



Genetic Divergence in Aromatic Rice Genotypes Under Problem Soil

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ABSTRACT

The existence of genetic divergence was assessed in 38 genotypes of scented rice and two checks by employing D^2 statistic on the basis of yield and quality traits in saline soil condition ($pH = 8.0$, $EC = 4.25 \text{ dSm}^{-1}$, $ESP = 13.0\%$). The Mahalanobis' D^2 analysis grouped 40 genotypes into eight distinct clusters. Maximum numbers of nine genotypes were present in cluster II, followed by cluster VII having eight genotypes, while cluster VIII had single genotype, IR-28. Clustering pattern of genotypes showed lack of correspondence between geographic origin and genetic diversity. Cluster II followed by cluster I, III, VI and VII recorded highest inter cluster distance from the monogenotypic cluster VIII. IR-28 was responsible for resulting best or second best cluster means in desirable direction for days to 50% flowering, plant height, spikelets per panicle, grains per panicle, spikelet fertility, 1000-grain weight and kernel width to cluster VIII. On the basis of inter-cluster distances, cluster means and mean performance of genotypes, the crossing of IR-28 of cluster VIII with promising genotypes of clusters exhibiting very high inter-cluster distance with it such as cluster II (Maleshiya and Juhi Bengal-B), cluster I (Katori Bhog, Lalmati and N-12), cluster III (Kanakjeer-A and Tilakchandani), cluster VI (Multani Basmati and Bas Surkh-161) and cluster VII (CSR-30) is recommended for isolating desirable recombinants for developing high yielding scented rice varieties suitable for saline conditions.

Key word: genetic divergence, scented rice, saline soil

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INTRODUCTION

Scented rice (*Oryza sativa* L.) constitutes a special sub-group of rice known for better grain quality and ability to emit pleasant aroma during cooking and eating. Scented 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 scented rice and its probable role in enhancing the farmer's income, the development of high yielding and widely adapted pure line as well as hybrid cultivars is needed.

Rice is cultivated in about 45 m ha in Uttar Pradesh in which scented rice shares more than 5.5 lac ha. Part of land where sodicity is a problem comes around 1.4 m ha. None of the scented rices, except CSR-30 is presently cultivated under high pH condition. Thus, there is urgent need to developing high yielding varieties of scented rice for stress environments like saline soil conditions. The information about the nature and magnitude of genetic divergence existing in the available germplasm of a particular crop is essential for selection of diverse parents, which upon hybridization may provide a wide spectrum of genetic recombinants for quantitatively inherited traits. In the present study, efforts have been made to identify suitable diverse genotypes for exploitation as parents in hybridization programme for developing high yielding scented rice varieties for saline conditions.

MATERIALS AND METHODS

Genetic divergence was assessed in 38 genotypes of scented rice and two checks (IR 28 and CSR-30) by employing D^2 statistic on the basis of yield and quality traits under saline condition ($pH = 8.0$, $EC = 4.25 \text{ dSm}^{-1}$, $ESP = 13\%$). These entries were evaluated in Randomized Complete Block Design with three replications during Kharif, 2010 at the Genetics and Plant Breeding Research Farm of N.D.U.A.T., Kumarganj, Faizabad. The observations were recorded on five randomly selected competitive plants in a plot in each replication for 13 characters viz., days to 50% flowering, plant height (cm), panicle bearing tillers per plant, spikelets per panicle, grains per panicle, spikelet fertility (%), 1000-grain weight (g),

kernel length (mm), kernel width (mm), L/B ratio, biological yield per plant (g), harvest-index (%) and grain yield per plant. The data was subjected to Mahalanobis D² analysis [2] to assess genetic divergence existing in the germplasm collections.

RESULTS AND DISCUSSION

The D² analysis grouped 40 genotypes into eight distinct clusters (Table 1). The discrimination of 40 rice genotypes into eight discrete and different clusters indicated existence of substantial genetic diversity in the material to suggest that it would serve as good source for providing suitable diverse parents for hybridization programme aimed at isolating superior segregants of scented rice for saline conditions. Maximum numbers of nine genotypes were present in cluster II, followed by cluster VII having eight genotypes, while cluster VIII with single entry, IR-28, had least number of genotypes. Cluster VI contained six entries, while cluster I and III possessed five genotypes each. Cluster IV and V were represented by three genotypes each. Clustering pattern of genotypes showed lack of correspondence between geographic origin and genetic diversity because genotypes originating or belonging to same geographical area were mostly found to be discriminated into different clusters though instances of being grouped together in same cluster were also there. Suman *et al.* [5] and Singh *et al.* [4] have also observed high degree of genetic diversity and absence of definite relationship between genetic and geographic diversity in scented rice to emphasize the need of selection of diverse parents for hybridization programme on the basis of genetic divergence analysis rather than their geographic origin. The estimates of intra-and inter-cluster distances presented Table 2, revealed that cluster II, followed by cluster I, III, VI and VII recorded highest inter-cluster distance from the monogenotypic cluster VIII, represented by IR-28. The minimum inter-cluster distance was observed between cluster VI and VII, followed by cluster V and VI, indicating thereby little genetic diversity between members of these cluster pairs. The highest intra-cluster distance was recorded for cluster IV (654.77) while lowest intra-cluster distance of 0.00 resulted for monogenotypic cluster VIII.

Table 1: Clustering pattern of 40 scented rice genotypes in saline soil on the basis of D² statistic

Cluster number	No. of genotypes	Name of genotypes
I	5	LALMATI, KAPOORCHINI, N-12, KATORI BHOG, T-3
II	9	JUHI BENGAL-B, MALESHIYA, KALANAMAK, LAUNGCHHOOR, NDR-6241, KANAKJEER, NDR-6242, TULSIPRASAD, SONACHOOR
III	5	TILAK CHANDAN, KESAR, RAMDHANI PAGAL, KANAKJEER-A, SAKKARCHINI
IV	3	LAUNGCHHOOR-A, SHYAMJEERA, BANTAPHOOL-B,
V	3	UPRI-93-60-3, VISNUPARAG, SABARMATI RAIBARELI
VI	6	BAS SHURKH-6113, BASMATI-A, BAS SHURKH-161, MULTANI BASMATI, KARNAL LOCAL, BASMATI RAIBARELI
VII	8	PUSA SUGANDHA-4, PUSA SUGANDHA-2, TARAORI BASMATI, CSR-30, PAKISTANI BASMATI, PUSA SUGANDHA-3, PUSA BASMATI-1, BASMATI SUFAID-106
VIII	1	IR-28

Table 2: Estimates of average intra-(diagonal and bold) and inter-cluster distances for eight clusters in scented rice

CLUSTER	I	II	III	IV	V	VI	VII	VIII
I	454.59	764.64	1411.08	2473.47	663.65	820.61	1224.96	33663.78
II		240.04	1204.53	3249.23	1655.55	2048.88	2778.40	38208.88
III			376.90	1250.29	1425.65	2220.29	3053.83	29267.01
IV				654.77	1568.01	2055.96	2645.82	20729.22
V					248.95	458.71	651.36	28020.38
VI						165.34	375.58	28563.14
VII							289.36	28218.10
VIII								0.000

IR-28 was responsible for resulting best or second best cluster means in desirable direction for days to 50% flowering, plant height, spikelets per panicle, grains per panicle, spikelet fertility, 1000-grain weight and kernel width to cluster VIII (Table 3). Cluster VII, with eight genotypes possessed highest or second highest cluster means for panicle bearing tillers per plant, spikelet fertility, 1000- grain weight, kernel length, L/B ratio, harvest – index and grain yield per plant besides having late flowering and lesser number of spikelets per panicle. Cluster VI showed highest on second highest cluster means for plant height, panicle bearing tillers per plant, kernel length, L/B ratio, biological yield per plant and grain yield per plant. Remaining five clusters also showed markedly different cluster means for different characters. On the basis of inter-cluster distances, cluster means and mean performance of genotypes, the crossing of IR-28 of cluster VIII with promising genotypes of clusters exhibiting very high inter-cluster distances and contrasting high means for different traits with it such as cluster II (Maleshiya and Juhi Bengal-B), cluster I (Katori Bhog, Lalmati and N-12), cluster III (Kanakjeer-A and Tilakchandani), cluster VI (Multani Basmati and Bas Surkh-161) and cluster VII (CSR-30) is recommended for isolating desirable recombinants for developing high yielding scented rice varieties suitable for saline conditions. Nayak *et al.* [1] and Singh *et al.* [3] have also advocated hybridization of genetically diverse parents for isolating transgressive segregates in scented rice. The crossing between promising genotypes of cluster II, III, VI and VII, mentioned above, also appears fruitful because these clusters had reasonably high inter-cluster distances from each other. Similarly, Shyamjeera (cluster IV) may be suitable for involving in hybridization with promising genotypes of clusters II, VII and VIII. The genotypes identified with high degree of genetic diversity and high mean performance for different characters may be used in developing suitable high yielding varieties for this stress ecology.

Table 3: Clusters means for 13 characters of eight clusters in scented rice

CLUSTER	Days to 50% flowering	Plant height (cm)	Panicle bearing tillers per plant	Spikelet per panicle	No. of grains per panicle	Spikelet fertility (%)	1000-grain weight (g)	Kernel length (mm)	Kernel width (mm)	L/B ratio	Biological yield per plant (g)	Harvest index (%)	Grain Yield per plant
I	98.07	130.43	6.17	106.68	64.99	60.58	15.38	6.22	1.53	4.08	39.33	26.74	10.47
II	117.56	143.20	5.72	120.08	64.64	52.96	13.45	5.11	1.47	3.49	48.52	24.11	11.57
III	105.20	125.67	5.87	98.50	53.70	55.07	12.89	4.45	1.70	2.63	37.93	23.54	9.08
IV	97.67	141.44	4.89	93.78	57.44	63.08	13.31	5.36	1.91	2.82	36.11	24.86	8.84
V	96.44	110.78	6.44	110.93	46.47	43.28	17.36	6.66	1.67	3.99	40.22	24.71	9.88
VI	98.11	145.39	7.19	72.78	39.78	56.97	19.72	7.31	1.65	4.43	43.50	26.59	11.58
VII	103.25	123.96	7.17	91.60	63.62	70.29	20.73	7.86	1.67	4.71	41.88	33.03	13.85
VIII	92.33	104.67	6.33	119.33	77.33	64.83	24.60	6.83	2.96	2.31	42.00	24.52	10.23

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