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Genetic diversity analysis of Basmati rice (*Oryza sativa*) genotypes for grain yield and quality traits

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ABSTRACT

The present study was carried out to determine the genetic diversity and association among 36 Basmati rice (*Oryza sativa* L.) genotypes based on morphological and quality traits. Different genotypes were evaluated in randomized block design (RBD) at Rice Research Station, Kaul (India) during rainy (*kharif*) season 2016 and 2017. Principle component analysis indicated that first five principle components (PC) accounted for more than 80% (PC1=35.33%, PC2=19.84%, PC3= 11.30, PC4=8.08 and PC5=6.81%) of the total variation. Principle component 1 was loaded with number of tiller per plant, panicle length, panicle weight, number of spikelets per panicle, thousand grain weight, grain yield per plant and harvest index while plant height, biological yield per plant, hulling per cent, milling per cent, head rice recovery per cent, alkali spreading value and amylose content were present in principle component 2. Cluster analysis divided the genotypes into five clusters and genotypes with earliness and yielding traits were present in cluster 1. A high positive and significant correlation of grain yield per plant was seen with number of tillers per plant, panicle length, panicle weight, number of spikelets per panicle, biological yield per plant, harvest index, alkali spreading value and amylose content. This study would be helpful in identifying the diverse and donor parents for important traits which can be used for genetic improvement programs of Basmati rice.

Keywords: Basmati, Correlation, Diversity, Principle components, Rice

Basmati rice (*Oryza sativa* L.) is a long scented grain rice which occupies a specific place in Indian sub-continent and is cultivated for more than 250 years by growers (Siddiq *et al.* 2012). The most important characteristics of Basmati rice include extra-long and slender grains, length breadth ratio, fluffy texture, good scent and excellent cooking and eating quality (Vemireddy *et al.* 2007). India is the leading producer as well as exporter of Basmati rice. During 2018–19, India exported nearly 4.4 million tonnes of Basmati rice worth 4.7 billion dollars (NCML 2019). Middle East countries Iran, Iraq, Saudi Arabia, United Arab Emirates and Kuwait are the major importers of Basmati rice from India (Mahajan *et al.* 2018). In spite of many traditional and evolved Basmati rice variety already under cultivation, research is still in progress for the development of high yielding, stable and good quality varieties to meet the consumers demand (Kaur *et al.* 2011). Large areas under cultivation dominated by a single or few varieties with related genetic background led to vulnerability to some insects, diseases or abiotic stresses (Pandey *et al.* 2011). Development of improved genotypes against these unfavourable conditions largely depends on genetic diversity present in the germplasm. Genetic diversity is an important criterion of parent selection in a crossing program. The availability of positive segregants with high yield and better quality depends largely on the genetic divergence between the parents. In comparison to other major food crops, an abundant amount of genetic diversity is present in the rice germplasm (Garris *et al.* 2005) which is a pre-requisite for starting a new genetic improvement program. However a small proportion of total diversity has been used in breeding which results in genetic relatedness among the modern varieties of rice crop (Das *et al.* 2013). Therefore, assessment of genetic diversity is very important for the identification of diverse donor parents for desirable traits. In present study, hierarchical clustering and principal component approaches were used to categorise the genotypes on the basis of similarity and dissimilarity among them and to identify the important traits explaining maximum amount of variation present in the germplasm.

MATERIALS AND METHODS

Thirty six Basmati rice genotypes, viz. Pusa Basmati 1121, Pusa Basmati 1509, Pusa Sugandh 2, Pusa Sugandh 3, Pusa Sugandh 5, Pusa Basmati 6, Pusa Basmati 1, Improved

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Pusa Basmati 1, HKR 98-476, HKR 03-408, HKR 06-434, HKR 06-443, HKR 06-487, HKR 06-417, HKR 08-425, Haryana Mahak 1, Haryana Basmati 1, Taraori Basmati, Super Basmati, CSR-30, Basmati 370, Pusa 1826-12-271-4, CSR TPB-1, Pusa 6295-2, Pusa 1734-8-3-85, HKR -11-509, Pusa 1475-03-42-45-119-1, SJR-70-3-2, HKR 11-447, HUBR-16, PAU-6297-1, UPR-386-9-1-1, Pusa 1656-10-705, Pusa 1637-2-8-20-5, Pusa 1884-3-9-175 and Pusa 1884-9-12-14 were grown in randomized block design with three replications at Rice Research Station, Kaul (India). Data on different morphological and quality traits were recorded for two seasons i.e. *kharif* 2016 and 2017. Plot size was maintained as 5 rows of 1 m length with spacing of 15 × 20 cm from plant to plant and row to row, respectively. Twenty seven days old seedlings were transplanted with 2–3 seedlings per hill. The inorganic fertilizers were applied @N (90 kg/ha), P (30 kg/ha) and K (30 kg/ha) and irrigation was applied at 3 days interval.

Data recording and analysis: Data for days to 50% flowering (DF) were recorded on whole plot basis and on five randomly selected plants for plant height (PH), number of tillers per plant (NTPP), panicle length (PL), panicle weight (PW), number of spikelets per panicle (NSPP), per cent filled spikelets per panicle (PFS), test grain weight (TGW), grain yield per plant (GYPP), biological yield per plant (BYPP) and harvest Index per cent (HI). Hulling per cent (H), milling per cent (M) and head rice recovery per cent (HRR) was measured according to the methods of Khush *et al.* (1979). Alkali spreading value (ASV) was measured on a 7 point scale as suggested by Little *et al.* (1958) and amylose content value was measured as per the protocol suggested by Juliano (1971). Principal component analysis (PCA) and cluster analysis was performed using PAST4.03 and JMP software version 15.2.

RESULTS AND DISCUSSION

Principal component analysis: Principal component analysis approach is the commonly used multivariate technique for the assessment of genetic diversity and identification of the most important traits which accounts for maximum variation among the genotypes (Ringner 2008). Eigen value estimated using principal component analysis revealed that first five principal components (PCs) with eigen value >1 represent more than 80% of total variation among the genotypes of rice (Table 1). The PC1 accounted 35.33% of the total variability and positively associated with number of tiller per plant, panicle length, panicle weight, number of spikelets per panicle, thousand grain weight, grain yield per plant and harvest index. The second PC accounted 19.84% of the total variation and positively defined by plant height, biological yield per plant, hulling per cent, milling per cent, head rice recovery per cent, alkali spreading value

Table 1 Eigen value, eigen vectors and genotypes of first five PCs for different morphological and quality traits

	PC1		PC2		PC3		PC4		PC5	
Eigen value	5.65		3.17		1.81		1.29		1.09	
Per cent	35.33		19.84		11.30		8.08		6.81	
Cumulative per cent	35.33		55.16		66.46		74.54		81.35	
Variable	*Eigen vectors*	*Genotype*	*Eigen vectors*	*Genotype*	*Eigen vectors*	*Genotype*	*Eigen vectors*	*Genotype*	*Eigen vectors*	*Genotype*
DF	-0.206	Pusa Basmati 1, Pusa Basmati 6, Pusa 1656-10-705, Pusa Basmati 1509, Pusa Basmati 1121, Improved Pusa Basmati 1 and Pusa 1637-2-8-20-5	0.241	HKR 98 476, HKR -11-509, Pusa Basmati 1121, Haryana Basmati 1, Taraori Basmati, Basmati 370, CSR-30	0.346	Pusa 1884-3-9-175, Pusa Basmati 6, Pusa 1734-8-3-85, Taraori Basmati and HKR-11-509	-0.169	Pusa Basmati 1121, Taraori Basmati, HKR 06-443, PAU-6297-1 and Pusa Basmati 1509	0.208	Pusa 6295-2, HKR 11-447, Pusa 1826-12-271-4 and Pusa 1734-8-3-85
PH	-0.163		0.368		0.172		0.385		-0.214	
NTPP	0.381		0.036		0.146		0.106		0.151	
PL	0.365		0.122		0.132		0.175		0.143	
PW	0.275		-0.175		0.027		-0.191		-0.117	
NSPP	0.354		0.076		0.166		-0.126		-0.114	
PFS	-0.072		-0.011		-0.138		0.731		0.256	
TGW	0.275		-0.054		-0.011		0.319		-0.214	
BYPP	0.136		0.281		0.530		0.034		0.178	
GYPP	0.393		0.030		0.159		-0.047		0.091	
HI	0.319		-0.201		-0.261		-0.061		-0.056	
H	0.105		0.420		-0.210		-0.215		0.287	
M	0.092		0.387		-0.419		-0.051		0.215	
HRR	0.110		0.361		-0.402		-0.022		0.009	
ASV	0.185		-0.337		-0.075		0.161		0.367	
AC	0.173		0.249		-0.058		0.109		-0.650	

Variable details given under Materials and Methods.

and amylose content. The third PC contributed 11.30% and variation of days to 50% flowering, biological yield per plant, milling per cent and head rice recovery per cent was related with this PC. The fourth principal component had 8.08% of total variability among genotypes and positively influenced by plant height and per cent filled spikelets. The PC5 accounted for 6.81 of the variation and positively associated with alkali spreading value and amylose content. Genotypes with high value in a particular principal component can be selected for the genetic improvement of variables selected in that particular PC. Therefore, genotypes having PC score more than one in positive direction are selected from each principal component (Table 1). Pusa Basmati 1, Pusa Basmati 6, Pusa 1656-10-705, Pusa Basmati 1509, Pusa Basmati 1121, Improved Pusa Basmati 1, Pusa 1637-2-8-20-5 had high value in PC1 indicated their positive association with grain yield and its component traits like number of tillers per plant, panicle length, panicle weight, number of spikelets per panicle, thousand grain weight, grain yield per plant and harvest index. High PC value of HKR 98-476, HKR 11-509, Pusa Basmati 1121, Haryana Basmati 1, Taraori Basmati, Basmati 370, CSR-30 in PC2 exhibited for quality traits, hulling per cent, milling per cent, head rice recovery per cent, alkali spreading value, amylose content, plant height and biological yield per plant. High PC value recorded by Pusa 1884-3-9-175, Pusa Basmati 6, Pusa 1734-8-3-85, Taraori Basmati and HKR -11-509 in PC3 for traits like days to 50% flowering, biological yield per plant and milling per cent and head rice recovery per cent. High value in PC4 was recorded by Pusa Basmati 1121, Taraori Basmati, HKR 06-443, PAU-6297-1 and Pusa Basmati 1509 for plant height and per cent filled spikelets. Genotypes Pusa 6295-2, HKR 11-447, Pusa 1826-12-271-4, Pusa 1734-8-3-85 had high PC value for alkali spreading value and amylose content. First two PCs accounted 71.47% of the total variation present in the 629 rice genotypes including landraces and breeding lines (Anandan *et al.* 2016). Nearly 78% of the total variation among 123 germplasm lines of *Oryza sativa* and *Oryza glaberrima* was also observed by Maji and Shaibu (2012). Similarly, maximum variation was observed in PC1 in 192 traditional and exotic rice genotypes (Nachimuthu *et al.* 2014).

Cluster analysis: Genetic improvement for grain yield and quality traits are major objectives in Basmati rice breeding, therefore means of different clusters for grain yield, its components and quality traits need to be taken into account for the selection of desirable genotypes (Table 2). The results revealed that cluster 1 (Pusa Basmati 1121, Pusa Basmati 1509, Pusa Sugandh 2, Pusa Sugandh 3, Pusa Sugandh 5, Pusa Basmati 6, Pusa Basmati 1, Improved Pusa Basmati 1, UPR-386-9-1-1, Pusa 1656-10-705, Pusa 1637-2-8-20-5) exhibited high mean for number of tillers per plant, panicle length, panicle weight, number of spikelets per panicle, thousand grain weight, grain yield per plant, harvest index and amylose content. Cluster 2 (HKR 06-434, Pusa 1826-12-271-4, Pusa 6295-2, Pusa 1734-8-3-85, HUBR-16 and Pusa 1884-3-9-175) had high mean for biological yield per plant and alkali spreading value. Cluster 3 (HKR 98-476, HKR 08-425, Haryana Basmati 1, Super Basmati, HKR -11-509, SJR-70-3-2 and HKR 11-447) recorded highest values for hulling%, milling% and head rice recovery% while cluster 4 (HKR 03-408, HKR 06-443, HKR 06-487, HKR 06-417, Haryana Mahak 1, Taraori Basmati, CSR-30 and Basmati 370) recorded high mean for percent filled spikelets. Cluster 1 and cluster 5 (CSR TPB-1, Pusa 1475-03-42-45-119-1, PAU-6297-1 and Pusa 1884-9-12-14) had lowest value for days to 50% flowering and plant height, respectively (Table 2). Genotypes with highly heritable traits like grain yield per plant, earliness and high mean value for other yield contributing traits were found in cluster 1 whereas genotypes with high mean for quality traits were grouped together in cluster 3. The genotypes with high value in PC1 and PC2 of important traits were correlated positively with genotypes in cluster 1 and 3. For the exploitation of heterosis, identification and selection of genetically diverse parent is the first step in hybrid breeding. Therefore genotypes from cluster 1 and cluster 3 can serve as donor parent for developing high yielding and good quality inbred lines in a crossing program. Hierarchical clustering grouped the Basmati rice genotypes into five distinct clusters in which Basmati 370, Taraori Basmati and CSR 30 were related closely with each other and carried in the same group (Sarhadi *et al.* 2011, Khare *et al.* 2014). Based on Ward's dissimilarity matrix, Mishra *et al.* (2019) divided the 35 rice genotypes into three clusters with four, sixteen and fifteen genotypes in cluster 1, cluster 2 and cluster 3, respectively. Likewise, Mahalanobis's D^2 method was used to divide 30 green gram genotypes into 6 clusters based on morphological (Garg *et al.* 2017a) and quality traits (Garg *et al.* 2017b) and 100 wheat plants of F2 population and their parents into 12 clusters (Yadav *et al.* 2018).

Correlation coefficient analysis: The knowledge of degree and direction of association between different component traits and grain yield as well as inter-relation

Table 2 Mean values of different clusters for different traits in Basmati rice

Cluster	DF	PH	NTPP	PL	PW	NSPP	PFS	TGW	BYPP	GYPP	HI	H	M	HRR	ASV	AC
1	94.16	106.82	15.41	30.03	2.48	113.91	83.71	26.99	43.13	16.97	39.41	78.70	67.96	55.33	6.32	23.96
2	102.01	106.74	15.12	29.84	2.45	105.11	83.82	25.57	46.83	16.65	35.74	77.62	65.98	51.98	6.42	21.76
3	104.27	123.11	14.22	29.76	2.13	106.16	83.75	24.78	46.04	16.09	34.90	80.41	70.01	56.71	5.13	23.49
4	102.64	134.29	12.62	28.72	1.97	88.85	85.54	24.88	42.71	13.98	32.92	77.62	66.60	53.59	5.21	23.23
5	99.08	100.53	11.48	27.87	2.02	79.98	84.59	24.50	39.96	13.25	33.12	77.74	66.92	53.94	6.03	21.13

among themselves will be helpful in designing the effective selection strategy for genetic improvement of grain yield (Kumar and Sharma 2006). Therefore, Pearson's correlation coefficient among different traits was analyzed and observed that days to 50% flowering showed a positive correlation with plant height (0.480**) and negative correlation with panicle weight (-0.367*), thousand grain weight (-0.462**), harvest index (-0.586**) and alkali spreading value (-0.421*). Grain yield per plant showed a highly positive correlation with number of tillers per plant (0.939**), panicle length (0.853**), panicle weight (0.523**), number of spikelets per panicle (0.811**), thousand grain weight (0.497**), biological yield per plant (0.491**), harvest index (0.696**), alkali spreading value (0.337*) and amylose content (0.331*). Number of tillers per plant correlated positively with panicle length (0.878**), panicle weight (0.425**), number of spikelets per panicle (0.691**) and thousand grain weight (0.580**). Hulling% correlated positively with milling per cent (0.766**) and head rice recovery per cent (0.592**). Number of tillers per plant (0.409*), panicle weight (0.335*), thousand grain weight (0.331*), grain yield per plant (0.337*), harvest index (0.496**) showed a significantly positive correlation with alkali spreading value whereas days to 50% flowering (-0.421*) and plant height (-0.522**) contributed negatively. Amylose content showed a positive and significant correlation with panicle length (0.400*), number of spikelets per panicle (0.445**), grain yield per plant (0.331*) and head rice recovery (0.360*). Correlation between number of tiller and panicle length with grain yield were reported significantly positive in earlier studies (Kole *et al.* 2008, Eidi *et al.* 2013, Sandhu *et al.* 2013, Oladosu *et al.* 2018).

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