

Genetic Divergence Studies in Basmati Rice (*Oryza sativa* L.)

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Received: 24.02.2017 | Revised: 5.03.2017 | Accepted: 6.03.2017

ABSTRACT

Twenty-five scented rice genotypes were grouped into six different clusters. Cluster I consisted of six genotypes followed by cluster II consist of seven genotypes, clusters III consist of eight genotypes, cluster IV consist of one genotypes and cluster V consist of one genotypes and cluster VI consist of two genotypes. The highest intra cluster distance for yield traits was found in cluster VI (301.94). The lowest values for intra cluster distances was recorded for cluster IV and V (0.00). The maximum inter cluster distance (D^2 -values) was found between cluster IV and I (4463.46), followed by cluster II and cluster I (3265.73). Length of main panicle had very low contribution (0.33%) towards total divergence whereas number of seeds per panicle had very high contribution (39.67%) toward total divergence and in quality traits kernel length after cooking had highest (37.33%) contribution.

Key words: Scented Rice, Intra Cluster Distances, Inter Cluster Distance, Divergence, quality traits.

INTRODUCTION

Over the past century selection of desirable parents for hybridization programme has been found as an effective operating implement in developing high yielding crop varieties upon which, the modern agriculture can rely. The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for successful lentil breeding programme. Developing hybrid rice varieties with desirable traits require a thorough knowledge about the existing genetic variability. The more genetic

diverse parents, the greater chances of obtaining higher heterotic expression in F_1 's and broad spectrum of variability in segregating population as already reported by earlier workers⁷. Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization⁶. Several genetic diversity studies have been conducted on different crop species based on quantitative and qualitative traits in order to select genetically distant parents for hybridization^{1,2,7}.

Cite this article: Supriya, Jaiswal, H. K. and Srivastva, A., Genetic Divergence Studies in Basmati Rice (*Oryza sativa* L.), *Int. J. Pure App. Biosci.* 5(2): 441-448 (2017). doi: <http://dx.doi.org/10.18782/2320-7051.2626>

Jagadev *et al.*³ reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization.

In views of these facts, the present study was undertaken with the aim of examining the magnitude of genetic diversity and characters contributing to genetic diversity among basmati rice genotypes for utilization in basmati rice breeding programme.

MATERIAL AND METHODS

In the present investigation, the experimental material comprised of 25 scented rice germplasm (*Oryza sativa* L.), representing diversity in yield and quality traits were sown on 17th June, and 25 days old seedlings were used for transplanting in the field in a Randomized Block Design with two replications. Each plot consisted of three rows

of 1.5m length with spacing (15 × 20) cm provided by, AICRIP, Department of Genetics and Plant Breeding, Banaras Hindu University, Varanasi, U.P (**Table-1**). Observations were recorded for fifteen traits *viz.*, days to 50% flowering, days to maturity, plant height, panicle length, effective panicle per plant, grain yield per plant, seeds per panicle, 100 seed weight, Test weight (gm), kernel length, kernel breadth, Kernel L/B Ratio, kernel length after cooking (KLAC), kernel breadth after cooking (KBAC) and alkali spread value.

Estimation of Alkali Digestion was done as per Standard Evaluation System for Rice given in **table-2**. Analysis of variance was done as per Randomized Block Design method given by Panse and Sukhatme⁴, genetic divergence was estimated based on Mahalanobis' generalized distance as described by Rao⁵ and distribution of genotypes into different clusters by Tocher's method.

Table 1: List of scented variety of rice used in the present investigation

S.No.	Germplasm	Origin
1.	Begum	Jammu & Kashmir
2.	Quadir	Jammu & Kashmir
3.	Mehvan	Jammu & Kashmir
4.	Mushkbudgi	Jammu & Kashmir
5.	Mazhat	Jammu & Kashmir
6.	Kamad	Jammu & Kashmir
7.	Majheradehradoon basmati-1	Uttarakhand
8.	Majheradehradoon basmati-2	Uttarakhand
9.	Majheradehradoon basmati-3	Uttarakhand
10.	Juhibengal 24-1	Bihar
11.	Kala namak 12-1	Uttar Pradesh
12.	Type-3	Uttarakhand
13.	Sarjoo -52	Uttar Pradesh
14.	NDR-359	Uttar Pradesh
15.	Tarori basmati	Haryana
16.	Basmati-370	Punjab
17.	Adam chini	Uttar Pradesh
18.	Badshahbhog	Uttar Pradesh
19.	Jeerabatti	Uttar Pradesh
20.	Tulsimangri	Madhya Pradesh
21.	Dubraj	Madhya Pradesh
22.	Jaya	Punjab
23.	Sonachur	West Bengal
24.	Laungchur	Uttar Pradesh
25.	Hariram 48	Uttar Pradesh

Table 2: Scale for alkali digestion value and GT for milled rice

Scale	Features	Alkali Digestion	Rating	GT (°C)
1	Not effected but chalky	Low	High	75-79
2	Kernel swollen	Low	High	75-79
3	Swollen with color incomplete and narrow	Low or Intermediate	High or Intermediate	70-74
4	Swollen with color incomplete and wide	Intermediate	Intermediate	70-74
5	Split or segmented with collar Complete and wide	Intermediate	Intermediate	70-74
6	Dispersed, merging with color	High	Low	65-69
7	Completely dispersed and Intermingled	High	Low	65-69

RESULTS AND DISCUSSION

Distribution of genotypes into different clusters by Tocher's method for yield traits is presented in **table 3**. The cluster diagram, indicating dispersion of genotypes under divergent clusters, is presented in **fig, 1 and 2**.

Yield traits

25 scented rice genotypes were grouped into six different clusters. Average intra and inter cluster distance among six clusters indicated presence of considerable diverse scented rice genotypes in the set of material under study (**table 4**). Cluster I consisted of six genotypes followed by cluster II consist of seven genotypes, clusters III consist of eight genotypes, cluster IV consist of one genotypes and cluster V consist of one genotypes and cluster VI consist of two genotypes.

The highest intra cluster distance for yield traits was found in cluster VI (301.94). The lowest values for intra cluster distances was recorded for cluster IV and V (0.00). The maximum inter cluster distance (D^2 -values) was found between cluster IV and I (4463.46), followed by cluster II and cluster I (3265.73).

A comparison of mean values of different clusters in respect to yield traits and quality traits are presented in tables **5 and 6**. Intra cluster means showed considerable differences among the clusters. Cluster I containing six genotypes with lowest value of days to flowering, plant height, days to

maturity, panicle length and seeds per panicle and it showed average performance for all other yield traits and cluster II containing seven genotypes with highest values for panicle length and lowest for yield per plant. Cluster III containing genotypes with highest value for test weight and grain yield per plant and lowest for number of effective panicles for yield traits and cluster IV containing only one genotype was characterized by highest value of number of seed per panicle for yield traits. Cluster V containing one genotype with highest value of number of effective panicle while cluster VI containing two genotypes was characterized by highest value of days to 50% flowering, days to maturity and plant height and lowest for test weight.

The relative contribution to total divergence in this study (**Table 7**) indicated that length of main panicle had very low contribution (0.33%) towards total divergence whereas number of seeds per panicle had very high contribution (39.67%) toward total divergence. Hence parent chosen on basis of yield (along with higher genetic advance) may not throw transgressive segregates for higher yield potential because it showed a very low contribution towards divergence. Therefore, in addition to yield, relatively simply inherited characters like plant height, days to 50% flowering and test weight should also be taken

in to account, while choosing the parents from genetically diverse clusters.

Quality traits

Cluster I consisted of eight genotypes followed by cluster II consist of nine genotypes, clusters III consist of four genotypes, cluster IV consist of one genotypes and cluster V consist of one genotypes and cluster VI consist of one genotypes. The highest intra cluster distance for quality traits was found in clusters I and lowest in cluster IV, V and VI. The maximum inter cluster distance (D^2 -values) was found between cluster I and V (721.858) followed by cluster IV and VI.

Cluster I containing genotypes was characterized with highest value for kernel length, kernel L/B ratio and kernel length after cooking and lowest for kernel breath and cluster II with genotypes was characterized with highest value for alkali spread value and average value for other quality traits. Cluster III containing genotypes was characterized

with average values for all quality traits while cluster IV containing one genotype was characterized with highest values for elongation ratio and lowest for kernel breath after cooking. Cluster V containing only one genotype was characterized with highest for kernel breadth after cooking and lowest for alkali spread value kernel length after cooking, kernel length and kernel L/B ratio among the clusters while cluster VI also containing one genotype was characterized with highest for kernel breadth and lowest for elongation ratio.

For quality traits relative contribution to total divergence indicated that elongation ratio had very low (4.33%) contribution and kernel length after cooking had highest (37.33%) contribution (**Table 8**) Therefore, in addition to quality, relatively simply inherited characters like kernel breath and kernel length should also be taken in to account, while choosing the parents from genetically diverse clusters.

Table 3: Distribution of 25 genotype of scented rice in different clusters by Tocher, s method in kharif 2013 (yield traits)

Cluster	Genotypes included	Number
1	Begum, Quadir, Mehvan, Mushkbudgi, Mazhat, Kamad	6
2	Adam chini, Tulsimanjri, Hariram 48, Dubraj, Badshahbhog, Basmati 370, kalanamak 12-1	7
3	Juhibengal 24-1, Type-3, Tarori basmati, Laungchur, Jaya, MDH-1, MDH-2, MDH-3	8
4	Jeerabatti	1
5	Sonachur	1
6	Sarjoo -52, NDR-359	2

MDH = Majhera Dehradon Basmati

Table 4: Average Intra and Inter Cluster distance (D_2 and D) values among six cluster of 25 scented rice genotype for Yield traits by Tocher,s method in kharif 2013

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	232.49 (15.24)	3265.73 (57.14)	1055.28 (32.48)	4463.46 (66.80)	2218.79 (47.10)	1354.08 (36.79)
Cluster 2		266.63 (16.32)	1003.88 (31.68)	461.85 (21.49)	678.71 (26.05)	1715.33 (41.41)
Cluster 3			293.15 (17.12)	1696.18 (41.18)	865.79 (29.42)	1034.92 (32.17)
Cluster 4				0.00 (0.00)	938.14 (30.62)	2331.81 (48.28)
Cluster 5					0.00 (0.00)	640.19 (25.30)
Cluster 6						301.94 (17.37)

Table 5: Mean value of different clusters in respect to 8 yield traits by Tocher,s method for kharif 2013

	Days to 50% Flowering	Days to Maturity	Plant Height(cm)	Effective Panicle (no.)	Panicle Length(cm)	Seeds/ panicle (no).	Test weight(gm)	Yield/Plant (gm)
1 Cluster	64.875*	92.900*	124.067*	8.250	22.342*	101.475*	2.339	11.686
2 Cluster	90.800	119.180	141.080	10.240	25.758**	129.980	2.157	8.874*
3 Cluster	95.750	124.950	124.075	7.750*	24.075	148.700	3.038**	21.508**
4 Cluster	94.367	123.133	143.033	10.800	25.400	254.433**	1.387	13.653
5 Cluster	118.467	147.250	145.750	11.433**	25.708	171.133	1.523	10.238
6 Cluster	126.933**	156.167**	190.033**	10.733	24.183	191.433	1.382*	12.173

*Lowest value;**highest value

Table 6: Mean value of different clusters in respect to 7 quality traits by Tocher,s methodfor kharif 2013

	Kernel Length	Kernel Breadth	L/B Ration	Kernel Length After Cooking	Kernel Breadth After Cooking	Elongation Ratio	ALKD
1 Cluster	7.299**	1.645*	4.464**	11.507**	2.469	1.571	4.300
2 Cluster	5.209	1.906	2.701	7.987	2.789	1.537	5.160**
3 Cluster	6.494	2.655	2.504	10.791	3.690	1.658	3.550
4 Cluster	4.735	1.695	2.810	9.665	2.620*	2.035**	3.600
5 Cluster	4.305*	2.160	1.985*	6.270*	4.235**	1.455	3.160*
6 Cluster	5.910	2.845**	2.070	6.680	3.235	1.125*	5.700

Table 7: Time ranked first and percentage contribution to total D²

Characters	Times Ranked 1st	Percentage contribution to total D ²
Days to 50% Flowering	27	9.00 %
Days to Maturity	0.01	0.00 %
Plant Height cm	19	6.33 %
No of Effective Panicle	6	2.00 %
Length of Main Panicle cm	1	0.33 %
No of Seeds In Main Panic	119	39.67 %
100 Seed Weight	40	13.33 %
Yield/ Plant	88	29.33 %

Table 8: Time ranked first and percentage contribution to total D²

Kernel Length	42	14.00 %
Kernel Breadth	64	21.33 %
L/B Ration	23	7.67 %
Kernel Length After Cooking	112	37.33 %
Kernel Breadth After Cooking	18	6.00 %
Elongation Ratio	13	4.33 %
ALKD	28	9.33 %

Phenotypical Correlations

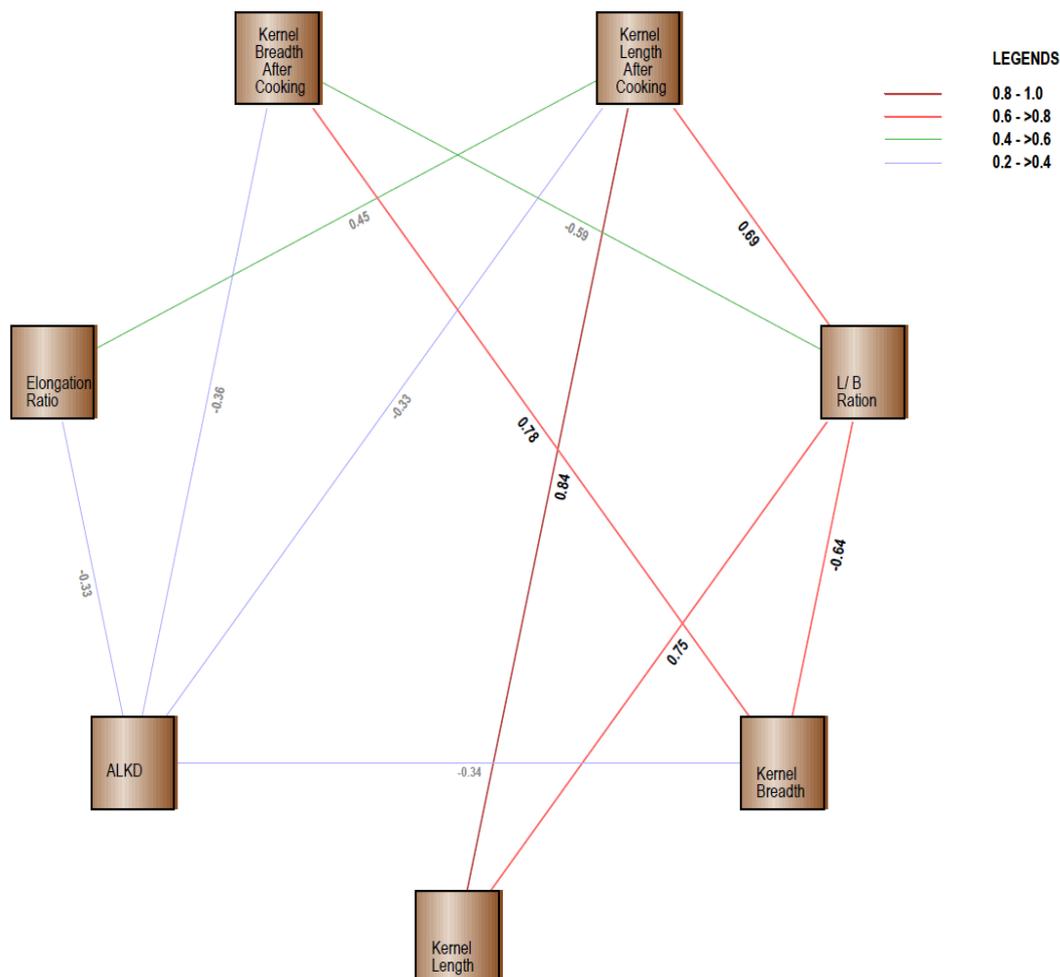


Fig. 2: Cluster diagram indicating dispersion of genotypes under divergent clusters for quality traits

CONCLUSION

D²- statistic (Tocher's method) was utilized and the 25 genotypes were grouped into 6 clusters. Genetic divergence studies also revealed that traditional basmati genotype were grouped into a single cluster, while the aromatic short grains were grouped into a separate cluster (II). The six japonica genotypes were clustered in a separate group (I) and the non -aromatic genotype were clustered (VI) separately. Clustering pattern revealed that they were not formed according to geographical distribution of the genotypes and the genotypes which originated even from

one place occupied their positions in different clusters. It is concluded that, clusters which are geographically isolated and are genetically diverse to each other may expect to give rise to novel recombinants and high heterotic combinations from crosses between these clusters to produce highly heterotic hybrids as well as superior transgressive segregates.

Acknowledgments

The corresponding author is very thankful to the Dr. H. K. Jaiswal, Professor and Sr. rice breeder, AICRIP, Department of Genetics and Plant Breeding, Banaras Hindu University,

Varanasi, U.P., India for providing rice germplasm, experimental field, laboratory facilities and other necessary guidance during the whole experiment.

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