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Variability, Heritability and Diversity Analysis for Some Morphological Traits in Basmati Rice (*Oryza sativa* L.) Genotypes

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Abstract

The present study was conducted at the research farm of Bangladesh Rice Research Institute (BRRI), Gazipur, during July to December (T. Aman season) 2016 to identify potential genotypes and suitable traits of Basmati rice (*Oryza sativa* L.) germplasm for breeding programs. Twenty-six genotypes were evaluated in a randomized complete block design with three replications. All genotypes exhibited a wide and significant variation for 13 morphological traits. Genotypic and Phenotypic co-efficient of variation were the highest for number of filled grains per panicle and 1000-grain weight. Higher heritability was observed for flag leaf width, plant height, number of filled grains per panicle, 1000-grain weight and yield per hill. Grain yield per hill was positively as well as significantly associated with number of filled grain per panicle and grain length. According to D^2 cluster analysis, 26 test genotypes were grouped into 5 clusters. Cluster IV was the largest consisting of 8 genotypes. The first two principal components of 13 traits accounted for about 41.06% of the total variation and indicated a wide variation among the genotypes. The selected best traits were the number of filled grains/panicle and 1000- grain weight which showed high heritability and high genetic advance. Therefore, these traits could be used as selection criteria for desired breeding materials. Moreover, the genotypes under cluster I, cluster II and cluster V might be selected for future hybridization programs.

Keywords: Genetic variability; heritability, correlation, path coefficients, character association, Basmati genotypes, yield and yield components.

1. Introduction

Basmati Rice (*Oryza sativa* L.) popularly known as ‘scented pearl’ is a natural gift exclusively to Indian sub-continent. It is a special type of aromatic rice known to the world for its extra-long grains, pleasant and distinct aroma (Allam *et al.*, 2015).

The Basmati fine rice and traditional aromatic rice have a great demand both in the national and international market (Mannan *et al*., 2012). In fact, aromatic long slender Basmati fine grain rice varieties are very popular in the world market (Yoshihashi, 2005). 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).

Most of the aromatic rice varieties in Bangladesh are of locally adapted, photoperiod-sensitive, and grown during Aman season under rainfed lowland ecosystem. The income potential is higher with aromatic fine rice cultivation, since its cultivation does not usually require additional expenditures whereas, demand is very high in both the domestic and internal market (Islam *et al*., 2016).

Therefore, Basmati rice genotypes can be considered as an export item for Bangladesh after selecting the better performing genotypes with superior traits. Grain yield is dependent on many contributing characters as well as on the environmental influence. Association of different characters is essential to determine their contribution towards yield. The knowledge about genetic variability of yield contributing characters presents the possibilities of the scope of improvement of individual characters.

Furthermore, knowledge of heritability is essential for selection based improvement, as it indicates the extent of transmissibility of a character into future generations (Sabesan *et al*., 2009). Before placing a strong emphasis on breeding for yield improvement traits, the knowledge on the association between yield and yield attributes will enable the breeder in the improvement of yield. The correlation coefficient may also help to identify characters that have little or no importance in the selection program. The existence of correlation may be attributed to the presence of linkage or pleiotropic effect of genes or physiological and development relationship or environmental effect or in a combination of all (Oad *et al*., 2002). The grain yield is the primary target for improvement of rice productivity in both favourable and unfavourable environments from its present level. Keeping in view the above facts, the present investigation was undertaken to assess the genetic variability, heritability, correlation and diversity among yield and its contributing traits in 26 rice germplasm accessions under rainfed ecosystem.

2. Materials and Methods

2.1 Experimental site, experimental design and plant material

The study was conducted at research farm of Bangladesh Rice Research Institute (BRRI), Gazipur, from July to December (T. Aman season), 2016. Geographically, the place is located at about 24.00°N latitude and 90.25°E longitude with an elevation of 8.4 meters from the sea level and is characterized by subtropical climate. The soil of the experimental site was clay loam in texture. The study was laid out as a randomized complete block design (RCBD) with three replications. Twenty-six Basmati type genotypes were selected from BRRI genebank (Table 1).

2.2 Transplantation and management practices

Sprouted seeds were sown in the seedbed. Thirty days-old seedlings were transplanted using single seedling per hill. Fertilizers were applied @ 60:20:40:10 kg N: P: K: S per hectare. However, except N, the other fertilizers were applied at final land preparation. Nitrogen was applied in three equal splits, at 15 days after transplanting (DAT), at 35 DAT, and just before flowering. Intercultural operations and pest control measures were done as and when necessary.

2.3 Data collection

Data were collected on flag leaf length (cm), flag leaf width (cm), culm diameter (mm), days to flowering, number of effective tiller, plant height (cm), panicle length (cm), days to maturity, number of filled grains per panicle, grain length (mm), grain breadth (mm), 1000-grain weight (g) and yield per hill (g).

2.4 Statistical analyses

The analysis of variance and comparison of means were performed by Statistix10 software. Diversity analysis, i.e. cluster analysis and principal component analysis (PCA) was conducted by GENSTAT software (version 5.5).

The genetic parameters, including the genotypic and phenotypic variance, the genotypic and phenotypic coefficient of variance, heritability (broad sense), and the expected genetic advance (GA) were calculated using the formula given by Burton and Devane (1953) and Johnson *et al*., (1955). Genetic advance in percent of mean was calculated by the formula of Comstock *et al*., (1952).

Simple correlations (Pearson) among yield contributing traits and correlation coefficient partitioning into components of direct and indirect effects by path coefficient analysis were accomplished by using R software (version 3.2.1). The genotypic and phenotypic correlations, biplot analysis for the first two principal components (PC1 and PC2) were done using META-R software (version 6.03) (Alvarado *et. al*., 2015).

Table 1. Name, accession number and origin of 26 basmati rice genotype

Sl No	Acc. No.	Genotype	Source/Origin
1	2517	BASH MATI TAPL -90	BRRI Genebank
2	2518	BASH MATI TAPL -91	BRRI Genebank
3	2519	BASH MATI TAPL -92	BRRI Genebank
4	2520	BASH MATI TAPL -93	BRRI Genebank
5	2521	BASH MATI TAPL -94	BRRI Genebank
6	2522	BASH MATI TAPL -95	BRRI Genebank
7	2523	BASH MATI TAPL -96	BRRI Genebank
8	2524	BASH MATI TAPL -97	BRRI Genebank
9	4488	BASMATI (IRGC-3647)	India
10	4489	BASMATI 370 (IRGC-3680)	India
11	4490	BASMATI T3 (IRGC-6447)	India
12	4494	BASMATI 370 (IRGC-10629)	India
13	4495	BASMATI (IRGC-27782)	Pakistan
14	4496	BASMATI NANOT 439 (IRGC-27788)	Pakistan
15	4497	BASMATI PARDNR442 (IRGC27790)	Pakistan
16	4500	BASMATI-1 (IRGC-27798)	Pakistan
17	4501	BASMATI-107 (IRGC-27803)	Pakistan
18	4502	BASMATI-134 (IRGC-27809)	Pakistan
19	4503	BASMATI-372 (IRGC-27823)	Pakistan
20	4504	BASMATI-372B (IRGC-27825)	Pakistan
21	4505	BASMATI-375A (IRGC-27827)	Pakistan
22	4506	BASMATI-376 (IRGC-27828)	Pakistan
23	4507	BASMATI-377 (IRGC-27833)	Pakistan
24	4508	BASMATI-406 (IRGC-27836)	Pakistan
25	4509	BASMATI-433 (IRGC-27836)	Pakistan
26	4510	BASMATI(BEGNI) (IRGC-53639)	India

3. Results and Discussion

3.1 Genetic variation study

The range, mean, variance, coefficients of variation, heritability and the genetic advance of 13 characters are presented in Table 2.

According to the results, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters considered indicating the presence of environmental influence to some degrees in the phenotypic expression of characters. This finding was similar for all the traits observed in another study by Osman *et al*. (2012). GCV was the highest (84.58) for number of filled grains per panicle followed by 1000 grain weight (42.99) and plant height (40.74), indicating a higher degree of genetic variability among the basmati genotypes for these traits. PCV values were also higher for the above mentioned traits. High GCV and PCV for number of filled grains per panicle were also recorded by Mazid *et al*. (2013) as well as by Pandey and Anurag (2010). Heritability (broad sense) ranged from 81.93 to 99.93%, which were relatively higher for almost all the traits studied except for number of effective tillers per hill and days to maturity. Hasan *et al*. (2011) also found similar results in case of effective tillers.

High heritability associated with high genetic advance were found in number of filled grains per panicle and 1000 grain weight, which indicated that the characters were simply inherited in nature and controlled by few major genes or possessed additive gene effects. The heritability estimates with low genetic advance were estimated for flag leaf width, grain breadth, and effective tiller. This implies that non additive gene action may be responsible for the expression of these traits.

Table 2. Estimation of genetic parameters of different quantitative characters in 26 Basmati rice landraces

Character	Mean	Range	V_p	V_g	PCV	GCV	h^2_b	GA (5%)	GAPM
LL	35.17	24.43-45.71	21.71	21.23	12.49	12.35	97.80	7.20	19.30
LW	1.08	0.93-1.25	3.35	3.34	1.74	1.71	99.93	2.88	2.70
CD	5.74	4.72-6.99	0.28	0.26	4.55	4.52	98.74	0.80	7.10
DF	103.87	97.00-114.00	21.97	20.84	3.62	3.53	94.86	7.03	5.43
ET	9.96	5.00-14.00	5.05	4.13	1.44	1.31	81.93	2.91	1.87
PH	159.00	134.75-178.86	111.52	110.43	40.94	40.74	99.02	16.52	64.05
PL	27.75	23.45-31.53	4.94	4.47	12.54	11.93	90.52	3.18	17.94
DM	138.91	129.00-145.00	13.94	12.04	35.58	33.06	86.32	5.09	48.53
FG	99.60	59.80-145.20	480.07	478.71	84.70	84.58	99.72	34.52	133.45
GL	9.18	7.34-11.34	5.10	4.83	3.48	3.39	94.67	3.38	5.21
GB	2.43	2.11-3.37	0.07	0.06	2.48	2.43	96.61	0.37	3.78
TGW	21.04	13.50-28.40	15.11	15.04	43.33	42.99	99.53	6.11	125.39
Y	11.50	5.94-18.32	8.41	8.39	14.24	14.22	99.69	4.57	22.43

V_p= Phenotypic variance, V_g =Genotypic variance, PCV = Phenotypic Coefficient of variation, GCV = Genotypic coefficient of variation, h^2_b = Heritability (Broad sense), GA = Genetic advance, GAPM = Genetic advance in percent of mean.

(LL= Flag leaf length, LW= Flag leaf width, CD= Culm diameter, DF= Days to flowering, ET= Number of effective tiller, PH=Plant height, PL= Panicle length, DM=Days to maturity, FG= Number of filled grain per panicle, GL= Grain length, GB=Grain breadth, TGW=1000-grain weight, Y= Yield per hill)

3.2 Correlation coefficient study

Pearson correlation analysis among yield and its contributing components are shown in Table 3. It revealed that 1000 grain weight possessed significant positive correlation with days to flowering, number of filled grain per panicle and grain breadth. For better understanding correlation coefficients are separated into the genotypic and phenotypic level (Table 4). The genotypic correlation coefficients in most cases were found higher than their phenotypic correlation coefficients indicating the genetic reason of association. In some cases, the phenotypic correlation coefficient was higher than genotypic correlation indicating the suppressing effect of the environment which modified the expression of the characters at phenotypic level. Effective tillers showed positive and significant relationship with culm diameter and days to flowering at both genotypic and phenotypic level.

In addition to that, days to flowering had positively significant association with days to maturity (Kumar *et al*., 2018), grain breadth and 1000 grain weight but significant negative association with panicle length. The aforesaid relationship was similar at both genotypic and phenotypic level. Filled grain per panicle was recorded with significant positive relationship with panicle length. However, thousand grain weight exhibited significant positive relationship with days to flowering, grain breadth and filled grain. Grain yield was positively associated with number of filled grains per panicle, grain length, thousand grain weight (Akter *et al*., 2018), flag leaf width and days to maturity. Association with number of filled grains per panicle and grain length was significant and rests are insignificant.

3.3 Path analysis

In correlation studies, with the increasing number of variables, the indirect association becomes complex and important. In such a situation, path coefficient analysis is useful to find out direct and indirect causes of associations. Path coefficient analysis permits a critical examination to specific factors acting to produce a given correlation and measures the relative importance of each factor. Path coefficient analysis (Table 5) revealed that number of filled grains per panicle and grain length possessed the highest positive effect on grain yield followed by thousand grain weight. This indicates that more filled grain in panicle is the highly reliable component of grain yield. Another important character with high direct effect on seed yield is panicle length which showed a positive direct effect on seed yield along with filled grains per panicle. Hence, number of filled grains per panicle should be given prior attention in rice improvement program because of their major influence on yield. This finding was in accordance with Hasan *et al.* (2010). Negative direct effect was observed for number of effective tillers/plant and plant height. The residual effect of the present study was 0.362, indicating variables studied in the present investigation explained 64% of the variability in yield and therefore, other attributes besides the characters studied are contributing for grain yield per plant.

3.4 Principal component analysis

Eigen values (latent roots) of five principal component axes and percentage of total variation accounted for them obtained from the component analysis are presented in Table 6. The result revealed that the first axis largely accounted for the variations observed among the genotypes (23.47%) followed by the second axis (17.59%). The first five axes accounted for about 77% of the total variations among the 13 characters describing 26 Basmati rice genotypes where only 41.06% variation was accounted for the first two axes. Islam *et al*., (2016) observed that the first nine axes accounted about 90% of the total variations by PCA in 113 aromatic and fine grain rice landraces. On the other hand, Akter *et al*. (2018) and Chakravorty *et al*. (2013) observed the contribution of 80.37% and 75.9% of the first five and four components, respectively to the total variation in rice.

Table 3. Pearson correlation coefficient among yield and yield contributing characters in Basmati rice genotypes

	LL	LW	CD	DF	ET	PH	PL	DM	FG	GL	GB	TGW
LL	1.000	-0.026	-0.324	0.219	0.099	0.009	-0.181	0.005	0.018	0.344	0.043	0.019
LW		1.000	-0.047	0.211	0.064	0.237	0.369*	0.301	0.305	0.233	-0.106	0.215
CD			1.000	0.276	0.613**	-0.013	-0.159	0.158	-0.042	-0.407*	0.465*	0.149
DF				1.000	0.502**	-0.076	-0.458*	0.569**	-0.178	0.011	0.437*	0.447*
ET					1.000	-0.021	0.063	-0.297	-0.097	0.290	-0.356	0.126
PH						1.000	0.285	-0.398*	-0.200	-0.009	0.174	0.163
PL							1.000	-0.199	0.551**	0.016	-0.318	-0.359
DM								1.000	0.129	0.085	-0.089	0.205
FG									1.000	-0.146	-0.356	0.397*
GL										1.000	-0.347	0.036
GB											1.000	0.396*
TGW												1.000

*, **Significant at 5% and 1% levels, respectively.

(LL= Flag leaf length, LW= Flag leaf width, CD= Culm diameter, DF= Days to flowering, ET= Number of effective tiller, PH=Plant height, PL= Panicle length, DM=Days to maturity, FG= Number of filled grain per panicle, GL= Grain length, GB=Grain breadth, TGW=1000-grain weight, Y= Yield per hill)

Table 4. Genotypic (G) and phenotypic (P) correlations among yield and yield contributing characters in Basmati rice genotypes

Traits		LL	LW	CD	DF	ET	PH	PL	DM	FG	GL	GB	TGW
LW	G	-0.029											
	P	-0.028											
CD	G	-0.326	-0.046										
	P	-0.337	-0.045										
DF	G	0.228	0.241	0.285									
	P	0.192	0.240	0.274									
ET	G	0.113	0.110	0.611**	0.517**								
	P	0.145	0.060	0.593**	0.457*								
PH	G	0.028	0.257	-0.013	-0.080	-0.061							
	P	0.027	0.225	-0.035	-0.196	-0.056							
PL	G	-0.184	0.401*	-0.164	-0.459*	0.049	0.288						
	P	-0.209	0.360	-0.176	-0.556**	0.097	0.247						
DM	G	0.007	0.306	0.164	0.587**	-0.318	-0.428*	-0.238					
	P	0.004	0.275	0.153	0.566**	-0.278	-0.473*	-0.255					
FG	G	0.018	0.334	-0.042	-0.167	-0.128	-0.200	0.560**	0.099				
	P	0.022	0.292	-0.040	-0.166	-0.135	-0.201	0.566**	0.102				
GL	G	0.396*	0.273	-0.451*	0.003	0.354	-0.010	0.024	0.108	-0.162			
	P	0.360	0.242	-0.405*	0.044	0.303	-0.020	0.036	0.084	-0.149			
GB	G	0.045	-0.129	0.467*	0.449*	-0.347	0.174	-0.326	-0.075	-0.356	-0.385		
	P	0.042	-0.108	0.464*	0.457*	-0.336	0.168	-0.329	-0.079	-0.353	-0.346		
TGW	G	0.019	0.254	0.150	0.449*	0.129	0.163	-0.367	0.216	0.398*	0.032	0.395*	
	P	0.045	0.227	0.167	0.556**	0.082	0.232	-0.335	0.240	0.411*	0.016	0.410*	
Y	G	0.045	0.269	-0.081	0.140	0.137	0.036	0.079	0.137	0.441*	0.438*	0.135	0.268
	P	0.042	0.232	-0.083	0.138	0.134	0.030	0.075	0.131	0.442*	0.396*	0.133	0.278

*, **Significant at 5% and 1% levels, respectively.

(LL= Flag leaf length, LW= Flag leaf width, CD= Culm diameter, DF= Days to flowering, ET= Number of effective tiller, PH=Plant height, PL= Panicle length, DM=Days to maturity, FG= Number of filled grain per panicle, GL= Grain length, GB=Grain breadth, TGW=Thousand grain weight, Y= Yield per hill)

Table 5. Path analysis showing direct and indirect effects of yield component on Basmati rice genotypes

	LL	LW	CD	DF	ET	PH	PL	DM	FG	GL	GB	TGW	Y
LL	**0.120**	**-0.007**	**0.012**	**0.001**	**-0.009**	**-0.004**	**-0.132**	**0.001**	**-0.016**	**0.069**	**0.007**	**0.002**	**0.045**
LW	-0.003	**0.254**	0.002	0.001	-0.006	-0.101	0.269	0.026	-0.274	0.047	-0.017	0.024	0.222
CD	-0.039	-0.012	**-0.038**	0.002	0.057	0.005	-0.116	0.014	0.038	-0.082	0.074	0.017	-0.080
DF	0.026	0.054	-0.011	**0.006**	0.047	0.032	-0.334	0.049	0.159	0.002	0.070	0.050	0.151
ET	0.012	0.016	0.023	-0.003	**-0.094**	0.009	0.046	-0.026	0.087	0.058	-0.057	0.014	0.087
PH	0.001	0.060	0.001	0.001	0.002	**-0.425**	0.208	-0.034	0.179	-0.002	0.028	0.018	0.036
PL	-0.022	0.094	0.006	-0.003	-0.006	-0.121	**0.729**	-0.017	-0.494	0.003	-0.051	-0.040	0.079
DM	0.001	0.077	-0.006	0.003	0.028	0.169	-0.145	**0.086**	-0.116	0.017	-0.014	0.023	0.123
FG	0.002	0.078	0.002	-0.001	0.009	0.085	0.402	0.011	**0.897**	-0.029	-0.057	-0.045	0.441*
GL	0.041	0.059	0.016	0.001	-0.027	0.004	0.012	0.007	0.131	**0.202**	-0.055	0.004	0.393*
GB	0.005	-0.027	-0.018	0.003	0.033	-0.074	-0.232	-0.008	0.319	-0.070	**0.160**	0.044	0.136
TGW	0.002	0.055	-0.006	0.003	-0.012	-0.069	-0.262	0.018	0.356	0.007	0.063	**0.112**	0.268

Residual Effect= 0.362904

*, **Significant at 5% and 1% levels, respectively.

(LL= Flag leaf length, LW= Flag leaf width, CD= Culm diameter, DF= Days to flowering, ET= Number of effective tiller, PH=Plant height, PL= Panicle length, DM=Days to maturity, FG= Number of filled grain per panicle, GL= Grain length, GB=Grain breadth, TGW=1000-grain weight, Y= Yield per hill)

Table 6. Latent roots (Eigen values) and their variation in five quantitative characters in 26 Basmati rice landraces

Principal component axes	Latent roots	% Variation	Cumulative % of variation
I	3.052	23.47	23.47
II	2.287	17.59	41.06
III	1.912	14.71	55.77
IV	1.650	12.69	68.46
V	1.114	8.57	77.03

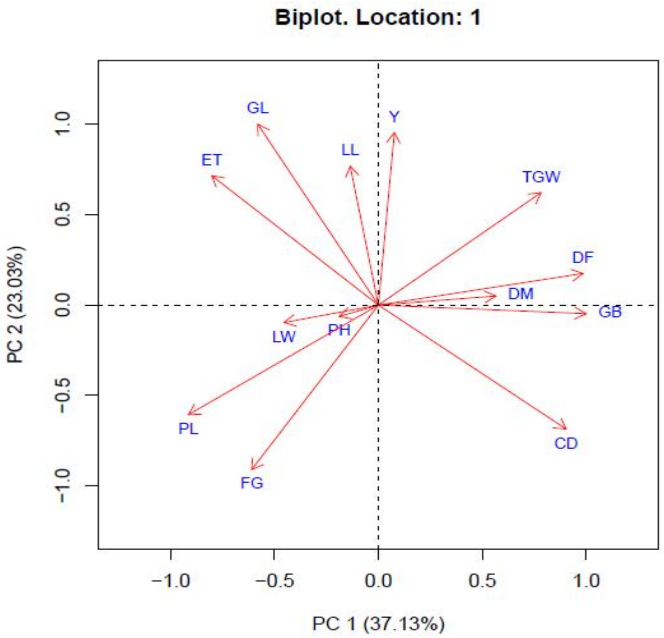

Figure1. Biplot analysis for the first two principal component PC1 and PC2

(LL= Flag leaf length, LW= Flag leaf width, CD= Culm diameter, DF= Days to flowering, ET= Number of effective tiller, PH=Plant height, PL= Panicle length, DM=Days to maturity, FG= Number of filled grain per panicle, GL= Grain length, GB=Grain breadth, TGW=1000-grain weight, Y= Yield per hill)

Biplot analysis indicates that yield is strongly influenced by flag leaf length, grain length, number of effective tiller, 1000 grain weight, days to flowering and days to maturity as those lines with arrow are close to yield. In addition to that, the first two principal component PC1 and PC2 accounted for 37.13% and 23.03% variation, respectively and combinedly they contribute for 41.06% of total variation.

Based on morphological diversity, twenty-six Basmati genotypes were grouped into five clusters (Table 7). Islam *et al*., (2014), Akter *et al*., (2016) and Ahmed *et al*. (2010) reported six clusters each. Besides that, Islam *et al*. (2017) and Siddique *et al*. (2013) reported five clusters each in their experiment with rice genotypes. The distribution pattern revealed maximum number of genotypes in cluster IV (eight genotypes) followed by six genotypes in cluster I and four in cluster II, III and V.

Intra- and inter cluster distances are presented in Table 8. There were no considerable variations in intra cluster distances which ranged from 0.54 in cluster II to 0.88 in cluster I indicating homogeneous nature of the genotypes within the cluster. The highest intra cluster distance was computed for cluster I (0.88) which was comprised of six genotypes followed by cluster V (0.66) with four genotypes. The genotypes under cluster I (with the highest intra cluster mean) were heterogeneous in some extent and genotypes under cluster II (with the lowest intra cluster mean) were comparatively homogenous.

The inter cluster distances ranged from 1.67 to 5.93 indicated a poor genetic diversity among the genotypes. Similar results were found by Salgotra *et al*., (2017). Regarding inter-cluster distance, cluster II showed the maximum genetic distance (5.93) from cluster V followed by cluster III (5.46) from cluster II and so on. Cluster V produced the highest inter-cluster distances (D^2 values) with all other clusters showing considerable diversity between the genotypes and the genotypes in these clusters could be used as parents in future hybridization programme.

Table 7. Distribution of 26 Basmati rice genotypes into five clusters

Cluster	Number of genotypes	% of total genotypes	Name of genotypes
I	6	23.09	BASH MATI TAPL-94, BASH MATI TAPL-97, BASMATI T3 (IRGC-6447), BASMATI-134 (IRGC-27809), BASMATI-375A (IRGC-27827), BASMATI-406 (IRGC-27836)
II	4	15.38	BASH MATI TAPL-92, BASMATI (IRGC-27782), BASMATI-1 (IRGC-27798), BASMATI (BEGNI) (IRGC-53639)
III	4	15.38	BASH MATI TAPL-90, BASH MATI TAPL-93, BASMATI NANOT 439 (IRGC-27788), BASMATI-107 (IRGC-27803)
IV	8	30.77	BASH MATI TAPL-91, BASH MATI TAPL-97, BASMATI 370 (IRGC-3680), BASMATI 370 (IRGC-10629), BASMATI PARDNR442 (IRGC27790), BASMATI-372B (IRGC-27825), BASMATI-377 (IRGC-27833), BASMATI-433 (IRGC-27836)
V	4	15.38	BASH MATI TAPL-95, BASMATI (IRGC-3647), BASMATI-372 (IRGC-27823), BASMATI-376 (IRGC-27828)

Table 8. Intra (bold) and inter-cluster distances (D^2) among 26 Basmati rice landraces

Cluster	I	II	III	IV	V
I	**0.8896**	2.791	2.363	1.669	3.305
II		**0.5480**	5.464	2.584	5.926
III			**0.6504**	2.256	4.560
IV				**0.6068**	4.379
V					**0.6621**

Table 9. Cluster means for 13 characters in Basmati rice genotypes

Characters	I	II	III	IV	V
LL	33.22(L)	36.90	42.02(H)	33.61	33.42
LW	1.07	1.12(H)	1.00(L)	1.10	1.04
CD	6.19(H)	5.80	5.33(L)	5.74	5.59
DF	108.67(H)	106.50	103.00	101.67	101.00(L)
ET	9.00	8.88(L)	11.00	10.17	11.14(H)
PH	159.30	162.67	140.12(L)	154.93	163.57(H)
PL	25.53 (L)	27.65	26.21	29.93(H)	27.37
DM	140.00 (H)	139.75	138.50	139.00	137.00(L)
FG	94.50	102.95	92.50	131.62(H)	85.40 (L)
GL	9.29	9.12	9.68(H)	9.05(L)	9.17
GB	2.78(H)	2.41	2.23(L)	2.34	2.42
TGW	25.82 (H)	17.95(L)	18.21	19.03	21.88
Y	15.15(H)	10.39(L)	13.85	10.77	11.16

(LL= Flag leaf length, LW= Flag leaf width, CD= Culm diameter, DF= Days to flowering, ET= Number of effective tiller, PH=Plant height, PL= Panicle length, DM=Days to maturity, FG= Number of filled grain per panicle, GL= Grain length, GB=Grain breadth, TGW=1000-grain weight, Y= Yield per hill)

The highest cluster means for yield, 1000 grain weight, culm diameter, days to flowering and grain breadth were obtained from cluster I (Table 9). The highest panicle length and filled grains per panicle were found in cluster IV. In addition to that, tallest plants, highest number of effective tillers along with shortest days to flowering and days to maturity were observed in cluster V. Furthermore, cluster III was characterized with the lowest cluster means for flag leaf width, culm diameter, plant height and grain breadth whereas possessed highest cluster means for flag leaf length and grain length. Cluster II had no highest class mean value other than for flag leaf width. Moreover, the cluster showed lowest mean values for number of effective tiller, 1000 grain weight and ultimately resulted in lowest yield.

Cluster means for the characters studied revealed that the maximum desirable characters were accumulated in cluster I and as a result higher grain yield (15.15 g/hill) was obtained in this cluster. However, considering the yield, 1000 grain weight, crosses involving cluster I and cluster II may exhibit high heterosis for yield. Again, considering growth duration and number of effective tiller, crosses between cluster I and V may exhibit higher heterosis for earliness and effective tiller.

It is assumed that a cross combination between parents of most divergent clusters will exhibit maximum heterosis. The objective of breeding is not only high heterosis but also to achieve a high level of yield and reducing the life duration. In the present study the maximum distances existed between cluster II and V. However, considering the cluster means and inter-cluster distances crosses between the genotypes of cluster I and cluster II, cluster I and cluster V would exhibit high heterosis as well as higher level of yield potential. So, based on this result, the genotypes under cluster I, cluster II and cluster V might be selected for hybridization program.

4. Conclusions

The highest GCV was recorded for number of filled grains per panicle followed by 1000 grain weight and plant height. High heritability associated with high genetic advance was observed in number of filled grains per panicle and 1000 grain weight. Moreover, grain yield had significant correlation with number of filled grains per panicle and grain length. The cluster analysis placed 26 Basmati rice genotypes into five groups. Considering the highest inter cluster distance, parent materials selected from cluster I, cluster II and cluster V might be judicious for crossing purpose.

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