14), flag leaf width (1.21), panicle length (24.51), number of spikelets per panicle (199.62), harvest index (49.88) and grain yield per hill (15.28). Harvest index (15.58%) and number of spikelets per panicle (7.61%) were found to be the maximum contributors towards the total divergence after plot yield.

Rice is the staple food in Asia and is the single biggest user of fresh water. It is mostly grown under submerged soil conditions and requires much more water compared with other crops. It is estimated that 5000 liters of water is needed to produce 1 kg of rice (Bouman 2009). The increasing scarcity of water threatens the sustainability of the irrigated rice production system and hence the food security and livelihood of rice producers and consumers. A new development in water saving technologies is the concept of "Aerobic Rice". The concept of aerobic rice was first developed in China (Bouman and Tuong 2001). The term "Aerobic Rice" was coined recently by IRRI (Bouman *et al.* 2002). Aerobic rice cultivation is a new method of growing rice characterized by direct seeding in non-puddled condition without standing water and soils are kept aerobic throughout the growing season. Intermittent water limitation in this cultivation approach results in yield reduction ranging between 15 and 40% which is not acceptable (George *et al.* 2002). Genetic diversity is a powerful tool for determination for genetic discrimination among the genotypes which is used to select appropriate plant genotype(s) for hybridization to develop high yielding potential variety (Bhatt 1970). Joshi and Dhawan (1966) reported that genetic diversity was very much important factor for any hybridization program aiming at genetic improvement of yield especially in self-pollinated crops. They also inferred that Mahalanobis's D^2 statistics was a powerful tool for choosing parents for hybridization aiming at hybrid improvement. Hence, keeping in view of the above factors, the experiment was proposed with 24 genotypes of aerobic rice to identify more diverse genotypes which can be used in hybrid development programme.

An experiment with 24 aerobic rice germplasm was carried out at the field experimentation center of Department of Genetics and Plant Breeding, Faculty of Agriculture, SHIATS (AAIDU) Allahabad using RBD with three replications. Field was thoroughly prepared and each genotype was raised in 3.2 m² by direct seeding in the main field. Row to row and plant to plant spacing

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*Author for correspondence: <mamta1233@gmail.com>.

were maintained at 20 cm × 15 cm. Standard package of practices were followed to raise good stand of crop. Surface irrigation was given as and when it was necessary. Observations were recorded for 13 quantitative characters along with plot yield *viz.,* days to 50 per cent flowering, plant height, flag leaf length, flag leaf width, number of tillers per hill, number of panicles per hill, panicle length, number of spikelets per panicle, biological yield per hill, days to maturity, test weight, harvest index, grain yield per hill and plot yield. Data for each trait were collected from five randomly selected plants from each genotype. The genetic distance between the genotypes was worked out using Mahalanobis D^2 analysis (1936) and grouping of genotypes into clusters was done following the Tochers method as detailed by Rao (1952).

The analysis of variance showed significant difference for all 13 characters under study at 5 and 1% level of significance suggesting that the genotypes were genetically divergent. Twenty four aerobic rice genotypes were grouped into 5 clusters following Mahalanobis D^2 analysis (Table 1). Clustering pattern indicated that cluster I is the largest cluster comprising 9 out of 24 genotypes followed by cluster II, comprising 8 genotypes. Cluster III comprised 4 genotypes whereas cluster IV comprised 2 genotypes and cluster V comprised 1 genotypes. The pattern of group constellation proved the existence of significant amount of variability. In the present investigation, the varietal composition of the clusters revealed that the genotypes did not follow their geographic distribution as varieties from diverse sources were grouped into the same cluster. Similar kind of observations of non-correspondence of geographic diversity and genetic diversity were reported earlier by Kumar (2007) and Akter *et al*. (2009).

Table 1. Clustering pattern of 24 genotypes.

Cluster	Number of genotypes	Name of genotypes
I	9	Vandana (check), IR78937-B-20-B-B-3, IR82589-B-B-51-4, IR82635-B-B-25-4, IR79966-B2-52-2, IR80021-3-86-3-4, IR82635-B-B-145-1, IR78913-B-22-B-B-B, CR2340-10
II	8	IR83748-B-B-86-3, BP234E-MR-11, IR79915-B-83-4-3, IR82635-B-B-93-2, IR83759-B-B-55-1, IR82589-B-B-63-2, IR82310-B-B-67-2, IR78937-B-4-B-B-B
III	4	IR83399-B-B-52-1, IR82693-36-4-1, IR82639-B-B-115-1, IR83639-B-B-3-3
IV	2	IR78944-B-8-B-B-B, IR78887-048-B-B-3
V	1	IR82098-B-B-18-1

Intra and inter cluster distances are presented in Table 2. Genotypes grouped into the same cluster diverge little from one another when the aggregate of characters were measured. Statistical distances represent the index of genetic diversity among clusters. Highest intra cluster distance was observed for cluster III (854.58) followed by cluster II (511.13) and cluster I (486.62). Minimum intra cluster distance was observed for cluster V (0.00). Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which can be used for improvement through inter-varietal hybridization (Joshi *et al.* 2008).

The inter cluster distances were higher than the intra-cluster distance reflecting wider genetic diversity among the genotypes of different groups. Maximum inter cluster distance (9116.90) was found between cluster II and V followed by cluster I and V (8173.51), cluster III and V (5687.15) and cluster III and IV (2680.69), which indicated that genotypes grouped in these clusters are

genetically diverse. Hybrids developed from selected genotypes of these clusters will lead to high heterosis and ultimately lead to improved yield. Hybridization programme involving genetically diverse parents belonging to different distant clusters would provide analysis opportunity for bringing together gene constellations of diverse nature, promising hybrids derivatives resulted probability due to complementary interaction of divergent genes in parents (Anand and Murthy 1968). Least inter cluster distance (706.54) was observed between clusters I and II, followed by cluster III and IV (1237.41) and I and III (1243.56) which indicates that genotypes grouped in these clusters are genetically similar and hybridization between these will not lead to satisfactory heterosis.

Table 2. Inter- and intracluster distances.

Cluster	I	II	III	IV	V
I	486.62	706.54	1243.56	2043.24	8173.51
II		511.13	1504.73	2680.69	9115.99
III			854.58	1237.41	5687.15
IV				267.38	2428.88
V					0.00

Mean performance of a cluster is the mean of overall values of individual correlated variables of all genotypes included in that cluster. The cluster mean was presented in Table 3. Cluster I showed least mean values for days to 50 per cent flowering (76.19), plant height (98.95), panicle length (21.75), biological yield per hill (23.09), grain yield per hill (10.72) as well as days to maturity (103.26). Cluster II containing eight genotypes, showed highest mean values fot days to 50 per cent flowering (81.46) and days to maturity (110.08) whereas, least mean values for harvest index (43.63), grain yield per hill (22.26) and plot yield (164.83). Cluster III which contains four genotypes showed highest mean values for most of the traits like plant height (106.35), flag leaf length (31.14), flag leaf width (1.21), panicle length (24.51), number of spikelets per panicle (199.62), harvest index (49.88) and grain yield per hill (15.28). Cluster IV exhibited high mean values for number of tillers per hill (6.55), number of panicles per hill (5.40), biological yield per hill (30.80) and test weight (24.17) whereas it showed least mean values for flag leaf length (27.13) and flag leaf width (1.09). Cluster V which has only one genotype, showed highest mean value for plot yield and least mean values for number of tillers per hill (5.53), number of panicles per hill (4.17) and number of spikelets per panicle (105.73). Early duration genotypes IR82635-B-B-145-1 (100.00), IR79966-B2-52-2 (101.00) and IR78913-B-22-B-B-B (102.33) were grouped in cluster I. IR82639-B-B-115-1 (17.31), IR82693-36-4-1 (12.93), IR83639-B-B-3-3 (18.15) showed more grain yield per hill and were grouped in cluster III.

None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. However, the cluster III recorded desirable mean value for maximum number of productive traits *viz*., plant height, flag leaf length, flag leaf width, panicle length, number of spikelets per panicle harvest index and grain yield per hill. Hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. Based on the per se performance of the aerobic rice genotypes within the clusters, they may be directly selected or may be used as potential parents in hybridization programme.

Table 3. Cluster means of 14 yield component characters.

	Days to 50% flowering	Plant height	Flag leaf length	Flag leaf width	No. of tillers/ hill	No. of panicles/ hill	Panicle length	No. of spikelets/ panicle	Days to maturity	Biological yield/ plant	Harvest index	Test weight	Grain yield/ plant	Plot yield
I	76.19	98.95	28.62	1.13	5.81	4.28	21.75	147.41	103.26	23.09	46.00	22.88	10.72	164.83
II	81.46	102.00	30.04	1.16	6.28	4.92	23.26	145.18	110.08	26.57	43.63	22.26	11.55	142.09
III	78.67	106.35	31.14	1.21	6.32	4.99	24.51	199.62	107.17	30.48	49.88	22.46	15.28	286.22
IV	77.33	100.24	27.13	1.09	6.55	5.40	23.67	141.75	104.50	30.80	46.17	24.17	14.22	366.73
V	79.00	105.43	28.27	1.17	5.53	4.17	23.65	105.73	107.67	30.62	43.96	22.60	13.46	567.38

Per cent contribution of each character towards genetic divergence is given in Table 4. Among 13 characters under study, maximum divergence was contributed by harvest index (15.58) after plot yield. Minimum contribution towards total divergence was by test weight (0.72), followed by days to 50 per cent flowering (1.09), flag leaf width (2.17), days to maturity (2.54), flag leaf length (3.26), grain yield per hill (3.99), biological yield per hill (5.80), plant height (6.52) and number of spikelets per panicle (7.61). Number of tillers per hill, number of panicles per hill and panicle length did not contributed towards total divergence. The characters like plot yield, harvest index, number of spikelets per panicle, plant height and biological yield per hill contributed 86.23 % of total divergence so they should be given priority while hybridization and selection during segregating generation.

Table 4. Percentage contribution of each character towards total divergence.

No. of characters	Source	Number of first rank	Contribution (%)
1	Days to 50% flowering	3	1.09
2	Plant height	18	6.52
3	Flag leaf length	9	3.26
4	Flag leaf width	6	2.17
5	Number of tillers/ hill	0	0.00
6	Number of panicles/ hill	0	0.00
7	Panicle length	0	0.00
8	Number of spikelets/ panicle	21	7.61
9	Days to maturity	7	2.54
10	Biological yield/ plant	16	5.80
11	Harvest index	43	15.58
12	Test weight	2	0.72
13	Grain yield/ plant	11	3.99
14	Plot yield	140	50.72

Significant amount of diversity was found among 24 aerobic rice germplasm. Plot yield contributed maximum towards total divergence followed by harvest index, number of spikelets per panicle, plant height and biological yield per hill, so these characters should be given priority during selection of parent as well as segregating generations.

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