



## Genetic variability, character association and divergence analysis for agro-morphological traits of local rice (*Oryza sativa* L.) germplasm in Bangladesh

Afsana Hannan<sup>1</sup>, Md. Rabiul Islam Rana<sup>1</sup>, Md. Najmol Hoque<sup>2</sup>, G. H. M. Sagor<sup>1</sup>✉<sup>1</sup>Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh 2202, Bangladesh<sup>2</sup>Department of Biochemistry and Molecular Biology, Khulna Agricultural University, Khulna 9100, Bangladesh

### ARTICLE INFO

#### Article history:

Received: 03 February 2020

Accepted: 29 March 2020

Published: 30 June 2020

#### Keywords:

Rice genotypes,  
Morphological traits,  
Genetic variability,  
Character association,  
Diversity analysis

#### Correspondence:

G. H. M. Sagor

✉: [sagorgpb@gmail.com](mailto:sagorgpb@gmail.com)

### ABSTRACT

Rice (*Oryza sativa*) contributes significantly to global food security and is a major food crop for almost half of the world's population. Forty seven local rice germplasm were collected and grown under normal field condition to evaluate the presence of genetic diversity among them. Analysis of variance (ANOVA) showed significant differences ( $P \leq 0.001$ ) among the genotypes for all the traits studied except leaf width reflecting broad spectrum of variability which offer an ample chances for selection. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for most of the traits except no. of filled grains panicle<sup>-1</sup> indicating that there was an influence of environment on majority of the studied traits. Similarly, moderate broad-sense heritability with high genetic advance as percent of mean of most of the traits such as seedling height, flag leaf area, flag leaf angle, grain length, 1000-grain weight also indicated the accumulation of additive gene effects and suggested direct selection for those characters for economic feasibility. Correlation analysis revealed significant positive and negative correlation among the traits. Principal component analysis showed that the first two principal components of the considered traits accounted for about 37.9% of the total variation and pointed out a wide variation among the genotypes. The dendrogram of cluster analysis grouped 47 rice genotypes into four clusters. Cluster II incorporated the highest number of genotypes followed by Cluster I. In terms of high yield potentiality cluster III had the highest cluster mean for rice yield, followed by cluster IV. Data from this study provide presence of sufficient genetic diversity among the traditional local rice germplasms which can be employed in future rice breeding program for either varietal improvement or developing new variety.

Copyright ©2020 by authors and BAURES. This work is licensed under the Creative Commons Attribution International License (CC By 4.0).

### Introduction

Rice is considered as world's third most important cereal crop after corn and it is grown on over 161.1 million hectares of land, yielding 487.5 metric tons milled rice worldwide (Statista, 2019). About 158.9 million people of Bangladesh are dependent on rice as a major staple food (BBS, 2017). So from the time immemorial Bangladesh has an assembly of profuse diversified rice landraces from when rice has a major role to play in the livelihood, cultural and socio-economic aspects of the people (Ahmed *et al.*, 2016). Actually, beyond four thousand landraces of rice are adopted in various regions of Bangladesh. However, now extensive cultivation of modern rice varieties throughout the country along with innumerable interference of rice territory adversely threatened the rice diversity in Bangladesh (Ahmed *et al.*, 2010). Exploring genetic diversity in available landrace and wild relatives is one of the most important way to improve the germplasms (Thomson *et al.*, 2007) using breeding programs. For preparing a breeding program sustainable, clear-cut knowledge on genetic diversity

related to yield and yield contributing traits is a vital one. Through systematic test and evaluation of germplasms, plant breeders are trying to exploit superior genetic stock for selection and production of cultivars with high yield potentiality (Iqbal *et al.*, 2018) as rice cultivation is not solely depends on cultural practices but also relies on inherent genetic variability among the germplasm (Augustina *et al.*, 2013). For enhancement of rice production, determining finest breeding procedures is a must and in this aspect it is crucial to have morpho-genetic diversity for different yield contributing traits in rice. Presence of wide genetic diversity for yield and its attributes in rice have been reported in the past in Bangladesh (Yesmin *et al.*, 2014; Ahmed *et al.*, 2016; Akter *et al.*, 2016; Akter *et al.*, 2018a,b,c; Islam *et al.*, 2018). To ascertain the polygenic relationships within and between species, agro-morphological traits have been widely used to study genetic variability and character association in rice.

However, morphological attributes are highly influenced by environmental factors, resulted differential pattern of

### Cite this article

Hannan, A., Rana, M.R.I., Hoque, M.N., Sagor, G.H.M 2020. Genetic variability, character association and divergence analysis for agro-morphological traits of local rice (*Oryza sativa* L.) germplasm in Bangladesh. *Journal of Bangladesh Agricultural University*, 18(2): 289–299. <https://doi.org/10.5455/JBAU.84906>

relationship in different degree (Selvi *et al.*, 2003), but still very much effective for selection in breeding program (Megloire *et al.*, 2005). Breeding strategies in rice rely mostly on the variation nature and interrelationship among yield attributes. It is therefore imperative to assess extent of genetic transmissibility and gain of yield contributing traits to predict selection response for further improvement. In this case, heritability estimate is necessary as it indicates the genetic involvement for the transmission of characters from one generation to other generations (Sabesan *et al.*, 2009). To improve yield attributing traits using different breeding approach, it is imperative to have knowledge on the association between yield and different yield attributing traits, which help the breeder to make suitable strategy for yield improvement. Correlation studies not only provide better vision towards the relationship among grain yield with other yield attributes (Oad *et al.*, 2002; Jayasudha *et al.*, 2010) but also assists plant breeders for more accurate and precise selection (Ratna *et al.*, 2015). Cluster analysis function for grouping different genotypes based on their similar performance in terms of different traits is now become very much popular tools for diversity analysis also (Vural *et al.*, 2007). Keeping all the information under consideration, the present study was designed to assess genetic variability among forty seven rice germplasm, to unravel the degree of association between yield and yield attributes and also to explore the diversity among different rice accession collected from different regions of Bangladesh.

## Materials and Methods

### Collection of the germplasms and experimental location

Forty seven rice genotypes (Table 1) were collected from Bangladesh Rice Research Institute (BRRI), local farmers of different districts and also from the Department of Genetics and Plant breeding, Bangladesh Agricultural University, Mymensingh.

Table 1. Name of the collected 47 rice germplasm used in the experiment

Sl.	Genotype	Sl.	Genotype	Sl.	Genotype
1	Katiabagdad	17	Jashore saran	33	Shafeeb sail
2	Peta	18	Sakkar khana	34	Jinga sail
3	Shuna onjona	19	Lalmatha	35	Chahlam
4	Supahar	20	Indra shail	36	Mathamota
5	Kataribug	21	Lalsharna	37	Daud sail
6	Lakkhidiga	22	Pakkiraj	38	Dula aman
7	Sadalakkhi	23	Karaja	39	Khawa
8	Mowlata	24	Jirashil	40	Molag baru
9	Naliuri	25	Sonaburion	41	Nandi dhan
10	Batraj	26	Nepali sorna	42	Narica
11	Kalijira 2	27	Miniket	43	Joila
12	Julaki	28	Biharijulon	44	Kalijira
13	L. shail	29	Kadam sail	45	Tulshimala
14	Sarna	30	Malibhug	46	Bismuri
15	Long	31	Pajam	47	China atap
16	Jobeshail	32	Binni		

### Experimentation

Seeds of all forty seven rice genotypes were sown on seed bed that was prepared by raising soil from the

surface about 10-15 cm. Seedlings were transplanted to the main experimental land after thirty days. The experiment was conducted following a randomized complete block design with three replications. Unit plot size was 1m × 1m. Genotypes were different in their maturity time. Harvesting was done when 90-95% plant population were reached to maturity.

### Data collection

Data were recorded from five randomly chosen plants from each genotype in each replication for the selected traits. Data on various morphological traits *viz.* 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<sup>-1</sup> (NTH), number of effective tiller hill<sup>-1</sup> (ETH), panicle length (PL), secondary branch in panicle (SB), no of filled grain panicle<sup>-1</sup> (FG), no of unfilled grain panicle<sup>-1</sup> (UFG), grain length (GL), grain breadth (GB), grain length and breadth ratio (GL/GB), ligule length (LIL), 1000-grain weight (GW) and yield plant<sup>-1</sup> (Y/P) were recorded at different growth stages of plants.

### Statistical analysis

The statistical analysis of the data recorded from forty seven rice genotypes was carried out using MINITAB<sup>®</sup>17 statistical software packages (Minitab Inc., State College, Pennsylvania, USA) and MSTAT computer software. A two-way analysis of variance (ANOVA) was executed for different agromorphological 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 as described by Johnson *et al.* (1955); GCV and PCV values as described by Burton and Devane (1953) and Singh and Chaudhury (1985); GA (%) was calculated as formula given by Comstock and Robinson (1952). Principal component analysis (PCA) and cluster analysis was performed using MINITAB<sup>®</sup>17 statistical software packages. Cluster analysis was performed using the average values for each trait of each genotype.

## Results and Discussion

### Analysis of Variance

Analysis of variance of different rice genotypes for quantitative traits revealed that the mean squares due to genotypes were highly significant ( $P \leq 0.001$ ) for all the studied traits except leaf width (Table 2) suggesting the presence of considerable variability among the genotypes for effective selection. Similarly, significant genetic differences were reported in other findings involved evaluation of different rice genotypes (Augustina *et al.*, 2013; Pradhan *et al.*, 2015; Iqbal *et al.*, 2018). Mean performances of forty seven genotypes for their morphological traits revealed significantly different performances among the rice genotypes (Table 3). Mean values for effective tillers hill<sup>-1</sup> ranged from 5.67 to

17.67, which is one of the most important yield attribute as tillers bearing effective panicle will obviously contribute to final yield. Karaja (17.67) produced utmost tillers hill<sup>-1</sup> followed by Naliuri (15.67) and Kalijira 2 (15.00) (Table 3a). As flag leaf is responsible to transfer assimilates from source to grains, therefore, its area is very much important to uphold yield. Maximum flag leaf area (65.00 cm<sup>2</sup>) was calculated for Julaki, followed by Katiabagdad (56.20 cm<sup>2</sup>) (Table 3a). Another important yield attribute is panicle length, as longer panicles have large number of grains that obviously lead higher yield. Highest panicle length was found for tulshimala and lowest in Sarna (Table 3b). Rice yield is also highly contributed by no of panicle per unit area, no of filled grain panicle<sup>-1</sup> and 1000-grain weight (Mehtre *et al.*, 1994; Samonte *et al.*, 1998). Improvement of these traits is vital for enhancing rice production. As depicted from Table 3b, mean values for panicle length ranged between 20.00 cm to 35.00 cm. The longest panicles (35.00 cm) were produced by Biharijulon and Kalijira 2. Supahar (162.3) produced highest no of filled grain whereas Katiabagdad (23.00) produced highest no of unfilled grain panicle<sup>-1</sup> (Table 3b). 1000-grain weight ranged from 10.43g to 26.80g. Maximum 1000-grain weight was calculated for Mathamota (26.80g) and Pakkiraj (26.42g). Development of high yielding rice cultivars along with their consistent performance in different condition is the real challenge of breeders (Iqbal *et al.*, 2018), which can be overcome only through the use of germplasm have wider genetic diversity. On the basis of mean performance, Sarna (55.56 g plant<sup>-1</sup>) followed by Pakkiraj (37.48 g plant<sup>-1</sup>), Long (30.79g), Jobeshail (30.59g). All the genotypes displayed considerable amount of differences with respect to all the characters (Table 3a, b). This result indicated that the existence of genetic divergent among the studied genotypes as mean performance of plant materials helps to determine the diversity of the genotypes (Iqbal *et al.*, 2018).

#### Coefficients of variability

The estimates of different genetic parameters are shown in Table 4. Phenotypic coefficient of variation (PCV) showed higher values (20%) for most of the studied traits except moderate values (10-20%) for leaf width, leaf angle, culm diameter and low values (<5%) for the trait no of filled grain panicle<sup>-1</sup>. Likewise, the genotypic coefficient of variation (GCV) was also high (>20%) for number of effective tiller, internode length, leaf length, flag leaf area, flag leaf angle, ligule length, culm length, no of unfilled grain panicle<sup>-1</sup>, grain length, grain breadth, grain length and breadth ratio, secondary branches in panicle, 1000-grain weight and yield plant<sup>-1</sup> (Table 4) suggesting the possibility of yield improvement through selection of these traits. The magnitude of PCV ranged from 3.65% (no of filled grain panicle<sup>-1</sup>) to 89.53% (flag leaf angle), while the magnitude of GCV ranged from

Table 2. Mean squares for studied agro-morpho-gical traits of 47 genotypes of rice

Characters	Mean sum of squares (MSS)			
	Replications (df = 2)	Genotypes (df = 46)	Error (df = 92)	CV (%)
Number of tillers hill <sup>-1</sup> (no.)	1.41	23.38***	0.59	5.67
Number of effective tillers hill <sup>-1</sup> (no.)	17.79	37.38***	5.71	8.04
Seedling height (cm)	24.95	1538.97***	9.93	2.62
Internode length (cm)	40.56	94.99***	4.56	8.86
Leaf length (cm)	52.94	332.45***	10.82	6.58
Leaf width (cm)	0.01	0.04 <sup>NS</sup>	0.005	6.68
Leaf angle (°)	315.11	78.94***	13.82	6.96
Flag leaf area (cm <sup>2</sup> )	53.77	338.92***	3.28	4.98
Flag leaf angle (°)	190.09	2842.53***	23.18	8.05
Ligule length (cm)	0.007	0.20***	0.005	8.19
Culm length (cm)	28.73	148.13***	4.55	9.19
Culm diameter (cm)	0.03	0.03***	0.006	6.41
Panicle length (cm)	17.79	37.38***	5.71	8.94
No. of filled grain panicle <sup>-1</sup>	0.66	5.71***	9.07	2.86
No. of unfilled grain panicle <sup>-1</sup>	12.60	48.44***	4.19	18.60
Grain length (cm)	0.02	0.06***	4.39	7.85
Grain breadth (cm)	0.0006	0.01***	0.0003	5.81
Grain length and breadth ratio	0.50	2.36***	0.11	10.26
Secondary branches in panicle (no.)	30.06	100.58***	5.95	10.33
1000-grain weight (g)	0.16	56.55***	0.06	1.26
Yield plant <sup>-1</sup> (g)	0.88	215.88***	0.54	17.97

\*\*\*= significant at ≤ 0.1% level of probability, NS= non-significant, df= degrees of freedom, CV= coefficient of variation

7.06% in culm diameter to 51.27% in flag leaf angle (Table 4). Similar results for no of filled grain panicle<sup>-1</sup> were earlier recorded by Gour *et al.*, (2017) and Summnaath *et al.*, (2017) respectively. The differences in PCV and GCV ranged from -8.35 to 57.87% (Table 4), indicating less influence of environment on these traits, therefore, selection for those traits to improve yield would be effective. The result is very much similar with the findings of other researchers (Bagati *et al.*, 2016; Prasad *et al.*, 2017; Iqbal *et al.*, 2018).

#### Heritability and genetic advance

For predicting whether selection procedures of succeeding generations will be easier or not, a brief knowledge on magnitude of transmissibility of a particular trait is essential for plant breeders (Khaliq *et al.*, 2009). Genetic advance represents the measure of genetic gain in selection. In this study, broad-sense heritability ranged from 7.59% (no of filled grain panicle<sup>-1</sup>) to 33.26% (yield plant<sup>-1</sup>), while corresponding values of genetic advance ranged from 0.57% (no of filled grain panicle<sup>-1</sup>) to 60.48% (flag leaf angle) (Table 4). Babu *et al.* (2012) found high genetic advance for grain panicle<sup>-1</sup> and flag leaf characters also. Traits like leaf width, leaf length, culm diameter and no of filled grain panicle<sup>-1</sup> exhibited moderate heritability (20-60%) with low genetic advance (0-10%). This result indicated non-additive gene action, thus selection should be practiced with care (Iqbal *et al.*, 2018).

Characterization of local rice genotypes

Table 3a. Mean performances of 47 rice genotypes for different morphological traits

Genotype	NTH	ETH	SH	IL	LL	LW	LAN	FLA	FLAN	LIL	CL
Katiabagdad	11.67i-m	5.67p	108.3kl	15.00rs	60.83b-f	1.33bc	40.67m	56.20b	40.67hi	1.13cd	11.67s
Peta	12.00h-k	5.67p	131.0ghi	13.33s	66.14ab	1.47a	45.00klm	45.53fgh	95.00a	0.83ghi	12.33s
Shuna onjona	12.00h-l	10.33e-i	122.7j	18.00pqr	56.00e-i	1.43ab	41.33lm	40.60jk	23.33klmn	0.73ij	12.33s
Supahar	10.33mn	6.67nop	110.0kl	21.00k-q	48.33klm	1.17de	20.33r	40.13jk	11.00p	1.13cd	10.67s
Kataribug	11.67i-m	9.33hijk	149.7a	22.33j-o	63.00bcd	1.17de	88.33a	48.53ef	93.33abc	1.13cd	12.00s
Lakkhidiga	12.00h-l	7.67lmno	120.3j	17.00qr	52.50h-k	1.13def	69.33bcd	47.00fg	84.33cde	1.03de	10.67s
Sadalakkhi	12.00h-l	9.33hijk	109.7kl	13.00s	46.00lmn	1.13def	85.67a	27.67opqr	20.67lmno	1.06de	11.00s
Mowlata	12.33g-k	7.67lmno	94.00op	19.00opq	38.33opq	1.07e-h	33.67mo	35.37l	25.00klm	1.36b	25.67g-k
Naliuri	18.67ab	15.67b	131.0ghi	30.33cdef	57.33c-h	1.13def	91.33a	42.47hijk	69.00g	0.56k	32.33b
Batraj	11.33j-m	6.33op	99.00no	24.00h-m	41.50nop	1.03e-h	53.33g-j	43.40hij	23.33klmn	1.03de	25.67g-k
Kaljira 2	19.33a	15b	149.7a	35.00ab	63.17bc	1.06e-h	47.67jkl	41.20jk	95.00a	1.03de	36.00a
Julaki	12.00h-l	8klmn	112.0k	25.67g-j	50.83i-l	1.06e-h	25.00pqr	65.00a	27.67kl	1.53a	22.33klmn
L. shail	12.33g-k	10.00fghi	148.7ab	17.00a	70.10a	0.97gh	74.00b	52.57cd	94.00ab	1.16cd	30.00b-f
Sarna	17.67b	1300c	94.00op	20.33m-q	45.83lmn	1.23cd	28.33opq	44.67ghi	21.67lmno	1.23c	21.00lmno
Long	14.33def	11.67de	136.3efg	30.67cde	56.67d-i	1.06e-h	70.00bcd	29.93nopq	95.00a	0.63jk	29.33b-g
Jobeshail	14.67de	12.67cd	141.0cde	31.33bcd	62.77bcd	1.03e-h	50.67g-k	47.37fg	70.67fg	1.03de	31.00bcd
Jashore saran	13.00f-i	11.33def	144.0a-d	29.33c-g	61.00b-f	1.03e-h	55.33f-i	35.33l	49.00h	1.03de	31.67bc
Sakkar khana	16.33c	13.67c	75.00h	19.00n-q	34.00qrs	1.17de	69.00bcd	21.00tu	91.67abc	0.63jk	19.00nop
Lalmatha	14.33def	11.33ef	92.67p	19.67cde	43.17mno	1.07e-h	21.67r	30.53nop	20.33lmno	0.63jk	19.67nop
Indra shail	13.00f-i	11.00efg	138.3def	30.67cde	52.33h-k	0.97gh	40.67m	39.97jk	25.00klm	1.16cd	30.33b-f
Lalsharna	12.33g-k	9.33hijk	80.33rh	11.67s	32.00rs	1.23cd	64.33de	21.03tu	86.33a-e	0.63jk	14.33qrs
Pakkiraj	13.33e-h	11.33def	143.0bcd	30.00c-f	62.00b-e	0.97gh	65.00cde	34.67lm	91.67abc	0.90fg	30.33b-f
Karaja	19.67a	17.67a	132.3ghi	25.67g-z	52.00h-l	1.03e-h	65.00cde	24.87rs	92.00abc	0.53k	27.33d-i
Jirashil	15.33cd	11.33ef	86.33q	24.00h-m	39.33opq	1.13def	19.33r	25.00rs	14.67nop	0.83ghi	13.67rs
Sonaburion	10.67lmn	6.33op	146.3abc	33.00abc	61.50b-f	1.10d-g	50.67g-k	41.53ijk	78.33ef	0.66jk	30.67bcde
Nepali sorna	14.33def	11.33def	121.3j	25.67g-j	46.00lmn	1.13def	57.00fg	43.33hij	81.67de	0.73ij	28.33b-h
Miniket	11.00klm	6.33op	89.33pq	23.33i-n	41.33nop	1.13def	23.00qr	36.00l	16.67mnop	0.86fgh	17.33o-r
Biharjulong	10.33mn	6.33op	142.3cd	32.33abc	60.83b-f	1.03e-h	30.67op	34.67lm	23.67klmn	1.13cd	28.00c-i
Kadam sail	11.67i-m	8.33jklm	117.7j	23.33i-n	46.00lmn	1.10d-g	71.67bc	54.00bc	84.33cde	0.66jk	22.67j-n
Malibhug	10.33mn	6.33op	134.7fgh	26.33f-j	54.13g-k	1.03e-h	70.67bcd	19.00u	89.00abcd	0.66jk	25.67g-k
Pajam	11.33j-m	8.00klmn	138.7def	23.67i-n	56.93c-i	1.03e-h	64.67.cde	50.53de	88.67abcd	0.66jk	27.67c-i
Binni	10.33mn	7.33mno	130.3hi	23.67i-n	49.33j-m	1.07e-h	65.33cde	23.00st	85.00bcde	0.66jk	24.67h-l
Shafeeb sail	10.33mn	6.67nop	139.3def	25.67g-j	56.67d-i	1.13def	70.00bcd	39.53k	93.33abc	1.06de	28.00c-i
Jinga sail	11.33j-m	6.33op	77.67s	18.00pqr	23.83t	1.23cd	24.67pqr	36.20l	25.00klm	0.96ef	16.33pqr
Chahlam	11.33j-m	8.33jklm	123.0j	27.00e-i	50.67i-l	1.13def	50.00h-k	31.67mn	42.00hi	0.40l	24.00i-m
Mathamota	10.33mn	7.33mno	128.3i	25.00h-k	51.17h-l	1.16de	49.67ijk	23.00st	45.67h	0.53k	24.33h-m
Daud sail	11.00klm	8.00klmn	107.7klm	23.33i-n	45.70lmn	1.13def	54.33f-j	35.73l	67.67g	0.73hij	20.33mno
Dula aman	11.33j-m	8.33jklm	102.7mn	23.33i-n	35.07qrs	1.17de	52.33g-j	30.77no	71.00fg	1.13cd	18.00opq
Khawa	9.33n	6.33op	149.7a	28.00d-h	59.40c-g	1.00fgh	59.33ef	35.60l	94.00ab	0.66jk	30.00b-f
Molag baru	13.33e-h	11.33def	90.33pq	19.67n-q	39.00opq	1.03e-h	23.67qr	27.17qr	13.67op	0.53k	19.67nop
Nandi dhan	11.33j-m	7.33mno	105.0lm	22.67j-o	36.63pqr	1.10d-g	39.00mn	31.77mn	36.67ij	0.56k	21.00lmno
Narika	14.33def	11.33def	146.0abc	27.00e-i	55.23f-j	0.97gh	71.67bc	42.67hijk	92.00abc	0.66jk	32.33b
Joila	13.33e-h	10.67efgh	149.3a	28.d-h	57.37c-h	0.93h	71.00bcd	35.43l	85.00bcde	0.66jk	30.00b-f
Kaljira	11.67i-m	8.00klmn	132.3ghi	24.67h-l	41.67nop	1.13def	51.00g-k	25.33rs	88.33abcd	0.66k	26.67e-j
Tulshimala	13.00f-i	9.67ghij	139.7def	25.67g-j	53.97ghijk	1.03e-h	56.67fgh	15.20v	71.67fg	0.56k	27.67c-i
Bismuri	12.67g-j	9.00ijkl	85.00qr	20.67l-q	30.27s	1.23cd	30.33op	30.60nop	45.67h	0.83ghi	21.33lmno
China atap	13.67efg	9.33hijk	117.7j	21.33k-p	41.60nop	1.13def	44.33klm	27.43pqr	31.00jk	0.86fgh	26.33f-k
Lsd (0.05)	1.174	1.22	5.111	3.46	5.336	0.1256	5.88	2.94	7.81	0.1147	3.46
SE (±)	0.11	0.11	0.46	0.31	0.48	0.01	0.53	0.26	0.07	0.01	0.31
Minimum	9.333	5.67	75.00	11.67	23.83	0.9333	19.33	15.20	11	0.400	10.67
Maximum	19.67	17.67	149.7	36	70.10	1.467	91.33	65	95	1.53	36
Mean	12.77	9.36	120.50	24.11	49.99	1.11	52.04	36.39	59.79	0.85	23.22
Level of significance	*	*	*	*	*	*	*	*	*	*	*
CV (%)	5.67	8.04	2.62	8.86	6.58	6.68	6.96	4.98	8.05	8.19	9.19

In single column values having common letter(s) indicate statistically non-significant difference as per DMRT, \* indicates significant at ≤ 5% probability, NTH= Number of tillers hill<sup>-1</sup>, ETH= Number of effective tillers hill<sup>-1</sup>, SH= Seedling height, IL= Internode length, LL= Leaf length, LW= Leaf width, LAN= Leaf angle, FLA= Flag leaf area, FLAN= Flag leaf angle, LIL= Ligule length, CL= Culm length.

Table 3b. Mean performances of 47 rice genotypes for different morphological traits (cont.)

Genotype	CD	PL	NFG	NUFG	GL	GB	GL/GB	SB	GW	Y/P
Katiabagdad	0.97h	28.67b-g	127.70c	23.00a	0.97ab	0.30b	3.22fgh	35.33b	10.43z	9.13op
Peta	1.07gh	28.33b-g	122.00def	13.67d-j	0.77cde	0.23cd	3.44efg	28.00c-f	21.72kl	16.35h-n
Shuna onjona	1.10fgh	26.67c-j	117.30fg	9.67j-q	0.83cd	0.27bc	3.22fgh	17.67n-q	24.21f	27.87cde
Supahar	1.10fgh	30.00b-e	162.3a	16.67cde	0.87bc	0.37a	2.41ijkl	48.33a	16.51st	18.60f-l
Kataribug	1.13efg	27.33b-i	74.33w	5.67q	0.83cd	0.30b	2.78hi	18.00n-q	20.55m	14.87j-o
Lakkhidiga	1.07gh	30.00b-e	127.7c	9.33k-q	0.87bc	0.30b	2.89ghi	28.33c-f	15.83u	14.20j-p
Sadalakkhi	1.07gh	24.33g-m	105.00jklm	11.33g-n	1.03a	0.40a	2.583hijk	19.00l-p	26.10bc	24.79c-f
Mowlata	1.30abcd	24.67f-m	103.7klm	7.67m-q	0.87bc	0.30b	2.89ghi	27.00d-i	16.63s	13.72k-p
Naliuri	1.43a	23.33h-m	118.70fg	14.33d-h	0.73def	0.20d	3.66def	26.00e-j	15.52z	19.90f-l
Batraj	1.23b-f	23.00i-m	99.33mnop	7.33n-q	1.03a	0.20d	5.16a	27.33d-h	22.29hi	13.72k-p
Kalijira 2	1.27bcde	35.00a	98.00nop	6.67pq	0.53h	0.30b	1.78m	17.33pq	19.68p	29.53cd
Julaki	1.33abc	27.33b-i	108.70ijk	11.00h-o	0.80cd	0.40a	2.00klm	26.33e-i	18.68q	15.41j-o
L. shail	1.33abc	29.33b-f	127.00cd	15.67c-f	0.97ab	0.20d	4.83ab	32.33bc	12.60y	16.74h-m
Sarna	1.20c-g	20.00m	134.70b	20.67ab	0.83cd	0.20d	4.16cd	29.00cde	25.97c	55.56a
Long	1.23b-f	26.33d-k	122.30cdef	17.00cd	0.83cd	0.20d	4.16cd	31.33bcd	13.12x	30.79c
Jobeshail	1.30abcd	26.33d-k	124.30cde	19.00bc	0.80cd	0.20d	4.00cde	34.33b	23.28g	30.59c
Jashore saran	1.33abc	31.00a-d	100.00mno	8.00m-q	0.67efg	0.40a	1.66m	23.33f-m	22.56h	29.48cd
Sakkar khana	1.23b-f	20.67m	97.33nop	7.67m-q	0.63fgh	0.30b	2.11jklm	24.67e-j	16.73s	15.81i-o
Lalmatha	1.17defg	24.00g-m	85.67tu	7.67m-q	0.83cd	0.20d	4.16cd	22.33h-o	20.30mno	21.01f-j
Indra shail	1.37ab	27.67b-i	95.33opq	6.67pq	0.87bc	0.30b	2.89ghi	26.00e-j	22.19hij	20.69f-k
Lalsharna	1.17defg	21.67k-m	102.00lmn	10.67h-p	0.80cd	0.30b	2.67hig	23.67f-l	22.03ijk	22.51e-i
Pakkiraj	1.20cdefg	22.33j-m	91.33qrst	7.67m-q	0.87bc	0.30b	2.89ghi	18.33m-q	26.42ab	37.48b
Karaja	1.17defg	29.33b-f	79.67v	7.33n-q	0.63fgh	0.20d	3.16fgh	17.33opq	19.92op	19.37f-l
Jirashil	1.17defg	21.00lm	89.33rstu	9.00k-q	0.63fgh	0.20d	3.16fgh	19.33k-p	19.92p	12.87l-p
Sonaburion	1.27bcde	26.33d-k	107.3ijkl	11.33g-n	0.63fgh	0.30b	2.50ijk	24.33e-k	24.67e	30.48c
Nepali sorna	1.23b-f	26.33d-k	111.30hi	11.33g-n	0.63fgh	0.30b	2.11jklm	27.67c-g	22.57h	13.29l-p
Miniket	1.13efg	27.33b-i	89.00rstu	8.00m-q	0.83cd	0.20d	4.16cd	13.67q	13.68w	7.69p
Biharijulon	1.27bcde	35.00a	91.67qrs	7.33n-q	0.57gh	0.20d	2.83ghi	23.67f-l	16.06u	13.24l-p
Kadam sail	1.23b-f	26.67c-j	108.70ijk	11.67g-m	0.63fgh	0.30b	2.11jklm	22.00i-p	21.83jkl	14.75j-o
Malibhug	1.37ab	26.67c-j	108.70ijk	11.00g-o	0.40i	0.20d	2.00klm	23.33f-m	20.03nop	19.70f-l
Pajam	1.30abcd	29.67b-e	117.3fg	11.67g-m	0.60gh	0.20d	3.00ghi	24.33e-k	17.86r	13.21l-p
Binni	1.23b-f	24.67f-m	101.00mn	9.00k-q	0.73def	0.20d	3.833cde	21.00j-p	22.53h	16.61h-m
Shafeeb sail	1.33abc	31.67ab	104.70klm	16.00c-f	0.63fgh	0.30b	2.11jklm	22.33h-o	21.52l	9.47nop
Jinga sail	1.17defg	23.00i-m	73.33w	7.00opq	0.87bc	0.20d	4.33bc	19.33k-p	12.30y	11.29m-p
Chahlam	1.17defg	26.00e-k	110.70hij	7.66m-q	0.83cd	0.20d	4.16cd	24.33e-k	20.35mno	13.30l-p
Mathamota	1.13efg	29.67b-e	94.00pqr	10.00i-p	0.83cd	0.20d	4.16cd	26.67b-i	26.80a	17.85g-m
Daud sail	1.17defg	25.33e-l	85.67u	9.00k-q	0.63fgh	0.20d	3.16fgh	25.67e-j	25.38d	25.10c-f
Dula aman	1.17defg	28.67b-g	121.00efg	13.00e-k	0.63gh	0.20d	3.16fgh	27.33d-h	21.60kl	14.34j-p
Khawa	1.20c-g	28.00b-h	105.00klm	14.00b-i	0.83cd	0.20d	4.16cd	27.67c-g	19.90op	18.78f-l
Molag baru	1.17defg	27.00b-j	87.00stu	8.67l-q	0.60gh	0.20d	3.00ghi	19.33k-p	23.39g	17.30g-m
Nandidhan	1.30abcd	21.00lm	109.30ijk	12.33f-l	0.83cd	0.20d	4.16cd	29.00cde	19.61p	23.79d-g
Narika	1.33abc	28.67b-g	111.30hi	11.00g-o	0.83cd	0.30b	2.78hi	23.67f-l	15.32v	16.95g-m
Joila	1.37ab	28.00b-h	112.00hi	15.00d-g	0.83cd	0.20d	4.16cd	22.67g-n	24.90	23.12b-h
Kalijira	1.33abc	31.33abc	115.7gh	16.33cde	0.37i	0.20d	1.83lm	25.33e-j	23.49g	22.52e-i
Tulshimala	1.67defg	24.00g-m	94.33pqr	9.67j-q	0.77cde	0.20d	3.83cde	22.67g-n	19.57p	16.79h-m
Bismuri	1.23b-f	20.67lm	89.33rstu	7.67m-q	0.63fgh	0.30b	2.11jklm	22.67g-n	20.44mn	16.55h-m
China atap	1.27bcde	25.67e-k	89.00rstu	7.67m-q	0.77cde	0.20d	3.83cde	22.33h-o	16.17tu	17.79g-m
Lsd (0.05)	0.13	3.855	4.89	3.336	0.10	0.05	0.5304	4.142	0.40	5.735
SE (±)	0.01	0.35	0.44	0.30	0.01	0.002	0.05	0.37	0.04	0.52
Minimum	0.97	20.00	73.33	5.67	0.37	0.2	1.67	13.67	10.43	7.693
Maximum	1.43	35.00	162.3	23.00	1.03	0.4	5.17	48.33	26.80	55.56
Mean	1.22	26.59	105.34	11.06	0.75	0.25	3.18	24.72	19.96	19.68
Level of sig.	*	*	*	*	*	*	*	*	*	*
CV (%)	6.41	8.94	2.86	18.60	7.85	5.81	10.26	10.33	1.26	17.97

In single column values having common letter(s) indicate statistically non-significant difference as per DMRT, \* indicates significant at  $\leq 5\%$  probability, CD= Culm diameter, PL= Panicle length, NFG= No of filled grains panicle<sup>-1</sup>, NUFG= No of unfilled grains panicle<sup>-1</sup>, GL= Grain length, GB= Grain breadth, GL/GB= Grain length and breadth ratio, SB= Secondary branches in panicle, GW= 1000-grain weight, Y/P= Yield plant<sup>-1</sup>.

Table 4. Estimation of different genetic parameters for various agro-morphological traits of 47 genotypes of rice

Characters	PCV	GCV	PCV-GCV	$\sigma^2_g$	$\sigma^2_p$	$h^2_b$	GA	GA (%)
Seedling height (cm)	32.66	18.73	13.93	509.68	1548.90	32.91	26.68	22.14
Leaf length (cm)	37.06	20.71	16.35	107.21	343.27	31.23	11.92	23.85
Leaf width (cm)	18.32	9.08	9.24	0.01	0.04	24.57	0.10	9.27
Leaf angle ( $^\circ$ )	18.51	8.95	9.56	21.71	92.76	23.40	4.64	8.92
Flag leaf area (cm <sup>2</sup> )	50.83	29.06	21.77	111.88	342.20	32.69	12.46	34.23
Flag leaf angle ( $^\circ$ )	89.53	51.27	38.26	939.78	2865.71	32.79	36.16	60.48
Culm length (cm)	53.21	29.79	23.42	47.86	152.68	31.35	7.98	34.36
Culm diameter (cm)	15.25	7.06	8.19	0.01	0.03	21.40	0.08	6.72
Internode length (cm)	41.38	22.77	18.61	30.14	99.55	30.28	6.22	25.81
Number of tillers hill <sup>-1</sup> (no.)	32.93	18.44	14.49	5.54	17.67	31.35	2.71	21.27
Number of effective tillers hill <sup>-1</sup> (no.)	52.29	29.44	22.85	7.60	23.96	31.70	3.20	34.15
Panicle length (cm)	24.69	12.22	12.47	10.56	43.09	24.50	3.31	12.46
Secondary branches in panicle (no.)	41.76	22.72	19.04	31.54	106.53	29.61	6.30	25.47
No of filled grain panicle <sup>-1</sup>	3.65	12.00	-8.35	1.12	14.78	7.59	0.60	0.57
No of unfilled grain panicle <sup>-1</sup>	65.61	34.74	30.87	14.75	52.63	28.03	4.19	37.88
Grain length (cm)	79.87	22.0	57.87	1.44	4.45	32.39	1.41	86.74
Grain breadth (cm)	44.07	24.86	19.21	0.80	0.01	31.82	0.07	28.88
Grain length and breadth ratio	49.32	27.22	22.1	0.75	2.46	30.45	0.98	30.94
Ligule length (cm)	53.27	30.01	23.26	0.06	0.20	31.74	0.30	34.83
1000-grain weight (g)	74.76	43.05	31.71	71.78	216.42	33.17	10.05	51.08
Yield plant <sup>-1</sup> (g)	37.70	21.74	15.96	18.83	56.62	33.26	5.16	25.83

GCV = genotypic coefficient of variance, PCV = phenotypic coefficient of variance,  $\sigma^2_g$  = genetic variance,  $\sigma^2_p$  = phenotypic variance,  $h^2_b$  = broad-sense heritability, GA = genetic advance, GA (%) = genetic advance as percent of mean.

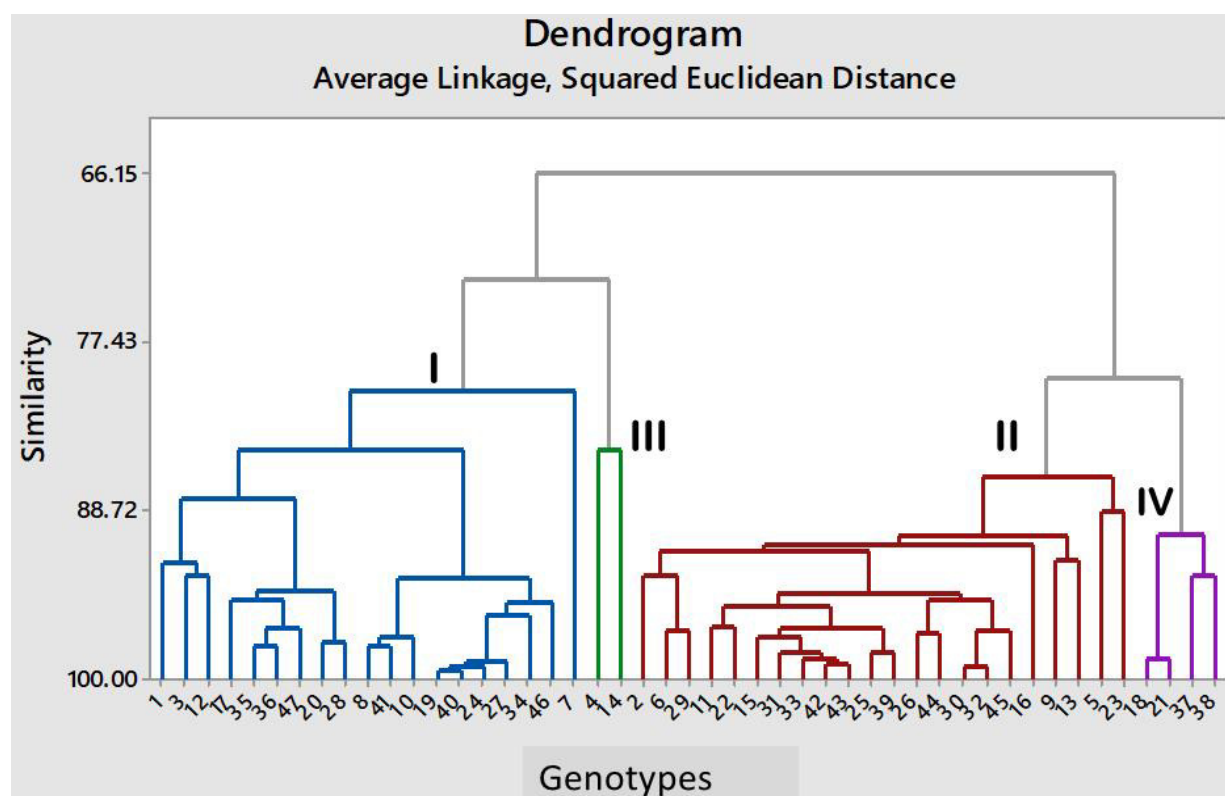


Fig. 1 Dendrogram of 47 rice genotypes from cluster analysis

Here, genotype 1=Katiabagdad, 2= Peta, 3= Shuna onjona, 4= Supahar, 5= Kataribug, 6= Lakkhidiga, 7= Sadalakkhi, 8= Mowlata, 9= Naliuri, 10= Batraj, 11= Kalijira 2, 12= Julaki, 13= L. shail, 14= Long, 16= Jobeshail, 17= Jashore saran, 18= Sakkar khana, 19= Lalmatha, 20= Indra shail, 21= Lalsharna, 22= Pakkiraj, 23= Karaja, 24= Jirashil, 25= Sonaburion, 26= Nepali sorna, 27= Miniket, 28= Biharijulon, 29= Kadam sail, 30= Malibhug, 31= Pajam, 32= Binni, 33= Shafeeb sail, 34= Jinga sail, 35= Chahlam, 36= Mathamota, 37= Daud sail, 38= Dula aman, 39= Khawa, 40= Molag baru, 41= Nandi dhan, 42= Narica, 43= Joila, 44= Kalijira, 45= Tulshimala, 46= Bismuri, 47= China atap

Moderate heritability (20-60%) with high genetic advance (>20%) was assessed for number of tiller plant<sup>-1</sup>, number of effective tiller plant<sup>-1</sup>, seedling height, internode length, leaf length, flag leaf area, ligule length, culm length, no of unfilled grain panicle<sup>-1</sup>, grain length, grain breadth, grain length-breath ratio, secondary branch in panicle, 1000-grain weight and yield plant<sup>-1</sup> (Table 4). Whereas, panicle length showed moderate heritability with moderate genetic advance (10-20%) (Table 4). Most of the characters showed moderate heritability indicated that these were less influenced by the environment and thus help in effective selection of these traits and suggested the opportunity of genetic improvement. Moderate heritability coupled with high genetic advance for rice yield have been reported by Abebe *et al.* (2017), supporting the present findings. 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 because of gathering higher additive genes results in further improvement (Edukondalu *et al.*, 2017).

#### *Phenotypic correlation*

Simple correlation results among the studied characters are presented in Table 5. As yield is a complex and dependable trait, so estimation of correlation among yield and different yield contributing traits is of great importance for breeders. Here, correlation studies revealed that seedling height had strong positive correlation ( $r = 0.874$ ) with leaf length but had a significant negative correlation with leaf width ( $r = -0.366$ ) (Table 5). Flag leaf area showed moderate positive correlation with ligule length ( $r = 0.529$ ) but negatively associated with 1000-grain weight ( $r = -0.288$ ) (Table 5). Sameera *et al.*, (2016) were also reported negative significant correlation between flag leaf area and 100-grain weight. Furthermore, no of filled grain panicle<sup>-1</sup> displayed strong positive correlation ( $r = 0.781$ ) with no of unfilled grain panicle<sup>-1</sup> and secondary branches in panicle, similar relation existed between culm length and internode length (Table 5). Yield plant<sup>-1</sup> showed significant positive correlation with number of tillers hill<sup>-1</sup> ( $r = 0.651$ ), number of effective tillers hill<sup>-1</sup> ( $r = 0.657$ ), 1000-grain weight ( $r = 0.543$ ), filled grain panicle<sup>-1</sup> ( $r = 0.216$ ), no of unfilled grain panicle<sup>-1</sup> ( $r = 0.243$ ) but displayed negative correlation with panicle length ( $r = -0.173$ ) (Table 5), similar results were also observed by Devi *et al.* (2017). Correlation study revealed some other significant positive and negative correlation among the considered agro-morphological traits of 47 rice genotypes showed in Table 5. The results showed some similarity and contradiction with the previous findings by Kalyan *et al.*, 2017; Akhter *et al.*, 2014 and Osundare *et al.*, 2017.

#### *Diversity analysis*

Eigen values and percentage of variation accounted for individual component are shown in Table 6. The result revealed that principal component 1 (PC1) explained 21.4% of total variations observed among the genotypes followed by PC2 (16.6%). The first seven principal components (Table 6) explained for about 79.5% of the total variations among all the studied traits describing 47 rice genotypes where only 37.9% variation was accounted for the first two components. Sameera *et al.* 2016 also observed a number of six principal components explained 83% variation for large number of quantitative traits. The most important traits for PC1 were: seedling height (0.406), internode length (0.383), culm length (0.379) and leaf length (0.339) with positive coefficients and leaf width (-0.243), 1000-grain weight (-0.124), grain length (-0.113) with negative coefficients (Table 6). The first component representing the significance of this PC for plant growth related traits. Whereas no of filled grain panicle<sup>-1</sup> (0.375), secondary branches in panicle (0.364), flag leaf area (0.356) and no of unfilled grain panicle<sup>-1</sup> (0.298) with positive coefficient and number of effective tiller hill<sup>-1</sup> (-0.275), leaf width (-0.243), number of tiller hill<sup>-1</sup> (-0.236) and 1000-grain weight (-0.235) with negative coefficients (Table 6) 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. Maximum number of genotypes (22) were clustered in group II, while minimum (02) into cluster III. Nineteen (19) and four (4) genotypes were grouped into cluster I and IV respectively (Fig. 1). For the improvement of various characters, superiority of cluster are generally assessed using clusterwise mean values of the studied traits (Ahmed *et al.*, 2014). Mean values of different clusters for the characters showed that genotypes which produced maximum flag leaf area, number of no of effective tillers hill<sup>-1</sup>, no of filled grain panicle<sup>-1</sup> and yield plant<sup>-1</sup> were accumulated in cluster III, whereas genotypes with maximum effective no of effective tillers hill<sup>-1</sup>, panicle length and leaf area were grouped in cluster II (Table 7). Similarly, genotypes which produced less seedling height and more grain weight were clubbed into cluster IV, whereas minimum effective tillers plant<sup>-1</sup>, low 1000-grain weight with low yielding genotypes were grouped into cluster I (Table 7). Cluster analysis showed that in terms of high yield potentiality cluster III (Supahar, Sarna) had highest cluster mean for rice yield (37.08g), followed by cluster IV (23.28g) (Sakkar khana, Lalsharna, Daud sail and Dula aman) (Table 7). Therefore, priority should be given to genotypes aggregated in cluster III and IV having high yield potentiality for future rice breeding.

Table 5. Phenotypic correlation co-efficient among different agro-morphological traits of 47 rice genotypes

	SH	LL	LW	FLA	LIL	CL	CD	NTH	ETH	PL	NFG	NUFG	GL	GB	GB/GL	SB	IL	LA	FLA	Y/p
SH																				
LL	0.847***																			
LW	-0.366***	-0.15																		
FLA	0.211**	0.411***	0.085																	
LIL	-0.055	0.1	0.087	0.529***																
CL	0.579***	0.362***	-0.55	0.003	-0.147															
CD	0.302***	0.126	-0.38	0.027	0.007	0.646***														
NTH	-0.029	0.041	-0.05	-0.036	-0.07	0.269***	0.135													
ETH	0.088	0.084	-0.196	-0.123	-0.173*	0.335***	0.177*	0.892***												
PL	0.525***	0.477***	-0.088	0.247**	0.153	0.243**	0.096	-0.125	-0.117											
FG	0.151	0.278***	0.164*	0.372***	0.193*	-0.089	-0.001	-0.064	-0.111	0.165*										
UFG	0.138	0.268***	0.166*	0.301***	0.124	-0.005	-0.029	-0.002	-0.062	0.07	0.718***									
GL	-0.115	0.064	0.059	0.282***	0.303***	-0.229**	-0.259**	-0.106	-0.109	-0.218**	0.154	0.089								
GB	0.037	0.104	0.051	0.316***	0.438***	-0.166*	-0.082	-0.04	-0.008	0.117	0.166*	-0.051	0.16							
GB/GL	-0.068	0.01	-0.033	-0.017	-0.124	0.027	-0.078	-0.047	-0.072	-0.219**	0.001	0.116	0.613***	-0.641***						
SB	0.022	0.144	0.07	0.299***	0.25**	-0.065	-0.051	-0.139	-0.183*	0.094	0.718***	0.57***	0.209*	0.089	0.09					
IL	0.638***	0.505***	-0.549	0.128	-0.011	0.781***	0.539**	0.177*	0.268***	0.352***	-0.009	0.003	-0.186*	-0.157	0.055	0.028				
LA	0.499***	0.379***	-0.187	0.008	-0.23**	0.247**	0.18**	0.094	0.217**	0.089	0.065	0.081	0.02	0.105	-0.071	-0.092	0.174*			
FLAN	0.551***	0.416***	-0.143	0.02	-0.303***	0.363**	0.183*	0.117	0.167*	0.212**	0.088	0.156	-0.299***	-0.045	-0.188*	-0.031	0.284***	0.72***		
Y/p	-0.039	-0.014	0.041	-0.041	0.036	0.099	0.029	0.651***	0.657***	-0.173*	0.216**	0.243**	-0.091	-0.029	-0.052	0.017	0.013	0.052	0.102	
GW	-0.204	-0.331	0.126	-0.288***	-0.059	-0.152	-0.129	0.033	0.048	-0.211*	-0.238**	-0.117	-0.175*	-0.097	-0.078	-0.271***	-0.246**	0.054	0.043	0.543***

\*\* and \*\*\* indicates significant at  $\leq 1\%$  and  $\leq 0.1\%$  level of probability respectively, 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 tillers hill<sup>-1</sup>, ETH= Number of effective tillers hill<sup>-1</sup>, PL= Panicle length, NFG= No of filled grain panicle<sup>-1</sup>, NUFG= No of unfilled grain panicle<sup>-1</sup>, GL= Grain length, GB= Grain breadth, GL/GB= Grain length and breadth ratio, SB= Secondary branches in panicle, IL= Internode length, LAN= Leaf angle, FLAN= Flag leaf angle, Y/p= Yield plant<sup>-1</sup>, GW= 1000-grain weight.



Table 6. Principal components and their coefficients of studied agro-morphological traits of 47 rice genotypes

Traits	Main components						
	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Seedling height	0.406	0.098	-0.108	-0.044	-0.111	0.128	-0.204
Leaf length	0.339	0.216	-0.007	-0.01	-0.062	0.228	-0.25
Leaf width	-0.243	-0.243	0.156	-0.127	-0.228	0.026	-0.203
Leaf angle	0.255	-0.029	0.033	-0.087	-0.34	0.407	0.407
Flag leaf area	0.092	0.356	0.093	-0.069	-0.069	0.146	-0.152
Flag leaf angle	0.297	-0.051	0.036	-0.137	-0.433	0.137	0.078
Culm length	0.379	-0.131	-0.056	0.131	0.163	-0.151	0.023
Culm diameter	0.266	-0.096	-0.064	0.047	0.216	-0.291	0.217
Internode length	0.383	-0.035	-0.094	0.138	0.215	-0.139	-0.1
No. of tillers hill <sup>-1</sup>	0.125	-0.236	0.439	0.021	0.203	0.103	0.049
No. of effective tillers hill <sup>-1</sup>	0.17	-0.275	0.4	0.017	0.178	0.178	0.105
Panicle length	0.218	0.176	-0.161	-0.2	-0.002	-0.121	-0.395
Secondary branch in panicle	0.019	0.364	0.182	0.147	-0.054	-0.287	0.229
No of filled grain panicle <sup>-1</sup>	0.071	0.375	0.286	0.053	-0.162	-0.228	0.159
No of nfilled grain panicle <sup>-1</sup>	0.074	0.298	0.303	0.151	-0.246	-0.234	0.027
Grain length	-0.113	0.226	0.057	0.323	0.171	0.514	0.046
Grain breadth	-0.015	0.185	0.072	-0.499	0.229	0.221	0.275
Grain length breadth ratio	-0.045	0.03	-0.025	0.652	-0.027	0.198	-0.191
Ligule length	-0.049	0.284	0.091	-0.163	0.431	0.035	-0.216
1000-grain weight	-0.124	-0.235	-0.124	-0.139	-0.124	-0.064	-0.478
Yield plant <sup>-1</sup>	0.054	-0.158	0.552	-0.019	0.009	-0.054	-0.239
Eigen values	4.49	3.48	2.47	2.03	1.76	1.41	1.05
% Total variation	21.4	16.6	11.7	9.6	8.4	6.8	5
Cumulative (%)	21.4	37.9	49.7	59.3	67.7	74.4	79.5

Table 7. Cluster mean for studied agro-morphological traits of 47 rice genotypes

Variables	Cluster means			
	Cluster I	Cluster II	Cluster III	Cluster IV
Seedling height	108.72	137.65	102.00	91.42
Leaf length	45.51	56.54	47.08	36.69
Leaf width	1.13	1.07	1.20	1.18
Leaf angle	38.47	64.67	24.33	60.00
Flag leaf area	35.68	38.15	42.40	27.13
Flag leaf angle	28.93	86.88	16.33	79.17
Culm length	21.18	26.62	15.83	17.92
Culm diameter	1.20	1.25	1.15	1.18
Internode length	22.54	26.65	20.67	19.33
No. of tillers hill <sup>-1</sup>	12.23	13.12	14.00	12.75
No. of effective tillers hill <sup>-1</sup>	8.61	9.86	9.83	9.75
Panicle length	25.98	27.71	25.00	24.08
Secondary branch in panicle	23.47	24.36	38.67	25.58
No of filled grains panicle <sup>-1</sup>	98.18	108.30	148.50	101.50
No of unfilled grains panicle <sup>-1</sup>	9.35	12.08	18.67	10.08
Grain length	0.81	0.72	0.85	0.68
Grain breadth	0.25	0.24	0.28	0.25
Grain length breadth ratio	3.36	3.09	3.29	2.78
Ligule length	0.91	0.78	1.18	0.78
1000-grain weight	19.03	19.70	21.24	24.23
Yield plant <sup>-1</sup>	15.74	20.37	37.08	23.28

## Conclusion

On summary, the present study confirmed the presence of adequate genetic diversity in the available rice genotypes tested. Moderate to high values of heritability and genetic advance for most of the yield attributes, offering the more opportunity for further improvement of those following breeding program. Positive significant correlation were observed for yield with number of effective tillers plant<sup>-1</sup>, 1000-grain weight, no of filled grains panicle<sup>-1</sup>, whereas, negative with panicle length.

Principal component analysis revealed most important traits contributing the genotypic variation. Cluster analysis manifested four clusters among which genotypes in cluster III (Supahar, Sarna) and cluster IV (Sakkar khana, Lalsharna, Daud sail, Dula aman) had high yield potentiality. Thus, the study can offer a valuable gene pool from the traditional local rice germplasms which can be further utilized in different breeding program for varietal improvement or development in future.

References

- Abebe, T., Alamerew, S. and Tulu, L. 2017. Genetic variability, heritability and genetic advance for yield and its related traits in rainfed lowland rice (*Oryza sativa* L.) genotypes at Fogera and Pawe, Ethiopia. *Advances in Crop Science and Technology*, 5: 272-279. <https://doi.org/10.4172/2329-8863.1000272>
- Ahmed, A., Shaon, S.G., Islam, M.S., Saha, P.S. and Islam, M.M. 2014. Genetic divergence analysis in HRDC rice (*Oryza sativa* L.) hybrids in Bangladesh. *Bangladesh Journal of Plant Breeding and Genetics*, 27: 25-32. <https://doi.org/10.3329/bjpbg.v27i2.27842>
- Ahmed, M. S. U., Khalequzzaman, M., Bashar, M. K. and Shamsuddin, A. K. M. 2016. Agro-morphological, physico-chemical and molecular characterization of rice germplasm with similar names of Bangladesh. *Rice Science*, 23: 211-218. <https://doi.org/10.1016/j.rsci.2016.06.004>
- Ahmed, M.S., Akter, K., Khalequzzaman, M., Rashid, E.S.M.H. and Bashar, M.K. 2010. Diversity analysis in Boro rice (*Oryza sativa* L.) accessions. *Bangladesh Journal of Agricultural Research*, 35: 29-36. <https://doi.org/10.3329/bjar.v35i1.5864>
- Akhter, M.S., Rizwan, M., Akhter, M., Naeem, M., Hussain, W., Elahi, F. and Latif, M. 2014. Genotypic and phenotypic condition coefficient analysis for yield and yield related components in basmati rice (*Oryza sativa* L.). *Americam-Eurasian Journal of Agricultural and Environmental Sciences*, 14: 1402-1404.
- Akter, N., Begum, H., Islam, M.Z., Siddique, M.A. and Khalequzzaman, M. 2018b. Genetic diversity in Aus rice (*Oryza sativa* L.) genotypes of Bangladesh. *Bangladesh Journal of Agricultural Research*, 43: 253-266. <https://doi.org/10.3329/bjar.v43i2.37329>
- Akter, N., Islam, M.Z., Chakrabarty, T. and Khalequzzaman, M. 2018a. Variability, Heritability and diversity analysis for some morphological traits in Basmati rice (*Oryza sativa* L.) genotypes. *The Agriculturists*, 16: 01-14. <http://dx.doi.org/10.3329/agric.v16i02.40338>
- Akter, N., Islam, M.Z., Siddique, M.A., Chakrabarty, T., Khalequzzaman, M. and Chowdhury, M.A. Z. 2016. Genetic diversity of Boro rice (*Oryza sativa* L.) landraces in Bangladesh. *Bangladesh Journal of Plant Breeding and Genetics*, 29: 33-40. <https://doi.org/10.3329/bjpbg.v29i2.33948>
- Akter, N., Khalequzzaman, M., Islam, M.Z., Mamun, M.A.A. and Chowdhury, M.A.Z. 2018c. Genetic variability and character association of quantitative traits in Jhum rice genotypes. *SAARC Journal of Agriculture*, 16: 193-203. <https://doi.org/10.3329/sja.v16i1.37434>
- Augustina, U.A., Iwunor, O.P. and Ijeoma, O.R. 2013. Heritability and character correlation among some rice genotypes for yield and yield components. *Journal of Plant Breeding and Genetics*, 1: 73-84.
- Babu, V.R., Shreya, K., Dangi, K.S., Usharani, G. and Nagesh, P. 2012. Genetic variability studies for qualitative and quantitative traits in popular rice (*Oryza sativa* L.) hybrids of India. *International Journal of Scientific and Research Publications*, 2(6): 1-5.
- Bagati, S., Singh, A.K., Salgotra, R.K., Bhardwaj, R., Sharma, M., Rai, S.K. and Bhat, A. 2016. Genetic variability, heritability and correlation coefficients of yield and its component traits in basmati rice. *SABRAO Journal of Breeding and Genetics*, 48: 445-452.
- BBS, 2017. Yearbook of Agricultural Statistics. Bangladesh Bureau of Statistics, Statistics and Informatics Division (SID), Ministry of Planning, Government of the People's Republic of Bangladesh, Dhaka. pp. 39.
- Burton, G.W. and Devane, D.E. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material 1. *Agronomy Journal*, 45: 478-481.
- Comstock, R.E. and Robinson, H.F. 1952. Genetic parameters, their estimation and significance. *Proceedings of the 6th international Grassland congress*, Pennsylvania State College, pp.248-291.
- Edukondalu, B., Reddy, V.R., Rani, T.S., Kumari, C.A. and Soundharya, B. 2017. Studies on variability, heritability, correlation and path analysis for yield, yield attributes in rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*, 6(10): 2369-2376. <https://doi.org/10.20546/ijcmas.2017.610.279>
- Gour, L., Koutu, G.K., Singh, S.K., Patel, D.D., Shrivastava, A. and Singh, Y. 2017. Genetic variability, correlation and path analyses for selection in elite breeding materials of rice (*Oryza sativa* L.) genotypes in Madhya Pradesh. *The Pharma Innovation Journal*, 6(11): 693-696.
- Iqbal, T., Hussain, I., Ahmad, N., Nauman, M., Ali, M., Saeed, S., Zia, M. and Ali, F. 2018. Genetic variability, correlation and cluster analysis in elite lines of rice. *Journal of Scientific Agriculture*, 85-91. <https://doi.org/10.25081/jjsa.2018.v2.900>
- Islam, M.Z., Akter, N., Chakrabarty, T., Bhuiya, A., Siddique, M.A. and Khalequzzaman, M. 2018. Agro-morphological Characterization and Genetic Diversity of Similar Named Aromatic Rice (*Oryza sativa* L.) Landraces of Bangladesh. *Bangladesh Rice Journal*, 22:45-56. <https://doi.org/10.3329/brj.v22i1.41836>
- Jayasudha, S. and Sharma, D. 2010. Genetic parameters of variability, correlation and path-coefficient for grain yield and physiological traits in rice (*Oryza sativa* L.) under shallow lowland situation. *Electronic Journal of Plant Breeding*, 1: 1332-1338.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimation of genetic and environmental variability in soybeans. *Agronomy Journal*, 47: 314-318.
- Kalyan, B., Radha Krishna, K.V. and Subba Rao, L.V. 2017. Correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*, 6: 2425-2430. <https://doi.org/10.20546/ijcmas.2017.604.287>
- Khaliq, I., Noorka, L.R. and Khaliq, R. 2009. Estimation of heritability and genetic advance for some quantitative characters in spring wheat. *International Journal of Applied Agricultural Sciences*, 1: 76-78.
- Megloire, N. 2005. The genetic, morphological and physiological evaluation of African cowpea genotypes. University of Free State.
- Mehetre, S.S., Mahajan, C.R., Patil, P.A., Lad, S.K. and Dhupal, P.M. 1994. Variability, heritability, correlation, path analysis, and genetic divergence studies in upland rice. *IRRN*. 19: 8-9.
- Oad, F.C., Samo, M.A., Hassan, Z.U., Pompe, S.C. and Oad, N. L. 2002. Correlation and path analysis of quantitative characters of rice ratoon cultivars and advance lines. *International Agricultural Biology*, 4: 204-207.
- Osundare, O.T., Akinyele, B.O., Fayeun, L.S. and Osekita, O.S. 2017. Evaluation of qualitative and quantitative traits and correlation coefficient analysis of six upland rice varieties. *Journal of Biotechnology and Bioengineering*, 1:17-27.
- Pradhan, B., Mishra T. K. and Das, S. R. 2015. Genetic basis of yield variations in Lowland rice. *International Journal of Basic and Applied Science*, 19: 306-318.
- Prasad, K.R., Radha-Krishna, K.V., Bhave, M.H.V. and Subba-Rao, L.V. 2017. Genetic variability, heritability and genetic advance in boro rice (*Oryza sativa* L.) germplasm. *International Journal of Current Microbiology and Applied Sciences*, 6:1261-1266.
- Ratna, M., Begum, S., Husna, A., Dey, S.R. and Hossain, M.S. 2015. Correlation and path coefficients analyses in basmati rice. *Bangladesh Journal of Agricultural Research*, 40:153-161. <https://doi.org/10.3329/bjar.v40i1.23768>

- Sabesan, T., Suresh, R. and Saravanan, K. 2009. Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamil Nadu. *Electronic Journal of Plant Breeding*, 1: 56-59.
- Sameera, S., Srinivas, T., Rajesh, A.P., Jayalakshmi, V. and Nirmala, P.J. 2016. Variability and path co-efficient for yield and yield components in rice. *Bangladesh Journal of Agricultural Research*, 41(2): 259-271.
- Samonte, S.O., Wilson, L.T. and McClung, A.M. 1998. Path analysis of yield and yield-related traits of fifteen diverse rice genotypes. *Crop Science*, 38: 1130-1136. <https://doi.org/10.2135/cropsci1998.0011183X003800050004x>
- Selvi, R., Muthiah, A.R., Maheswaran, M. And Shanmugasundaram 2003. Genetic diversity in the genus *Vigna* based on morphological traits and isozyme markers. *SABRAO Journal of Breeding and Genetics*, 35: 103-112.
- Statista. 2018. Grain Production Worldwide by Type, 2017/2018. Cited July 7, 2018.
- Sumanth, V., Suresh, B.G., Ram, B.J. and Srujana, G. 2017. Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, 6(4): 1437-1439.
- Thomson, M.J., Septiningsih, E.M., Suwardjo, F., Santoso, T.J., Silitonga, T.S. and McCouch, S.R. 2007. Genetic diversity analysis of traditional and improved Indonesian rice (*Oryza sativa* L.) germplasm using microsatellite markers. *Theoretical and Applied Genetics*, 114: 559-568. <http://dx.doi.org/10.1007/s00122-006-0457-1>
- Vural, H. And Karasu, A. 2007. Variability studies in cowpea (*Vigna unguiculata* L. Walp.) varieties grown in Isparta, Turkey. *Revista UDO Agricola*, 7:29-34.
- Yesmin, N., Elias, S.M., Rahman, M., Haque, T., Mahub Hasan, A.K.M. and Seraj, Z.I. 2014. Unique genotypic differences discovered among indigenous Bangladeshi rice landraces. *International Journal of Genomics*, 2014. <https://doi.org/10.1155/2014/210328>