Genetic divergence in selected indigenous aromatic rice of Odisha

AK Kar, SR Das and D Bastia

Orissa University of Agriculture and Technology, Bhubaneswar-751 003
*Email: srdas2002@gmail.com

ABSTRACT

The demand for aromatic rice has increased over the past two decades. In the present study 65 indigenous aromatic rice genotypes collected from different parts of Odisha were evaluated for divergence analysis. The genotypes were grouped into thirteen clusters. A wide variation was observed in cluster means for all the characters studied. Based on clustering pattern, the maximum genetic distance among genotypes existed between cluster IV, V and XI. The clusters V and X were ascertained outstanding on the basis of higher cluster means for most of the component characters. The most divergent clusters have been isolated as V containing Acharmati, Kanikabhog and Bashuabhog and Cluster X having Nalidhan.

Key words: Odisha, genetic divergence, indigenous aromatic rice

Genetic improvement of short grain indigenous aromatic rice largely depends upon the amount of the genetic variability present in the population. In order to generate variability, hybridization between genotypes of diverse origin is suggested to unlock new recombinations. Genetic divergence has been used as an indirect parameter of moderate effectiveness in selecting parents to produce high yielding progenies. Success of hybridization depends largely on the selection of parents with high genetic diversity for traits of interest. In the present study, attempt was made to classify and understand the nature and magnitude of genetic diversity in a set of 65 elite genotypes of indigenous aromatic rices by using Mahalanobis (1936) D^2 statistics.

Sixty five genotypes of indigenous aromatic rice collected from different parts of Odisha including four aromatic rice varieties as checks were evaluated in a randomized block design with two replications with an intra and inter row spacing at 15 and 20 cm., respectively. The observations were recorded on five randomly selected plants for eight metric traits and eleven different growth parameters *viz*. days to 50% flowering, panicle length, panicle number plant^{-1}, grains panicle^{-1}, fertility percentage, 100-grain weight, harvest index, grain yield plant^{-1}, relative growth rate (RGR), crop growth rate (CGR), net assimilation rate (NAR), leaf area index (LAI), leaf area ratio (LAR), leaf weight ratio (LWR), specific leaf area (SLA), relative leaf growth rate (RLGR), relative leaf area growth rate (RLAGR), leaf area duration (LAD) and total dry matter (TDM) production. The replicated data were subjected to genetic divergence analysis using Mahalanobis D^2 statistics as suggested by Rao (1952) and all the genotypes were grouped in to respective clusters following Tocher's method.

The analysis of variance revealed highly significant variation in respect of all the nineteen characters studied. Days to 50 % flowering, 100 grain weight, relative leaf area growth rate and to some extent grain yield plant^{-1}, grain number and leaf area duration were found to be major characters contributing to varietals divergence. Similiar findings for characters like days to 50% flowering and 100-grain weight contributing substantially towards genetic diversity was reported by Pradhan and Mani (2005) and Gupta and Govind (2006). Based on the analysis all 65 indigenous aromatic rice genotypes were grouped into thirteen clusters (Table 1). Cluster I was the biggest cluster having 40 genotypes which was followed by clusters II, IV, V with 6, 3, 3 genotypes, respectively. The cluster III, VI, VII, and VIII had 2 genotypes, whereas the cluster IX, X, XI, XII and XIII were monogenotypic

Table 1. Clustering pattern of all the test genotypes

Cluster	Number of genotypes	Genotypes
I	40	Gangeikalli, Shrabanimasi, Acharmati, Dubraj, Galeigutti, Magurphulla-B, Manasi, Jhillipanjari, Barangamalli, Gangaballi, Gatia, Dhoiabankoi, Jaiphulla Khosakani, Thakursuna, Tulasiphulla, Heerakani (58), Ratnasundari, Basuabhava, Mahulakuchi, Jala, Jalaka, Karpurakalli, Sheetakeshari, Barikunja, Basnaparijat, Kalajeera, Basmati, Maguraphulla, Kalakanhu (30), Lajkulibadan, Parijatak, Kalajeevan, Sremula, Bhatagundi, Badsahbhog, Thakurnana, Kalikati, Kalajauvan, Neelabati
II	6	Lalkanhu, Dubrajsena, Nanu , Sheetabhog, Jhingisialli, Thakurbhog
III	2	Durgabhog , Basnadhan
IV	3	Type-3, T-Basumati, Basmati-370
V	3	Acharmati-B , Kanikabhog , Bishnubhog
VI	2	Baranamagomoti , PB-1
VII	2	Kalakrishna , Basumati
VIII	2	Deulabhog , Dhobaluchi
IX	1	Pimpudibasa
X	1	Nalidhan
XI	1	Bhulasapuri
XII	1	Sujata
XIII	1	Krushnabhog

cluster having one genotype only. The present study revealed that different clusters include genotypes originating from different geographical regions, indicating that there is no relationship between clustering pattern and geographical distribution of genotypes.

Previous studies of Roy and Panwar (1993), Manonmani and Fazluah Khan (2003), Ravindra Babu et. al. (2006) and Sharma et al. (2008) in rice also supported this view. The distribution also indicated that the genotypes originating from similar geographical regions were classified in different clusters. Therefore, the kind of genetic diversity found among the genotypes belonging to same geographical region might be due to differences in adaptation, selection criteria, selection pressure and environmental conditions (Nayak et al., 2004).

The average intra- and inter-cluster D^2 values (Table 2) indicated that maximum intra cluster distance was observed in cluster VIII (120.93) and the minimum intra cluster distance (0.00) in cluster IX, X, XI, XII and XIII indicating limited genetic diversity on these clusters. This cluster was the most divergent group and genotypes falling in these clusters could be utilized as parents for hybridization. The relative magnitude of each cluster from other clusters (inter cluster distance) indicated greater genetic divergence between cluster IV and V (727.7) followed by cluster IV and XI (723.00).Parents selected from individual groups showing maximum inter-cluster distance are likely to produce superior recombinants.

Cluster means based on all the nineteen characters revealed that Cluster III, IV, VII, VIII, IX and XII were characterized by mid-early in maturity duration where as the clusters I, II, V, VI, X, XI and XIII classified under medium maturity group (Table 3). Cluster IV was distinguished for earliest in flowering

Table 2. Average intra- and inter- cluster D^2 values for 65genotypes of aromatic rice

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	83.81	104.2	155.2	417.3	238.7	224.3	126.4	242.7	141.8	108.3	181.4	165.8	122.8
II		77.67	246.0	613.2	174.2	301.8	191.7	356.8	159.1	118.0	125.1	165.9	165.3
III			42.74	278.0	337.3	369.6	158.1	235.2	181.9	177.1	396.0	184.6	189.9
IV				76.84	727.7	266.2	266.7	214.7	457.8	517.9	723.0	514.8	394.7
V					60.71	506.2	364.9	466.7	352.6	319.2	195.7	101.6	401.6
VI						83.83	145.5	196.8	296.1	294.7	307.0	391.7	204.9
VII							99.47	218.0	199.2	161.3	248.2	233.3	140.0
VIII								120.93	296.5	307.8	372.9	270.0	214.1
IX									0	123.5	312.9	210.9	138.9
X										0	218.0	236.2	177.3
XI											0	180.1	263.6
XII												0	191.7
XIII													0

with cluster means of 88.66 days where as the genotypes in cluster XI were late in maturity duration (cluster means 106.50 days). Cluster I was characterized for its higher value of fertile grain number with improved fertility and expressed higher values for physiological parameters like LAR, SLA and RGR. Cluster II was distinguished for its lowest value for 100-grain weight, and moderate to high values for panicle number, panicle length, and fertile grain number with improved fertility, RLGR, CGR, RGR, NAR and TDM. Cluster III indicated higher values for fertility percentage, LAR and SLA.

Cluster IV was characterized for high panicle number, panicle length, 100-grain weight, and harvest index, LWR, SLA, RGR and NAR. It exhibited lowest value for fertile grain number .Cluster V was characterized for its higher value for some biometric traits like panicle length, fertile grain number with improved fertility along with physiological parameters *viz*. LAI, LWR, SLA, RLAGR, RLGR, LAD, CGR, RGR and NAR.

Cluster VI had higher values for panicle number, panicle length, 100-grain weight, LWR and NAR. Cluster VII was characterized for its higher value for panicle number, panicle length, LAR, LWR

and LAD. Cluster VIII was characterized for higher values for panicle number, 100- grain weight, harvest index, grain yield plant^{-1}, LAR, LWR, SLA, RLAGR, RLGR and LAD. Cluster IX had exhibited higher values for panicle length, fertile grain number with improved fertility, CGR, RGR and NAR

Cluster X had the highest panicle number, longest panicle length, highest number of fertile grains, fertility percentage and highest values for leaf weight ratio, leaf area duration, and total dry matter. Cluster XI was distinguished for higher fertile grain number with improved fertility, LAR, LWR, SLA, RLAGR, RLGR and TDM. Cluster XII had the highest values for grain yield plant^{-1}, leaf area ratio specific leaf area, relative leaf area growth rate and exhibited higher values for panicle number, fertile grain number with improved fertility, harvest index, LAI, LWR, RLGR, LAD, RGR and TDM. Cluster XIII was characterized a with higher values for panicle number, harvest index, grain yield plant^{-1}, LAR, and TDM.

Average mean values of clusters, it is revealed that different clusters exhibited superior performance for various traits and no single cluster could be identified promising combining all desirable trait. On the basis of higher cluster mean for almost all component characters,

Table 3. Cluster means for different characters in 65 genotypes of aromatic rice

Characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
Days to 50 % flowering	100.50	104.58	91.00	88.66	100.16	104.00	99.00	96.00	99.50	104.56	106.50	95.50	101.00
Panicle number	7.49	8.33	6.15	8.46	6.87	9.87	8.37	8.39	6.13	13.00	5.86	9.00	10.13
Panicle length	24.86	25.93	23.50	26.11	24.00	26.38	26.71	20.30	26.37	27.65	23.15	24.66	24.07
Fertile grain number	143.24	156.93	101.95	59.90	165.90	95.35	79.55	105.55	160.40	173.90	148.40	139.90	109.90
Fertility percentage	87.77	85.89	87.71	79.91	91.46	76.67	76.32	79.09	85.95	93.09	85.79	90.00	72.75
100-grain weight	1.36	1.14	1.39	2.49	1.31	2.21	1.69	2.21	1.30	1.23	1.53	1.41	1.34
Harvest index	0.37	0.35	0.39	0.42	0.35	0.37	0.23	0.54	0.38	0.38	0.31	0.52	0.53
Leaf area index	2.41	2.74	2.98	2.74	4.54	2.27	3.26	3.61	1.43	3.49	3.82	4.39	1.61
Leaf area ratio	101.86	98.47	105.72	87.53	97.22	99.16	114.42	138.95	40.61	104.02	149.81	220.32	103.19
Leaf weight ratio	0.44	0.46	0.45	0.39	0.42	0.42	0.43	0.53	0.33	0.55	0.49	0.54	0.46
Specific leaf area	256.51	247.24	273.15	250.40	284.40	230.55	230.82	314.03	203.34	244.34	270.00	319.33	240.83
Relative leaf area growth rate	0.23	0.25	0.22	0.24	0.41	0.22	0.21	0.32	0.10	0.09	0.53	0.55	0.08
Relative leaf growth rate	0.27	0.33	0.29	0.27	0.49	0.22	0.14	0.39	0.27	0.16	0.44	0.35	0.12
Leaf area duration	3.91	4.30	4.80	4.34	6.32	3.67	5.40	5.41	2.61	6.42	4.71	5.37	2.98
Crop growth rate	219.12	301.56	214.00	296.44	613.33	207.00	157.83	174.50	42.67	119.33	135.67	211.00	52.34
Relative growth rate	0.30	0.36	0.24	0.33	0.57	0.30	0.16	0.20	0.47	0.10	0.15	0.35	0.08
Net assimilation rate	0.29	0.37	0.23	0.36	0.52	0.32	0.15	0.16	0.82	0.09	0.14	0.21	0.09
Total dry matter	24.01	26.53	23.51	23.96	24.12	23.85	21.88	12.52	29.48	42.78	28.75	26.66	25.86
Grain yield plant^{-1}	7.86	8.15	5.35	7.01	7.43	8.24	4.78	14.21	8.17	9.21	8.20	17.13	15.10

most divergent clusters have been isolated as V containing genotypes like Acharmati B, Kanikabhog and Bishnubhog and cluster X consists of a single genotype Nalidhan. It is interesting to note that the clusters V and X consisted of genotypes combining many desirable quantitative and physiological traits and could be successfully employed in a breeding programme for genetic enhancement in yield.

The selection of divergent genotypes from above clusters would produce broad spectrum of variability for yield and quality traits, which may enable further selection and genetic improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregates that would be useful in rice breeding programme.

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