

## DIVERGENCE ANALYSIS FOR YIELD AND QUALITY TRAITS IN SOME INDIGENOUS BASMATI RICE GENOTYPES [*Oryza sativa* L.]

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**ABSTRACT:** Genetic divergence was assessed among 23 genotypes of basmati rice representing different regions of India on the basis of yield and quality characteristics utilizing Mahalanobis D<sup>2</sup> analysis. Based on the genetic distance (D<sup>2</sup> values), the rice genotypes were grouped into six clusters. Of the six clusters formed cluster VI consisted of maximum eight genotypes followed by cluster V accommodating six genotypes, cluster I with four genotypes, cluster III and IV with three genotypes each and cluster II with one genotype. The results indicated that there was some degree of similarity of genotypes clustered together on the basis of their origin. However, the pattern of distribution of some genotypes from different eco-geographical regions was found random, indicating that geographical diversity and genetic diversity were not related. The maximum intra cluster distance was observed for the cluster III. The highest genetic divergence was observed between the clusters IV and I exhibiting wide diversity. The genotypes representing cluster VI are more yielding combined with excellent cooking quality. Among different traits, plant height, kernel length, elongation ratio and amylose content had maximum contribution towards total divergence may be used as selection parameters in segregating generations. Intelligent selection of genotypes from the clusters may be used as potential donors for future hybridization programmes to develop varieties and hybrids of high yield without much compromise on quality.

**Key words:** Genetic divergence, *Oryza sativa* L., Cluster, Basmati rice, Amylose, Quality traits.

### INTRODUCTION

Basmati Rices, indigenous to the Indian sub-continent and endowed with unique quality traits are palatal delights of the rice connoisseurs' world over. These virtues of Basmati Rices command them premium price in domestic and international markets (Siddiq E.A et al., 2012). India is leading exporter of basmati rice to global market. The country has exported 37,57,271.44 MT of basmati rice to the world for the worth of Rs. 29,299.96 crores during the year 2013-2014 ([www.apeda.gov.in](http://www.apeda.gov.in)). Improving productivity and quality traits of basmati rice always remain crucial. It is of no value to increase the production potential of genotypes compromising on quality. To sustain the leading position of basmati exports and to further improve the export potential of country amid stiff competition, basmati improvement should necessarily aim to recover transgressive segregants and hybrids without compromise on basmati traits is needed. Traditional basmati rice varieties are very low yielding due to their poor harvest index, tendency to lodging and increasing susceptibility to foliar diseases; hence there is a need to develop new varieties combining the grain quality attributes of basmati with high yield potential (Amarawathi et al., 2008). Genetic improvement of any crop mainly depends upon the genetic variability present in the population. The nature and magnitude of genetic divergence would help the plant breeder in choosing right choice of parents in order to obtain high amount of heterotic expression in F<sub>1</sub>s and broad spectrum variability in subsequent generations (Vivekanandan and Subramanian, 1993). Keeping this in view, the present investigation was undertaken to study the nature and degree of genetic divergence among some indigenous basmati rice genotypes. A meaningful classification of experimental material depending upon different characters helps to distinguish genetically close and diverse genotypes which is a prerequisite for any genetical study.

## MATERIALS AND METHODS

The experimental material used in the study comprised of twenty three basmati rice genotypes grown in different agro-ecological zones of India. Two non-basmati genotypes were also included in study to know their relatedness to basmati genotypes. The details of the genotypes are presented in Table 1. All genotypes were evaluated for grain yield and its attributing characters following randomized complete block design (RBD) with three replications during *kharif* season of two consecutive years of 2010 and 2011 at Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India. Transplanting was done 25 days after sowing of seeds in nursery bed in a 4m<sup>2</sup> plot. Plant to plant distance was 15cm, row to row distance was 20cm and the crop was raised as per recommended package of practices to ensure normal crop. Observations were recorded on ten yield attributes viz., days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), effective panicles per plant (no.), spikelets per panicle (no.), filled grains per panicle (no.), spikelet fertility (%), test weight (gm) and yield per plant (gm) of ten randomly selected plants in each entry in a replication. Observations were also recorded to study grain quality characters viz., brown rice length (mm), brown rice breadth (mm), brown rice L/B ratio, kernel length (mm), kernel breadth (mm), kernel L/B ratio, kernel length after cooking (mm), elongation ratio, alkali spread value (Little et al., 1958) and amylose content (Juliano 1971). For statistical analysis, INDOSTAT software was used. The mean of the 25 genotypes were analyzed statistically by the method outlined by Ostle (1966). The analysis of variance for different characters was carried out in order to assess the genetic variability among genotypes as given by Cochran and Cox (1950). The level of significance was tested at 5% and 1% using F table values given by Fisher and Yates (1963). The genetic diversity between the genotypes was worked out using Mahalanobis D<sup>2</sup> analysis (1936) and grouping of genotypes into clusters was carried out following Tocher's method (Rao, 1948 and 1952).

## RESULTS AND DISCUSSIONS

The analysis of variance revealed a significant difference among twenty five genotypes for all ten yield characters indicating the existence of high variability among the genotypes (Table 2). However, there is little variation exist for quality traits since basmati quality traits are unique and should not vary (Table 3). Based on the relative magnitude of D<sup>2</sup> estimates, twenty five genotypes were grouped in to six clusters (Table 4). Cluster VI was the largest, consisting of eight genotypes followed by six genotypes in cluster V, four genotypes in cluster I, three genotypes each in clusters III and IV and one genotype in cluster II. The clustering pattern indicated that there was some degree of similarity of genotypes clubbed together in a cluster on the basis of their origin. Similar findings were reported by Singh et al., 2008. However, some genotypes were placed in clusters independent of geographical origin. Similar kind of results were also reported in other studies (Sharma et al., 2002; Datt and Mani, 2003; Pradhan and Mani, 2005; Sharma et al., 2008 and Sharma et al., 2011).

Average intra and inter cluster distance (D<sup>2</sup> and D) values among six clusters were presented in Table 5 and cluster diagram depicted in Fig 1. The average intra cluster D values ranged from 0 to 54.217. The highest intra cluster distance (D=54.217) was observed in the cluster III, indicating wide genetic variation among the genotypes included in the cluster. This cluster included traditional basmati varieties viz Basmati 370 and Type-3 or Dehradoni basmati. Emphasis should be given to this cluster while selection of parents for hybridization programme since traditional basmati cultivars are excellent in basmati cooking qualities. The inter cluster D values ranged from 66.770 to 120.259. The maximum genetic distance was between cluster IV and I (D=120.259) followed by cluster III and II (D=113.08), cluster III and I (D=111.83) and cluster VI and III (D=106.715), revealing that genotypes included in these clusters are genetically diverse and may give rise to superior recombinants and high heterotic response. However, it was noted that cluster II included only one genotype which is a non-basmati. This cluster should not used for basmati breeding since to isolate good basmati quality genotype, both parents in a cross should possess basmati quality traits.

Percentage contribution of the characters towards total divergence (Fig 2) revealed that maximum percentage of contribution came from the trait plant height (34%), followed by kernel length (14%), elongation ratio (14%), alkali spread value (12%), brown rice L/B ratio (8%), amylose content (7%) and spikelets per panicle (5%). Relative importance of some of these characters in inter varietal divergence on basmati rice was reported in other study (Datt and Mani, 2003; Pradhan and Mani, 2005; and Singh et al., 2008). The other traits had very low contribution to genetic divergence. Contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the first rank (Table 6). Hence, plant height, spikelets per panicle, kernel length, elongation ratio, alkali spread value and amylose content may be used as selection parameters in the segregating generations.

The cluster mean values showed a wide range of variation for all the yield traits under study (Table 7) however, variation among quality traits was less (Table 8). The cluster I exhibited higher days to 50% flowering, days to maturity, spikelets per panicle and lowest panicle length, spikelet fertility and test weight.

Genotypes in this cluster can be used to improve number of spikelets per panicle which have bearing on yield. Cluster II designated with lower days to 50% flowering, days to maturity, effective panicles, spikelets per panicle, filled grains and yield per plant. However, this cluster is ignored as it contains a single non-basmati genotype. Cluster III was marked for its highest plant height, panicle length and filled grains and lowest brown rice breadth. This cluster includes traditional basmati cultivars with tall plant type which is an undesirable character for high yield however; these genotypes can be utilized for grain quality traits.

**Table 1 List of basmati varieties under study**

S.no	Variety	Parentage	Origin
1	TBD-1	Mutant of Taroari Basmati	BHU
2	TBD-2	Mutant of Taroari Basmati	BHU
3	TAROARI BASMATI	Pureline selection from local Basmati	Haryana
4	BASMATI 370	Pureline selection from local agro commercial group	Punjab
5	KASTURI BASMATI	Basmati 370/CR 88-17-1-5	DRR, Hyderabad
6	SONASAL BASMATI	-	Jammu & Kashmir
7	RANBIR BASMATI	Selection from Bas 370-90-95	Jammu & Kashmir
8	PUSA 2517-2-51-1	-	IARI, New Delhi
9	PUSA BASMATI-1	Pusa 167/Kernal local	IARI, New Delhi
10	PUSA BASMATI-1S-97	Selection from Pusa Basmati-1	BHU
11	PUSA 44	IARI 5901-2/IR-8	IARI, New Delhi
12	PUSA SUGANDH-3	-	IARI, New Delhi
13	PUSA SUGANDH-5	Pusa 3A/Haryana Basmati	IARI, New Delhi
14	HUBR-2-1	HBR 92/Pusa Basmati-1/Kasturi	BHU
15	BASMATI-24-1	Local land race	Maharaj ganj, U.P
16	BASMATI-24-5	Local land race	Partawal, U.P
17	BASMATI-24-7	Local land race	Siddardh nagar, U.P
18	VASUMATI	-	
19	PUSA SUGANDH-2	-	IARI, New Delhi
20	CSR-30(YAMINI)	Selection from Taroari Basmati	
21	JP-2	Collection from Basti	Uttar Pradesh
22	PUSA 1460	Improved Pusa Basmati-1	IARI, New Delhi
23	PUSA 1121(Pusa Sugandh-4)	Pusa 614-1-2/Pusa 614-2-4-3	IARI, New Delhi
24	MAHI SUGANDHA	BK 79/Basmati 370	Rajasthan
25	TYPE-3	Selection from Dehradun Basmati	Uttar Pradesh

**Table 2. Analysis of variance for yield attributing characters in Basmati rice**

Source	df	Days to 50% Flowering	Days to maturity	Plant Height (cm)	Panicle Length (cm)	Effective Panicles (no.)	Spikelets/Panicle (no.)	Filled Grains (no.)	Spikelet Fertility (%)	Test Weight (gms)	Yield per plant(gms)
Replication	2	0.413	0.093	0.982	1.279	0.213	0.373	25.120	0.492	0.010	0.538
Treatment	24	204.120**	202.396**	1117.06**	24.205**	11.264**	2425.97**	1734.05**	23.470**	0.315	18.988**
Error	48	0.705	0.675	0.573	0.353	0.074	5.901	11.38	2.969	0.013	0.447

\*\*Significance at p=0.01

**Table 3. Analysis of variance for quality characters in Basmati rice**

Source	df	Brown Rice Length(mm)	Brown Rice Breadth(mm)	Brown Rice L/B Ratio	Kernel Length(mm)	Kernel Breadth(mm)	Kernel L/B Ratio	KLAC(mm)	Elongation Ratio	Alkali Spread Value	Amylose Content(%)
Replication	2	0.005	0.000	0.000	0.000	0.003	0.042	0.036	0.000	0.053	0.108
Treatment	24	2.330**	0.005	0.596	2.187*	0.034	0.606	6.048**	0.075	7.692**	4.296**
Error	48	0.004	0.002	0.000	0.001	0.002	0.016	0.025	0.000	0.025	0.083

\*\*Significance at p=0.01 \*Significance at p=0.05

**Table 4. Distribution of 25 genotypes of Basmati rice into different clusters**

Cluster	Genotypes included	Number
I	TBD-1, TBD-2, Pusa 44, Basmati 24-1.	4
II	J.P-2.	1
III	Basmati 370, Sonasal Basmati, Type-3.	3
IV	Taroari Basmati, Ranbir Basmati, Mahi Sugandha.	3
V	HUBR-2-1, Basmati 24-5, Basmati 24-7, Vasumati, Kasturi Basmati, CSR-30.	6
VI	Pusa 2571-1-51-1, Pusa Basmati-1, Pusa Basmati-1S-97, Pusa Sugandha-3, Pusa Sugandha-5, Pusa Sugandha-2, Pusa 1460, Pusa 1121.	8

**Table 5. Average intra (diagonal, bold) and Inter Cluster distance ( $D^2$  and D) values among six clusters**

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	<b>2560.624</b> <b>(50.602)</b>	5023.218 (70.874)	12507.210 (111.835)	14462.350 (120.259)	6216.438 (78.844)	9804.567 (99.018)
Cluster 2		<b>0.000</b> <b>(0)</b>	12787.240 (113.080)	11060.010 (105.166)	5425.273 (73.656)	6470.942 (80.442)
Cluster 3			<b>2939.550</b> <b>(54.217)</b>	4498.574 (67.07)	5818.756 (76.280)	11388.150 (106.715)
Cluster 4				<b>1290.658</b> <b>(35.925)</b>	4458.332 (66.770)	5479.328 (74.022)
Cluster 5					<b>2187.157</b> <b>(46.767)</b>	4661.551 (68.275)
Cluster 6						<b>2057.086</b> <b>(45.355)</b>

D values are in parenthesis.

**Table 6. Times ranked first and percentage contribution to total  $D^2$** 

	CHARACTERS	TIMES RANKED 1 <sup>ST</sup>	PERCENTAGE CONTRIBUTION TO TOTAL $D^2$
1	Days to 50% Flowering	4	1.33
2	Days to Maturity	0	0.00
3	Plant Height (cm)	102	34.00
4	Panicle Length(cm)	0	0.00
5	Effective Panicles	1	0.33
6	Spikelets/ Panicle	14	4.67
7	Filled Grains	0	0.00
8	Spikelet Fertility %	0	0.00
9	Test Weight (100 Grain Wt)	0	0.00
10	Yield/ Plant (gm)	0	0.00
11	Brown Rice Length (mm)	2	0.67
12	Brown Rice Breadth (mm)	0	0.00
13	Brown Rice L/B Ratio	23	7.67
14	Kernel Length (mm)	41	13.67
15	Kernel Breadth (mm)	0	0.00
16	Kernel L/B ratio	0	0.00
17	KLAC(mm)	15	5.00
18	Elongation Ratio	41	13.67
19	Alkali Spread Value	36	12.00
20	Amylose Content (%)	21	7.00

Table 7. Mean values of different clusters with respect to 10 yield traits

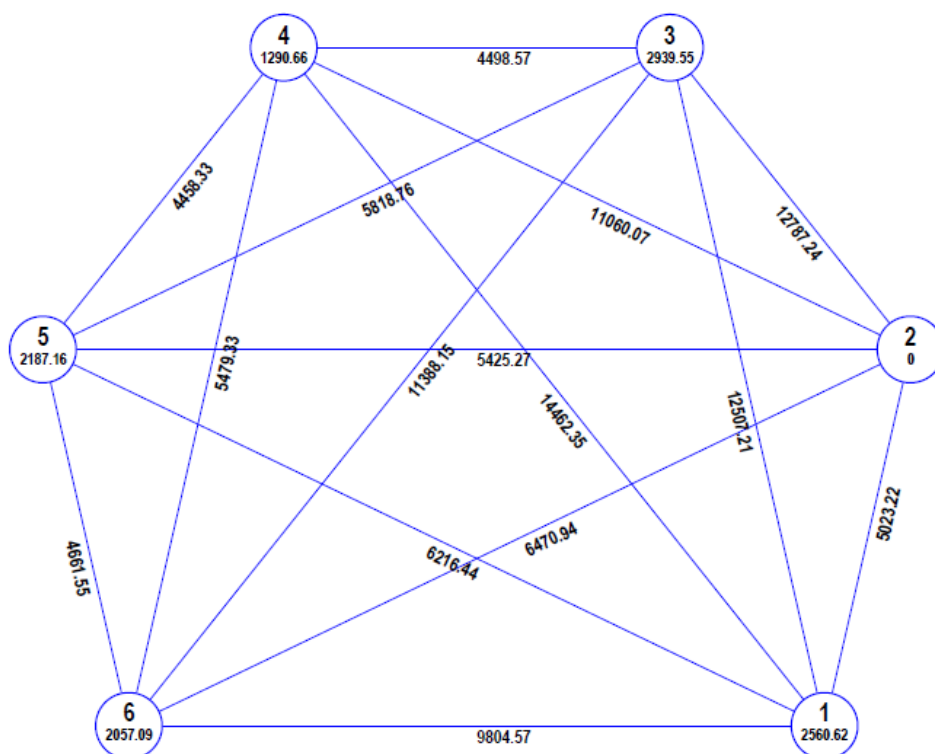
	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Panicle Length(cm)	Effective Panicles	Spikelets/ Panicle	Filled Grains	Spikelet Fertility %	Test Weight (100 Grain Wt.)	Yield/ Plant (gm)
1 Cluster	105.833**	135.833**	95.658*	24.383*	10.083	195.250**	165.917	85.167*	1.772*	9.992
2 Cluster	89.667*	119.667*	108.667	28.000	6.000*	135.333*	118.333*	87.400	2.307	5.923*
3 Cluster	94.444	124.444	150.856**	30.844**	10.444	193.667	169.444**	86.983	2.003	11.647
4 Cluster	97.444	127.444	139.589	29.089	10.667**	159.889	141.667	88.552**	2.296	11.882**
5 Cluster	99.111	128.944	114.717	27.583	9.667	155.611	135.000	86.783	2.181	9.793
6 Cluster	99.875	129.875	105.792	29.333	8.500	168.000	147.208	87.765	2.472**	10.724

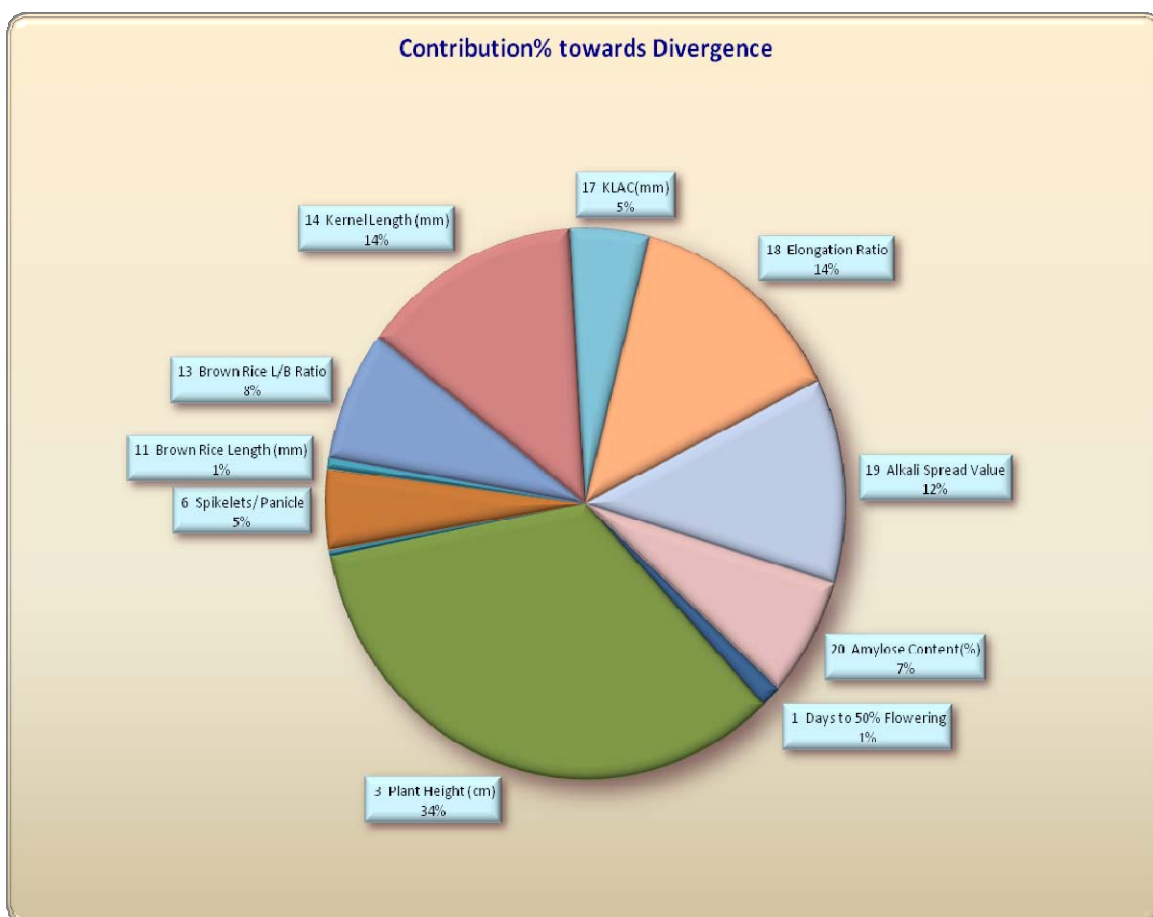
\*LOWEST VALUES; \*\*HIGHEST VALUES

Table 8. Mean values of different clusters with respect to 10 quality traits

	Brown Rice Length (mm)	Brown Rice Breadth (mm)	Brown Rice L/B Ratio	Kernel Length (mm)	Kernel Breadth (mm)	Kernel L/B ratio	KLAC (mm)	Elongation Ratio	Alkali Spread Value	Amylose Content (%)
1 Cluster	6.583*	2.000*	3.292*	6.500*	1.717	3.752*	12.783	1.956**	6.000	22.898
2 Cluster	8.000	2.200**	3.600	7.767	2.000**	3.883	12.400*	1.590*	6.000	20.560*
3 Cluster	6.944	2.000*	3.467	6.700	1.756	3.850	13.594	1.930	3.667	23.973
4 Cluster	8.200	2.020	4.117	7.967	1.700*	4.702**	15.633**	1.951	3.889	24.167**
5 Cluster	7.500	2.000*	3.750	7.367	1.750	4.213	13.247	1.777	3.333*	23.883
6 Cluster	8.692**	2.000*	4.346**	8.429**	1.817	4.637	14.892	1.722	6.458**	23.713

\*LOWEST VALUES; \*\*HIGHEST VALUES

Fig. 1 Relative disposition of clusters showing average genetic distance ( $D^2$ ) between and within them



**Fig. 2 Percentage contribution towards total Divergence**

Cluster IV genotypes are designated by more number of effective panicles and spikelet fertility also having excellent basmati cooking qualities viz highest kernel L/B ratio and kernel length after cooking. Cluster V genotypes represent lowest alkali spreading value. Cluster VI represents highest test weight which has direct bearing on yield. This cluster is also possessing excellent basmati grain qualities like highest brown rice length, kernel length and lowest brown rice breadth and low kernel breadth. All the genotypes included in this cluster possessing a good combination of highest grain yield without compromising on quality which shows importance of using genotypes in this cluster as one of the parents in breeding programme. For instance, Pusa basmati-1, in addition to remaining as a landmark variety, it served as donor variety for developing many progressively improved basmati quality varieties and hybrids (Siddiq et al., 2012). It was observed that except cluster VI, no other cluster contained the combination of both yield and quality features together in its member. Considering the importance of genetic distance, relative contributions of characters towards total divergence, the present investigation suggests that parental lines selected from cluster VI for plant height, test weight, kernel length, alkali spread value and amylose content; cluster IV for effective number of panicles, spikelet fertility, kernel L/B ratio and kernel length after cooking; cluster III for panicle length and filled grains could be used in breeding programme to isolate superior recombinant genotypes with higher yield and best basmati quality. However, it was noted that, unlike the development of non-basmati hybrids, the task of developing basmati quality hybrids was challenging as the development of parental lines was required to be incorporated with the basmati quality traits in order to improve the yield potential without sacrificing the special quality features of basmati.

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