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Morpho-genetic Evaluation of Rice Genotypes (*Oryza sativa* L.) Including Some Varieties and Advanced Lines Based on Yield and Its Attributes

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ABSTRACT

In breeding programs, direct selection based on yield is very difficult due its polygenic nature. Therefore, breeders need to consider association of numerous yield related attributes with yield and among themselves. In this study, 43 rice genotypes including some released varieties and advanced lines were evaluated based on morpho-genetic parameters. A field experiment was conducted at the field laboratory of Genetics and Plant Breeding Department, Bangladesh Agricultural University using a randomized complete block design with three replications. Analysis of variance revealed that all genotypes exhibited significant variations ($P \leq 0.001$) for all considered traits except leaf length indicating a wider extent of variability for selection. Greater phenotypic coefficient of variation (PCV) compared to corresponding genotypic coefficient of variation (GCV) for all the traits representing environmental influence on the studied traits. High GCV and PCV values were observed for the most important yield related traits like seedling height, leaf length, flag leaf area, flag leaf angle, number of effective tiller hill^{-1}, 1000-grain weight and yield plant^{-1}. These results suggested that selecting genotypes with these traits could be way for attaining enhancement in rice yield. Majority of the traits displayed high heritability (>60%) with high genetic advance (>20%) pointing towards non-additive gene action suggesting selection should be practiced carefully. Correlation study explored significant positive and negative association among yield and related attributes. Principal component analysis revealed the most important traits contributing to the variations among the genotypes. According to cluster analysis, 43 genotypes were grouped into 4 clusters among which genotypes within cluster I and cluster III might be selected for future rice breeding programs regarding yield potentiality and other related traits.

Introduction

The social as well as economic livelihood of Bangladeshi people are dominated by rice cultivation. Enhancement in yield is the key factor for achieving food security in Bangladesh as about 158.9 million people of Bangladesh depends on rice for their major food source (BBS, 2017). Therefore, development of high yielding rice genotypes associated with anticipated agronomic traits and adaptation capacity in diverse environment is the crying necessity for coping with the increasing demand. But the complex polygenetic character of yield that is affected by its component traits misleads the plant breeders for its direct selection. Therefore, it is very urgent to know the association among yield and its component traits (Akinwale *et al.,* 2011). Broad spectrum diversity in agro-climatic, physiographical, soil and hydrological condition makes this country a great source of endemic landraces especially of rice with distinctive phenotypic and genetic characteristics (Sweeney *et al.,* 2007). Exploring this existing diversity in rice germplasm surely leads to identify the novel genes and speads up the progress in rice breeding (Thomson *et al.,* 2007). For selecting the best breeding procedures in rice, it is essential to know the morpho-genetic variation in different yield related traits (Hannan *et al.,* 2020). Actually noticable genetic variability among the individuals in breeding materials helps to find out the most efficient selection procedure (Ragvendra *et al.,* 2011). Morphological traits are being diversely used as a parameter for variability and trait association in rice. Although having high environmental influences, evaluation based on morphplogical traits are are still feasible for selection (Megloire *et al.,* 2005). Genetic parameters like the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) are useful biometric tools for measuring genetic variability (Aditya

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et al., 2011). 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 (Jayasudha *et al.,* 2010). In this aspect correlation studies assist plant breeders in the process of more precise selection (Ratna *et al.,* 2015) whereas heritability estimates express the extent of transmissibility of a character into future generations (Sabesan *et al*., 2009). Cluster analysis is a tool for diversity analysis which differentiates the genotypes into groups based on their similar performance in terms of different traits (Vural *et al.,* 2007). Previous literatures revealed that in Bangladesh there exists greater genetic diversity in rice for yield and its related attributes (Yesmin *et al.,* 2014; Ahmed *et al.,* 2016; Akter *et al.,* 2016; Akter *et al.,* 2018a,b,c; Islam *et al.,* 2018, Hannan *et al.,* 2020). However, even thousands of important allelic variants of economic value features remain unexplored. So these diversities need to be explored for facing the current and future challenge in rice breeding. Therefore, the present study was planned to evaluate a set of 43 rice genotypes based on morpho-genetic parameters with an aim to characterize these different rice accessions for providing a solid basis for selection and ultimately for the improvement of rice yield.

Materials and Methods

Experimental site and materials

This field experiment was performed at the "Genetics and Plant breeding Field Laboratory" of Department of Genetics and Plant Breeding, Bangladesh Agricultural University. The experimental site was located in the sub-tropical climate zone, characterized by heavy rainfall during the months from May to September and scanty rainfall in the rest of the year.

Table 1. List of the studied 43 rice genotypes including some varieties and advanced lines

Sl.	Genotype	Sl.	Genotype	Sl.	Genotype
1	BAU-280-80-28	17	BRRI dhan 54	33	BR12
2	BRRI dhan 47	18	Binadhan-3	34	BRRI dhan 68
3	BRRI dhan 3	19	BAU 6-246	35	Binadhan-7
4	ACE-441	20	BRRI dhan 52	36	BRRI dhan 72
5	Binadhan-8	21	ACE-4126	37	BRRI dhan 54
6	BRRI dhan 33	22	BRRI dhan 44	38	BRRI dhan 39
7	BRRI dhan 51	23	Binadhan-9	39	IR09F534
8	Binadhan-10	24	BRRI dhan 28	40	BR10
9	Kalijira 2	25	BAU104-33-36-7	41	BAU-125-4-69-28
10	BRRI dhan 40	26	ACE-6106	42	BRRI dhan 34
11	BRRI dhan 62	27	BRRI dhan 48	43	ACE-4148
12	BR11	28	BRRI dhan 46		
13	BRRI dhan 41	29	BR23		
14	BR26	30	ACE-4496		
15	Binadhan-17	31	BAU 125		
16	BRRI dhan 57	32	BRRI dhan 51		

The experimental materials consisted of forty three rice genotypes including some varieties and advanced lines (Table 1) and all are collected from "Genetics and Plant breeding Field Laboratory" of Department of Genetics and Plant Breeding, Bangladesh Agricultural University.

Experimental design and plant growth

A randomized complete block design along with three replications was used for this study. Seedlings of fourty three rice genotypes were sown in raised seedbed on 20 July, 2018. Seedbeds were prepared by raising the soil from the field surface to 5-10 cm above and then puddling. Transplantation to the main plot was performed when seedlings were thirty days old. One seedling was transplanted per hill for all rice genotypes. Plot size was 1m × 1m. Row to row and plant to plant distances were maintained as 20 cm and 15 cm, respectively. Maturity time varies among the genotypes. Harvesting was done at the time of 90-95% of the plant population of each plot reached to maturity.

Data collection

For each genotype of each replication, five plants were chosen randomly. From them data were taken on the selected traits. The studied yield and related attributes were seedling height (SH), leaf length (LL), leaf width (LW) leaf angle (LAN), flag leaf area (FLA), flag leaf angle (FLAN), culm length (CL), culm diameter (CD), internode length (IL), number of tiller hill^{-1} (NTH), number of effective tiller hill^{-1} (ETH), panicle length (PL), secondary branch in panicle (SB/P), filled grain panicle^{-1} (FG), unfilled grain panicle^{-1} (UFG), grain length (GL), grain breadth (GB), grain length-breadth ratio (GL/GB), ligule length (LIL), 1000-grain weight (TGW) and yield plant^{-1} (Y/P).

Statistical analysis

The collected data from 43 rice genotypes for various morphological traits related to yield were statistically analysed by MINITAB$^{®}$17 statistical software packages (Minitab Inc., State College, Pennsylvania, USA) and MSTAT computer software. Two-way Analysis of Variance (ANOVA) was performed for studied traits following a general linear model (GLM) to find out the variation among genotypes. MSTAT computer software was used for *posthoc* analyses. Genotypic and phenotypic variances, heritability (%), genetic advance were estimated according to the formula given by Johnson *et al.* (1955); GCV and PCV values were estimated according to the formula given by Burton and Devane (1953) and Singh and Chaudhury (1985); GA (%) was calculated by the formula of Comstock and Robinson (1952). Diversity analysis, i.e. principal component analysis (PCA) and cluster analysis was executed using MINITAB$^{®}$17 statistical software packages. Cluster analysis was accomplished by using the average values for each trait of each genotype following Squared Euclidean Distance method.

Results and Discussion

Analysis of Variance

The analyses of variances of 43 rice genotypes for quantitative traits showed that the mean squares due to genotypes were highly significant ($P \leq 0.001$) for all the studied traits except leaf length (Table 2). The result indicated possible amount of variability among the genotypes. This gives the rice breeder an opportunity to improve these traits through selection and hybridization. In previous studies of evaluating different rice genotypes, similar significant genetic differences were reported (Augustina *et al.,* 2013; Pradhan *et al.,* 2015; Abebe *et al.,* 2017; Iqbal *et al.,* 2018, Hannan *et al.,* 2020). Mean performances of the genotypes for their studied morphological traits exposed significantly different performances among the rice genotypes (Table 3). The current study revealed that mean values for number of effective tillers hill^{-1} ranged from 5.33 to 15.00. Effective tiller is one of the considered yield contributing traits, because panicle bearing tillers will obviously bring upsurge in the final yield. Kalijira 2 (15.00) produced utmost number of effective tillers hill^{-1} followed by BRRI dhan 44 (14.33) (Table 3a). Flag leaf area is very important character as it is responsible for transferring assimilates to developing grains. Perusal of Table 3a revealed that the maximum flag leaf area (57.57 cm^2) was calculated for IR09F534, followed by BRRI dhan 41 (54.92 cm^2) and BR11 (51.33 cm^2). Panicle length is also one of the major traits assessed by rice breeders in yield related research since longer panicles with more filled grains will obviously lead to higher return. Furthermore, research studies conducted previously found that rice yield is the product of number of panicles per unit area, percentage of filled grains panicle^{-1} and 1000-grain weight (Garcia *et al.,* 2015; Li *et al.,* 2019). Rice production can be enhanced by improving these traits. As represented in Table 3b, mean values for panicle length ranged between 18.00 cm to 35.00 cm. The longest panicles (35.00 cm) were produced by Kalijira 2, BR26, BAU104-33-36-7 and ACE-6106 (Table 3b). Whereas ACE-441 (147.3) produced highest filled grain per panicle and Binadhan-10 (20.67), BRRI dhan 33 (20.00), BRRI dhan 41 (19.33), BAU-280-80-28 (18.67), BAU 125 (18.00) produced highest unfilled grain per panicle (Table 3b). Highest 1000-grain weight was calculated for BRRI dhan 3 (27.98g) followed by BRRI dhan 52 (27.53g) and BR26 (27.14g) whereas the range arranged within 9.27g to 27.98g (Table 3b). Rice breeders give sharp focus on the development of high yielding rice cultivars with consistent yield performance (Iqbal *et al.,* 2018). On the basis of mean performance of yield plant^{-1}, BR26 (39.93g) produced highest yield followed by BRRI dhan 34 (32.70g), BRRI dhan 52 (30.94g) and Kalijira 2 (29.81g) (Table 3b). It is formerly known that mean performance of plant materials aids the determination of genotypic diversity (Iqbal *et al.,* 2018). In present study significant amount of differences among the studied rice genotypes regarding all the considered traits (Table 3a, b) indicated divergence of the genotypes under study. This result had similarities with the finding of Hannan *et al.* (2020).

Phenotypic and Genotypic Coefficients of Variation

For being a polygenic trait, rice grain yield is largely influenced by environment and determined by the nature and magnitude of their genetic variability in which they grow (Singh *et al.,* 2000). The knowledge of genetic variability is essential in breeding for selecting the desired types. Studying the genetic variability is pre-requisite in rice breeding program because effective breeding depends on the presence of the existing variability. Therefore, in the beginning of any rice breeding programs, assessing the genetic variability through appropriate parameters like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is very important (Abebe *et al.,* 2017). In present study, assessment of genetic variability parameters revealed that majority of the studied traits had higher values (>20%) for PCV except moderate values (10-20%) for leaf width, culm diameter, number of tiller hill^{-1}, panicle length, secondary branch in panicle, filled grain panicle^{-1} and grain length (Table 2). In the same manner, the magnitude of GCV was also high (>20%) for seedling height, leaf length, leaf angle, flag leaf area, flag leaf angle, culm length, internode length, number of effective tiller, unfilled grain panicle^{-1}, grain breadth, grain length-breadth ratio, ligule length, 1000-grain weight and yield plant^{-1} (Table 2) suggesting that rice yield could be enhanced through selecting these traits. The extent of PCV fluctuated from 11.16% (culm diameter) to 55.62% (flag leaf angle), while the extent of GCV varied from 9.41% in culm diameter to 54.95% in flag leaf angle (Table 2). The differences in PCV and GCV ranged from 0.04% (1000-grain weight) to 6.25% (unfilled grain panicle^{-1}) (Table 2) representing the appreciable role of genotypes over environment thus indicating less environmental effect on these attributes. It also suggested the effectiveness of the selection process based on these traits. The result had unison and some contradiction with some former findings (Kole *et al.,* 2008; Bagati *et al.,* 2016; Prasad *et al.,* 2017; Abebe *et al.,* 2017; Gour *et al.,* 2017; Sumanth *et al.*, 2017; Iqbal *et al.,* 2018 and Hannan *et al.,* 2020).

Broad-sense heritability and genetic advance

For easy prediction of selection procedures in succeeding generations, plant breeders must have brief idea about the magnitude of transmissibility of a particular trait (Khaliq *et al.,* 2009). Heritability estimate is the proportion of variation transmissible to the progenies in subsequent generations where genetic advance measures the genetic gain in a selection process. According to Johnson *et al.* (1955), heritability was classified as low (<30%), medium (30-60%) and high (>60%). Knowledge on heritability coupled with genetic advance produce more reliable selection value because heritability alone does not indicate the amount of genetic improvement (Johnson *et al.,* 1955; Abebe *et al.,* 2017). In present study, extent of broad-sense heritability ranged from 61.83% (panicle length) to 99.59% (1000-grain weight) (Table 2). Almost all the studied traits showed high heritability (>60%) with high genetic advance (>20%). Except traits like leaf width, culm diameter and panicle length exhibited high heritability (>60%) with moderate genetic advance (10-20%). This result pointed out non-additive gene action suggesting careful selection practice (Iqbal *et al.,* 2018). Most of the traits displayed high heritability indicating less influence of environment upon these traits (Babu *et al.,* 2012). Traits with high heritability and genetic advance were mostly governed by additive gene effects, so direct selection of these traits depending on phenotypic expression would be effective (Edukondalu *et al.,* 2017). This knowledge assisted for effective selection of these traits and explored the opportunity of genetic improvement. Earlier high heritability along with high genetic advance for rice yield has been reported by Nandan *et al.* (2010); Sravan *et al.* (2012) and Toshimenla and Sapuchangkija (2013).

Table 2. Mean square values of genotypes from analysis of variance and assessment of genetic parameters for studied morphological traits of 43 genotypes of rice

Characters	**Genotype MSS (df= 42)**	**σ^2g**	**σ^2p**	**h^2_b (%)**	**GA**	**GA%**	**PCV%**	**GCV%**	**PCV-GCV**
Seedling height (cm)	1851.47***	614.38	622.71	98.66	50.72	44.11	21.70	21.56	0.14
Leaf length (cm)	1144.62NS	378.55	387.52	97.69	39.61	74.79	37.17	36.73	0.44
Leaf width (cm)	0.04***	0.01	0.02	67.38	0.17	16.10	11.60	9.52	2.08
Leaf angle (^{0})	828.16***	269.53	289.10	93.23	32.66	73.43	38.23	36.92	1.31
Flag leaf area (cm^2)	291.87***	93.60	99.95	93.65	19.29	53.62	27.80	26.90	0.9
Flag leaf angle (^{0})	2573.78***	850.97	871.84	97.61	59.37	111.84	55.62	54.95	0.67
Culm length (cm)	156.00***	50.40	55.20	91.30	13.97	60.23	32.02	30.60	1.42
Culm diameter (cm)	0.045***	0.01	0.02	71.05	0.20	16.34	11.16	9.41	1.75
Internode length (cm)	116.44***	36.67	43.10	85.09	11.51	48.88	27.89	25.72	2.17
Number of tiller hill^{-1} (no.)	11.93***	3.68	4.56	80.87	3.56	28.42	17.06	15.34	1.72
Number of effective tiller hill^{-1} (no.)	17.35***	5.57	6.21	89.62	4.60	49.47	26.79	25.36	1.43
Panicle length (cm)	35.08***	9.70	15.68	61.83	5.04	19.08	14.98	11.78	3.2
Secondary branch in panicle (no.)	42.56***	12.64	17.28	73.15	6.26	27.83	18.47	15.79	2.68
Filled grain panicle^{-1} (no.)	600.37***	196.26	207.85	94.42	28.04	27.83	14.31	13.90	0.41
Unfilled grain panicle^{-1} (no.)	47.04***	13.94	19.16	72.78	6.56	63.79	42.55	36.30	6.25
Grain length (cm)	0.05***	0.02	0.02	81.65	0.23	29.54	17.56	15.87	1.69
Grain breadth (cm)	0.01***	0.00	0.00	92.42	0.11	41.02	21.54	20.71	0.83
Grain length-breadth ratio	2.17***	0.70	0.76	92.41	1.66	54.76	28.76	27.65	1.11
Ligule length (cm)	0.21***	0.07	0.07	94.31	0.53	60.10	30.93	30.04	0.89
1000-grain weight (g)	51.72***	17.22	17.29	99.59	8.53	41.42	20.19	20.15	0.04
Yield plant^{-1} (g)	124.80***	41.34	42.12	98.16	13.12	67.46	33.36	33.05	0.31

MSS= Mean sum of square, df= degrees of freedom, ***= significant at ≤ 0.1% level of probability, NS= non-significant, GCV= genotypic coefficient of variance, PCV= phenotypic coefficient of variance, σ^2g= genetic variance, σ^2p= phenotypic variance, h^2_b= broad-sense heritability, GA= genetic advance, GA (%)= genetic advance as percent of mean.

Table 3a. Mean performances of 43 rice genotypes regarding studied yield and yield related attributes

Genotype	SH	LL	LW	LAN	FLA	FLAN	CL	CD	IL	NTH	ETH
BAU-280-80-28	86.43op	34.50kl	1.20cd	43.33ij	29.28n-q	51.67ef	12.33lm	0.87j	18.93l-p	10.33kl	8.00k-n
BRRI dhan 47	110.7i	60.33b-g	1.37a	33.00lm	31.53l-p	20.67mno	11.00lm	1.07gh	11.33s	11.67g-l	5.33p
BRRI dhan 3	99.33kl	53.67b-k	1.23bc	23.33o-r	39.33f-k	11.33pq	11.67lm	100hi	18.00nop	10.67jkl	7.67lmn
ACE-441	116h	56.33b-i	1.33ab	73.33ab	38.67f-m	44.67fgh	11.33lm	1.13e-h	22.33h-n	11.33h-l	11.00d-g
Binadhan-8	115.3hi	50.33b-l	1.13cde	71.67abc	43.03d-h	42.67gh	10.33lm	0.93ij	11.67rs	12.33f-j	10.33f-i
BRRI dhan 33	84.33p	42.33e-l	1.07d-g	68.00b-e	38.67f-m	91.67ab	9.33m	0.93ij	10.00s	11.67g-l	10.67e-h
BRRI dhan 51	66.33q	41.33g-l	0.93g	29.67l-p	18.00r	13.00opq	22.00efg	1.27b-e	16.00pqr	13.00e-h	8.33j-m
Binadhan-10	94.33m	40.33h-l	1.07d-g	44.00ij	38.33f-m	26.33j-m	32.33b	1.43a	22.33h-n	13.67ef	11.67c-f
Kalijira 2	149.7bc	63.17bc	1.07d-g	47.67g-j	41.20e-i	95.00a	36.00a	1.27b-e	35.00a	19.33a	15.00a
BRRI dhan 40	87.33nop	39.60h-l	1.17cde	25.00n-r	24.00pqr	8.00q	20.33g-j	1.27b-e	22.00h-o	11.00i-l	8.00k-m
BRRI dhan 62	102.7jk	43.50d-l	1.13cde	33.33lm	45.00c-f	21.33lmn	23.67efg	1.37ab	24.67e-i	11.33h-l	8.00k-m
BR11	146.3bcd	63.83b	1.03efg	28.33l-q	51.33abc	29.67jkl	31.33b	1.27b-e	33.00ab	11.33h-l	9.00i-l
BRRI dhan 41	119h	53.33b-j	1.17cde	41.33jk	54.92ab	95.33a	23.67efg	1.33abc	23.67f-l	12.00f-k	9.00i-l
BR26	136.3g	58.00b-h	1.07d-g	45.00hij	49.33bcd	47.33fgh	30.00b	1.30a-d	30.00bcd	16.33b	13.67ab
Binadhan-17	101jk	44.60b-l	1.20cd	49.33g-j	50.00bcd	91.67ab	21.67e-h	1.23b-f	23.00g-m	11.67g-l	9.33h-k
BRRI dhan 57	91.33mno	39.50h-l	1.17cde	20.00qr	37.60f-m	49.33fg	20.67g-j	1.23b-f	19.33j-p	13.67ef	11.67c-f
BRRI dhan 54	88.33nop	42.17e-l	1.17cde	25.00m-r	38.67f-m	21.67k-n	20.67g-j	1.20c-g	19.33k-p	10.67jkl	7.00mno
Binadhan-3	118.3h	51.33b-l	1.03efg	43.67ij	32.00k-o	41.67gh	21.33f-i	1.33abc	21.33i-o	12.33f-j	7.33mno
BAU 6-246	142def	55.67b-j	0.97fg	62.33ef	22.33qr	91.67ab	30.67b	1.20c-g	28.00c-f	10..l	6.67nop
BRRI dhan 52	91.33mno	41.33g-l	1.17cde	76.00a	40.00e-k	93.67ab	20.00g-j	1.30a-d	17.33opq	16.00bc	12.67bc
ACE-4126	91.67mno	44.67b-l	1.07d-g	16.67r	21.97qr	25.00j-n	17.67h-k	1.13e-h	13.33qrs	12.33f-j	10.67e-h
BRRI dhan 44	142def	61.43b-e	0.93g	65.00cde	36.67g-n	85.00bc	31.00b	1.27b-e	30.67a-d	16.67b	14.33a
Binadhan-9	101.3jk	44.00c-l	1.03efg	35.00kl	29.43n-q	30.00jk	17.33ijk	1.13e-h	18.33m-p	12.67e-i	9.67g-j
BRRI dhan 28	92.33mn	44.00c-l	1.07d-g	27.67l-q	43.67d-g	25.67j-m	17.00jk	1.23b-f	17.33opq	12.33f-j	10.67e-h
BAU104-33-36-7	141.3d-g	58.33b-h	0.93g	65.00cde	33.13i-o	91.67ab	30.33b	1.20c-g	27.67d-g	14.33cde	12.33bcd
ACE-6106	150.3abc	128.2a	0.97fg	61.67ef	34.33i-o	91.67ab	30.33b	1.27b-e	31.33a-d	14.33cde	12.00cde
BRRI dhan 48	148.3bc	58.37b-h	0.97fg	49.00g-j	37.03f-n	71.67d	29.33bc	1.23b-f	29.67bcd	10.33kl	6.00op
BRRI dhan 46	141d-g	55.60b-j	0.93g	47.00hij	19.00r	58.33e	31.67b	1.23b-f	30.00bcd	11.00i-l	6.00op
BR23	91mno	40.00h-l	1.07d-g	21.67pqr	38.17f-m	18.33m-p	14.33kl	1.10fgh	22.33h-n	11.33h-l	6.00op
ACE-4496	151.3ab	61.87bcd	0.93g	55.67fg	33.00j-o	81.67c	29.67b	1.17d-g	28.00c-f	10.33kl	7.33mno
BAU 125	155a	63.73b	0.93g	51.00ghi	47.13cde	78.33cd	36.33a	1.27b-e	32.67abc	11.00i-l	8.33j-m
BRRI dhan 51	145cde	57.50b-h	0.93g	62.00ef	35.40h-n	90.67ab	28.33bcd	1.27b-e	29.00b-e	13.33efg	8.33j-m
BR12	105.3j	41.93f-l	1.13cde	45.00ij	36.13g-n	33.33ij	23.33efg	1.37ab	21.00i-o	12.33f-j	8.00k-n
BRRI dhan 68	105j	32.33l	1.07d-g	31.67l-o	40.53e-j	41.67gh	21.67e-h	1.37ab	22.33h-n	11.33h-l	7.00mno
Binadhan-7	94.67lm	36.33jkl	1.17cde	32.00lmn	31.00m-p	45.33fgh	24.00efg	1.27b-e	24.33e-j	10.00l	6.00op
BRRI dhan 72	88.67nop	34.00l	1.20cd	43.33ij	24.13pqr	41.00ghi	25.33def	1.27b-e	23.33f-l	12.33f-j	8.00k-n
BRRI dhan 54	140.7efg	50.33b-l	0.97fg	63.33def	19.67r	82.00c	25.67cde	1.33abc	27.00d-h	13.33efg	11.00d-g
BRRI dhan 39	100.3jk	37.33i-l	1.23bc	41.00jk	34.43i-o	40..hi	23.00efg	1.23b-f	27.00d-h	12.67e-i	8.33j-m
IR09F534	139.3fg	57.33b-h	1.03efg	24.33n-r	57.57a	44.67fgh	30.67b	1.33abc	24.00f-k	14.33de	11.33c-f
BR10	139.3fg	42.73d-l	1.07d-g	25.00m-r	19.60r	16.67nop	17.33ijk	1.13e-g	24.00f-k	15.67bcd	11.33c-f
BAU-125-4-69-28	117.7h	46.50b-l	1.07d-g	41.67jk	35.02h-o	30.00jk	22.67efg	1.10fgh	24.67e-i	11.33h-l	8.33j-m
BRRI dhan 34	150.3abc	60.87b-f	0.97fg	53.33gh	48.90bcd	86.67abc	28.67bcd	1.33abc	35.00a	12.67e-i	11.00d-g
ACE-4148	115.7h	44.33c-l	1.10c-f	71.00a-d	27.34opq	85.00bc	21.67e-h	1.33abc	22.00i-o	11.67g-l	7.67lmn
Lsd (0.05)	4.724	15.54	0.11	7.18	6.67	7.42	3.57	0.12	4.12	1.52	1.31
SE (±)	0.44	0.44	0.01	0.67	0.62	0.71	0.33	0.01	0.39	0.14	0.12
Minimum	66.33	32.33	1.37	16.67	18.00	8.00	9.33	0.87	10.00	10.00	5.33
Maximum	155	128.2	0.93	76.00	57.57	95.33	36.33	1.43	35.00	19.33	15.00
Mean	116.142	50.67	1.08	44.47	35.97	53.09	23.20	1.12	23.54	12.51	9.30
Sig. level	*	*	*	*	*	*	*	*	*	*	*
CV (%)	2.50	18.89	6.63	9.95	11.38	8.61	9.46	6	10.77	7.46	8.68

In single column, figures having common letter(s) indicate statistically non-significant difference as per DMRT, * indicates significant at ≤ 5% probability, lsd= least significant difference, SE= Standard error, CV= Coefficient of variance, SH= Seedling height, LL= Leaf length, LW= Leaf width, LAN= Leaf angle, FLA= Flag leaf area, FLAN= Flag leaf angle, CL= Culm length, CD= Culm diameter, IL= Internode length, NTH= Number of tiller hill^{-1}, ETH= Number of effective tiller hill^{-1}.

Table 3b. Mean performances of 43 rice genotypes regarding studied yield and yield related attributes

Genotype	PL	SB/P	FG	UFG	GL	GB	GL/GB	LIL	TGW	Y/P
BAU-280-80-28	22.10k-o	27.67abc	110.3de	18.67ab	1.00a	0.27de	0.39l	1.23bc	21.59hi	23.40g
BRRI dhan 47	25.00e-n	26.67abc	107.0def	11.33def	0.83cd	0.33c	2.53hij	0.87hi	26.52d	17.59n-q
BRRI dhan 3	27.00c-k	19.67h-k	101.7f-i	8.00d-h	0.97ab	0.30cd	3.22efg	0.77ij	27.98a	16.34qr
ACE-441	24.00g-n	30.33a	147.3a	7.67e-h	0.77c-f	0.30cd	2.56hi	0.63kl	19.47m	28.63de
Binadhan-8	30.00bcd	18.33h-k	99.00h-m	7.00fgh	0.83cd	0.30cd	2.78gh	1.13cde	20.10l	20.94h
BRRI dhan 33	28.67b-g	22.00e-h	120.0c	20.00ab	0.97ab	0.30cd	3.22efg	1.00fg	16.95qr	20.47hij
BRRI dhan 51	22.67j-n	20.00g-j	101.3f-j	7.33e-h	0.83cd	0.30cd	2.78gh	0.40 o	20.80j	17.44opq
Binadhan-10	26.33c-m	24.33c-f	103.0fgh	20.67a	0.87bc	0.23ef	4.33b	1.03efg	9.27x	11.16vwx
Kalijira 2	35.00a	17.33jk	98.00h-m	6.67gh	0.53j	0.30cd	1.78k	1.03efg	19.95l	29.81cd
BRRI dhan 40	24.33f-n	20.00g-j	101.7f-i	7.00fgh	0.97ab	0.20f	4.83a	0.65kl	22.82g	19.08j-n
BRRI dhan 62	29.00b-f	24.33c-f	99.67g-l	7.33e-h	1.00a	0.30cd	3.33ef	1.12cd	18.98n	14.36st
BR11	29.33b-e	28.67ab	113.0d	12.33cd	0.83cd	0.30cd	2.78gh	1.03efg	17.32q	18.67k-o
BRRI dhan 41	29.00b-f	29.33ab	129.7b	19.33ab	0.97cde	0.20f	4.83a	1.13cde	16.47st	19.92h-k
BR26	32.33ab	24.33c-f	106.0efg	9.00d-h	0.80cde	0.30cd	2.67h	1.03efg	27.14bc	39.93a
Binadhan-17	23.00i-n	22.33d-h	102.0f-i	8.00d-h	0.83cd	0.20f	4.17bc	1.03efg	21.38i	19.58h-k
BRRI dhan 57	26.33c-m	17.67ijk	80.67q	6.33h	0.80cde	0.20f	4.00bc	1.10def	23.18g	22.40g
BRRI dhan 54	26.33c-m	22.00e-h	87.33op	7.33e-h	0.73d-g	0.40b	1.83k	0.70jk	20.19kl	13.26tu
Binadhan-3	23.67h-n	21.67e-i	96.00i-m	8.67d-h	0.83cd	0.30cd	2.78gh	0.97gh	23.05g	15.78rs
BAU 6-246	23.00i-n	22.00e-h	101.7f-i	8.33d-h	0.83cd	0.30cd	2.78gh	0.63kl	16.74rs	12.57uv
BRRI dhan 52	21.67mno	15.00k	83.00pq	7.67e-h	0.87bc	0.30cd	2.89fgh	1.07d-g	27.53b	30.94c
ACE-4126	20.33no	24.00c-g	100.3g-k	10.67d-h	0.63g-j	0.20f	3.17efg	0.63kl	16.03tu	17.89m-q
BRRI dhan 44	25.67d-m	18.33h-k	83.33pq	10.00d-h	0.67f-i	0.30cd	2.22ijk	0.97gh	23.07g	26.69f
Binadhan-9	23.00i-n	19.00h-k	93.33l-o	8.00d-h	0.63g-j	0.30cd	2.11k	0.43no	17.31q	16.84pqr
BRRI dhan 28	29.67b-e	18.33h-k	87.33op	9.33d-h	0.63g-j	0.30cd	2.11k	1.17cd	12.62w	12.48uv
BAU104-33-36-7	31.00abc	18.00h-k	95.00j-m	8.67d-h	0.63g-j	0.20f	3.17efg	0.80ij	16.11tu	18.68k-o
ACE-6106	30.67abc	18.33h-k	94.00k-m	7.00fgh	0.60hij	0.20f	3.00fgh	0.83i	15.30v	11.88uvw
BRRI dhan 48	26.33c-m	25.67b-e	94.00k-m	11.00d-h	0.70e-h	0.20f	3.50de	0.97gh	24.81f	14.64st
BRRI dhan 46	28.33b-h	25.67b-e	86.67pq	9.67d-h	0.63g-j	0.20f	3.17efg	0.53lmn	18.36o	10.11x
BR23	26.73c-l	21.67e-i	88.33nop	10.33d-h	0.67f-i	0.20f	3.33ef	0.97gh	22.69g	13.20tu
ACE-4496	30.33bcd	27.67abc	107.0def	8.33d-h	0.77c-f	0.20f	3.83cd	1.13cde	24.63f	19.26i-m
BAU 125	29.33b-e	27.67abc	130.7b	18.00ab	0.83cd	0.20f	4.17bc	0.47mno	19.36mn	20.73hi
BRRI dhan 51	27.33c-j	29.00ab	111.7de	16.00bc	0.83cd	0.20f	4.17bc	0.87hi	21.98h	19.69h-l
BR12	29.00b-f	21.67e-i	93.67l-o	11.67de	0.67f-i	0.20f	3.33ef	0.97gh	15.93u	12.36uv
BRRI dhan 68	24.33f-n	21.67e-i	98.33h-m	10.00d-h	0.57ij	0.20f	2.83gh	0.57lm	20.58jk	17.55n-q
Binadhan-7	18.00o	20.00g-j	83.33pq	7.67e-h	0.63g-j	0.20f	3.17efg	1.37a	19.94l	10.54wx
BRRI dhan 72	25.67d-m	19.33hij	93.33l-o	9.33d-h	0.87c	0.30cd	2.89fgh	1.17cd	25.33e	17.90m-q
BRRI dhan 54	22.00l-o	21.00f-j	93.00mno	9.00d-h	0.87c	0.30cd	2.89fgh	1.30ab	26.76cd	27.70ef
BRRI dhan 39	27.33c-j	26.33a-d	101.3f-j	10.33d-h	0.77c-f	0.20f	3.83cd	0.63kl	17.80p	18.26l-p
IR09F534	28.67b-g	21.33f-j	103.7fgh	8.33d-h	0.63g-j	0.50a	2.11ijk	1.13cde	24.75f	28.27e
BR10	24.33f-n	22.33d-h	85.00pq	7.33e-h	0.77c-f	0.30cd	2.56hi	0.40 o	19.14mn	17.53n-q
BAU-125-4-69-28	27.67b-i	21.67e-i	88.33nop	6.67gh	0.63g-j	0.30cd	2.11ijk	0.47mno	17.85p	19.39h-m
BRRI dhan 34	27.33c-j	24.33c-f	129.3b	16.33b	0.87bc	0.30cd	2.89fgh	0.87hi	22.72g	32.70b
ACE-4148	25.00e-n	22.33d-h	103.3fgh	10.00d-h	0.67f-i	0.20f	3.33ef	0.53lmn	24.98ef	20.87h
Lsd (0.05)	4.03	3.50	5.53	3.708	0.89	0.05	0.39	0.10	0.44	1.38
SE (±)	0.38	0.33	0.52	0.35	0.01	0.004	0.04	0.01	0.04	0.13
Minimum	18.00	15.00	80.67	6.33	0.53	0.20	0.39	0.40	9.27	10.11
Maximum	35.00	30.33	147.3	20.67	1.00	0.50	4.83	1.37	27.98	39.93
Mean	26.44	22.51	100.76	10.29	0.77	0.26	3.03	0.88	20.29	19.48
Sig. level	*	*	*	*	*	*	*	*	*	*
CV (%)	9.32	9.57	3.38	22.02	7.53	11.66	7.92	7.37	1.31	4.36

In single column, figures having common letter(s) indicate statistically non-significant difference as per DMRT, * indicates significant at ≤ 5% probability, lsd= least significant difference, SE= Standard error, CV= Coefficient of variance, PL= Panicle length, SB/P= Secondary branch in panicle, FG= Filled grain panicle^{-1}, UFG= Unfilled grain panicle^{-1}, GL= Grain length, GB= Grain breadth, GL/GB= Grain length-breadth ratio, LIL= Ligule length, TGW= 1000-grain weight, Y/P= Yield plant^{-1}

Table 4. Estimates of phenotypic correlation coefficient among yield and its related traits of 43 rice genotypes

Traits	SH	LL	LW	FLA	LIL	CL	CD	NTH	ETH	PL	FG	UFG	GL	GB	GL/GB	SB/P	IL	LAN	FLAN	TGW
LL	0.59***																			
LW	-0.48***	-0.28**																		
FLA	0.26***	0.13	0.10																	
LIL	0.05	-0.02	0.14	0.33***																
CL	0.67***	0.35***	-0.55***	0.14	0.04															
CD	0.23**	0.07	-0.19*	0.18*	0.06	0.59***														
NTH	0.17	0.21*	-0.17	0.09	0.08	0.30***	0.20*													
ETH	0.17*	0.24**	-0.14	0.23*	0.15	0.22*	0.11	0.79***												
PL	0.41***	0.35***	-0.20*	0.42***	0.11	0.33***	0.09	0.28***	0.29***											
FG	0.24**	0.12	0.11	0.37***	-0.08	-0.02	-0.07	-0.20*	0.01	0.12										
UFG	0.05	-0.06	-0.08	0.23**	0.13	0.07	-0.07	-0.12	-0.01	0.04	0.51***									
GL	-0.24**	-0.20*	0.24**	0.07	0.23*	-0.26**	-0.16	-0.23*	-0.13	-0.10	0.39***	0.35***								
GB	-0.12	-0.08	0.15	0.04	0.04	-0.22*	-0.19*	0.17	0.19*	0.00	0.00	-0.18*	0.19*							
GL/GB	0.04	0.00	-0.04	0.11	-0.02	0.18*	0.33***	-0.17	-0.16	0.04	0.19*	0.21*	0.32***	-0.62***						
SB/P	0.24**	0.02	0.04	0.16	-0.06	0.11	0.00	-0.33***	-0.28***	0.09	0.58***	0.50***	0.22*	-0.17	0.16					
IL	0.72***	0.40***	-0.44***	0.18*	0.00	0.80***	0.44***	0.21*	0.19*	0.35***	0.11	0.06	-0.22*	-0.19*	0.08	0.22*				
LAN	0.43***	0.28***	-0.18*	0.06	0.08	0.15	-0.02	0.13	0.26**	0.11	0.26**	0.13	0.05	-0.03	0.02	0.02	0.19*			
FLAN	0.59***	0.37***	-0.34***	0.21*	0.21*	0.42***	0.14	0.24**	0.31***	0.18*	0.22*	0.23**	-0.04	-0.24**	0.15	0.03	0.41***	0.73***		
TGW	0.09	-0.10	0.15	0.01	0.17	-0.11	-0.06	0.05	-0.11	-0.14	-0.07	-0.25**	0.20*	0.17*	-0.08	-0.09	0.00	0.06	0.08	
Y/P	0.27***	0.00	0.03	0.34***	0.16	0.09	0.05	0.50***	0.59***	0.13	0.33***	0.02	0.12	0.27**	-0.21*	0.01	0.19*	0.32***	0.33***	0.50***

*, **, ***= significant at ≤ 5%, ≤ 1% and ≤ 0.1% level of probability, SH= Seedling height, LL= Leaf length, LW= Leaf width, FLA= Flag leaf area, LIL= Ligule length, CL= Culm length, CD= Culm diameter, NTH= Number of tiller hill^{-1}, ETH= Number of effective tiller hill^{-1}, PL= Panicle length, FG= Filled grain panicle^{-1}, UFG= Unfilled grain panicle^{-1}, GL= Grain length, GB= Grain breadth, GL/GB= Grain length-breadth ratio, SB/P= Secondary branch in panicle, IL= Internode length, LAN= Leaf angle, FLAN= Flag leaf angle, TGW= 1000-grain weight, Y/P= Yield plant^{-1}.

Table 5. Principal components and their coefficients of studied morphological traits of 43 rice genotypes

Traits	Main components						
	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Seedling height	0.388	-0.047	0.052	-0.207	-0.041	-0.222	0.020
Leaf length	0.108	-0.070	-0.133	-0.415	0.131	-0.044	0.380
Leaf width	-0.247	-0.035	-0.256	0.215	0.011	-0.094	0.024
Leaf angle	0.236	-0.029	-0.173	-0.247	-0.368	0.291	0.014
Flag leaf area	0.182	-0.093	-0.228	0.318	0.317	-0.131	0.197
Flag leaf angle	0.341	-0.051	-0.083	-0.120	-0.348	0.234	0.137
Culm length	0.370	0.001	0.259	0.048	0.040	-0.158	0.005
Culm diameter	0.200	0.014	0.246	0.388	-0.049	-0.183	-0.102
Internode length	0.368	-0.032	0.168	-0.065	0.049	-0.280	-0.037
No. of tiller hill^{-1}	0.217	0.378	-0.088	0.189	0.071	0.224	-0.175
No. of effective tiller hill^{-1}	0.238	0.306	-0.197	0.147	0.137	0.356	-0.113
Panicle length	0.240	0.020	-0.019	0.119	0.372	-0.014	0.097
Secondary branch in panicle	0.075	-0.426	-0.074	-0.098	0.177	-0.204	-0.214
Filled grain panicle^{-1}	0.121	-0.370	-0.299	-0.053	0.112	0.012	-0.316
Unfilled grain panicle^{-1}	0.095	-0.379	-0.157	0.005	0.148	0.286	0.014
Grain length	-0.087	-0.263	-0.324	0.191	-0.162	-0.012	-0.009
Grain breadth	-0.081	0.254	-0.314	-0.140	0.227	-0.210	-0.114
Grain length-breadth ratio	0.057	-0.319	0.179	0.428	-0.272	0.148	-0.067
Ligule length	0.074	0.014	-0.219	0.273	-0.071	-0.071	0.697
1000-grain weight	-0.006	0.123	-0.228	0.033	-0.466	-0.510	-0.044
Yield plant^{-1}	0.212	0.171	-0.408	0.081	-0.127	-0.122	-0.284
Eigen values	4.53	2.92	2.65	1.63	1.50	1.33	1.14
% Total variation	21.6	13.9	12.6	7.7	7.1	6.3	5.4
Cumulative (%)	21.6	35.5	48.1	55.8	63.0	69.3	74.8
Variety	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
Replication	<0.001	0.005	0.004	0.181	0.001	0.340	0.407

Table 6. Distribution pattern of the studied 43 rice genotypes into different clusters according to cluster analysis

Cluster name	Genotypes
Cluster I	BAU-280-80-28
Cluster II	BRRI dhan 47, BRRI dhan 37, BRRI dhan 51, BRRI dhan 40, BR10, ACE-4126, BRRI dhan 54, BRRI dhan 28, BR23, Binadhan-10, BRRI dhan 62, Binadhan-9, BR12, BRRI dhan 39, BRRI dhan 68, Binadhan-3, BAU-125-4-69-28, BRRI dhan 57, Binadhan-7, BRRI dhan 72
Cluster III	ACE-441, Binadhan-8, BRRI dhan 33, Binadhan-17, ACE-4148, BRRI dhan 52, Kalijira 2, BAU 6-246, BAU104-33-36-7, ACE-4496, BRRI dhan 51 , BRRI dhan 44, BRRI dhan 54, BRRI dhan 48, BRRI dhan 46, BRRI dhan 41, BAU 125, BRRI dhan 34, BR11, BR26, IR09F534
Cluster IV	ACE-6106

Table 7. Cluster mean for studied morphological traits of 43 rice genotypes

Variables	**Cluster means**			
	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**
Seedling height	86.43	96.82	131.97	150.33
Leaf length	133.20	42.78	55.27	128.17
Leaf width	1.20	1.12	1.04	0.97
Leaf angle	43.33	31.88	55.70	61.67
Flag leaf area	29.28	32.93	39.25	34.33
Flag leaf angle	51.67	28.02	75.19	91.67
Culm length	12.33	20.37	26.08	30.33
Culm diameter	0.87	1.22	1.23	1.27
Internode length	18.93	20.62	26.18	31.33
No. of tiller hill^{-1}	10.33	12.12	12.91	14.33
No. of effective tiller hill^{-1}	8.00	8.45	10.05	12.00
Panicle length	22.10	25.34	27.50	30.67
Secondary branch in panicle	27.67	21.57	23.37	18.33
Filled grain panicle^{-1}	110.33	94.55	106.54	94.00
Unfilled grain panicle^{-1}	18.67	9.27	11.02	7.00
Grain length	1.00	0.77	0.78	0.60
Grain breadth	0.27	0.26	0.26	0.20
Grain length-breadth ratio	0.39	3.05	3.14	3.00
Ligule length	1.23	0.82	0.92	0.83
1000-grain weight	21.59	19.90	21.46	15.30
Yield plant^{-1}	23.47	16.07	22.85	11.88

Phenotypic correlation among yield and related attributes

Estimates of trait association ascertain the comparative significance of independent character(s) that may be beneficial as indicator(s) for one or more characters (Mustafa *et al.,* 2007). Being a polygenic trait, direct selection based on yield always misleads the breeder. So, it is very precious to know about the direction and magnitude of relation among yield and yield related traits for appropriate selection of traits. Furthermore, these traits can be exploited for yield enhancement through suitable breeding techniques (Oad *et al*., 2002; Jayasudha *et al.,* 2010; Ratna *et al.,* 2015). Correlation coefficients from correlation study assess the relationship among yield and its related attributes. In present study, assessment of correlation revealed that seedling height registered a highly significant positive correlation with leaf length (r= 0.59), flag leaf area (r= 0.26), culm length (r= 0.67), panicle length (r= 0.41), internode length (r= 0.72), leaf angle (r= 0.43), flag leaf angle (r= 0.59), yield plant^{-1} (r= 0.27) and showed a negative correlation with leaf width (r= -0.48) and grain length (r= -0.24) (Table 4). Flag leaf area exhibited highly significant positive correlation with ligule length (r= 0.33), panicle length (r= 0.42), number of filled grain panicle^{-1} (r= 0.37) and yield plant^{-1} (r= 0.34). Furthermore, number of filled grain panicle^{-1} displayed highly significant positive correlation with number of unfilled grain panicle^{-1} (r= 0.51), grain length (r= 0.39), secondary branch panicle^{-1} (r= 0.58), yield plant^{-1} (r= 0.33) and similar relation existed among number of unfilled grain panicle^{-1}, grain length and secondary branch panicle^{-1} (Table 4). Number of effective tiller hill^{-1} had highly significant positive correlation with number of tiller hill^{-1} (r= 0.79) and negative correlation with secondary branch panicle^{-1} (r= -0.28) (Table 4). Yield plant^{-1} exhibited significant positive correlation with seedling height (r= 0.27), flag leaf area (r= 0.34), number of tiller hill^{-1} (r= 0.50), number of effective tiller hill^{-1} (r= 0.59), filled grain panicle^{-1} (r= 0.33), grain breadth (r= 0.27), internode length (r= 0.32), leaf angle (r= 0.33), 1000-grain weight (r= 0.50), but displayed negative correlation with grain length-breadth ratio (r= -0.21) (Table 4). This result indicated that the characters positively associated with yield had an influence on increasing the grain yield. Thus these characters can be used as a selection criterion for better yield performance. Correlation study revealed some other significant positive and negative correlation among the considered morphological traits of 43 rice genotypes represented in Table 4. The result showed some similarity and contradiction with the previous findings by Kalyan *et al.* (2017); Akhter *et al.* (2014); Osundare *et al.* (2017) and Hannan *et al.* (2020).

Principal Component Analysis (PCA)

PCA is a multivariate technique which extracts the significant information from a data set and expresses the information as a new set of orthogonal variables known as principal components (Abdi and Williams, 2010). PCA revealed the most appropriate combination of the studied traits. In this study, PCA exhibited seven principal components with Eigen values greater than one and all seven PCs showed significant difference for genotype ($P < 0.001$) (Table 5). The criterion used by Clifford and Stephenson (1975) and corroborated by Guei *et al.* (2005) suggest that the first three principal components are often the most important in reflecting the variation patterns among accessions and the characters associated with these are more useful in distinguishing accessions. In this study, principal component 1 (PC1) explained 21.6% of total variations observed among the genotypes followed by PC2 (13.9%) and PC3 (12.6%) (Table 5). The first seven principal components explained for about 74.8% of the total variations among all the studied traits describing 43 rice genotypes where only 35.5% variation was accounted for the first two components (Table 5). The most important traits for PC1 were: seedling height (0.388), culm length (0.370) and internode length (0.368) with positive coefficients and leaf width (-0.247), grain length (-0.087) and grain breadth (-0.081) with negative coefficients (Table 5). The first component representing the significance of this PC for plant growth related traits. Whereas number of tiller hill^{-1} (0.378), number of effective tiller hill^{-1} (0.306) and grain breadth (0.254) with positive coefficient and secondary branches in panicle (-0.426), unfilled grain panicle^{-1} (-0.379) and filled grain panicle^{-1} (-0.370) with negative coefficients (Table 5) were the important traits of PC2 indicating usefulness of this PC for yield related traits. The result revealed the most important traits that contributed to the variations occurred among the rice genotypes under study.

Cluster analysis

For effective hybridization program, genetic divergence is a crucial factor for discerning the genetically diverse parents (Thippeswamy *et al.,* 2016) as only hybridization between divergent parents produces wider variability and segregants with high heterotic effects (Bhati *et al.,* 2015). Cluster analysis usually done to select parents for getting high heterotic gain. In presen study, cluster analysis using average values of all the studied traits of all 43 rice genotypes computed the genotypes in four clusters following Squared Euclidean Distance method (Table 6). Distribution pattern indicated that maximum genotypes (21) were accomodated in cluster III followed by cluster II (20), while minimum (01) genotypes were presented in cluster I and cluster IV (Table 6). Cluster wise mean values of the studied traits were utilized for superiority assessment of the cluster thus could be accounted in improvement of various characters (Ahmed *et al.,* 2014). Mean performance of different clusters for the considered traits in this study manifested that the genotypes which produced higest filled grain panicle^{-1}, 1000-grain weight, yield plant^{-1} and minimum seedling height were accumulated in cluster I (Table 7). Whereas genotypes with maximum flag leaf area with second highest yield plant^{-1}, 1000-grain weight, filled grain panicle^{-1}, panicle length and number of effective tiller panicle^{-1} were grouped in cluster III (Table 7). Similarly, genotypes which produced less seeding height and more grain weight were clubbed into cluster I, whereas low yielding genotypes with maximum seedling height and effective tillers plant^{-1} but minimum 1000-grain weight were grouped into cluster IV (Table 7). From cluster analysis it was suggested that in terms of yield potentiality and other yield related traits genotypes aggregated in cluster I and cluster III should be more prominently considered in future rice breeding.

Conclusion

The present study revealed the existence of sufficient genetic variability in the tested genotypes. The extent of heritability and genetic advance were moderate to high for the traits, offering more chance for advancement. Yield plant^{-1} exhibited significant positive correlation with seedling height, flag leaf area, number of tiller hill^{-1}, number of effective tiller hill^{-1}, filled grain panicle^{-1}, grain breadth, internode length, leaf angle, 1000-grain weight, but showed negative correlation with grain length-breadth ratio. This result indicated that the characters positively associated with yield had an influence on increasing grain yield. Thus selection based on these traits can improve the yield performance of rice. The first two principal components from principal component analysis described 35.5% of total variation. Among four clusters obtained from cluster analysis, cluster I and cluster III were the most feasible for selection based on yield potentiality. This study provided genetic differences among genotypes based on yield and its attributes which might be utilized for future varietal development programs.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

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