

Genetic Assessment of Selected Rice (*Oryza sativa* L.) Genotypes Based on Agro-Morphological Traits in Tropical Climate: Malaysia

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Abstract

Rice contributes significantly to global food security and is a major food crop for half of the world's population. Sixty-five traditional and improved rice genotypes were collected and grown in pot condition to evaluate the presence of genetic diversity. Analysis of variance showed significant difference among the genotypes for all traits. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for the most of the traits. 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 and pointed out a wide variation among the genotypes. The dendrogram of cluster analysis grouped 65 rice genotypes into eight clusters. Data from this study provide presence of sufficient genetic diversity among the traditional and improved rice genotypes which can be employed in future rice breeding program for either varietal improvement or developing new variety.

Keywords: Genetic variability; Heritability; Genetic advance; Correlation coefficient

Introduction

Rice (*Oryza sativa* L.) is an important, staple food crop and one of the oldest crop for more than half of the world's human population. One hundred and sixty seven million and twenty five thousand hectares of cultivated area yielded a global production of approximately 770 million tons [1] with Asia producing 90%, Africa and Americas producing 4.8% and 4.6 respectively. The human population is expected to rise 10 billion by 2050 and 50% increase in food production is expected in order to feed this expected population. Rice is a security crop in Malaysia, as it provides a staple diet for the majority of the population and a source of income for rural farmers. Around 150,000 farmers in Malaysia rely only on rice agriculture for their livelihood [2]. The average rice productivity in Malaysia is low (1.88 million metric ton). Whereas, China's paddy rice production amounted to over 209.6 million metric ton, while India's production volume exceeded 177 million metric tons. The rice is grown in the world 165.25 million hectares with a yield of about 756 million tons [1]. Rice is the most important food in Malaysia, and it is grown in 12 rice-growing areas that encompass roughly 0.6 million hectares of land across the country. Annually, around 2.6 million tons of rice are produced, accounting for 70% of self-sufficiency, with the remaining 30% being supplied by imports from neighboring countries [3]. In irrigated wetland rice areas account for approximately 321,696 ha of the total area in Malaysia is equipped with extensive irrigation and drainage

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systems of wetland rice, while the rainfed upland area 276,787 ha [4].

Exploring genetic diversity in available landrace and wild relatives is one of the most important way to improve the germplasm [5] using breeding program. For 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 potentiality [6] as rice cultivation is not solely depends on cultural practices but also relies on inherent genetic variability among the germplasm [7]. For enhancement of rice production, determining finest breeding procedures is necessary and in this aspect, it is crucial to have morphological genetic diversity for different yield contributing traits in rice. However, morphological attributes are highly influenced by environmental factors, resulted differential pattern of relationship in different degree [8], but still very much effective for selection in breeding program [9]. Breeding strategies in rice rely mostly on the variation nature and inter relationship 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 the case, heritability estimate is necessary as it indicates the genetic involvement for the transmission of characters from one generation to other generations [10]. 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 [11] but also assists plant breeders for more accurate and precise selection [12]. 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 [13]. Keeping all the information under consideration, variability among sixty-five rice genotypes, to unravel the degree of association between yield and yield attributes and to explore the diversity among different rice genotypes collected from different regions.

Method and Materials

Experiment location

The pot experiment was carried out in the field 10 of the net house, University Putra Malaysia (UPM), Malaysia. The experiment was conducted two seasons, the first season being from February 2019 to June 2019 and the second season from August 2019 to December 2019. The experimental place is situated at around 3°02'N latitude and 101°42'E longitude on the altitude of 31m above sea level and in humid tropical climate.

Plant materials

65 rice genotypes were selected in this study. The genotypes are obtained from different sources: Four genotypes were from International Rice Research Institute (IRRI), Philippines; 37 genotypes were from Bangladesh Rice Research Institute (BRRI), Bangladesh, and 2 genotypes were Indian Agricultural Research Center, India and twenty 2 genotypes from the Department of Crop Science at University Putra Malaysia's Gene Bank. The genotypes names, origin, and status of the genotypes are represented in Table 1.

Table 1: List of 65 traditional and improved rice genotypes.

Sl. No.	Name of Genotype	Source Country	Grain Size and Shape	Status of Sample
1	Pukhi	Bangladesh	Medium, Slender	Traditional cultivar
2	Panbira	Bangladesh	Short, Bold	Traditional cultivar
3	Dharial	Bangladesh	Medium, Bold	Traditional cultivar
4	Utri	Bangladesh	Medium, Slender	Traditional cultivar
5	Luanga	Bangladesh	Medium, Slender	Traditional cultivar
6	Kaisa panja	Bangladesh	Medium, Slender	Traditional cultivar
7	Vandana	Bangladesh	Medium, Slender	Traditional cultivar
8	Dular	Bangladesh	Medium, Bold	Traditional cultivar
9	Sonhumoni	Bangladesh	Medium, Bold	Traditional cultivar
10	Hasikamli	Bangladesh	Medium, Slender	Traditional cultivar
11	Dumai	Bangladesh	Medium, Slender	Traditional cultivar
12	Parija	Bangladesh	Medium, Slender	Traditional cultivar
13	Kaktara	Bangladesh	Medium, Slender	Traditional cultivar
14	Balirdia	Bangladesh	Short, Bold	Traditional cultivar
15	Binnatoa	Bangladesh	Medium, Slender	Traditional cultivar
16	Parangi	Bangladesh	Medium, Bold	Traditional cultivar
17	Chengri	Bangladesh	Medium, Slender	Traditional cultivar
18	Dhala saitta	Bangladesh	Short, Bold	Traditional cultivar

19	Morich boti	Bangladesh	Short, Bold	Traditional cultivar
20	Saitta	Bangladesh	Medium, Bold	Traditional cultivar
21	Lal Dular	Bangladesh	Medium, Slender	Traditional cultivar
22	Nayan moni	Bangladesh	Medium, Slender	Traditional cultivar
23	Kalabokra	Bangladesh	Medium, Bold	Traditional cultivar
24	HUA1003	Philippines	Medium, Slender	Improved cultivar
25	Takanari	Philippines	Medium, Bold	Improved cultivar
26	Kachalath	India	Medium, Slender	Traditional cultivar
27	Wkhi1	Philippines	Medium, Bold	Improved cultivar
28	Hukurikul193	Philippines	Medium, Bold	Improved cultivar
29	ML6	Malaysia	Long, Slender	Breeding and mutant line
30	ML9	Malaysia	Long, Slender	Breeding and mutant line
31	Wanxiam-P10	Malaysia	Medium, Slender	Traditional cultivar
32	RENGAN WANG	Malaysia	Long, Slender	Traditional cultivar
33	PETEH PERAK	Malaysia	Long, Bold	Traditional cultivar
34	WANGI PUTEH	Malaysia	Medium, Bold	Traditional cultivar
35	KUNYIT	Malaysia	Medium, Slender	Traditional cultivar
36	GHAU	Malaysia	Long, Slender	Traditional cultivar
37	LALAMG	Malaysia	Medium, Slender	Traditional cultivar
38	MGAWA	Malaysia	Medium, Slender	Traditional cultivar
39	SUNGKAI	Malaysia	Medium, Slender	Traditional cultivar
40	UGAN	Malaysia	Long, Slender	Traditional cultivar
41	TADOM	Malaysia	Medium, Slender	Traditional cultivar
42	BANGKUL	Malaysia	Medium, Slender	Traditional cultivar
43	NMR151	Malaysia	Long, Slender	Improved cultivar
44	NMR152	Malaysia	Long, Slender	Improved cultivar
45	MR297	Malaysia	Long, Slender	Improved cultivar
46	Putra 1	Malaysia	Long, Slender	Improved cultivar
47	Putra 2	Malaysia	Long, Slender	Improved cultivar
48	MR 303	Malaysia	Long, Slender	Improved cultivar
49	MR 309	Malaysia	Long, Slender	Improved cultivar
50	BR24	Bangladesh	Medium, Slender	Improved cultivar
51	BRR1 dhan48	Bangladesh	Medium, Slender	Improved cultivar
52	BRR1 dhan82	Bangladesh	Medium, Slender	Improved cultivar
53	BRR1 dhan72	Bangladesh	Medium, Slender	Improved cultivar
54	BRR1 dhan28	Bangladesh	Medium, Slender	Improved cultivar
55	BRR1 dhan39	Bangladesh	Medium, Slender	Improved cultivar
56	BRR1 dhan42	Bangladesh	Medium, Slender	Improved cultivar
57	BRR1 dhan43	Bangladesh	Medium, Slender	Improved cultivar
58	BRR1 dhan46	Bangladesh	Short, Bold	Improved cultivar
59	BRR1 dhan75	Bangladesh	Medium, Slender	Improved cultivar
60	BRR1 dhan55	Bangladesh	Medium, Slender	Improved cultivar
61	BRR1 dhan69	Bangladesh	Medium, Slender	Improved cultivar
62	B370	India	Long, Slender	Improved cultivar
63	BINASAIL	Bangladesh	Medium, Bold	Improved cultivar
64	BINA dhan7	Bangladesh	Medium, Bold	Improved cultivar
65	BINA dhan5	Bangladesh	Medium, Slender	Improved cultivar

Settings and design of the experiment

Experiment was designed as a randomized complete block design (RCBD) with three replications. Twenty-day-old seedlings of each test genotypes were transplanted, and using two seedlings per hill in 24cm diameter and 30cm height plastic pot with 15kg soil and 20cm spacing between plant to plant.

Fertilizer application and intercultural operation

Fertilizers were applied @150:60:60kg N: P: K per hectare. However, except N, the other fertilizers were applied at final soil preparation on pot. Nitrogen was applied in three equal splits, at 15 days after transplanting (DAT), at 35 DAT, and just before flowering. Intercultural operations and pest control measures were done as and when necessary.

Table 2: An analysis of variance was used to compare the morphological, physiological, and yield parameters of 65 rice genotypes examined over two seasons (mean squares).

SV	Blocks (Season)	Seasons (S)	Genotypes (G)	G×S	Error
df	4	1	64	64	256
PH	188.37**	137.78**	3433.63**	1.92ns	0.92
DM	92.24**	188.00**	1082.44**	2.44**	0.62
NT	21.66ns	227.57**	54.74**	0.94**	0.59
NFG	1476.35ns	1884.81**	8967.37**	32.94**	11.56
NUFG	1110.73ns	1146.12**	1982.55**	16.30**	3.06
NP	12.53ns	147.20**	28.44**	0.90**	0.58
TGW	7.79**	5.79**	152.32**	0.27**	0.16
SF	1540.08ns	382.53**	760.06**	3.50**	2.08
SP	379.42**	163.97**	7475.42**	1.94**	0.69
FLA	108.72**	29.14**	1600.57**	0.72**	0.49
CD	0.05**	1.01**	22.71ns	0.04ns	0.02
PL	7.87**	0.46ns	125.48**	2.50**	0.74
HI	0.007**	0.005**	0.200**	0.002**	0.005
SY	86.66**	124.79**	159.08**	1.14**	0.96
CC67	0.15ns	34.73ns	150.43**	0.48ns	0.1
CC97	0.06ns	37.75ns	199.42**	0.24ns	0.02
GL	0.0034*	0.0009**	23.22**	0.0034*	0.0036
GB	0.0021*	0.0073**	0.59**	0.0002*	0.0001
GLBR	0.01**	0.04**	8.88**	0.002**	0.002
DF	151.64ns	1665.65ns	1104.08**	3.03**	0.82
YP	1.71**	75.21**	186.68**	0.88**	0.38

Statistical analysis

All morphological, yield, and yield component data were analyzed with using Statistical Analysis Software (SAS) version 9.4, we used the ANOVA process to see if there are any major differences, as well as the least significant differences (LSD) approach to compare among the significant characteristic means. The multiple variance components, such as genotypic variance (σ^2_g), phenotypic variance (σ^2_p), and error variance (σ^2_e) were estimated from the mean square for all examined characteristics using SAS' PROC VARCOMP technique with restricted maximum likelihood (REM).

Collection of data

Table 2 shows the morphological, physiological, and yield characteristics, a total of twenty-one quantitative attributes were recorded. The quantitative trait such as days to flowering (DF), days to maturity (DM), plant height (PH, cm), culm diameter (CD, mm), flag leaf area (FLA, cm²), total number of tiller plant⁻¹ (NT, no.), total number of panicle plant⁻¹ (NP, no.), spikelet panicle⁻¹ (SP, no), number of filled grains panicle⁻¹ (NFG, no), number of unfilled grains panicle⁻¹ (UNFG, no), spikelet fertility (SF,%), chlorophyll content 67&97 days after transplanting (CC67 &CC97 DAT), grain length (GL, mm), grain breadth (GB, mm), grain length breadth ratio (GLBR), 1000 grain weight (TGW, g), grain yield plant⁻¹ (YP, g), straw yield plant⁻¹ (SY, g) and harvest index (HI,%).

The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV, broad-sense heritability (h^2_B) and genetic advance (GA) were estimated following [14]. The genetic variability of 21 quantitative variables was assessed using cluster analysis. The Euclidian distance method, as well as Dice's and Jaccard's similarity coefficients, were used to assess the genetic variability data. The cluster analysis between rice genotypes was Ward Hierarchical Clustering (WHC) method using JMP version 1.6SAS program. For the analysis NTSYS version 2.1 (Numerical Taxonomy Multivariate Analysis System), exeter soft-were, Setauket, NY, USA software

were used the principal component analysis (PCA) and was done to produce two dimensional (2D) plots through, multivariate statistical packages (MVSP) was used for OCA biplot loading (Table 2,3).

Table 3: Explanation of 65 rice genotypes dignified quantitative characteristics.

Characters	Method of Evaluation
Days to flowering (DF, days)	The duration of days from seeding to 50% flowering day
Plant height (PH, cm)	The average of height from the base to the tip of last leaf (flag leaf)
Panicle length (PL, cm)	From base of the lowest spikelet to the top of latest spikelet on panicle
Flag leaf area (FLA, cm ²)	flag leaf length (cm) x maximum width (cm) x 0.75
Number of tillers per plant (NT, no.)	Counting of the tillers per hill
Number of panicles per plant (NP, no.)	Counting the panicles per hill
Culm diameter (CD, mm)	Outer diameter internodes of the culms were measured
Chlorophyll content of leaf (CC67)	The chlorophyll content of leaf was measured at 67 days after transplanting
Chlorophyll content of leaf (CC 97)	The chlorophyll content of leaf was measured at 97 days after transplanting
Spikelet per panicle (SP, no.)	Counting the spikelet per panicle
Number of filled grains per panicle (NFG, no.)	Counting the number of filled grains on panicle-1
Number of unfilled grains per panicle (UNFG, no.)	Counting the number of unfilled grains on panicle-1
Grain length (GL, mm)	Length of grain was measured
Grain breadth (GB, mm)	Breadth of grain was measured
Grain length breadth ratio (GLBR)	Dividing grain length by grain breadth
Spikelet fertility (SF, %)	Dividing ripped spikelet to all spikelet
Yield per plant (YP, g)	Weighting total grains per plant
One thousand grain weight (TGW, g)	Fully developed 100 whole grains were weighted then 1000 weight grains were calculated from these weights
Days to maturity (DM, days)	The duration of days from seeding to 90% or above maturing day
Harvest Index (HI, %)	Ratio of grain yield to biological yield
Straw Yield (SY, g)	Weighting of straw per plant

Result

Analysis of variance on morpho-physiological and yield characters

The combined analysis of variance for the two seasons showed significant differences among the growth characters evaluated (Table 1). Significant differences ($P \leq 0.001$ or 0.05) were observed in seasons, genotype, and genotype by season interaction for all the evaluated traits except culm diameter were non-significant differences were observed for genotype and genotype by season interaction. Similarity, no significant differences were observed

plant height, chlorophyll content at 67 DAT and chlorophyll content at 97 DAT for genotype by season interaction (Table 1). The CV% for yield and yield related components vary from 7.04 to 29.85% indicating a high variability among the studied traits. Out of 21 traits, number of unfilled grains panicle⁻¹, flag leaf area, number of tiller per plant⁻¹, number of panicles plant⁻¹ and number of filled grains panicle⁻¹ found with relatively higher coefficient of variation (26.74, 22.37, 20.46, 19.53 and 17.80%, respectively) than the other traits shown in Table 4. These possibly happened because of characters and/or sampling error were more influenced by the environmental factors.

Table 4: Variability in 65 rice genotypes for several quantitative parameters.

Characters	Range	Mean	Std Dev	Std Error	CV (%)
PH (cm)	168.53-118.67	138.25	13.99	0.409	10.15
DM	104-136	112.9	7.98	0.233	7.04
NT	6.78-13.76	10.08	2.15	0.063	20.46
NFG	114.55-204.27	131.26	23.14	0.677	17.8
NUFG	71.47-90.63	42.74	11.16	0.326	26.74
NP	6.22-15.55	8.86	1.66	0.049	19.53
TGW	15.36-25.48	21.26	3.01	0.088	14.09
SF (%)	13.55-51.72	69.46	7.14	0.209	10.19

SP	92.16-159.61	129.44	20.48	0.599	15.78
FLA (cm ²)	29.78-62.59	43.18	9.63	0.282	22.37
CD (mm)	9.75-5.86	7.71	1.17	0.034	15.25
PL (cm)	17.65-24.72	22.07	2.86	0.083	12.95
HI (%)	0.36-0.68	0.52	0.11	0.003	21.39
SY (g)	16.82-27.68	22.94	3.48	0.102	14.97
CC67	30.86-45.40	38.09	2.9	0.085	7.58
CC97	33.20-49.16	39.65	3.32	0.097	8.33
GL (mm)	7.20-11.23	9.23	1.13	0.033	12.24
GB (mm)	1.56-2.52	2.04	0.18	0.005	8.91
GLBR	3.16-6.28	4.57	0.7	0.02	15.29
DF	80-114	86.88	8.22	0.24	9.33
YP (g)	7.03-18.12	10.81	3.31	0.097	29.85

Note: PH: Plant Height; DM: Days to Maturity; NT: Number of Tiller; NFG: Number of Filled Grain; NUGF: Number of Unfilled Grain; NP: Number of Panicle; TGW: 1000 Grain Weight; SF: Spikelet Fertility; SP: Spikelet Per Panicle; FLA: Flag Leaf Area; CD: Culm Diameter; PL: Panicle Length; HI: Harvest Index; SY: Straw Yield; CC67: Chlorophyll Content after 67 days after Transplanting; CC97: Chlorophyll Content after 97 days after Transplanting; GL: Grain Length; GB: Grain Breadth; GLBR: Grain Length Breadth Ratio; DF: Days to Flowering; YP: Yield Per Plant; Std Dev: Standard Deviation; Std error: Standard Error; CV: Coefficient of Variation.

The plant height varied from 118.67-168.53cm with genotypes Kalabokra having the highest mean value while the lowest height was recorded in BRRi dhan75 (Table 5). The days to 50% flowering ranged from 80 to 114 days, as observed in early flowering in Sondhamoni (80 days) and late flowering observed in BRRi dhan28 (121 days). The growth duration ranged from (SUNGKAI) 104 days to (BRRi dhan55)136 days. The highest no. of tillers per plant observed in genotype HUA 1003 (13) and lowest no of tillers observed in genotype Panbira (6). The highest no. of grains per panicle produced in genotype BRRi dhan72 (204) and lowest grains produced in genotype TADOM (114). The highest no. of panicles per plant observed in genotype BRRi dhan55 (15) and lowest panicles produced in genotype Panbira (6) (Table 5). The flag leaf area ranged from 29.78cm² (TADOM) to 62.59cm² (BRRi dhan48). The longest panicle length observed in genotype BRRi dhan55 (24.72cm) and shortest in genotype Hasikamla (17.65cm).

Chlorophyll content 67 DAT ranged from 30.86 (RENGAN WANG) to 45.4 (BRRi dhan72) and Chlorophyll content 97 DAT ranged from 33.20 (GHUA) to 49.16 (BRRi dhan72).The culm diameter ranged between 5.86mm (Saitta) to 9.75mm (Putra1) (Table 6). The 1000 grains weight ranged from 15.26-25.48g. MR309 had the highest value of 1000-grain weight (25.48g), which was not significantly different from Putra2, BR24, BRRi dhan82, BRRi dhan72 and MR297.The lowest grain weight was recorded in genotype Panbira (15.36g). The grain length breadth ratio ranged from 6.28 (RENGAN WANG) to G19 (3.16) (Morich boti). The Straw yield ranged from 16.82g (Vandana) to 27.68g (BRRi dhan82. The highest yield per plant was recorded in genotype MR297 (18.12g) which was statistically similar to BR24, BRRi dhan72, Putra 2, HUA1003, Putra 1 and BRRi dhan75. The lowest yield was observed in genotype Kalabokra (7.03g) (Table 7).

Table 5: Mean performance of 65 rice genotypes for different morpho-physiological and yield traits.

Genotype	PH	DF	DM	NT	NFG	NUGF	NP
G1	138.86stu	83.44b-e	106.27abz	10.21mno	156.16m	87.87c	7.33bc
G2	158.19de	81.01ij	105.75ab	6.78z	134.27ef	85.54h	6.22d
G3	140.61pqr	81.11ij	106.71axyz	9.27opqr	147.83v	87.23e	7.22bc
G4	144.72ij	85.13r-w	108.48q-u	10.17lmn	155.16o	85.18jhi	7.88a
G5	156.92e	84.41abw-z	108.29s-v	8.61rst	134.61de	81.55xy	8.77wx
G6	166.10b	86.49op	110.53m	8.23t-x	132.27h	82.90st	7.06c
G7	158.34d	83.32c-f	107.89t-w	9.11qrs	119.27s	77.43h	10.11st
G8	142.82klm	83.71a-dz	108.24stuv	10.29k-n	161.16i	84.42lmn	8.88w
G9	145.93hi	80.68j	106.03abz	9.56n-q	156.72l	86.91ef	8.55wxy
G10	143.81jkl	85.34q-w	108.35r-v	10.25k-n	151.38t	85.15ij	9.44v
G11	137.90uv	82.60h-g	105.48bc	10.39j-m	153.61q	86.87ef	10.33sr
G12	158.96d	83.16c-f	106.72axyz	8.36s-w	131.61i	80.76ab	10.88opq
G13	167.37ab	85.52q-v	109.76mno	7.54w-z	127.94l	84.21mn	8.55wxy

G14	143.83jk	84.78t-z	109.42mno	11.26f-k	154.05p	89.15b	8.33yz
G15	145.14ij	81.69ghi	105.83abz	10.82g-l	152.38r	81.39yz	11.22mno
G16	150.35f	84.75t-z	107.37v-y	10.53i-m	150.94u	86.37g	7.14c
G17	143.22klm	82.74d-g	108.50p-t	11.37f-j	146.05x	83.53r	8.44xy
G18	146.61gh	84.10acx-z	108.74o-t	11.42d-h	160.16j	87.36d	10.77pq
G19	142.48lmn	86.03o-r	109.38n-q	10.76g-l	155.72n	84.64kl	9.33v
G20	163.09c	83.67a-e	108.32r-v	8.37s-w	134.83d	85.47hi	10.32rs
G21	146.94gh	85.70p-t	110.17mn	11.38e-h	153.56q	84.06nop	8.13az
G22	161.78c	84.81s-y	109.03o-s	7.43u-y	126.05o	83.84opq	10.77pq
G23	168.53a	83.12cdef	106.44abx-z	9.29o-r	134.055g	79.51f	9.55uv
G24	124.36b	81.64hij	105.52bc	13.76a	121.94r	85.14ij	8.55wxy
G25	131.24x	84.83s-y	108.40q-u	11.46d-h	146.52w	86.61fg	10.77pq
G26	138.46tuv	86.16o-r	110.21mn	10.67h-m	151.83s	85.03jk	9.42v
G27	142.89mno	86.12o-r	109.28n-s	8.55r-u	118.05t	83.05s	9.33v
G28	139.86qrs	86.21opq	109.52m-p	11.45d-h	119.38s	85.25hij	7.44b
G29	133.48w	104.52c	127.16e	11.72cdef	134.27ef	84.56lm	12.66de
G30	130.90x	103.04d	126.53e	10.26lmn	125.45p	83.51qr	11.55j-m
G31	146.57h	85.72p-t	107.47u-x	7.52w-z	136.27c	81.42y	12.23f-i
G32	140.46pqr	87.88n	109.69mno	7.19yz	127.16m	84.20mno	11.44klm
G33	146.98gh	88.10n	109.65mno	8.24t-x	128.16l	87.77c	13.13bcd
G34	143.21klm	85.63p-u	106.59wxyz	7.69u-y	133.83g	85.53h	11.44klm
G35	141.13opq	84.67au-z	106.38abyz	7.24xyz	122.94q	83.59qr	10.88poq
G36	137.22v	87.09no	108.54p-t	8.43r-v	121.83r	87.11de	12.11fgh
G37	139.37rst	90.64m	112.17l	9.25p-s	131.38ij	82.64tu	12.22fg
G38	150.70f	83.82abcyz	105.60bc	8.21t-w	117.38u	83.23s	12.33ef
G39	146.97gh	82.31fgh	104.55c	7.65v-y	134.82d	84.55lm	11.41nop
G40	141.11nop	84.17abcx-z	105.84abz	8.45r-v	126.61n	87.33d	9.88tu
G41	151.40f	85.84p-s	109.12n-s	8.06t-x	114.55v	82.36uv	11.16nop
G42	147.94g	88.04n	109.45n-r	7.58u-y	126.61n	90.63a	11.88g-j
G43	134.27w	106.26b	132.34b	11.09f-j	131.05j	85.11ij	10.55qr
G44	130.04xyz	105.71b	130.22c	11.45d-h	127.83l	83.78pq	11.55j-m
G45	129.36zy	94.23h	118.06hij	13.48a	191.72c	83.50qr	14.66b
G46	130.41xy	92.87ijk	117.52ijk	13.64a	180.16e	82.10vw	13.22c
G47	128.75z	91.58lm	116.56k	13.73ab	173.61f	80.20de	13.25c
G48	126.27a	93.56hi	118.23ghi	11.38f-j	170.94g	79.45fg	12.11fgh
G49	126.78a	92.43jkl	117.18jk	12.47bc	167.72h	80.60bc	11.33lmn
G50	120.85cde	84.12abcx-z	108.75o-t	12.64cd	184.52d	80.35cd	10.77pq
G51	120.29d-g	84.52av-z	108.38r-v	12.36cde	180.56e	82.23v	10.74pq
G52	123.73b	83.20cdef	107.36v-y	11.74c-f	192.38b	81.07az	11.66i-l
G53	121.69c	93.73hi	118.71gh	11.54c-g	204.27a	80.02e	10.88opq
G54	119.27hg	114.21a	132.728b	11.37e-i	157.27k	77.27h	12.11f-i
G55	120.56c-g	95.46fg	119.32g	12.36bc	145.16y	79.10g	12.13fgh
G56	120.43c-g	93.48hij	117.45ijk	10.74g-l	144.72z	74.13l	11.77h-k
G57	121.60cd	94.45hg	119.17g	10.65h-m	138.38b	76.56i	10.77pq
G58	119.78e-h	95.83f	120.46f	9.86m-p	145.51y	75.14k	11.88g-j
G59	118.67h	97.49e	121.32f	12.37bc	141.166a	77.63h	11.22mno
G60	120.79cde	113.54a	136.41a	10.08mno	140.94a	81.84wx	15.55a
G61	119.33fgh	104.33c	129.18d	11.34f-k	130.45k	79.10g	11.22mno

G62	124.14b	94.41g	118.23ghi	9.43pqrs	136.55c	76.18j	11.23mno
G63	121.31cd	92.37kl	117.25ijk	9.87mnop	138.05b	79.28fg	10.55qr
G64	120.66c-f	94.32h	119.08gh	10.29k-n	126.16o	75.07k	12.22fg
G65	120.62c-f	95.78f	120.43f	10.27lmn	117.61u	71.47m	12.11fgh
Mean	138.25	86.88	112.9	10.08	131.26	42.74	8.86
LSD (p=0.05)	1.34	1.32	1.02	0.82	0.08	0.37	0.38
Season							
S1	138.24a	86.87b	112.89b	10.07b	128.71b	40.76b	8.15b
S2	137.56b	89.26a	113.69a	10.95a	131.25a	42.74a	8.86a
LSD (p=0.05)	0.11	0.1	0.09	0.07	0.39	0.2	0.09

Means with the same letter in each column are not significantly different at p=0.05 using Duncan’s new multiple range test (DNMRT), PH: Plant height; DF: Days to flowering; DM: Days to maturity; NT: Number of tiller; NFG: Number of filled grain; NUFG: Number of unfilled grain; NP: Number of panicle.

Table 6: Mean performance of 65 rice genotypes for different morpho-physiological and yield traits.

Genotype	SF	SP	FLA	CD	PL	CC67	CC97
G1	21.83k	115.94b	45.42jkl	8.10i	20.16q	37.25k	39.22wx
G2	21.94k	127.83sr	34.13az	5.96bcd	20.16q	35.38p	37.30f
G3	22.16k	121.61v	49.46h	8.33h	18.83t	38.25ij	39.29wv
G4	27.38x	110.72g	45.91i-l	7.58q	21.83m	40.22f	44.17f
G5	30.72s	119.72y	34.10az	6.07ab	20.52p	36.28lm	38.06c
G6	27.94w	115.32c	32.16b	6.06abc	21.83m	33.06r	34.14l
G7	35.83n	105.38l	34.96xyz	5.89d	18.83t	37.43k	39.08y
G8	29.92t	117.38a	45.50jkl	7.95ijk	19.16s	40.39f	43.91g
G9	23.94fg	110.33g	44.30no	7.73m-p	20.55p	39.37gh	39.36uv
G10	26.16y	109.31h	42.69qr	7.37r	17.65v	38.00j	40.92p
G11	23.38ihj	111.94f	43.96op	7.16s-v	20.58p	36.34lm	39.18x
G12	30.61s	103.38no	35.27wxy	5.93bcd	19.75r	34.46q	36.25i
G13	24.16ef	117.51a	30.31c	5.94bcd	20.51p	36.12mn	37.25f
G14	18.05n	127.38s	43.18pqr	7.90i-l	20.83o	40.12f	39.42u
G15	35.56no	118.05z	49.08h	7.76lmn	19.56r	39.47gh	42.24k
G16	23.72hg	125.52t	46.01i-l	7.30rs	21.35n	37.49k	38.31b
G17	28.72v	120.54w	44.37mno	7.88j-m	18.52u	37.33k	39.23wx
G18	23.61ihg	118.38z	42.62qr	7.97ij	19.59r	36.58l	38.39ab
G19	28.61v	122.94u	46.79i	7.15tuv	19.26s	40.23f	43.22h
G20	23.38ihj	103.83n	33.78a	5.86d	20.17q	35.41p	36.45h
G21	29.27u	119.82yx	46.34ij	7.06vw	20.16q	39.34gh	42.25k
G22	24.38de	112.05f	32.41b	5.88d	20.83o	37.16k	38.41a
G23	34.38p	106.38j	30.53c	5.91cd	21.61mn	35.39p	37.13g
G24	21.83k	120.27wx	58.27d	9.39ef	20.52op	41.55e	44.13f
G25	23.27ij	128.24qr	46.13ijk	8.40h	19.57r	39.23h	40.17s
G26	27.38x	120.05wxy	43.15pqr	7.23rstu	19.16s	39.36gh	41.29n
G27	24.38de	100.61p	30.59c	7.61opq	20.56p	37.39k	36.42h
G28	21.38l	98.57q	45.49jkl	9.05g	20.16q	41.35e	42.31jk
G29	25.54z	92.16s	36.56vw	7.76l-o	22.94ghi	39.31gh	38.58z
G30	25.05a	102.94o	36.78uv	7.74m-p	22.72ij	38.41i	38.10c
G31	31.53r	105.38l	33.85a	6.91wxy	22.16l	35.87no	36.30i
G32	24.16fe	96.53r	35.28wxy	7.62n-q	21.38n	30.86u	34.10l

G33	18.72m	119.94yx	31.89b	7.14uv	22.38kl	32.47s	33.37m
G34	23.05j	115.05c	35.71wx	7.58q	21.54n	35.28p	34.37k
G35	24.53cde	106.16jk	30.45c	6.96wx	22.38lk	36.27lm	37.65e
G36	18.72m	108.72i	35.36wxy	6.96wx	22.83ih	31.34t	33.20n
G37	27.94w	104.38m	40.06t	7.29rst	21.75n	34.17q	37.13g
G38	23.72gh	113.94d	34.61ayz	6.88xy	22.65jk	38.43i	39.31wv
G39	24.94ab	98.52q	35.65wx	6.18a	22.53jk	37.44k	38.41a
G40	18.94m	109.72h	37.178u	7.29r-u	21.57n	33.03r	35.15j
G41	24.61bcd	112.72e	29.78c	6.19a	20.83o	35.54op	36.49h
G42	13.55o	105.83lk	31.82b	6.77y	22.53jk	36.32lm	37.32f
G43	23.27ij	112.27ef	43.20pqr	7.89i-l	21.85n	37.45k	38.06c
G44	24.83abc	112.38ef	41.02s	7.93jk	23.16fg	37.15k	39.23wx
G45	38.27l	158.16b	59.77c	9.50cde	24.57a	42.27d	44.32e
G46	39.05k	151.38d	53.68f	9.75a	24.16b	39.49gh	41.17o
G47	42.83h	159.61a	60.17c	9.47de	23.61de	41.37e	42.39j
G48	43.72fg	135.94m	55.94e	9.30f	23.16fg	38.06ij	41.12o
G49	40.27j	128.61q	60.22c	9.69ab	24.05bc	39.36gh	39.56t
G50	45.05e	154.94c	62.25ab	9.55bcd	23.83cd	42.34d	43.11i
G51	39.27k	149.05e	62.59a	9.48cde	23.16fg	41.53e	45.55d
G52	45.27e	146.54h	61.42b	9.39ef	23.05gh	43.39c	48.44b
G53	51.72a	155.23c	58.47d	9.051g	23.16fg	45.40a	49.16a
G54	46.94d	147.72g	51.67g	9.36ef	24.611a	40.28f	43.23h
G55	39.16k	140.05k	53.26f	9.44def	24.16fg	39.42gh	41.42m
G56	51.38a	136.72l	45.26kl	7.81klm	23.38ef	41.31e	41.54l
G57	43.45g	143.94i	43.52opq	7.66n-q	22.38df	40.19f	40.78q
G58	49.16b	131.72p	45.17lmn	7.60pq	23.88ef	37.41k	38.09c
G59	41.27i	146.72 h	61.42b	9.62abc	23.13cd	43.83b	46.52c
G60	32.38q	148.27f	41.02s	7.37r	24.72a	41.40e	40.31r
G61	35.38o	133.94n	43.98op	7.24rstu	24.05bc	39.67g	41.10o
G62	43.94f	133.27o	39.72t	6.96xw	21.61mn	35.41p	37.08g
G63	37.38m	140.83j	34.06az	6.41z	22.57jk	37.41k	37.76d
G64	42.83h	127.94r	42.46r	7.28rstu	23.05gh	39.39gh	40.35r
G65	47.83c	147.61g	45.22lm	7.31rs	22.16l	37.42k	39.427u
Mean	129.44	69.46	43.18	7.71	22.07	38.09	39.65
LSD (p=0.05)	0.36	0.54	0.9	0.1138	0.23	0.381	0.088
Season							
S1	69.46b	129.43b	43.17b	7.706a	22.03a	38.09b	39.64b
S2	70.6a	130.18a	43.49a	7.64b	22.07a	38.43a	40a
LSD (p=0.05)	0.17	0.1	0.08	0.02	0.1	0.04	0.01

Means with the same letter in each column are not significantly different at p=0.05 using Duncan’s new multiple range test (DNMRT), SF: Spikelet fertility; SP: Spikelet per panicle; FLA: Flag leaf area; CD: Culm diameter; PL: Panicle length; CC67” Chlorophyll content after 67 days after transplanting; CC97: Chlorophyll content after 97 days after transplanting.

Table 7: Mean performance of 65 rice genotypes for different morpho-physiological and yield traits.

Genotype	GL	GB	GLBR	1000-GW	YP	SY	HI
G1	8.53xy	1.88yz	4.37tuv	18.92ayz	12.01jkl	24.16k-o	0.56kl
G2	7.53e	2.18h	3.44f	15.36h	8.51q-t	17.84b-e	0.53mn
G3	9.14r	2.52a	3.55e	20.28qrs	11.99kl	24.68i-l	0.54lm

G4	8.93tu	2.07op	4.35v	19.98tu	11.57l	23.56m-r	0.54lmn
G5	7.88c	2.23s	3.89b	18.13c	7.58wxy	18.04a-d	0.46o-r
G6	8.60wx	2.06no	4.19x	17.28d	7.43ayz	18.29abc	0.44s-v
G7	9.71m	1.91a	5.08ij	16.73e	7.03za	16.82e	0.46o-r
G8	8.63w	2.15ij	4.00a	18.52b	12.44jkl	24.05k-p	0.56kl
G9	8.89u	2.18h	4.06yz	19.41vw	12.46h-k	24.56j-m	0.57jkl
G10	8.42az	1.84cd	4.56r	20.36tu	12.19ijk	23.41n-s	0.58h-k
G11	8.41a	1.78f	4.69q	19.28vwx	12.57hij	21.73uvw	0.60efg
G12	8.54xy	1.56i	5.59c	15.81g	7.59wxy	17.91a-d	0.48o
G13	9.13qr	1.80e	5.05ij	15.57gh	8.97opq	17.52cde	0.57ijk
G14	7.71d	2.31d	3.35g	19.85u	12.71hi	23.47n-s	0.61ef
G15	8.10b	2.02uv	4.04az	19.27v-y	12.34h-k	23.49n-s	0.59g-j
G16	8.59wx	2.28e	3.80c	20.03stu	12.47h-k	23.67p-s	0.61efg
G17	9.80n	2.02st	4.74pq	20.82op	12.67hi	23.31n-s	0.59f-i
G18	7.40f	2.37c	3.16h	19.78w-z	13.37g	23.48n-s	0.63de
G19	7.72d	2.48b	3.16h	21.64lm	12.84gh	22.57r-v	0.65de
G20	8.60wx	2.13kl	4.09y	16.38f	8.68o-s	17.43cde	0.55lm
G21	9.44o	2.04tu	4.69q	22.19k	12.37h-k	23.57o-s	0.58h-k
G22	8.35a	1.66h	5.09i	16.57ef	8.72o-s	18.38abc	0.52n
G23	8.51yz	2.02uvw	4.27w	20.39rst	7.46xyz	17.05de	0.47opq
G24	9.45o	1.78f	5.29f	22.76j	16.34abc	26.57b-e	0.67abc
G25	7.76d	2.16i	3.59e	21.92kl	13.42g	23.56m-r	0.63de
G26	7.43f	1.77g	4.39tuv	21.24n	12.38ijk	23.61l-q	0.56kl
G27	7.20h	2.15ij	3.37g	19.37vwx	7.91u-y	19.78yz	0.42vwxy
G28	8.75v	2.17j	4.09yz	21.94kl	12.71hi	24.38h-k	0.56kl
G29	10.40g	2.09klm	4.98k	21.53n	8.64o-s	22.36s-v	0.44s-v
G30	10.30h	2.07n	4.97k	21.13no	8.37rstu	22.86qrst	0.41w-z
G31	9.08sr	2.09klm	4.33v	21.38mn	7.75v-y	22.73q-u	0.39abcz
G32	11.23a	1.79f	6.28a	20.62pq	7.16az	21.74uvw	0.36d
G33	10.13i	2.33d	4.46st	19.50v	8.63o-s	21.58vwxy	0.44rst
G34	9.95j	2.27g	4.45s	18.57ab	7.71v-y	21.83t-w	0.39abcz
G35	9.30p	1.89b	4.91l	20.13rstu	8.53p-t	21.35wx	0.44rstu
G36	11.05bc	2.03uvw	5.51d	20.42qr	8.05t-w	22.92qrs	0.39abcz
G37	10.31h	2.07rs	5.06ij	19.02xyz	9.15mno	21.23wx	0.48op
G38	9.77lm	2.09n	4.71q	19.78tu	7.48v-y	18.92za	0.45p-s
G39	9.66n	1.95yz	4.93kl	18.65ab	6.85a	20.61xy	0.37bcd
G40	10.77e	1.88c	5.77b	18.76abz	8.73o-s	20.54xy	0.47opq
G41	9.19q	2.08no	4.46s	17.86c	7.53w-z	19.76yz	0.42t-x
G42	9.01st	1.97y	4.60r	19.38xyz	7.46yxz	18.58ab	0.454qrs
G43	11.04bc	2.09m	5.29f	23.53i	8.23s-v	23.46n-s	0.39abyz
G44	11.01c	2.05opq	5.35e	23.63i	9.23mno	22.94qrs	0.45qrs
G45	10.92d	2.11klm	5.22g	25.18abc	16.68ab	26.47b-e	0.68a
G46	10.98cd	1.99vw	5.50d	24.86cde	16.18bcd	25.69e-i	0.68a
G47	10.94d	2.04qr	5.34e	25.39ab	16.25bcd	26.32c-f	0.67ab
G48	11.10b	2.15ij	5.16h	24.73de	15.28ef	25.69e-i	0.65bcd
G49	11.09b	2.19h	5.07ij	25.48ab	16.38cd	26.17defg	0.63a
G50	9.88k	1.85cd	5.31ef	25.36a	16.84a	27.19a-d	0.68a
G51	8.11b	1.88cd	4.36uv	25.12abc	15.82cd	26.94a-d	0.63bcd

G52	8.09b	1.87d	4.32tuv	25.36a	15.71de	27.68a	0.63de
G53	9.70m	2.03s	4.78op	25.32a	16.38bcd	27.59a	0.65cd
G54	10.01j	1.99wx	5.03j	24.68ef	9.70m	26.34c-f	0.42u-x
G55	9.86k	2.07pq	4.82no	24.96b-e	14.89f	27.45ab	0.60fgh
G56	9.56n	1.95y	4.89lm	24.27g	9.05n-q	25.32e-h	0.40axyz
G57	9.85kl	2.02s	4.85mn	24.68ef	8.71o-s	25.80e-h	0.37bcd
G58	7.44f	2.25f	3.30g	24.37fg	8.93o-r	25.62e-i	0.38abc
G59	9.11r	1.94z	4.69q	25.16abc	15.43f	27.31abc	0.61efg
G60	9.63n	2.10k	4.57r	25.03a-d	9.16omn	25.18g-j	0.42u-x
G61	9.31p	2.09klm	4.45s	24.73de	8.56p-t	25.34f-j	0.37bcd
G62	10.68f	1.90b	5.62c	23.64i	8.02t-x	24.32j-n	0.37cd
G63	7.32g	1.98x	3.69d	23.85hi	8.93o-r	22.68s-v	0.42u-x
G64	7.97c	2.29d	3.46f	24.15gh	9.52mn	23.56m-r	0.43s-w
G65	9.19q	2.10lm	4.40tu	24.07gh	9.67nop	22.81q-t	0.44s-v
Mean	9.23	2.04	4.57	21.26	10.81	22.94	0.52
LSD (p=0.05)	0.07	0.01	0.04	0.34	0.57	1.04	0.023
Season							
S1	9.22a	2.03b	4.58a	21.26b	10.8b	22.93b	0.51b
S2	9.22a	2.03a	4.56b	21.4a	11.31a	23.59a	0.52a
LSD (p=0.05)	0.01	0.001	0.005	0.05	0.07	0.11	0.003

Means with the same letter in each column are not significantly different at $p=0.05$ using Duncan's new multiple range test (DNMRT), GL: Grain length; GB: Grain breadth; GLBR: Grain length breadth ratio; TGW: 1000 grain weight; YP: Yield per plant; SY: Straw yield; HI: Harvest index.

Genetic factors and genotype variation

In this study, yield and yield component traits lower PCV compared to most of the growth traits showed higher are presented in Table 8. However, lower PCV belonged to days to maturity (7.12%) though yield plant⁻¹ (30.80%) were recorded with higher value. Number of unfilled grains panicle⁻¹ (27.56%), and flag leaf area (22.46%) were noted with higher values of PCV. Although, CC67 (7.67%), CC97 (8.43%) and grain breadth (8.98%) were found with lower values. The higher GCV was associated with yield per plant (29.74%) whereas the value was low in circumstance of days to maturity (6.85%). These results also showed constricted differences between PCV and GCV for the most of the traits. The heritability ranged from 54.30 to 99.70%. The heritability of highest and lowest were recorded at grain length and grain length breadth ratio. Grain breadth, chlorophyll content 67 and 97, spikelet per panicle and plant height were extremely heritable, all with an estimated $H^2 > 0.90$ whereas other characters presented

relatively low heritability. The genetic advance as present of mean (GA %) ranged from 13.60% in days to maturity to 59.17% in yield per plant. In this study, number of filled grain per panicle, number of unfilled grain per panicle, flag leaf area, harvest index, grain length breadth ratio and yield per plant presented high heritability and high genetic advance indicated the presence of additive genes governing these characters. The relative difference (RD) is the ratio of GCV in association with the respective PCV and the estimated RD values varied from 0.15% (grain length) to 26.36% for number of panicles (Table 8). Relatively low difference value between GCV and PCV was recorded for the traits like FLA (2.91%), PH (2.10%), SP (1.27%), CC67 (1.08%), GB (0.74%), CC97 (0.43%) and GLBR (0.29%) and noticed that the variation present among the traits due to the effect gene and have a better response to direct selection. On the other hand, the traits with higher difference in between their PCV and GCV values indicated the wider genetic variability due to environmental effect and not better feedback to direct selection for the improvement of traits.

Table 8: Variance components, relative difference, heritability and genetic advance of 21 quantitative traits in 65 rice genotypes.

Traits	Mean	σ^2_e	σ^2_g	σ^2_p	PCV (%)	GCV (%)	RD (%)	h^2_b (%)	GA (%)
PH	138.25	8.26	190.3	198.56	10.19	9.98	2.1	95.84	20.12
DM	112.9	4.66	59.88	64.53	7.12	6.85	3.67	92.79	13.6
NT	10.08	1.7	2.95	4.65	21.39	17.03	20.36	63.43	27.95
NFG	131.26	47.25	495.56	542.81	18.1	17.29	4.45	91.3	34.04
NUFG	42.74	17.01	109.2	126.21	27.56	25.63	6.98	86.52	49.12
NP	8.86	1.27	1.51	2.78	20.45	15.07	26.31	54.3	22.87

TGW	21.26	0.72	8.42	9.14	14.22	13.65	4	92.16	26.99
SF	69.46	4.39	41.98	46.37	9.8	9.33	4.85	90.54	18.28
SP	129.44	10.7	414.71	425.41	15.93	15.73	1.27	97.49	32
FLA	43.18	5.4	88.62	94.02	22.46	21.8	2.91	94.26	43.6
CD	7.71	0.14	1.25	1.39	15.3	14.53	4.99	90.27	28.44
HI	0.52	0	0.01	0.01	21.59	20.3	5.97	88.41	39.32
PL	22.07	1.27	1.51	2.78	20.45	15.07	26.31	54.3	22.87
SY	22.94	3.39	8.65	12.04	15.13	12.82	15.24	71.84	22.39
CC67	38.09	0.18	8.35	8.53	7.67	7.58	1.08	97.86	15.46
CC97	39.65	0.1	11.07	11.17	8.43	8.39	0.43	99.14	17.22
GL	9.23	0	1.29	1.29	12.33	12.31	0.15	99.7	25.32
GB	2.04	0	0.03	0.03	8.98	8.92	0.74	98.52	18.23
GLBR	4.57	0	0.49	0.5	15.38	15.33	0.29	99.42	31.5
DF	86.88	7.55	60.92	68.47	9.52	8.98	5.67	88.98	17.46
YP	10.81	0.75	10.33	11.08	30.8	29.74	3.43	93.27	59.17

Note: σ^2_e , Error variance; σ^2_g , Genotypic variance; σ^2_p , Phenotypic variance; GCV, Genotypic coefficient of variation; PCV, Phenotypic coefficient of variation; RD, Relative differences; h^2_b , Broad sense heritability; GA; Genetic advance.

Affiliation amongst traits

The results of utilizing proc corr SAS software version 9.4 to calculate simple Pearson’s phenotypic correlation coefficients for vegetative, yield, and yield contribute traits shows in Table 9. Most traits does not exist in isolation, rather it is an association with one another, which forms a complex relationship that ultimately influence the yield. This relationship might be whichever positive or negative. The correlation coefficient r- value gives the idea of the relationship between two distinct traits through identification of an association. The phenotypic correlation coefficient of characters ranged from -0.82 to 0.91 which indicated that there is higher magnitude of phenotypic variation. The r- value of -1, 0 and +1 indicates negative linear relationship, no liner relationship, and perfect positive linear association respectively. Strong, moderate, and low negative linear relationships are indicated by values ranging from 0.7 to 1, 0.3 to 0.7, and 0 to 0.3, respectively [15]. The levels of association among the 21 traits varied significantly at different points (Table 8). The greatest positive r-value (0.87; $p < 0.01$) indicated a very strong correlation between days to

flowering and days to maturity. The morphological characteristics of day to flowering (0.35**) and days to maturity (0.48**) were highly significantly positive correlated with yield plant⁻¹; In contrast plant height, number of unfilled grains panicle⁻¹, flag leaf area and grain length breadth ratio were highly significantly negatively correlated with yield plant⁻¹. In this combined analysis, it was noticed that the physiological trait harvest index was highly significantly related to nearly all of the studied traits with exceptions of the non-significant associations of this trait: Culm diameter, grain length, grain breadth and grain length breadth ratio. Importantly, the characteristics with the strongest contribution to yield, number of filled grains panicle⁻¹ was highly significantly positively correlated with number of tiller plant⁻¹, 1000-grain weight, harvest index, straw yield plant⁻¹ and yield plant⁻¹. Consideration of higher value of genotypic coefficient of variation along with higher heritability and genetic advance is the powerful tools of selection for crop improvement than the consideration of individual genetic matrix or measuring unit. However, these traits were governed by additive genes having limited response to environment and suggestively notable for the selection procedure.

Table 9: A combined analysis for correlation coefficients among 21 quantitative traits was performed of 65 rice genotypes.

	DM	NT	NFG	NUFG	NP	TGW	SF	SP	FLA	CD	PL	HI	SY	CC67	CC97	GL	GB	GLBR	DF	YP
PH	0.59**	0.36**	0.41**	0.09ns	0.44**	0.82ns	0.25**	0.51**	-0.60ns	-0.63ns	-0.65**	-0.42**	-0.68ns	0.53*	0.49**	-0.25ns	0.05ns	-0.14ns	-0.58ns	-0.39**
DM	1	0.43**	-0.01ns	0.22*	0.21ns	0.55ns	-0.05*	0.02ns	-0.16ns	0.23*	0.21ns	-0.31**	0.32ns	0.26ns	-0.15ns	0.37**	-0.11**	0.20**	0.87**	0.48**
NT		1	0.70**	-0.37ns	-0.91ns	0.62**	0.62ns	0.69**	0.70**	0.66ns	-0.59**	0.50ns	0.63**	0.61ns	0.59**	0.11ns	0.03ns	0.05ns	0.21**	0.75**
NFG			1	-0.57**	-0.67**	0.56ns	0.82**	0.72**	0.78**	0.77ns	0.67**	0.68**	0.66ns	0.70**	0.75**	-0.01ns	0.02ns	-0.03ns	-0.06*	0.88**
NUFG				1	-0.35ns	-0.10**	-0.50ns	-0.56ns	-0.46**	-0.35**	-0.28**	-0.56**	-0.23**	-0.42ns	-0.46ns	0.10**	-0.09**	0.04ns	0.30ns	-0.53**
NP					1	0.59ns	0.58ns	0.67**	0.68**	0.65ns	0.58ns	-0.48**	0.62**	0.54**	-0.55ns	0.16ns	0.04ns	0.08*	0.18**	0.67ns
TGW						1	0.36**	-0.63ns	-0.69ns	0.70**	0.63**	0.22ns	0.73**	0.59*	0.56*	0.29*	0.08*	0.15**	0.51**	0.81**
SF							1	-0.78ns	-0.74ns	-0.66**	-0.59*	0.74**	-0.57ns	-0.57**	-0.63**	-0.04ns	0.06*	-0.07*	0.11**	0.61**
SP								1	0.91**	-0.84ns	0.79**	0.76**	0.69**	-0.68*	-0.72**	0.11**	-0.01ns	0.06ns	-0.03ns	0.54**
FLA									1	0.85**	-0.81**	-0.66ns	-0.75ns	0.72**	0.78ns	0.15ns	0.03ns	0.09**	0.10**	-0.79ns
CD										1	0.77ns	0.54ns	0.77ns	0.62**	0.61**	0.30**	0.11**	-0.15ns	0.20**	0.55**
PL											1	0.53**	0.69**	-0.64*	0.67**	0.16*	0.03ns	0.09ns	0.18**	0.57**

HI																				1	0.25**	0.53**	0.59**	0.07ns	0.02ns	0.07ns	0.27**	0.73**
SY																					1	0.58ns	-0.57**	0.19ns	0.10**	-0.08*	0.28**	0.69**
CC67																						1	0.92ns	0.09ns	0.06*	0.13ns	0.19ns	0.62**
CC97																							1	-0.08*	-0.06*	-0.05ns	0.10*	0.60**
GL																								1	0.09**	0.82**	0.41**	0.04ns
GB																									1	-0.63**	0.09ns	0.05*
GLBR																										1	0.24**	-0.01ns
DF																											1	0.35**

Note: *Significantly at 0.05 probability level; **highly significant at 0.01 probability level; ns: not significant; PH: Plant height; DM: Days to maturity; NT: Number of tiller; NFG: Number of filled grain; NUFG: Number of unfilled grain; NP: Number of panicle; TGW: 1000 grain weight; SF: Spikelet fertility; SP: Spikelet per panicle; FLA: Flag leaf area; CD: Culm diameter; PL: Panicle length; HI: Harvest index; SY: Straw yield; CC67: Chlorophyll content after 67 days after transplanting; CC97: Chlorophyll content after 97 days after transplanting; GL: Grain length; GB: Grain breadth; GLBR: Grain length breadth ratio; DF: days to flowering; YP: Yield per plant.

Clustering pattern

One of the criteria for parental selection is genetic divergence analysis, in which the extent among genotype is estimated on existing diversity. Accurate information on the degree and nature of genetic variability is vital in selecting a desirable parent. In this present study, 65 rice genotypes had been magnificently clustered into eight major groups based on their quantitative traits to differentiate genotypes in population. A dendrogram was fortified based on the Ward Hierarchical Clustering (WHC) method using JMP version 1.6 SAS program. Conferring the dendrogram constructed (Figure1), the genotypes were clustered into eight groups. The dendrogram showed the similar genotypes tend to cluster together. Among the eight groups, largest number of genotypes (18) had in cluster VII, followed by cluster I with 11 genotypes and cluster III with 9 genotypes. Cluster V and VI had six genotypes. Cluster

II and VIII had five genotypes and cluster IV had four genotypes presented in Table 10. Mean of the values of different clusters for the characters showed that genotypes which produced maximum flag leaf area, no. of tillers plant⁻¹, no. of filled grains panicle⁻¹, spikelet fertility, and yield plant⁻¹ were accumulated in cluster V, whereas genotypes with maximum no. of panicles plant⁻¹, panicle length, and flag leaf area were grouped in cluster VI (Table 11). The genotypes which produced less plant height and harvest index were clubbed into cluster IV, whereas minimum no. of tillers plant⁻¹, low 1000-grain weight with low yielding genotypes were grouped into cluster VII (Table 11). Cluster analysis showed that in terms of high yield potentially cluster V (G24, G50, G51, G52, G53 and G59) had highest cluster mean of yield (16.49g), followed by cluster VI (G45, G46, 47, G48, G49 and G55 (16.37g) (Table 11). Therefore, priority should be given to genotypes aggregated in cluster V and VI having high yield potentiality for future rice breeding.

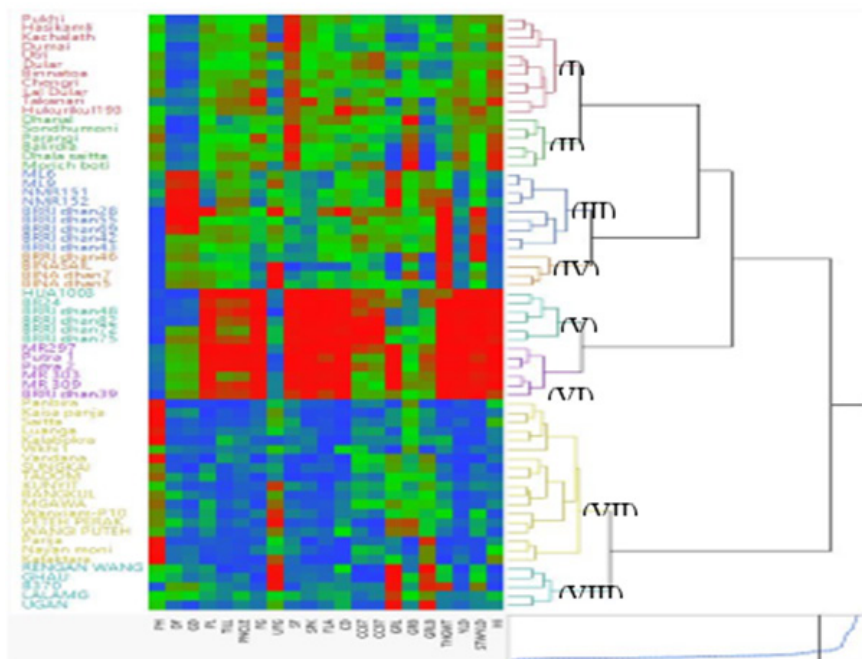


Figure 1: The association between 65 rice genotypes based on 21 variables was examined using Ward Hierarchical Clustering (WHC) method using JMP version 1.6 SAS program.

Table 10: Distribution of 65 rice genotypes into eight clusters.

Cluster	No. Of Genotypes	Name of Genotypes
I	11	Pukhi (G1), Hasikamli (G10), Kachalath (G26), Dumai (G11), Utri (G4), Dular (G8), Binnatoa (G15), Chengri (G17), Lala Dular (G21), Takanari (G25) and Hukurikul 193 (G28)
II	5	Dharial (G3), Sondhamoni (G9), Parangi (G16), Balirdia (G14) and Dhala saitta (G18)
III	9	ML6 (G29), ML9 (G30), NMR 151 (G43), NMR 152 (G44), BRRi dhan28 (G54), BRRi dhan55 (G60), BRRi dhan69 (G61), BRRi dhan42 (G56) and BRRi dhan43 (G57)
IV	4	BRRi dhan46 (G58), BINASAIL (G63), BINA dhan7 (G64) and BINA dhan5 (G65)
V	6	HUA1003 (G24), BR24 (G50), BRRi dhan48 (G51), BRRi dhan82 (G52), BRRi dhan72 (G53) and BRRi dhan75 (G59)
VI	6	MR297 (G45), Putra 1 (G46), Purta 2 (G47), MR303 (G48), MR 309 (G49) and BRRi dhan39 (G55)
VII	18	Panbira (G2), Kaisa panja (G6), Saitta (G20), Luanga (G5), Kalabokra (G23), Wkhi 1(G27), Vandana (G7), SUNGKAI (G39), TADOM (G41), KUNYIT (G35), BANGKUL (G42), MGAWA (G38), Wanxiam-10 (G31), PETEH PERAK (G33), WANGI PUTEH (G34), Parija (G12), Nayan moni (G22) and Kataktara (G13)
VIII	5	RENGAN WANG (G32), GHAU (G36), B370 (G62), LALAMG (G37) and UGAN (G40)

Table 11: Mean values of quantitative traits for 8 groups revealed by cluster analysis.

Trait	Cluster							
	Group I	Group II	Group III	Group IV	Group V	Group VI	Group VII	Group VIII
	G1, G10, G26, G11, G4, G8, G15, G17, G21, G25, G28	G3, G9, G16, G14, G18	G29, G30, G43, G44, G54, G60, G61, G57, G56	G58, G63, G64, G65	G24, G50, G51, G52, G53, G59	G45, G46, G47, G48, G49, G55	G2, G6, G20, G5, G23, G27, G7, G39, G41, G35, G42, G38, G31, G33, G34, G12, G22, G13	G32, G36, G62, G37, G40
PH	140.8	145.29	125.35	120.36	121.15	126.86	153.76	136.12
DM	108.68	108.02	128.15	119.78	111.84	118.1	108.27	111.56
NT	11.11	10.56	11.4	10.54	12.7	13.13	8.55	8.77
NFG	143.68	137.9	121.26	115.99	167.08	162.85	108.82	108.01
NUFG	34.5	41.6	47.12	57.14	32.43	30.94	44.15	52.98
NP	8.95	8.56	8.99	8.35	10.15	10.51	7.06	7.51
TGW	20.51	19.88	23.65	24.13	24.86	25.05	18.22	20.58
SF	75.43	76.17	67.46	64.21	77.96	78.06	63.74	63.78
SP	136.92	134.04	120.07	119.97	167.72	164.48	110.77	116.01
FLA	45.37	45.28	42.57	42.03	61	57.36	33.04	37.67
CD	7.81	7.89	7.91	7.24	9.39	9.5	6.47	7.29
PL	22.74	22.28	22.04	22.54	25.97	26.25	19.16	20.63
HI	0.59	0.6	0.44	0.41	0.66	0.68	0.46	0.42
SY	23.79	23.77	24.83	24.3	27.52	26.61	19.49	22.54
CC67	39.12	38.53	39.52	38.06	43.11	40.23	36.09	33.22
CC97	41.51	39.21	40.24	39.05	46.26	41.84	37.09	35.6
GL	8.56	8.33	10.12	7.97	9.05	10.81	8.89	10.8
GB	1.98	2.33	2.05	2.15	1.88	2.08	2	1.91
GLBR	4.33	3.59	4.94	3.72	4.81	5.19	4.5	5.67
DF	82.97	81.79	103.15	93.6	86.02	92.18	83.72	88
YP	12.6	12.93	9.17	9.35	16.49	16.37	8.01	8.28

Note: PH: Plant height; DM: Days to maturity; NT: Number of tiller; NFG: Number of filled grain; NUFG: Number of unfilled grain; NP: Number of panicle; TGW: 1000 grain weight; SF: Spikelet fertility; SP: Spikelet per panicle; FLA: Flag leaf area; CD: Culm diameter; PL: Panicle length; HI: Harvest index; SY: Straw yield; CC67: Chlorophyll content after 67 days after transplanting; CC97: Chlorophyll content after 97 days after transplanting; GL: Grain length; GB: Grain breadth; GLBR: Grain length breadth ratio; DF: days to flowering; YP: Yield per plant.

Valuation of principal component analysis

Based on the result from Table 12 it that the principal component 1 (PC1) accounted for close 56.2% of the total variation and the characters responsible for genotypes separation along this axis NP (highest 0.27), SP, FLA, NT, NFG, CD, PL and YP (gm palnt⁻¹) with high and positive value of coefficient variation. The second principal component 2 (PC2) associated with the traits DM (maximum 0.43), NUFG, TGW, SY, GL and DF accounted for 17.19% of the total variation. About 9.24% of the total variation was detected for principal component 3 (PC3) and displayed differences based on PH, GL and GLBR (largest 0.62). The principal component 4 (PC4) accounted 4.84% of the total variation and

consisted mostly of the traits NUFG, SF, SP, CD, HI, GL, GB (maximum 0.58), and YP (gm plant⁻¹). Most of the genotypes were dispersed at low distances whereas the few were dispersed at high distances as reflected by eigenvector (Figure 2). The farthest genotypes from centroid was G2, G20, G6, G41, G33, G32, G54, G59, G51 and G24 whereas other genotypes were near to centroid. The proportion of variation for principal component (PC1) and (PC2) were 56.17% and 17.19%. respectively, in which the first principal component occupied the topmost position of the total variation excited (Table 12). PCA biplot loaded the both variables and cases (genotypes) at the same time shows how strongly each trait influences as PC and correlated to each other it also shows the how distances the genotype from each other.

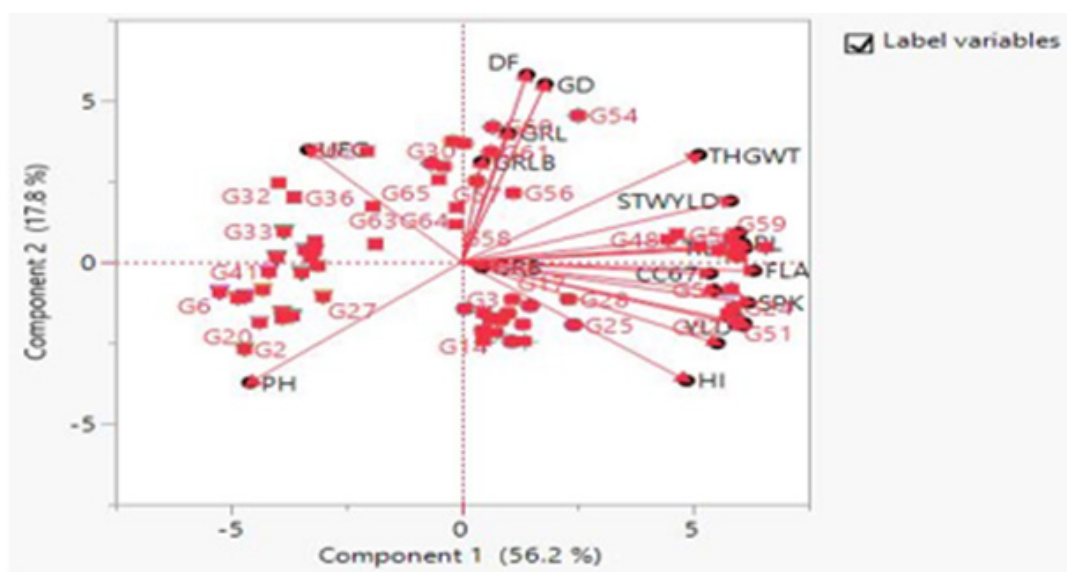


Figure 2: Principal component analysis showing the relationship among 65 rice genotypes in two-dimensional graph.

Table 12: Estimation of principal components of 21 traits in 65 rice genotypes.

Variables	PC1	PC2	PC3	PC4
Eigen values	11.79	3.73	1.94	1.01
Proportion	56.17	17.19	9.24	4.84
Cumulative	56.17	73.97	83.21	88.05
PH	-0.2	-0.29	0.12	0.05
DM	0.07	0.43	-0.15	-0.14
NT	0.26	0.03	-0.01	-0.06
NFG	0.26	-0.14	0.02	0.01
NUFG	-0.14	0.27	-0.15	0.18
NP	0.27	0.03	0.02	0.03
TGW	0.22	0.26	-0.09	-0.03
SF	0.24	-0.19	0.02	0.11
SP	0.27	-0.09	0.08	0.11
FLA	0.27	-0.02	0.03	0.03
CD	0.26	0.07	0.03	0.22
PL	0.26	0.04	0.001	0.06
HI	0.21	-0.28	0.1	0.12

SY	0.25	0.14	-0.08	0.06
CC67	0.23	-0.02	-0.15	-0.37
CC97	0.24	-0.06	-0.05	-0.39
GL	0.04	0.31	0.41	0.4
GB	0.01	-0.01	-0.53	0.58
GLBR	0.01	0.24	0.62	0.002
DF	0.06	0.45	-0.13	-0.11
YP	0.26	-0.15	0.05	0.12

Note: PC1: First principle component; PC2: Second principle component; PC3: Third principle component; and PC4: Fourth principle component.

Discussion

In the present study, all the traits showed highly significant ($P < 0.01$) variations among 65 rice genotypes, which originated in different countries. Results are in close settlement with those of [16] who noted highly significant variability among the different rice genotypes [17]. Also gives parallel support to the present judgements. The judgements of [18] and [19] further strengthen the current judgements, who also found highly and valuable significant and positive variability among their studied genotypes. The reliance of grain yield on other traits has been reported for many crops [20]. Yield is a complex and quantitatively inherited trait that depends on other yield contributing characteristics that are influenced by genetic effects. Therefore, knowledge of the correlation coefficient between different traits is essential for the design of an effective hybridization programme. The highly significant and strong positive correlations between days to flowering and days to maturity positive correlated with yield plant⁻¹ in contrast plant height, number of unfilled grains panicle⁻¹, flag leaf area and grain length breadth ratio were highly significantly negatively correlated with yield plant⁻¹. A positive (0.32**) and significant correlation was also found between the day to flowering and the days to maturity by [21]. The number of filled grain panicle⁻¹ was positively and highly significantly correlated with the number of tiller plant⁻¹, 1000-grain weight, harvest index, straw yield plant⁻¹ and yield plant⁻¹, and these findings were consistent with and supported by those of [22] and [21]. The vital plant characteristics yield plant⁻¹ was significantly and positively correlated with nearly all of the traits. Similar findings have also been observed by many researchers [23,24]. These researchers have recorded significant positive correlations of the majority on morphological traits with yield in rice plants. Correlations between traits are important because they help the breeder to select important characteristics from the studied traits [25]. The majority of traits, including yield and yield contributing traits are influenced by interactions the genotype and environment, and therefore, the use of correlation coefficients make selection easy or plant breeders [25]. The correlation coefficients implied that days to flowering and days to maturity, straw yield plant⁻¹, harvest index, number of tiller plant⁻¹, number of filled grains panicle⁻¹ and 1000-grain weight should be considered during selection to improve yields and other desirable agronomic characteristics.

The genetic analysis of quantitative traits is a pre-requisite for plant breeding pro-programmes and can lead to a systematic method of design and the appropriate planting of plant breeding strategies. The current study suggests that the phenotypic coefficient of variance was greater than the genotypic coefficient of variance for all the traits. Similar results were reported for all the traits observed in another study [26]. This study reported that the trait is magnitude of the differences between the genotypic and phenotypic coefficients of variation, that is, large of differences reflect a substantial environmental effect, and small differences indicate a strong genetic influence. In the present study, the small differences between the phenotypic coefficient of variance and genotypic coefficient of variance for most of the traits. These small differences also suggest that selection based of these characters will not be effective in future crossing pro-programmes. The other traits, which showed a higher difference between phenotypic coefficient of variance and genotypic coefficient of variance, indicated that the environmental effect on the expression of those traits was higher and that selection based on these characters will not be effective for further yield improvement. The highest phenotypic coefficient of variance was recorded for yield plant⁻¹ and number of unfilled grain panicle⁻¹ in the present study. These traits were recorded by the following researchers [27-29].

The variables number of filled grain per panicle, number of unfilled grain per panicle, flag leaf area, harvest index, grain length breadth ratio and yield plant⁻¹ exhibited grater higher heritability's and thus indicated the presence of additive gene actions. This characteristics exhibited very high heritability's coupled with the greatest genetic advance, which suggested that these traits were mainly under genetic control and that they can be scored according to their phenotypic performances [10]. estimated high heritability and genetic advances for the parameters of days to 50% heading, days to maturity, flag leaf area, panicle length, no. of branches panicle⁻¹, no. of seeds panicle and seed weight panicle⁻¹ at seed yield. The 65 traditional and commercial rice genotypes clustered into eight groups based on the dendrogram from the cluster analysis and principal component analysis. The groupings from the hierarchical cluster analysis exhibited a dendrogram topology and cluster memberships that were similar to those produced based on the principal component analysis, which confirmed the accuracy of the constructed dendrogram. Fifty-eight rice varieties were grouped

into four clusters based on 18 morphological characters in a study by [30]. Similarly, [31] calculated a similar clustering pattern based on hierarchical cluster analysis and principal component analysis for 24 rice genotypes. Principal component analysis indicated diversity among 65 rice genotypes. "Proper values" measure the importance and contribution of each component to total variance, whereas each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated. The higher the coefficients are, regardless of the direction (positive or negative), the more effective they will be in discriminating between genotypes. In the present study, the first four principal components accounted for 56% of the total variation, which indicated very strong correlations between the examined characteristics. Similarly, [32] explained 61.2% of the total variability using the first and second principal components. Approximately 82.7% of the total variation of rice varieties was also explained by [33]. The present investigation highlighted that the genotypes originated from the Bangladesh could be hybridized with the genotypes from Malaysia, Philippines, India and vice versa to create broader genetic variation to improve yield and other favourable characteristics.

Conclusion

Knowledge of the performance of rice genotype individually is crucial in selecting the best genotypes for varietal improvement. The sixty-five studied rice genotypes varied with respect to their morpho-physiology and yield performances as well as pungency level. The extent of genetic variation indicated that they might be derived from multiple origins. The development of rice genotypes that could lead to sustainable yield production rests on exploring genetic aspects of its morphological traits. This is because genetic variability provides room for recombinant that is crucial in varietal development. The 65 studied rice genotypes varied with respect to their morpho-physiology and yield performance as well as pungency level. The extent of genetic variation indicated that they might be derived from multiple origins, indicating their different sources. The prevalence of genetic variance for morpho-physiological traits studied such as 1000-grain weight, number of filled grain panicles⁻¹, number of empty grain panicles⁻¹, flag leaf area, grain length, harvest index, grain length breadth ratio, and yield plant⁻¹ can be exploited through selection exhibited by the estimate of high heritability and high genetic advance. These findings provide an insight into genetic diversity for future references. Considering diversity pattern and other morphological performances Clusters V and VI may be further utilized in different breeding program for varietal improvement or development in future.

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Author's contributions

Conceptualization, Mohammad Anisuzzaman and Mohd Rafii; Data curation, Mohammad Anisuzzaman; Formal analysis, Mohammad Anisuzzaman and Md Mahmudul Hasan Khan; Funding acquisition, Mohammad Anisuzzaman and Mohd Rafii; Investigation, Shairul Izan Ramlee and Noraini M. Jaafar; Methodology, Mohammad Anisuzzaman and Mohd Rafii; Supervision, Mohd Rafii; Validation, Mohd Rafii; Writing-original draft, Mohammad Anisuzzaman; Writing-review & editing, Mohammad Anisuzzaman, Ferdouse Iqbal, Azadul Haque and Md Mahmudul Hasan Khan.

Conflict of Interest

There is no conflict of interest.

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