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

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ARTICLE INFO	ABSTRACT
Article history: Received: 03 February 2020 Accepted: 29 March 2020 Published: 30 June 2020	Rice (<i>Oryza sativa</i>) contributes significantly to global food security and is a major food crop for almost half of the world's population. Fourty 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 ($P \le 0.001$) among the genotypes for all the traits studied
Keywords: Rice genotypes, Morphological traits, Genetic variability, Character association, Diversity analysis	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 ⁻¹ 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
Correspondence: G. H. M. Sagor ⊠: sagorgpb@gmail.com	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
open	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.

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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 morphogenetic 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

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Characterization of local rice genotypes

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

S1.	Genotype	S1.	Genotype	S1	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 $1m \times 1m$. 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⁻¹ (NTH), number of effective tiller hill⁻¹ (ETH), panicle length (PL), secondary branch in panicle (SB), no of filled grain panicle⁻¹ (FG), no of unfilled grain panicle⁻¹ (UFG), grain length (GL), grain breadth (GB), grain length and breadth ratio (GL/GB), ligule length (LIL), 1000-grain weight (GW) and yield plant⁻¹ (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[®]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[®]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 ($P \le 0.001$) 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⁻¹ ranged from 5.67 to

Hannan et al.

17.67, which is one of the most important yield attribute as tillers bearing effective panicle will obviously contribute to final vield. Karaja (17.67) produced utmost tillers hill⁻¹ 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 cm²) was calculated for Julaki, followed by Katiabagdad (56.20 cm²) (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⁻¹ and 1000-grain weight (Mehetre 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⁻¹ (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 $(55.56 \text{ g plant}^{-1})$ followed by Pakkiraj (37.48 g plant⁻¹), 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⁻¹. 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⁻¹, grain length, grain breadth, grain length and breadth ratio, secondary branches in panicle, 1000-grain weight and yield plant⁻¹ (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⁻¹) to 89.53% (flag leaf angle), while the magnitude of GCV ranged from

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

of 47 genotypes of	of rice			
	Mean sun	1 of squares	(MSS)	
Characters	Replications		Error	CV
	(df = 2)	(df = 46)	(df = 92)	(%)
Number of tillers hill-1				
(no.)	1.41	23.38***	0.59	5.67
Number of effective				
tillers hill ⁻¹ (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 ^{NS}	0.005	6.68
Leaf angle (⁰)	315.11	78.94^{***}	13.82	6.96
Flag leaf area (cm ²)	53.77	338.92***	3.28	4.98
Flag leaf angle (⁰)	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 ⁻¹	0.66	5.71***	9.07	2.86
No. of unfilled grain				
panicle ⁻¹	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 ⁻¹ (g)	0.88	215.88^{***}	0.54	17.97
***= significant at ≤ 0.19	6 level of pro	bability, NS	= non-sig	nificant,

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⁻¹ were earlier recorded by Gour *et al.*, (2017) and Summnath *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⁻¹) to 33.26% (yield plant⁻¹), while corresponding values of genetic advance ranged from 0.57% (no of filled grain panicle⁻¹) to 60.48% (flag leaf angle) (Table 4). Babu et al. (2012) found high genetic advance for grain panicle⁻¹ and flag leaf characters also. Traits like leaf width, leaf length, culm diameter and no of filled grain panicle⁻¹ 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

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L shail 12.33g-k 10.00fpin 148.7ab 36.00a 70.10a 0.97gh 74.00b 52.57cd 94.00ab 1.16cd 30.00b 3arna 17.67b 1300c 94.00ap 20.33m-q 45.83mn 1.23cd 28.33opq 44.67pi 21.671mn 1.23c 21.001m 14.33dcf 11.67dc 13.65cf 30.07cd 56.7d-i 1.06c-h 70.00bcd 29.93nopq 95.00a 0.63jk 29.33b 10bcshail 14.67dc 12.67cd 141.0cd 31.33bcd 62.77bcd 1.03c-h 50.67g-k 47.37g 70.67fg 1.03de 31.00b 3abcro sarna 13.00f-i 11.33dcf 144.0vd 29.33g-g 61.00b-f 1.03c-h 55.37jk 47.37g 70.67fg 1.03de 31.00b 130dr 44.0vd 29.33c-g 61.00b-f 1.03c-h 55.37jk 90.0bcd 21.001u 91.67ab 0.63jk 19.07m 20.331mo 0.63jk 19.67m 13.00f-i 11.33dcf 144.0vd 29.33c-g 61.00b-f 1.03c-h 55.37jk 90.0bcd 21.001u 91.67ab 0.63jk 19.67m 3abcro sarna 12.33g-k 9.33hjk 80.33rh 11.67s 32.07s 12.37d 64.33de 21.03tu 85.33-e 0.63jk 14.33qb 14.33def 14.3.0de 30.00e-f 62.00b-e 0.97gh 65.00cde 34.67lm 91.67ab 0.93jk 14.33qb 14.33def 1.33def 25.67g-z 52.00h-1 1.03e-h 65.00cde 24.87rs 92.00abc 0.53jk 14.33qb 13.67a 1.32.3ghi 25.67g-z 52.00h-1 1.03e-h 65.00cde 24.87rs 92.00abc 0.53jk 12.33de 0.61,50b-f 1.004z 50.67c+k 41.53jk 78.33de 0.63jk 13.67b 0.97gb 30.33b 50.0bcd 0.53b 14.67nop 0.83ghi 13.67b 0.97gb 30.57b 14.67nop 0.83ghi 13.67b 0.97gb 30.57b 14.67nop 0.83ghi 13.67b 0.97gb 40.001m 1.13def 57.007g 43.33hj 81.67de 0.73ij 28.33b-0.06k k3.0abcu 0.61,50b -1 1.004z 50.67c+k 41.53jk 78.33de 0.66jk 22.67j-9 1.03c-h 65.33cd 23.004z 0.66jk 22.67j-9 1.63c-h 0.53b 14.67nop 0.86fgh 17.33o 11.033m 0.33m 13.87def 23.671-h 56.32-i 1.03c-h 65.33cde 23.004c 0.66jk 22.67j-9 24.13ji 1.33jm 8.00klm 13.87def 23.671-h 56.33c 24.670p 34.671m 23.53de 1.66jk 22.67j-9 24.13ji 1.33de 1.033m 6.330p 1.23df 25.67g-j 56.67d-i 1.33de 50.33b 150.60dc 38.500bcd 0.66jk 22.67j-9 1.03c-h 65.33cd 23.00b 38.500bcd 0.66jk 22.67j-9 2.67dj 3.671m 1.33de 1.000klm 0.33m 7.33mo 120.3hi 23.671-h 59.33c 1.03c-h 63.70cd 19.000 8.800bcd 0.66jk 22.67j-9 1.03c-h 63.33c 1.23d 1.030m 6.330b 1.23df 2.56jg-1.13def 50.00h-k 31.671m 1.23def 1.033m 6.330p 1.23df 2.56jg-1.13def 50.00h-k 31.671m 2.33db 1.040k 24.03b-1.040k 24.00b-1.040k 24.00	Kalijira 2	19.33a	15b	149.7a	35.00ab	63.17bc	1.06e-h	47.67jkl	41.20jk	95.00a	1.03de	36.00a
Sama 17.67b 1300c 94.000p 20.33m-q 45.81m 1.23cd 28.33opq 44.67b 1.23c 1.23b 29.33m-q 0.63jk 1.03de 31.00b Lahmatha 14.33def 11.33cf 140.04d 29.33m-q 140.75 1.07e-h 21.677 30.53m-q 20.33m-q 0.63jk 19.07m Lahmatha 13.30cf 11.00erg 138.3def 30.07c-f 52.03h-l 0.07g h 65.00cde 24.87m 92.03b-q 0.03jk 14.63a Laisharaa 13.35a-h 11.33def 14.33q 32.00b-f 52.00b-l 0.05rb-f 1.10d-g 50.67g-k 41.33jk 78.167mo 0.83ghi 13.67r 75.00b 80.33p 42.30kf 1.30br 1.67mop	Julaki	12.00h-l	8klmn	112.0k	25.67g-j	50.83i-1	1.06e-h	25.00pqr	65.00a	27.67kl	1.53a	22.33klmn
Long 14.33def 11.67de 12.67cd 13.33bcd 62.77bcd 1.03bch 70.00bcd 29.33b- 95.00a 0.63jk 92.33b- lobeshail 14.67de 12.67cd 141.06de 12.33bcg 61.00bc+ 10.3ch 53.33i- 43.30de 1.03bcf 11.33bcg 13.37bc 75.00h 19.00hc 10.7bc+ 15.353i- 35.33i 49.00h 1.03bc 31.37bc 05.37bc 10.7bc+ 15.354i- 35.33i 49.00h 1.03bc 31.03bc 31.00bc 32.37bc 10.7bc+ 15.7bc+ 10.7bc+ 75.7bc 10.7bc+ 17.7bc 10.7bc+ 17.7bc+ 11.0bc+ 32.33bc 0.7bc+ 10.7bc+ 32.50bc+ 11.7bc+ 32.0bc+ 12.3cd 14.33dc 11.33bc+ 13.3bc+ 13.0bc+ 30.0bc+ 12.0bc+ 14.07bc+ 15.7bc+ 14.03bc+ 15.7bc+ 11.0bc+ 50.0bc+ 34.67bc+ 10.7bc+ 52.0bc+ 13.3bc+ 13.7bc+ 52.0bc+ 13.3bc+ 13.7bc+ 52.0bc+ 13.3bc+ 13.7bc+ 52.0	L. shail	12.33g-k	10.00fghi	148.7ab	36.00a	70.10a	0.97gh	74.00b		94.00ab	1.16cd	30.00b-f
Indeschail 14.67de 12.67de 141.0cde 31.33bcd 62.77bcd 1.03e+ 50.77g-k 47.37g 70.67fg 1.03de 31.00bc Iashore saran 13.00f-i 11.33def 11.67b 52.33h-k 0.97gh 40.67m 39.97jk 25.00klm 11.67b 30.33b- Lalmatha 12.33gek 9.33hijk 80.33rh 11.67b 52.03h-k 0.97gh 40.67m 39.97jk 25.00klm 11.67b 30.33b- Laishara 12.33gek 11.33def 13.23cf 12.767g 52.00h-m 10.32-6 52.00h-m 39.33pq 1.13def 19.67a 0.63jk 17.37a Sonaburion 10.67lmn 6.33op 12.32 25.67g-z 52.00h-m 1.13def 19.33de 14.67ao 0.33b Karaja 11.33def 11.33def 12.32def 52.57g-g 52.00h-m 31.33h 1.13def 1	Sarna	17.67b	1300c	94.00op	20.33m-q	45.831mn	1.23cd	28.33opq	44.67ghi	21.671mno	1.23c	21.001mno
Iashore saran 13.00f-i 11.33def 14.40a-d 29.33c-g 61.00b-f 1.03ch 55.33c-i 35.33c-i 49.00h 1.03de 31.67b Sakar khana 16.33c-i 13.67c 75.00h 19.00r-q 34.00qrs 1.17de 69.00bcd 21.07b 0.57cb 0.57cb 0.57cb 0.57cb 43.75b 0.75cb 0.57cb 0.57cb 43.75b 0.57cb 0.57cb 43.75b 0.57cb 0.	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
Sakkar khana 16.33c 13.67c 75.00h 19.00n-q 34.00qrs 1.17de 69.00bcd 21.00tu 91.67abc 0.63jk 19.00nc Lalmatha 14.33def 11.00efg 13.30e1- 11.00efg 13.30e1- 11.00efg 33.33e1- 0.72h 0.67jk 0.72h	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
Lalmatha 14.33def 11.33ef 92.67p 19.67cde 43.17mo 1.07e-h 21.67r 30.53nop 20.33lmo 0.63jk 19.67nc fndra shail 13.00ri 11.00cfg 138.3def 30.67cde 52.33h-k 0.97gh 40.67m 39.97jk 25.00km 1.16cd 30.33b 12.33g-k 9.33hijk 80.33h 11.57s 32.00rs 1.23cd 64.33de 21.03tm 86.33a- 0.63jk 14.33q 24.87rs 92.00km 0.63jk 72.33m 70.75r 12.32gh 46.33de 21.03tm 91.67ac 0.63jk 72.32gh 25.00bc 0.97gh 65.00cde 34.67lm 91.67ac 0.53jk 72.33k 72.33hi 72.30jk 72.50km 1.03e-h 65.00cde 24.87rs 92.00ab 0.53k 72.33d 73.50km 11.33def 11.33def 121.3j 25.67g-z 52.00h 1.103e-h 65.00cde 24.87rs 92.00ab 0.53k 72.33d 73.50km 14.53nop 0.83ph 13.5dr 73.50km 12.33d 74.50km 79.33jk 74.53km 74.5	Jashore saran	13.00f-i	11.33def	144.0a-d	29.33c-g	61.00b-f	1.03e-h	55.33f-i	35.331	49.00h	1.03de	31.67bc
indra shail 13.00Fi 11.00efg 138.3def 30.67cd 52.33h-k 0.97gh 40.67m 39.97jk 25.00km 1.16cd 30.33b- Lalshama 12.33g-k 9.33hjk 80.33h 11.67s 32.00rs 1.23cd 64.33e 21.03u 86.33e 0.65jk 14.33g Pakkiraj 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 Sonaburion 10.671m 6.33og 14.63abc 33.00abc 61.50b-f 1.10deg 50.67g-k 41.53ik 78.33e 0.66jk 27.33d Sonaburion 10.33mn 6.33og 89.33pq 23.33i-n 41.33nog 1.13def 53.00rg 43.33hij 81.67dc 0.73ij 28.30b Siharijulon 10.33mn 6.33og 142.3dt 23.31-n 41.33nog 1.13def 73.0b 84.32dc 0.66jk 22.67g-g Binarijulon 10.33mn 6.33og 142.3dt 23.67i-n 56.93e-i 1.03e-h 70.67bcd 19.00u 89.00abcd 0.66jk 22	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
Lalsharnan 12.33 g-k 9.33 hijk 80.33 rh 11.67s 32.00rs 12.32 de 64.33 de 21.03 u 86.33 e-e 0.63 jk 14.33 pr Pakkiraj 13.33 e-h 11.33 def 143.0bcd 30.00 c-f 62.00 b- 0.79 gh 65.00 cde 24.87 s 92.00 be 0.73 st 30.33 b- Birashil 15.33 cd 11.33 def 18.3 gpi 25.07 g-z 52.00 st 14.67 nop 0.83 ghi 13.67 r. Sonaburion 10.67 lm 6.33 op 140.53 pc 25.07 g-z 52.00 st 41.57 jk 78.33 ef 0.66 jk 30.67 bc Sonaburion 14.33 def 11.33 cf 80.3 p 23.33 r 60.08 b-f 1.03 e-h 30.67 lm 23.00 r 36.01 16.67 nm op 0.86 gh 17.33 o Biharijulon 10.33 m 6.33 op 144.7 gb 26.33 rj 54.1 g-k 1.03 e-h 70.67 bc 54.00 te 50.03 ts 50.06 te 45.67 lm 23.67 klm 1.13 cd 28.00 c- 53.8 te 26.06 jk 27.67 c- Malibhug 10.33 m 7.33 mo 130.3hi 23.67 rlm 13.	Lalmatha	14.33def	11.33ef	92.67p	19.67cde	43.17mno	1.07e-h	21.67r	30.53nop	20.331mno	0.63jk	19.67nop
Lalsharnan 12.33 g-k 9.33 hijk 80.33 rh 11.67s 32.00rs 12.32 de 64.33 de 21.03 u 86.33 e-e 0.63 jk 14.33 pr Pakkiraj 13.33 e-h 11.33 def 143.0bcd 30.00 c-f 62.00 b- 0.79 gh 65.00 cde 24.87 s 92.00 be 0.73 st 30.33 b- Birashil 15.33 cd 11.33 def 18.3 gpi 25.07 g-z 52.00 st 14.67 nop 0.83 ghi 13.67 r. Sonaburion 10.67 lm 6.33 op 140.53 pc 25.07 g-z 52.00 st 41.57 jk 78.33 ef 0.66 jk 30.67 bc Sonaburion 14.33 def 11.33 cf 80.3 p 23.33 r 60.08 b-f 1.03 e-h 30.67 lm 23.00 r 36.01 16.67 nm op 0.86 gh 17.33 o Biharijulon 10.33 m 6.33 op 144.7 gb 26.33 rj 54.1 g-k 1.03 e-h 70.67 bc 54.00 te 50.03 ts 50.06 te 45.67 lm 23.67 klm 1.13 cd 28.00 c- 53.8 te 26.06 jk 27.67 c- Malibhug 10.33 m 7.33 mo 130.3hi 23.67 rlm 13.	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
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-lirashil Sonaburion 10.67lmn 6.33op 146.3abc 33.00abc 61.50b-f 1.10d-g 50.67g-k 41.53ijk 78.33ef 0.66jk 30.67bc Sonaburion 10.67lmn 6.33op 142.3def 11.33def 13.30p 1.13def 57.00fg 43.33hij 81.67de 0.73j (28.33bi) Winiket 11.00klm 6.33op 142.3cd 23.33i-n 40.00lmn 1.10d-g 71.67bc 54.00bc 84.37bc 0.66jk 22.67je- Malibhug 10.33mn 6.33op 142.7gb 26.37i- 56.92c-i 1.03e-h 70.67bc 19.00u 89.00abcd 0.66jk 22.67je- Malibhug 10.33mn 6.33op 134.7fgb 26.37i-g 96.67c-i 1.13def 70.00tcd 39.33bc 0.06kjk 27.67c- Binai 10.33mn 6.33op 77.67s 18.00pq 23.83t 1.23cd 24.67pq 36.201 25.00kk 16.33pc 23.31a- </td <td>Lalsharna</td> <td>12.33g-k</td> <td>9.33hijk</td> <td>80.33rh</td> <td>11.67s</td> <td>32.00rs</td> <td>1.23cd</td> <td>64.33de</td> <td>-</td> <td>86.33a-e</td> <td>0.63jk</td> <td>14.33qrs</td>	Lalsharna	12.33g-k	9.33hijk	80.33rh	11.67s	32.00rs	1.23cd	64.33de	-	86.33a-e	0.63jk	14.33qrs
Hirrshil 15.33cd 11.33ef 86.33q 24.00i-m 39.33op 1.13def 19.33r 25.00rs 14.67nop 0.83ghi 13.67rs Sonaburion 10.67lmn 6.33op 146.3adef 121.3j 25.67g-j 46.00lmn 1.13def 77.07g-k-k 41.53igk 78.33ef 0.66jk 30.07bc Nepali sorma 14.33def 1121.3j 25.67g-j 46.00lmn 1.13def 57.00fg 43.33hij 81.67 e 0.73j 28.30cr Biharijulon 10.33mn 6.33op 142.3cd 23.33bc 60.83b-f 1.03e-h 70.67bc 54.00bc 84.33cde 0.66jk 22.67j- Pajam 11.33j-m 8.30klm 138.7def 23.67i-n 56.93c-i 1.03e-h 70.67bc 50.00bc 86.67abcd 0.66jk 22.67j- Binni 10.33mn 7.35mn 130.3bi 25.67g-j 56.67d-i 1.13def 70.00bcd 39.53k 93.33abc 10.62 k 20.00c- Shafeeb sail 10.33mn 7.35m 130.9j 27.00e-i 50.67i-i 1.13def 70.00bcd 39.53k 93.33abc </td <td>Pakkiraj</td> <td>13.33e-h</td> <td>11.33def</td> <td>143.0bcd</td> <td>30.00c-f</td> <td>62.00b-e</td> <td>0.97gh</td> <td>65.00cde</td> <td>34.671m</td> <td>91.67abc</td> <td>0.90fg</td> <td>30.33b-f</td>	Pakkiraj	13.33e-h	11.33def	143.0bcd	30.00c-f	62.00b-e	0.97gh	65.00cde	34.671m	91.67abc	0.90fg	30.33b-f
Hirashil 15.33cd 11.33ef 86.33q 24.00i-m 39.33opq 1.13def 19.33r 25.00rs 14.67nop 0.83ghi 13.67rs Sonaburion 10.671mn 6.33op 146.3ae 33.00abc 61.50b-f 1.10d-g 50.67g+k 41.53igk 78.33ef 0.66jk 30.07bc Nepali soma 14.33def 11.21.3j 25.67g+j 40.00lmn 1.13def 57.00fg 43.33hj 81.67de 0.73j 28.30cr Biharjulon 10.33mn 6.33op 142.3cd 23.33i-a 40.00lmn 1.1def 23.00qr 36.00l 16.67mnop 0.86gh 17.33o- Biharjulon 10.33mn 6.33op 144.7fgh 26.33f-j 54.13g-k 1.03e-h 70.67bc 49.00b 84.33cde 0.06jk 22.67j- Binni 10.33mn 7.35m 130.3bi 25.67g-j 56.67d-i 1.13def 70.00bcd 39.33bk 80.0bcde 26.06jk 24.67b- Shafeeb sail 10.33mn 7.67s 18.00pr 23.83t 1.23cd 24.67p- 36.20l 25.00km 0.63jk 24.00i-i	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
Sonaburion 10.67lmn 6.33 op 146.3abc 33.00abc 61.50b-f 1.10d-g 50.67g-k 41.53ijk 78.3acf 0.66jk 30.67bc Nepali sorna 14.33def 11.33 12.3j 25.67g-j 46.00lm 1.13def 57.00fg 43.33hij 81.67de 0.73ij 28.33b- Miniket 11.00klm 6.33 op 142.3cd 32.33b- 41.03nop 1.13def 57.00fg 44.67lm 23.67klm 1.13def 57.00fg 44.67lm 23.67klm 1.13def 57.00fg 44.7bu 88.67abcd 0.66jk 22.67j- Malibhug 10.33mn 6.33op 134.7fgh 23.67i-n 49.33j-m 1.07e-h 65.33cd 88.67abcd 0.66jk 24.67h Shafeeb sail 10.33mn 6.33op 77.67s 18.00pqr 23.83t 1.23cd 24.67pqr 36.201 25.00klm 0.96ef 16.33pc Chahlam 11.33j-m 8.33jklm 123.0j 27.0ce-i 50.67i-l 1.13def 50.00b-k 31.67mn 42.0	Jirashil	15.33cd	11.33ef	•		39.33opq	1.13def	19.33r	25.00rs	14.67nop	0.83ghi	13.67rs
Nepali sorna 14.33def 11.33def 121.3j 25.67g-j 46.00lmn 1.13def 57.00rg 43.33hij 81.67de 0.73ij 28.33b- Miniket 11.00klm 6.33op 89.33pq 23.33i- 41.33nop 1.13def 23.00rg 36.00l 16.67mop 0.86fgh 17.35o- Biharijulon 10.33mn 6.33op 142.3cd 32.33abc 60.83b-f 1.03e-h 30.67p 34.67lm 28.36rklmn 1.13cd 28.00cr Kadam sail 11.671-m 8.33klm 117.7j 23.33i-n 46.00lmn 1.10d-g 71.67bc 54.00bc 84.33cde 0.66jk 22.67j- Malibhug 10.33mn 6.33op 138.7def 23.67i-n 56.93ci-l 103e-h 64.67.cde 50.53de 88.67abcd 0.66jk 27.67c- Shafeeb sail 10.33mn 7.67s 18.00pqr 23.83t 1.22cd 24.67pq 36.20l 25.00klm 0.96ft 16.33pc Chaham 11.33j-m 8.33jklm 123.0j 27.00e-i 50.67i-1 1.13def 50.00c-k 31.67m 45.67h 0.53k	Sonaburion			-						-		30.67bcde
Minket11.00klm $6.33op$ $89.33pq$ $23.33i-n$ $41.33nop$ $1.13def$ $23.00qr$ $36.00l$ $16.67mnop$ $0.86fgh$ $17.33o-Biharjulon$ Biharjulon $10.33mn$ $6.33op$ $142.3cd$ $22.33abc$ $60.83b-f$ $1.03e-h$ $30.67op$ $34.67lm$ $23.67lmn$ $1.13def$ $22.67j-$ Malibhug $10.33mn$ $6.33op$ $134.7fgh$ $22.37i 54.13g+h$ $1.03e-h$ $70.67bc$ $19.00bc$ $89.00abcd$ $0.66jk$ $22.67j-$ Pajam $11.33j-m$ $8.00klmn$ $138.7def$ $23.67i-n$ $56.93c-i$ $1.03e-h$ $64.67.cdc$ $50.53de$ $88.67abcd$ $0.66jk$ $24.67b-$ Shafeeb sail $10.33mn$ $6.67nop$ $139.3def$ $22.67j 56.67d-i$ $1.13def$ $70.00bcd$ $39.53k$ $93.33abc$ $1.06de$ $28.00c-$ Chaplam $11.33j-m$ $6.33op$ $77.67s$ $18.00pq$ $23.83t$ $1.23cd$ $24.00t-j$ $36.67m$ $42.00hi$ $0.40l$ $24.00i-j$ Chaplam $11.33j-m$ $8.33jklm$ $122.0j$ $27.00e-i$ $50.67i-l$ $1.13def$ $50.00h-k$ $31.67mn$ $42.00hi$ $0.40l$ $24.00i-j$ Daud sail $11.0klm$ $8.00klmn$ $107.7km$ $23.33i-h$ $5.70lm$ $1.13def$ $54.37j-j$ $37.70r$ $71.00fg$ $1.32d$ $46.7hgq$ $35.00l$ $45.67h$ $0.53k$ $24.33h-$ Dula sama $11.33j-m$ $8.33jklm$ $122.0j$ $27.00e-i$ $50.67i-j$ $1.13def$ $54.67h$			-					-				28.33b-h
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CV (%) 5.67 8.04 2.62 8.86 6.58 6.68 6.96 4.98 8.05 8.19 9.19	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 \leq 5% probability, NTH= Number of tillers hill⁻¹, ETH= Number of effective tillers hill⁻¹, 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.)

Table 3b. Mear	-				-	-		CD	CW	V/D
Genotype	CD	PL	NFG	NUFG	GL 0.07ab	GB	GL/GB 3.22fgh	SB 25.22b	GW	Y/P
Katiabagdad	0.97h	28.67b-g	127.70c	23.00a 13.67d-j	0.97ab 0.77cde	0.30b	3.221gn 3.44efg	35.33b	10.43z 21.72kl	9.13op
Peta	1.07gh	28.33b-g	122.00def	-		0.23cd 0.27bc	3.44efg 3.22fgh	28.00c-f	24.21f	16.35h-n 27.87cde
Shuna onjona	1.10fgh	26.67c-j	117.30fg	9.67j-q 16.67ada	0.83cd		-	17.67n-q	24.211 16.51st	18.60f-1
Supahar Kataribua	1.10fgh	30.00b-e	162.3a 74.33w	16.67cde	0.87bc	0.37a	2.41ijkl 2.78hi	48.33a		
Kataribug	1.13efg	27.33b-i		5.67q	0.83cd	0.30b		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	19.001-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	10.52z	19.90f-1
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-1	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-1
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-1	16.06u	13.24l-p
Kadam sail	1.23b-f	26.67с-ј	108.70ijk	11.67g-m	0.63fgh	0.30b	2.11jklm	22.00i-p	21.83jkl	14.75j-o
Malibhug	1.37ab	26.67с-ј	108.70ijk	11.00g-o	0.40i	0.20d	2.00klm	23.33f-m	20.03nop	19.70f-1
Pajam	1.30abcd	29.67b-е	117.3fg	11.67g-m	0.60gh	0.20d	3.00ghi	24.33e-k	17.86r	13.211-p
Binni	1.23b-f	24.67f-m	101.00mn	9.00k-q	0.73def	0.20d	3.833cde	21.00ј-р	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	21.521	9.47nop
Jinga sail	1.17defg	23.00i-m	73.33w	7.00opq	o.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-е	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-1	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	8.671-q	0.60gh	0.20d	3.00ghi	19.33k-p	23.39g	17.30g-m
Nandidhan	1.30abcd	21.00lm	109.30ijk	12.33f-1	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-1	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
Mean Level of sig.	1.22	26.59 *	105.34	11.06 *	0.75 *	0.25 *	3.18	24.72 *	19.96	19.68

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⁻¹, NUFG= No of unfilled grains panicle⁻¹, 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⁻¹.

Characterization of local rice genotypes

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_b^2	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 (⁰)	18.51	8.95	9.56	21.71	92.76	23.40	4.64	8.92
Flag leaf area (cm ²)	50.83	29.06	21.77	111.88	342.20	32.69	12.46	34.23
Flag leaf angle $(^{0})$	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 ⁻¹ (no.)	32.93	18.44	14.49	5.54	17.67	31.35	2.71	21.27
Number of effective tillers hill ⁻¹ (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 ⁻¹	3.65	12.00	-8.35	1.12	14.78	7.59	0.60	0.57
No of unfilled grain panicle ⁻¹	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 ⁻¹ (g)	37.70	21.74	15.96	18.83	56.62	33.26	5.16	25.83

 $\overline{\text{GCV}}$ = genotypic coefficient of variance, PCV = phenotypic coefficient of variance, $\sigma^2 g$ = genetic variance, $\sigma^2 p$ = phenotypic variance, h_b^2 = broad-sense heritability, GA = genetic advance, GA (%) = genetic advance as percent of mean.

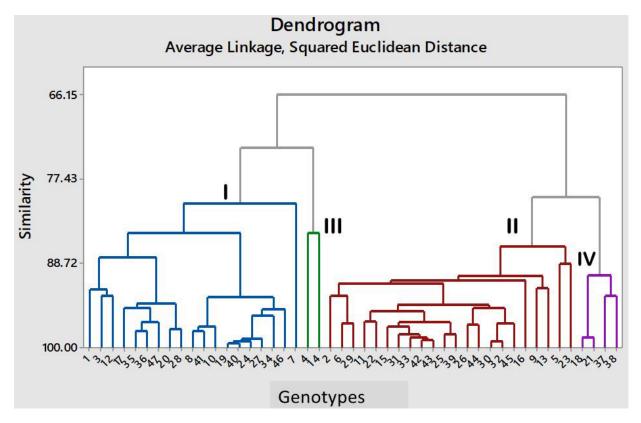


Fig. 1 Dendrogram of 47 rice genotypes from cluster analysis

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= Sarna, 15= 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 ¹, number of effective tiller plant⁻¹, seedling height, internode length, leaf length, flag leaf area, ligule length, culm length, no of unfilled grain panicle⁻¹, grain length, grain breath, grain length-breath ratio, secondary branch in panicle, 1000-grain weight and yield plant⁻¹ (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⁻¹ displayed strong positive correlation (r =0.781) with no of unfilled grain panicle⁻¹ and secondary branches in panicle, similar relation existed between culm length and internode length (Table 5). Yield plant⁻¹ showed significant positive correlation with number of tillers hill⁻¹ (r = 0.651), number of effective tillers hill⁻¹ (r = 0.657), 1000-grain weight (r = 0.543), filled grain panicle⁻¹ (r = 0.216), no of unfilled grain panicle⁻¹ (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⁻¹ (0.375), secondary branches in panicle (0.364), flag leaf area (0.356) and no of unfilled grain panicle⁻¹ (0.298) with positive coefficient and number of effective tiller hill⁻¹ (-0.275), leaf width (-0.243), number of tiller hill⁻¹ (-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⁻¹, no of filled grain panicle⁻¹ and yield plant⁻¹ were accumulated in cluster III, whereas genotypes with maximum effective no of effective tillers hill⁻¹, panicle length and leaf area were grouped in cluster II (Table 7). Similarly, genotypes which produced less seeding height and more grain weight were clubbed into cluster IV, whereas minimum effective tillers plant⁻¹, 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.

5. Phenoty	ypic corre	elation	co-efficie	ent among	g differen	it agro-m	orpholog	ical traits	of 47 ric	e genotyp	bes								
SH	LL	LW	FLA	LIL	CL	CD	NTH	ETH	PL	NFG	NUFG	GL	GB	GB/GL	SB	IL	LA	FLA	Y/p
0.847***																			
-0.366***	-0.15																		
0.211**	0.411***	0.085																	
-0.055	0.1	0.087	0.529***																
0.579***	0.362***	-0.55	0.003	-0.147															
0.302***	0.126	-0.38	0.027	0.007	0.646***														
-0.029	0.041	-0.05	-0.036	-0.07	0.269***	0.135													
0.088	0.084	-0.196	-0.123	-0.173*	0.335***	0.177*	0.892***												
0.525***	0.477***	-0.088	0.247**	0.153	0.243**	0.096	-0.125	-0.117											
0.151	0.278***	0.164*	0.372***	0.193*	-0.089	-0.001	-0.064	-0.111	0.165*										
0.138	0.268***	0.166*	0.301***	0.124	-0.005	-0.029	-0.002	-0.062	0.07	0.718***									
-0.115	0.064	0.059	0.282***	0.303***	-0.229**	-0.259**	-0.106	-0.109	-0.218**	0.154	0.089								
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							
-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***						
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					
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				
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*			
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***		
-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	

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

SH LL LW FLA LIL CLCD NTH ETH PL FG UFG GL GB GB/GL SB IL LA FLAN Y/p

GW

-0.204

-0.331

0.126

-0.288***

-0.059

-0.152

-0.129

0.033

0.048

** 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⁻¹, ETH= Number of effective tillers hill⁻¹, PL= Panicle length, NFG= No of filled grain panicle⁻¹, NUFG= No of unfilled grain panicle⁻¹, 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⁻¹, GW= 1000-grain weight.

-0.211*

-0.238**

-0.117

-0.175*

-0.097

-0.078

-0.271***

-0.246**

0.054

0.043 0.543***

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-1	0.125	-0.236	0.439	0.021	0.203	0.103	0.049					
No. of effective tillers hill ⁻¹	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 ⁻¹	0.071	0.375	0.286	0.053	-0.162	-0.228	0.159					
No of nfilled grain panicle ⁻¹	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 ⁻¹	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 trait	s 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-1	12.23	13.12	14.00	12.75					
No. of effective tillers hill ⁻¹	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 ⁻¹	98.18	108.30	148.50	101.50					
No of unfilled grains panicle ⁻¹	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 ⁻¹	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⁻¹, 1000-grain weight, no of filled grains panicle⁻¹, 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.

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