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Genetic divergence analysis for yield and quality traits in scented rice

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ABSTRACT

Genetic divergence in 62 genotypes of scented rice was assessed on the basis of grain yield, yield components and quality traits using Mahalanobis D^2 analysis. Based on the genetic distance (D^2 values) genotypes were grouped into a distinct clusters of which cluster VII with 14 genotypes was the largest followed by cluster IV with 11 genotypes. Clustering pattern was of genotypes showed lack of corresponding between geographic origin and genetic divergence. Maximum inter-cluster distance was observed between clusters VIII and IX. Very high inter-cluster distances were also shown by cluster II and IV from cluster IX; cluster I from VIII and III and cluster III from VIII.

Key words: *aromatic rice, genetic divergence, yield and yield components, quality traits*

Scented rices constitute a special sub-group of rice known for better grain quality and ability to emit pleasant aroma during cooking and eating. India is bestowed with a rich genetic diversity of aromatic rice ranging from indigenous short grain types to long and slender grain Basmati types. Aromatic rice gets more than twice the prices of non-aromatic long grain rice because of being extremely popular in India, Pakistan and Middle East besides being getting popular in Europe and other continents as well. However, scented rice varieties are characterized by lower productivity levels and narrow adaptation as compared to non-aromatic rice. Considering the rising demand of aromatic rice and its probable role in enhancing the farmer's income, the development of high yielding and widely adapted pureline as well as hybrid cultivars is needed. The selection of suitable diverse parents for hybridization is an important pre-requsite for the success of recombination as well as heterosis breeding programme in any crop as well in rice because crosses between diverse parents have been found to provide superior transgressive segregants in segregating generations. Therefore, an attempt was made to assess genetic diversity for 18 important characters in 62 lines of aromatic rice germplasm (*O. sativa* L.) by employing Mahalanobis D^2 analysis.

MATERIAL AND METHODS

Sixty two lines of scented rice germplasm along with three check (Pusa Basmati-1, Pusa sugandha-2 and Taraori Basmati) were evaluated for 18 yield and quality traits in a randomized complete block design with three replications at N.D.U.A.T., Faizabad, Uttar Pradesh during wet season, 2008. Each plots consisted of a single row of 3m length following inter and intra-row spacing of 20 cm and 15 cm, respectively. Recommended cultural practices were followed to raise a good rice crop. The observations were recorded on five randomly selected competitive plants from each plot for 18 characters *viz*., days to 50% flowering, days to maturity, flag leaf area, plant height, effective tillers plant^{-1}, panicle length, sterile spikelets panicle^{-1}, fertile spikelets panicle^{-1}, spikelet fertility, 1000-grain weight, biological yield plant^{-1}, harvest-index, kernel length), kernel width, L:B ratio kernel elongation ratio alkali digestion value and grain yield plant^{-1}. The data recorded on above characters were subjected to genetic divergence analysis using Mahalanobis D^2 statistic (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance of randomized complete block design revealed the existence of highly significant genetic variance for all the eighteen characters studied. Based on D^2 analysis, 65 genotypes of scented rice were grouped into 9 different non-overlapping clusters as presented in Table 1. This indicated existence of substantial genetic diversity in the scented rice lines, evaluated. Cluster VII contained highest number of 14 genotypes, followed by cluster IV with 11 genotypes and cluster V with 10 genotypes. Cluster I and III possessed 7 entries each, while cluster VI and VIII were comprised of 5 entries each. Cluster II and IX were constituted 3 entries each. Bhatt, (1970), Arunachalam (1981), Ratho (1984), Sharma *et al.* (2002) and Nayak *et al*. (2004) also reported existence of substantial genetic divergence in scented rice materials. The grouping genotypes collected / originated from different places into same cluster and distribution of genotypes from same place into different cluster, suggested that the pattern of grouping of genotypes was independent of their geographical distribution.

The estimates of intra- and inter-cluster distances represented by D^2 values have been given in Table 2. The intra-cluster distances ranged from 2.284 (Cluster IV) to 2.849 (Cluster II). The maximum inter-cluster distance was observed between cluster IX and cluster VIII, followed by cluster VIII and II. The inter-cluster distance between cluster I and III, cluster IV and IX, cluster I and VIII and cluster III and VIII were also high. The minimum estimate for inter-cluster distance was recorded between cluster IV and VIII (2.897), followed by cluster V and VII (3.053). Therefore, the chance of obtaining good recombinants

Table 1. Clustering pattern of 65 genotypes on the basis of Mahalanobis' D^2 statistics

Cluster Number	Number of genotypes	Genotypes
I	7	Harikesh , Kanakjeer A, Moongphali D, Lalsar , Tilakchandan Moongphali B, Bansphool B.
II	3	Maleshiya, Sonachoor, Shakkarchini.
III	7	Pusa Basmati-1, Bas Shurkh 161, UPRI -93-60-3, Bas Shurkh 6113, Pusa Sughanda 3, Pusa Sughanda 2, Taraori Basmati.
IV	11	NDR-6242, Kanakjeer, Tulsi manjri, Tulsiprasad , Ramdhani Paugal, Dhaniya B, Kalanamak A, ST 10, Juhi Bengal B, Laungchoor B, Kalanamak (Nichnaul).
V	10	T-1 Bansphool A, Lalmati, Lalkahwa, Ramziawan, Dulhania, Kapoorchini, Basmati C, Admachini B, Kasturi Chandauli.
VI	5	Shyamjira, , Kataribhog , Rambhog B, Rambhog, Bas 213.
VII	14	Basmati B, Vishmaparag , Keshar, Basmati 370, Basmati cuttack, Chinnor A, N 12, Vishnubhog, Basmati A, Multani Basmati, Sabarmati (Raibareli), Karnal Local, Basmati Sufaid 06, Palwan.
VIII	5	NDR-6241, Badshah Pasand A, Laungchoor A, T-3, Karnal Local A.
IX	3	Basmati (Raibareli), Pakistani Basmati, Pusa Sughanda 4.

Table 2. Average of intra- and inter-clusters D^2 values for 9 clusters

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX
I	2.730	5.623	6.582	5.334	4.513	5.244	4.222	6.612	5.657
II		2.849	5.467	3.912	5.728	5.559	4.959	4.710	6.691
III			2.816	6.093	5.213	5.861	4.093	6.207	3.535
IV				2.284	5.417	4.319	4.138	2.897	6.240
V					2.726	3.846	3.053	5.594	5.334
VI						2.830	3.163	4.176	5.350
VII							2.765	4.639	3.512
VIII								2.764	6.970
IX									2.621

in segregating generations by crossing the member of the same cluster are very low. Therefore, crosses should be attempted between the genotypes belonging to clusters separated by large inter-clusters distance Chaudhary and Sarawgi (2002); Sharma *et al*., (2002); Nayak *et al*., (2004); Awasthi *et al*., (2005) and Deepak *et al*., (2006) also proposed hybridization between lines belonging to clusters separated by large inter-clusters distances in scented rice.

The intra-cluster group means for eighteen characters revealed marked differences between the clusters in respects of cluster means for different characters (Table 3). Cluster I showed highest cluster means for spikelet fertility and kernel width but, exhibited lowest cluster means for effective tillers plant^{-1}, sterile spikelets panicle^{-1}, kernel length and L/B ratio. Cluster II, exhibited lowest cluster means for plant height and panicle length. Cluster III included genotypes with highest cluster means for effective tillers plant^{-1}, panicle length, harvest-index and grain yield plant^{-1}. The entries of cluster IV were responsible for highest cluster mean for days to 50% flowering (128.64 days) and days to maturity (158.45 days) but this cluster was characterized by low mean for 1000-grain weight, kernel width and average means for rest of the characters. Cluster V possessed highest cluster mean for flag leaf area and lowest cluster means for days to 50% flowering, days to maturity and biological yield plant^{-1}. Cluster VI had lowest cluster means for spikelet fertility and grain yield plant^{-1}. Cluster VII, showed lowest mean for alkali digestion value. Cluster VIII, possessed highest cluster means for plant height, number of sterile spikelets panicle^{-1}, number of fertile spikelets panicle^{-1} and biological yield plant^{-1} but it exhibited lowest means for harvest-index and kernel elongation ratio. Cluster IX having 3 genotypes, exhibited highest cluster means for 1000-grain weight, kernel length, L/B ratio, kernel elongation ratio and alkali digestion value but it showed lowest cluster means for flag leaf area and number of fertile spikelets panicle^{-1}.

The maximum contribution towards expression of genetic divergence was exhibited by days to 50% flowering (25.62%), followed by days to maturity (18.26%). Flag leaf area, plant height and number of effective tillers plant^{-1}, also played considerable role in conditioning the genetic divergence. Panicle length, number of sterile spikelets panicle^{-1}, number for fertile

Table 3. Intra-cluster group means for yield attributing and quality characters.

Clusters	Days to 50% flowering	Days to maturity	Flag leaf area (cm^2)	Plant height (cm)	No. of effective tillers plant^{-1}	Panicle length (cm)	No. of sterile spikelets panicle^{-1}	No. of fertile spikelets panicle^{-1}	Spikelet fertility percentage	1000-grain weight (g)	Biological yield plant^{-1}(g)	Harvest index (%)	Kernel length (mm)	Kernel width (mm)	L/B ratio	Kernel elongation ratio	Alkali digestion value	Grain yield plant^{-1} (g)
I	92.62	121.38	34.07	125.26	07.07	22.54	08.03	108.81	93.09	15.20	28.90	38.75	04.68	01.78	02.63	01.84	04.53	11.16
II	119.22	148.78	39.47	111.39	10.56	22.49	32.78	181.02	84.59	12.40	43.33	40.60	04.82	01.58	03.13	02.01	04.20	17.45
III	108.67	137.76	33.39	114.81	12.48	27.76	18.22	125.92	87.21	21.05	43.29	42.87	07.56	01.69	04.49	01.98	05.20	18.43
IV	128.64	158.45	30.04	141.62	08.25	25.43	22.47	152.99	86.89	12.16	41.73	30.19	04.88	01.54	03.18	01.88	04.48	12.45
V	91.97	120.27	56.04	117.68	08.35	26.85	27.37	120.35	81.53	16.25	28.67	39.82	06.13	01.60	03.84	01.84	04.43	11.41
VI	109.97	138.27	32.23	132.71	08.01	25.59	31.84	80.53	71.39	15.28	34.27	29.67	06.32	01.68	03.78	01.87	04.48	09.77
VII	108.64	137.83	37.50	130.65	07.48	25.71	18.20	109.67	85.23	19.65	34.12	36.73	06.81	01.66	04.11	01.88	04.35	12.47
VIII	122.20	151.13	31.38	154.06	8.19	26.90	44.36	189.73	80.81	14.02	46.33	28.33	05.62	01.62	03.51	01.82	04.50	12.97
IX	107.67	136.33	22.59	125.50	09.13	24.96	09.22	79.82	89.52	21.89	31.56	41.91	07.90	01.67	04.73	02.10	05.48	13.34

spikelets panicle^{-1}, spikelet fertility percentage), 1000-grain weight, biological yield plant^{-1}, harvest-index and kernel length exhibited low contribution towards total genetic divergence, while remaining five characters played negligible role (<1.0%) in contributing genetic diversity.

This study indicated that genetic divergence in scented rice are mainly contributed by traits like days to 50% flowering, days to maturity, flag leaf area, plant height and effective tillers plant^{-1} and panicle length. These are the traits which are directly contributing towards yield, may boost the quality rice improvement breeding program either through recombinant or heterosis breeding.

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