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Genetic Variability Analysis for Yield Contributing Traits in Rice (*Oryza sativa* L.) in Hilly Areas of Bangladesh

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ABSTRACT

A field experiment was carried out with six genotypes of Boro season rice at Sadar upazila of Khagrachhari district, Bangladesh. The study evaluated the genetic variability, heritability, correlations among the studied traits, and their direct effect on yield. The research result revealed that the phenotypic variance was higher than the genotypic variance for all the measured traits. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values were observed for grain yield (GY), thousand-grain weight (TGW), days to flowering (DTF), days to maturity (DTM), plant height (PH), panicle length (PL), number of filled grains per plant (FG), and number of unfilled grains per plant (UFG), indicating a very high heritability estimate. The calculated genetic advance as a percent of the mean for all traits was also very high. The GY was positively correlated with PH, DTM, and the number of total tillers per hill (NTH), PL, FG, UFG, and TGW; and negatively correlated with DTF and the number of non-effective tillers per hill (NETH). Principal component analysis revealed that PC1 exhibited the highest standard deviation (267.95) and proportion of variance (88%), with subsequent principal components showing gradual reduction. However, in terms of cumulative proportion, the contributions of the principal components were similar, except for PC1. Path analysis revealed that DTM, number of effective tillers per hill (ETH), PL, FG, UFG, and TGW directly affect GY. FG (0.526), PL (0.394), UFG (0.205), and ETH (0.192) showed a highly significant positive correlation contributed to the GY in path analysis; indicating that selecting these traits might be effective in improving grain yield in the future breeding programmes.

Key words: Genetic variability, correlation coefficients, path analysis, rice (*Oryza sativa* L.)

INTRODUCTION

Oryza sativa L., the most extensively farmed rice, is an indispensable food for an assessed 3.5 billion people globally and is the major crop in Asia, where around 90% of the globe's rice is growing and eaten up (Muthayya *et al.,* 2014 and Debsharma *et al.,* 2022). As a result of ever-rising inhabitants, the primary goal of plant breeders is to upturn rice production. However, several significant drivers have prevented the world from ending hunger and malnutrition in all its forms by 2030 (Byerlee and Fanzo, 2019).

Regarding global rice production, Bangladesh ranks third and is the fourth-largest rice user (Mottaleb *et al.,* 2020), with rice being the leading staple food. It is cultivated by 90% of the total net crop areas of the nation, and over 99% of the country's populace consumes 367.2 g of rice per person per day (HIES, 2016). Rice is grown in Bangladesh during three distinct seasons - Aus, Aman, and Boro, with Boro being the most important and leading season for rice in Bangladesh in terms of production volume in recent years. The Boro rice cultivation comprises about 61% of the total cropped area which is about 55% of the total rice

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production (BBS, 2019). Proper improved crop management practices such as balanced irrigation, fertilizer, and pesticide application have strengthened its production.

Rice cultivation in Khagrachari district, one of the three hill districts of Bangladesh, has great potential in the Boro season despite the less profitable traditional jhum cultivation. Specifically, the study aims to conduct trait-specific statistical varietal selection among the district's most cultivated inbred rice cultivars. The achievements of genetic variability by choice turn on the genetic progression of heredity, individual traits, and crop development, which rely on genetic diversity in the base population (Govintharaj *et al.,* 2016; Gupta et al., 2022). Once genetic variability is established, appropriate selection methods can improve crop yields by selecting yield components. Environmental factors play a significant role in the observable fluctuations of quantitative attributes. Therefore, partitioning overall variation is obligatory for a fruitful breeding platform. Heritability estimation helps predict the most effective selection strategy and breeding methods, as well as the profit from selection. A character with a high PCV and a low GCV has a high environmental effect on its manifestation (Singh, 2015). Although correlation estimates can reveal the positive or negative influence of factors on a trait, they are not capable of providing accurate insights into the relative significance of direct and indirect effects of intricate attributes like yield. Path analysis utilizes standard partial regression coefficients to differentiate the correlation coefficients between the direct and indirect effects of multiple attributes on the reliant variable. In this analysis, crop yield is regarded as the reliant variable, while residual characters are reflected as liberated variables.

Several researchers have used morphological traits for variability assessment and characterization of Bangladesh rice germplasm (Siddique et al., 2011; Banik et al., 2012; Khalequzzaman et al., 2012; Baktiar et al., 2013; Siddique et al., 2013; Islam et al., 2014; Ahmed et al., 2015a, 2015b; Kulsum et al., 2015; Akter et al., 2016; Biswash et al., 2016; Siddique et al., 2016; Akter et al., 2017; Islam et al., 2017; Akter et al., 2018; Islam et al., 2018; Siddique et al., 2018; Islam et al., 2019; Muti et al., 2020; Khalequzzaman et al., 2022; Khalequzzaman et al., 2023), but research exploring Boro rice is scanty. Thus, it is imperative to conduct this research with Boro rice to explore the genetic variation, correlation coefficients linked to characteristics that impact yield favourably or unfavourably, and the connection between yield components and their direct and indirect influences on grain yield via path coefficient analysis. As a result, this investigation was performed to assess the genetic variation, heritability, and correlation between diverse quantitative traits and their direct impact on yield via path analysis. This examination will establish the groundwork for rice selection and yield enhancement.

MATERIALS AND METHODS

An experiment was carried out during the Boro season of 2018-19 (December 2018 to May 2019) at a farmer's field located in Sadar upazila of Khagrachhari district, Bangladesh. The field belongs to the Northern and Eastern hills, which are categorized as the AEZ-29 (Agro-Ecological Zone) (Ahmmed *et al.,* 2018). The randomized complete block design (RCBD) was implemented in the trial, which comprised six inbred rice cultivars, specifically Binadhan-5, Binadhan-10, Binadhan-12, Binadhan-18, BRRI dhan28, and BRRI dhan29, with four replications. The experimental plot had a total area of 208 m^2, with individual plots measuring 2 × 2 m^2. Pre-germinated seeds were sowed, and 2-3 seedlings were transplanted per hill at a spacing of 20 cm × 20 cm after 35 days of sowing. Fertilizer application involved administering urea, triple superphosphate (TSP), muriate of potash (MOP), gypsum, and zinc at the rate of 210-100-150-80-6 kg ha^{-1}. To control weeds, pre-emergence herbicide Rifit 500 EC @ 988 ml/ha was used, and two-hand weeding was done 30 and 45 days after transplanting. Pest infestation was prevented by applying Granular Carbofuran-5G @ 10 Kg/ha and spraying Amistar Top @ 500 ml/ha and Ripcord 10 EC @ /988 ml/ha. Harvesting was done when 80% of the grains matured and turned golden. Data were collected from five randomly selected competitive plants from each plot, including plant height (PH), number of total tillers per hill (NTH), number of effective tillers per hill (ETH), number of non-effective tillers per hill (NETH), panicle length (PL), number of filled grain per plant (FG), number of unfilled grain per plant (UFG), thousand grain-weight (TGW), days to maturity (DTM), days to flowering (DTF), and grain yield (GY) measured in ton per hectare.

Statistical Analysis

The Agricolae package of R statistical software in R Studio (Team R, 2017) was used for statistical analysis of various genetic parameters, including genetic variance, phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2b), genetic advance (GA), and genetic advance as a percentage of the mean (GAM), as well as correlation coefficients and path analysis. Principal component analysis (PCA) was also performed using the GGally package in R Studio.

RESULTS

Performance of varieties

Recommendation of a variety for cultivation, considering the overall varietal performance, including grain yield and quality, is crucial for sustainable production. To evaluate the performance of six popular boro rice varieties, yield and growth characteristics were assessed. Variations in plant height (PH), days to flowering (DTF), days to maturity (DTM), total tillers per hill (NTH), effective tillers per hill (ETH), non-effective tillers per hill (NETH), panicle length (PL), filled grains per plant (FG), unfilled grains per plant (UFG), thousand grain-weight (TGW), grain yield (GY) were observed among the varieties. Analyzing the ANOVA (Table 1) and mean performance (Table 2) of different yield-related traits of six varieties of the best-performing varieties were identified.

Table 1. Analysis of variance (mean sum of squares) for yield and its component characters of six popular Boro rice varieties.

Source of variation	df	PH (cm)	DTF	DTM	NTH	ETH	NETH	PL (cm)	FG (No.)	UFG (No.)	TGW (g)	GY (t/ha)
Varieties	5	142.64***	233.76***	384.38***	3.58***	6.76***	16.15***	21.54***	27.80***	25.37***	851.58***	31.24***
Replication	3	1.24	10.20***	9.13***	2.83**	2.45	2.06	1.76	2.36	2.08*	9.02***	5.33**
Error	15	4.14***	*	*	2.03**	1.70	1.02	0.97	3.86***	2.85***	2.75***	*

*, ** and *** indicates significant at 0.05, 0.01 and 0.001 probability, respectively.

PH: plant height, NTH: number of total tillers per hill, ETH: number of effective tillers per hill, NETH: number of non-effective tillers per hill, PL: panicle length, FG: number of filled grains per plant, UFG: number of unfilled grains per plant, TGW: thousand grain-weight, DTM: days to maturity, DTF: days to flowering and GY: grain yield.

Table 2. Mean performance of six varieties based on different morphological traits related to yield.

Varieties	PH (cm)	DTF	DTM	NTH (no.)	ETH (no.)	NETH (no.)	PL (cm)	FG (no.)	UFG (no.)
Binadhan-5	115.20 a	127.50 c	161.00 b	11.05 b	10.25 b	0.80 cd	23.58 ab	888.13 bc	347.00 ab
Binadhan-10	107.25 b	106.25 e	139.00 d	12.65 ab	11.50 b	1.15 bcd	22.96 ab	835.74 cd	180.83 d
Binadhan-12	94.70 c	126.00 c	159.00 b	14.30 a	13.85 a	0.45 d	24.35 a’	1262.75 a	379.75 a
Binadhan-18	93.50 cd	130.75 b	151.00 c	14.10 a	10.00 b	4.10 a	20.12 d	722.50 d	258.50 c
BRRI dhan28	92.25 cd	119.75 d	143.75 c	13.60 ab	11.65 ab	1.95 bc	20.90cd	693.75 d	160.37 d
BRRI dhan29	91.25 d	134.25 a	166.50 a	12.75 ab	10.45 b	2.30 b	22.27 bc	1001.50 b	288.75 bc
P value									
Varieties	0.000	0.000	0.000	0.135	0.012	0.000	0.000	0.000	0.000
Replication	0.738	0.288	0.441	0.233	0.236	0.154	0.188	0.490	0.295
CV (%)	9.82	6.72	7.65	23.32	24.59	106.32	9.51	29.05	41.66
SEM	0.89	0.87	0.95	0.28	0.25	0.17	0.19	23.9	10.2
Mean	99.03	124.08	154.88	13.08	11.28	1.79	22.36	900.70	269.20

The same letter indicates no significant differences and the different letter indicates significant differences among the varieties for each trait. PH: plant height, NTH: number of total tillers per hill, ETH: number of effective tillers per hill, NETH: number of non-effective tillers per hill, PL: panicle length, FG: number of filled grains per plant, UFG: number of unfilled grains per plant, TGW: thousand grain-weight, DTM: days to maturity, DTF: days to flowering and GY: grain yield. CV: Coefficient of variation, SEM: Standard error mean.

Estimation of Genetic Variability

Improvement of field crops (like rice) through breeding, the level of diversity for each given trait is necessary. Table 3 presents the assessments of genotypic variation (σ^2g), phenotypic variation (σ^2p), error variance (σ^2e), GCV, PCV, heritability, GA, and GAM for the previously mentioned eleven traits. Using only genotypic variance as a comparison to total phenotypic variance, we determined the extent of the role of genotype in rice varietal development.

For all traits considered, genotypic variance exceeded environmental variance at the mean level excluding the NTH of σ^2g=5.20 and σ^2p=13.25. In the present study, GCV value varied from 14.00% for DTM to 160.43% for the NETH, whereas PCV varied from 14.12% for DTM to 180.37% for the NETH. The greater PCV and GCV values were recorded for GY, PH, ETH, NETH, FG, UFG, and TGW where not extreme GCV and PCV values had been obtained for DTM, DTF, and PL. Among the studied traits, TGW, DTM, DTF, PH, PL, GY, FG, and UFG revealed more than 80% of heritability estimates.

Table 3. Assessment of genetic factors for GY and yield attributes.

Character	σ^2g	σ^2p	σ^2e	CV		h^2b	GA	GAM (%)
				GCV (%)	PCV (%)			
DTF	484.92	493.25	8.33	17.76	17.91	98.31	44.97	36.27
DTM	470.72	479.04	8.31	14.00	14.12	98.26	44.30	28.59
PH	481.46	495.06	13.60	22.16	22.47	97.25	44.58	45.02
NTH	5.20	13.25	8.05	17.44	27.84	39.25	2.94	22.51
ETH	8.67	14.69	6.02	26.10	33.97	59.02	4.66	41.30
NETH	8.26	10.44	2.18	160.43	180.37	79.11	5.27	293.94
PL	12.35	14.75	2.40	15.71	17.17	83.70	6.62	29.61
FG	212281.28	243964.66	31683.38	51.15	54.84	87.01	885.35	98.29
UFG	36908.63	42966.00	6057.37	71.37	77.00	85.90	366.80	136.26
TGW	95.86	96.31	0.45	43.65	43.75	99.53	20.12	89.71
GY	1.73	1.96	0.23	21.43	22.81	88.32	2.54	41.50

σ^2g: Genotypic variance, σ^2p: Phenotypic variance, σ^2e: Environmental variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h^2b: broad sense heritability, GA: Genetic advance and GAM: GA as a percent of the mean.

Here, PH: plant height, NTH: number of total tillers per hill, ETH: number of effective tillers per hill, NETH: number of non-effective tillers per hill, PL: panicle length, FG: number of filled grains per plant, UFG: number of unfilled grains per plant, TGW: thousand grain-weight, DTM: days to maturity, DTF: days to flowering and GY: grain yield.

Likewise, moderately high heritability (60-79%) was documented for the NETH. Instead, a moderate broad sense heritability estimate (40-59%) was perceived for the ETH and less H^2 (<39%) was shown for the NTH. The estimated GA as a GAM in the current study was higher and it was about >20% for all the traits. The uppermost value of GAM (293.94) was detected in the NETH, tracked by 136.26 in the UFG, 98.29 in the FG, 89.71 in TGW, and 45.02 in PH.

Principal component analysis (PCA)

For summarizing the information of large data, principal component analysis effectively decreases the measurement dimensions while retaining data accuracy. In principal component analysis, the largest standard deviation and proportion of variance were found in PC1 (267.95 and 88%, respectively) and for others PC was gradually reduced but in the case of cumulative proportion, the PCs were similar except PC1 (Table 4).

In PC1, the variable FG has a high negative coefficient (-0.97) and UFG has a low negative coefficient (0.23). This suggests that PC1 is capturing information related to the contrast between filled and unfilled grains. PC2 has notable positive coefficients for DTF, DTM, and UFG, suggesting that PC2 may be associated with the timing of growth stages and unfilled grains. PC3 has a high positive coefficient for PH, ETH, PL, UFG, TGW, and GY indicating that PC3 may represent variations related to plant height, effective tiller per hill, panicle length, unfilled grain per plant, thousand-grain weight, and grain yield. On the other hand, PC3 has a high negative coefficient to DTM and DTF. Again, PC4 has a high negative coefficient to PH, DTM, and DTF which represents variability. Similarly, the other principal components (PC5 to PC11) capture specific patterns or relationships among the variables (Table 5).

The PCA results provide a way to understand the relationships and patterns in the data, reducing the dimensionality of the original variables while retaining important information. The coefficients in each principal component indicate the contribution of each variable to the overall variation captured by that component.

Table 4. Standard deviation, proportion of variance and cumulative proportion of each principal components for the principal components of six rice varieties.

Parammeter	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Standard deviation	267.95	96.23	13.50	8.31	3.69	3.35	1.81	1.60	1.25	0.50	0.00
Proportion of variance	0.88	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Cumulative proportion	0.88	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Table 5. Principal component analysis for quantitative traits of six rice varieties.

Variable	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
PH (cm)	0.00	0.01	0.48	-0.85	0.14	0.06	0.10	-0.05	-0.06	0.03	0.00
DTM	0.00	0.04	-0.58	-0.43	-0.03	-0.12	-0.30	0.18	0.57	-0.14	0.00
NTH	0.00	0.00	0.00	0.10	0.73	-0.27	0.10	0.19	0.05	-0.01	-0.58
ETH	0.00	0.00	0.05	0.08	0.59	0.02	-0.52	-0.22	-0.05	0.00	0.58
NETH	0.00	0.00	-0.04	0.02	0.15	-0.30	0.61	0.41	0.10	0.00	0.58
DTF	0.00	0.03	-0.64	-0.26	0.13	0.06	0.19	-0.18	-0.64	0.15	0.00
PL (cm)	0.00	0.00	0.06	-0.03	-0.06	0.20	-0.36	0.82	-0.39	-0.06	0.00
FG	-0.97	-0.23	-0.01	-0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
UFG	-0.23	0.97	0.04	0.04	0.00	-0.01	0.00	0.00	0.00	0.00	0.00
TGW	0.01	-0.01	0.10	-0.06	-0.25	-0.88	-0.27	-0.07	-0.27	-0.03	0.00
GY (t/ha)	0.00	0.00	0.01	0.00	-0.03	-0.05	-0.10	0.11	0.15	0.98	0.00

Here, PH: plant height, NTH: number of total tillers per hill, ETH: number of effective tillers per hill, NETH: number of non-effective tillers per hill, PL: panicle length, FG: number of filled grains per plant, UFG: number of unfilled grains per plant, TGW: thousand grain-weight, DTM: days to maturity, DTF: days to flowering and GY: grain yield.

Coefficients of Correlation Analysis

The association among the physiological and yield-attributing traits was calculated through a correlation study concerning them (Table 6). The GY was positively correlated with PH, NTH, ETH, PL, FG, UFG, TGW, DTM and negatively correlated with DTF and NETH. Among the traits, GY has a positive significant correlation with ETH, PL, FG, and UFG and simultaneously, a negative significant correlation with DTF and NETH.

Table 6. Coefficients of correlations among diverse yield attributing characters of six rice genotypes.

Traits	**PH**	**DTF**	**DTM**	**NTH**	**ETH**	**NETH**	**PL**	**FG**	**UFG**	**TGW**
DTF	-0.321***									
DTM	-0.126	0.918***								
NTH	-0.162	-0.001	-0.037							
ETH	0.001	-0.156	-0.121	0.790***						
NETH	-0.261**	0.226*	0.118	0.450***	-0.192*					
PL	0.332***	-0.127	0.042	-0.115	0.170	-0.431***				
FG	-0.021	0.155	0.312***	0.189*	0.392***	-0.269**	0.435***			
UFG	0.106	0.441***	0.519***	-0.008	0.132	-0.205*	0.389***	0.480***		
TGW	0.251**	-0.438***	-0.391***	-0.084	-0.275**	0.266**	-0.289***	-0.478***	-0.444***	
GY	0.091	-0.205*	0.006	0.055	0.192*	-0.191*	0.394***	0.526***	0.205*	0.011

Path Coefficient Analysis of the Concerned Traits

Determining the direct and indirect effects allowing for ten characters viz. PH, DTM, NTH, ETH, NETH, DTF, PL, FG, UFG, and TGW, the path coefficient analysis was performed utilizing a correlation coefficient. The traits PH, DTM, NTH, ETH, PL, FG, UFG, and TGW had positive direct effects on GY (Table 7). The high values of direct positive effects of FG (0.526) displayed a highly significant positive correlation and this trait contributed the maximum for GY. Besides, the direct effects of other considered characters on grain yield were optimistic, resilient, and significant for the characters like PL (0.394), UFG (0.205), and ETH (0.192). In contrast, a negative direct influence on grain yield per plant was exercised by NETH (-0.191) and DTF (-0.205).

Table 7. Partitioning of phenotypic correlations into direct and indirect influences of ten important traits by path analysis.

Traits	**PH**	**DTM**	**NTH**	**ETH**	**NETH**	**DTF**	**PL**	**FG**	**UFG**	**TGW**	**Correlation to GY**
PH	-0.382	-0.481	0.157	0.000	-0.170	0.892	0.046	-0.006	0.003	0.031	0.091
DTM	0.092	**2.005**	0.137	-0.268	0.131	-2.196	-0.021	0.009	0.009	-0.037	0.006
NTH	0.061	-0.281	**-0.979**	0.729	0.294	0.206	-0.015	0.056	0.000	-0.010	0.055
ETH	0.000	-0.581	-0.774	**0.923**	-0.124	0.641	0.024	0.114	0.003	-0.035	0.192*
NETH	0.099	0.401	-0.441	-0.175	**0.654**	-0.618	-0.059	-0.079	-0.005	0.034	-0.191*
DTF	0.149	1.924	0.088	-0.258	0.176	**-2.288**	-0.036	-0.020	0.007	-0.042	-0.205*
PL	-0.126	-0.301	0.108	0.157	-0.281	0.595	**0.138**	0.126	0.010	-0.036	0.394***
NFG	0.008	0.060	-0.186	0.360	-0.176	0.160	0.059	**0.292**	0.013	-0.060	0.526***
NUFG	-0.042	0.682	0.010	0.120	-0.131	-0.595	0.054	0.140	**0.027**	-0.055	0.205*
TGW	-0.095	-0.601	0.078	-0.258	0.176	0.778	-0.040	-0.140	-0.012	**0.125**	0.011
Residual Effect = 0.421											

*, **, and *** indicate significance at 5%, 1%, and 0.1% levels, respectively. Bold figures indicate the direct influence.

DISCUSSION

Success in crop breeding programmes is largely determined by genetic variability and the transmission of desired traits. Exploring the genetic variability, and trait associations of a species with the intervention of plant breeders may result in the improvement of desired varieties. The grain yield is a complicated product affected by many interdependent quantitative characters. Plant breeders have a blueprint for selection if they understand how other traits affect yield and how genetic and non-genetic components interact.

Explanation of quantitative traits for crop improvement

The assessment of genotypic and environmental variances provided valuable insights into the underlying factors influencing the observed trait variations. Notably, the genotypic variance exceeded environmental variance at the mean level, excluding the NTH with $\sigma^2g=5.20$ and $\sigma^2p=8.05$. This suggests a predominant genetic influence on the traits under investigation, highlighting the significance of genetic factors in determining phenotypic expressions. The GCV and PCV values further elucidated the variability within the studied traits. Substantial variations were observed, with GCV ranging from 14.00% for DTM to 160.43% for NETH, and PCV ranging from 14.12% for DTM to 180.37% for NETH. Notably, traits such as GY, PH, ETH, NETH, FG, UFG, and TGW exhibited higher PCV and GCV values, indicating a greater potential for genetic improvement in these traits. Conversely, DTM, DTF, and PL displayed lower GCV and PCV values, suggesting a comparatively lower genetic variability in these traits. The outcomes described by Sravan *et al.* (2012) and Karim *et al.* (2007) comply with the very low alteration between PCV and GCV, which indicates that the environment has little influence on the manifestation of the trait or that genotypes are less sensitive to the environment. The findings from earlier studies (Bitew, 2016; Hossain *et al.,* 2015) are consistent with the findings of our investigation, demonstrating that ecological influence is not discernible in the expression of phenotypic traits. As a result, features with lesser fluctuation by the environment and choice attributed to the phenotype reasonably than the genotype may be suitable for improving such potentials (Karad and Pol, 2008). Studies have also shown that on the part of generating high-yielding cultivars over and done with hybridization and selection, cultivars with high GCV of yield-contributing traits are essential. The characters' having high and low PCV with GCV differences reveal their vulnerability to environmental change and their differential influence with it. The PCV and GCV values of more than 20% are high, less than 10% are low, and 10% to 20% are considered medium, according to Girma *et al.* (2018). According to Bose *et al.* (2007), a high level of GCV results in varied offspring in the segregating generations. For the parameters, FG, test weight, and yield, the degree of PCV and GCV were moderate to high (Roy *et al.,* 2001; Thirumala *et al.,* 2014). For FG, test weight and yield. Thirumala *et al.* (2014) once more reported high PCV. The PCV and GCV were moderate to high (Lingaiah *et al.,* 2014).

The heritability estimates provided further insights into the genetic control of the traits, with TGW, DTM, DTF, PH, PL, GY, FG, and UFG demonstrated heritability estimates exceeding 80%. NETH showed moderately high heritability (60-79%), while ETH exhibited a moderate broad-sense heritability estimate (40-59%), and NTH showed low heritability (<39%). These findings underscore the potential for successful selection for breeding programs, particularly for traits with high heritability. In this study, the poor heritability of NTH (39.25%) was attributed to the substantial environmental influence on this character expression. Genetic advance as a percentage of the mean values indicated substantial genetic variability, with NETH exhibiting the highest GAM (293.94), followed by UFG, FG, TGW, and PH. These values suggest ample scope for genetic improvement through selection. The heritability assessments besides GA can be suitable for calculating the effect of selection in a breeding programmes. Vaithiyalingan and Nadarajan (2006) stated that the traits viz. NGP (number of grains per plant), test weight, yields, and PH revealed a high level of GA as a percent of the mean. Lingaiah *et al.* (2014) stated that high heritability united with high GAM for the traits' number of grains per panicle, TGW, and yield representing the role of the additive genes in leading these characters. The PH, seeds per plant, and number of spikelets per panicle demonstrated high heritability in combination with high to moderate GAM, representing the preponderance of additive gene action in the development of these features (Yadav *et al.,* 2011). According to the current study's findings of higher heritability and high GAM, selection would be successful because of additive gene action in the expression of character (Hossain *et al.,* 2015).

Therefore, the comprehensive analysis of genotypic and environmental variances, along with GCV, PCV, heritability, and genetic advance values, provides a robust foundation for understanding the genetic basis of the studied traits. The identified traits with high heritability and substantial genetic variability offer promising avenues for targeted breeding efforts aimed at enhancing rice cultivars.

Principal component analysis (PCA)

For six varieties 11 principal components emerged as a robust method for summarizing information from a large dataset for explaining the varietal traits where the cumulative proportion of variation ranged from 88% to 100%. However, cumulative variance with maximum variability for three major PCs was stated by Basavaraj *et al.* (2022). Neeru *et al.* (2016) also acknowledged 11 principal components (PCs) which explained about 75% variability in mustard.

The analysis revealed that PC1 played a prominent role, exhibiting the largest standard deviation (267.95) and accounting for 88% of the total variance (Table 4). Rahangdale *et al.* (2021) and Debsharma *et al.* (2024) reported a maximum variation percentage in PC1 in their study on 67 rice lines. Similar findings were reported by Shivani *et al.* (2021), Manohara *et al.* (2020), and Sahu *et al.* (2016).

This signifies the dominance of PC1 in capturing the overall variability in the dataset (Table 4). Examining the loadings within PC1 provided valuable insights into the information encapsulated by this principal component. The variable FG displayed a high negative coefficient (-0.97), while UFG had a low negative coefficient (0.23); suggesting that PC1 primarily captures information related to the contrast between filled and unfilled grains. This aligns with the notion that PC1 serves as a key indicator of grain characteristics. Moving to PC2, the presence of notable positive coefficients for DTF, DTM, and UFG implies an association with the timing of growth stages and the occurrence of unfilled grains. This suggests that PC2 may provide insights into the temporal aspects of plant development, particularly regarding grain filling. The subsequent principal components (PC3 to PC11) further contributed to the understanding of specific patterns or relationships among the variables (Table 5). Similar findings were observed by Kishore et al. (2007), and Babar et al. (2009). Using path analysis, the eight traits were estimated to contribute 58 percent of grain yield variability where the residual influence was 0.42.

Coefficients of correlation for the studied associated traits

Positive correlations were observed between GY and PH, NTH, ETH, PL, FG, UFG, TGW, and DTM; while negative correlations were noted with DTF and NETH. Specifically, GY exhibited significant positive correlations with ETH, PL, FG, and UFG, concurrently displayed significant negative correlations with DTF and NETH among the studied traits. These findings highlight the interconnectedness of physiological attributes and yield-related characteristics, providing valuable insights into the complex relationships that influence overall grain yield. The positive associations suggest that enhancements in certain traits, such as ETH, PL, FG, and UFG, may contribute positively to grain yield, while negative correlations with DTF and NETH indicate potential trade-offs that need consideration in breeding or management strategies (Table 6). In the correlation coefficient among the grain yield per plant and additional measurable characters contributing to yield, Yadav *et al.* (2011) found that the GY was significantly and positively related to the NTH, PH, the number of panicles per plant, the number of spikelets per panicle and TGW at in cooperation to genotypic and phenotypic levels. According to Debsharma et al. (2020) and Eidikohnaki et al. (2013), there is a significant positive association between ETH and GY. The positive connection of GY with filled grains per panicle was reported by Perween *et al.* (2020) and Eidikohnaki *et al.* (2013). These mentioned research results are similar to the current study.

Path coefficient analysis of the studied associated traits

Plant breeders have utilized path analysis in agriculture to help them uncover features to increase crop yield which is the most important trait for the crop breeders (Milligan *et al.,* 1990). In this analysis, the direct and indirect stimuli on grain yield were examined. Based on these studied associated traits, the selection efficiency might be improved where it expedites the selection process and save time and money. By exploiting variable cultivars and retaining effective selection practices to enhance yield through yield traits, breeding initiatives attempt to raise rice production. Correlation analysis is a crucial step in determining the association between the yield and yield-contributing traits but path analysis, which separates a trait's influence into direct and indirect influences, is even more vital for the choice of yield-contributing traits (Dhavaleshvar *et al.,* 2019). According to Yadav *et al.* (2011), NTH, PL, NSP, and PH are the primary factors that affect yield since they have a direct beneficial impact on seed production per hill. According to Satheeshkumar and Saravanan (2012), path analysis demonstrated the greatest direct benefits for kernel length, FG, total grains produced, and ETH. Positive direct influences and correlation coefficients suggested that choice for these characters could be used to increase yield. Makwana *et al.* (2010) observed similar findings. The current study found that DTM, ETH, PL, FG, UFG, and TGW traits should be considered in choosing the genotypes for increased GY of rice is crucial. The top-most significant characters that directly contributed to GY are the DTM, ETH, PL, FG, UFG, and TGW, according to the findings of correlation and path analysis.

CONCLUSION

The studied genotypes possess promising characteristics and have the potential to be integrated into the breeding of diversified rice cultivars for the hilly ecosystem of Bangladesh. The PCV was observed to be marginally greater than the GCV indicating the minimum influence of the environment on the expression of the traits. The existence of additive genetic mechanisms and negligible environmental effects, as evidenced by the high heritability combined with a high GAM and genotypic correlation coefficients that were superior to their phenotypic correlation coefficients, further enhances inherent genetic associations. Therefore, it is advisable to choose these genetic parameters as a high priority in selection for further development, which could be utilized in future rice breeding programmes for the hilly areas.

AUTHORS' CONTRIBUTIONS

R.G.: Design, formulation, and supervision of experiment, writing of manuscript, performing the field and collection and analysis of data. S.K.D.: Analysis of data and writing of the manuscript. N.J.: writing of the manuscript. M.H. R.: supervision of experiment, and review of manuscript.

DECLARATION OF INTERESTS

The authors have declared that no competing interest exists.

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REFERENCES

Ahmed, M S, S Parveen, M H K Baktiar and M A Siddique. 2015a. Study of qualitative agro-morphological characters of Dhaliboro rice germplasm. *Journal of Eco-friendly Agriculture,* 8(8): 91-96.

Ahmed, M S, S Parveen, M Z Islam and M A Siddique. 2015b. Characterization of Dhaliboro rice (*Oryza sativa* L.) germplasm of Bangladesh for morpho-physicochemical traits. *International Journal of Biological Research,* 19(1): 1-11.

Ahmmed, S, M Jahiruddin, M R Sultana, R R A Begum, R A J C Biswas and J C A S M M Rahman. 2018. Fertilizer Recommendation Guide. *Bangladesh Agricultural Research Council (BARC)*, Farmgate, Dhaka, 01-223.

Akter, N, H Begum, M Z Islam, M A Siddique and M Khalequzzaman. 2018. Genetic diversity in Aus rice (*Oryza sativa* L.) genotypes of Bangladesh. *Bangladesh Journal of Agricultural Research,* 43(2): 253-266. DOI: https://doi.org/10.3329/bjar.v43i2.37329

Akter, N, M Z Islam, A Bhuiyan, M A Siddique and M Khalequzzaman. 2017. Distinctness of 45 irrigated rice (*Oryza sativa* L.) landraces of Bangladesh through agro-morphological traits. *Journal of Eco-friendly Agriculture,* 10(7): 100-107.

Akter, N, M Z Islam, M A Siddique, T Chakrabarty, M Khalequzzaman and M A Z Chowdhury. 2016. Genetic diversity of Boro rice (*Oryza sativa* L.) landraces of Bangladesh. *Bangladesh Journal of Plant Breeding and Genetics,* 29(2): 33-40. DOI: https://doi.org/10.3329/bjpbg.v29i2.33948

Babar, M, A A Khan, A Arif, Y Zafar and M Arif. 2009. Path analysis of some leaf and panicle traits affecting grain yield in double haploid lines of rice (*Oryza sativa* L.). *Bangladesh Journal of Agricultural Research,* 45 (4):245-252.

Baktiar, M H K, M A Samad, M Khalequzzaman, N Sharma and M A Siddique. 2013. Morphological characterization of local Aus rice germplasm (*Oryza sativa* L.). *Journal of Eco-friendly Agriculture,* 6(10): 238-242.

Banik, S, M Z Islam, M A Haque, M A Siddique, A Mallik and M A Siddiquee. 2012. Physico-chemical properties based genetic diversity of T. Aman rice genotypes. *Journal of Eco-friendly Agriculture,* 5(7): 69-72.

Basavaraj, P S, C Gireesh, M Bharamappanavara, C A Manoj, L V G Ishwaryalakshmi, P Senguttuvel, R M Sundaram, L V Subbarao and M S Anantha. 2022. Genetic analysis of introgression lines of *Oryza rufipogon* for improvement of low phosphorous tolerance in indica rice. *Indian Journal of Genetics and Plant Breeding,* 82(2): 135-142. DOI: https://doi.org/10.31742/IJGPB.82.2.1

BBS (Bangladesh Bureau of Statistics). 2019. 45 Years Agriculture Statistics of Major Crops (Aus, Amon, Boro, Jute, Potato & Wheat). Bangladesh Bureau of Statistics. Ministry of Planning, Government of the People's Republic of Bangladesh, Dhaka, Bangladesh. http://www.bbs.gov.bd/site/page/453af260-6aea-4331-b4a5-7b66fe63ba61/Agriculture

Biswash, M R, M Sharmin, N M F Rahman, T Farhat and M A Siddique. 2016. Genetic diversity in modern T. Aman rice varieties of Bangladesh (*Oryza sativa* L.). *Sains Malaysiana*, 45(5): 709–716. Available at: http://www.ukm.my/jsm/pdf_files/SM-PDF-45-5-2016/06%20M.R.%20Biswash.pdf

Bitew, J M. 2016. Estimation of genetic parameters, heritability and genetic advance for yield related traits in upland rice (*Oryza sativa* L. and *Oryza glaberrima* Steud) genotypes in northwestern Ethiopia. *World Scientific News,* 47(2): 340-350.

Bose, L K, S Das, S K Pradhan, H Subudhi, S Singh and O Singh. 2007. Genetic variability of quality characters and grain yield in lowland rice genotypes of Eastern India. *Korean Journal of Breeding Science,* 39(1): 1-6.

Burton, G W and D E Devane. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal,* 45(10): 478-481. DOI: https://doi.org/10.2134/agronj1953.00021962004500100005x

Byerlee, D and J Fanzo. 2019. The SDG of zero hunger is 75 years on Turning full circle on agriculture and nutrition. *Global Food Security,* 21: 52-59. DOI: https://doi.org/10.1016/j.gfs.2019.06.002

Debsharma, S K, M A Syed, M H Ali, S Maniruzzaman, P R Roy, M Brestic, A Gaber and A Hossain. 2022. Harnessing on Genetic Variability and Diversity of Rice (Oryza sativa L.) Genotypes Based on Quantitative and Qualitative Traits for Desirable Crossing Materials. *Genes,* 14:10. DOI: https://doi.org/10.3390/genes14010010

Debsharma, S K, R F Disha, M M E Ahmed, M Khatun, M Ibrahim, and T L Aditya. 2020. Assessment of Genetic Variability and Correlation of Yield Components of Elite Rice Genotypes (*Oryza sativa* L.). *Bangladesh Rice Journal,* 24(1): pp.21-29. DOI: https://doi.org/10.3329/brj.v24i1.53237

Debsharma, S K, Rahman M A, Khatun M, Disha R F, Jahan N, Quddus M R, Khatun H, Dipti S S, Ibrahim M, Iftekharuddaula, K M, Kabir, M S. 2024. Developing climate-resilient rice varieties (BRRI dhan97 and BRRI dhan99) suitable for salt-stress environments in Bangladesh. *PLoS ONE.* 19;19(1):e0294573. DOI: https://doi.org/10.1371/journal.pone.0294573

Dhavaleshvar, M, C Malleshappa and B M Dushyanth-Kumar. 2019. Variability, correlation and path analysis studies of yield and yield attributing traits in advanced breeding lines of rice (*Oryza sativa* L.). *International Journal of Pure & Applied Bioscience,* 7(1): 267-273.

DOI: http://dx.doi.org/10.18782/2320-7051.7308

Eidi kohnaki, M, G Kiani and G Nematzadeh. 2013. Relationship between Morphological Traits in Rice Restorer Lines at F3 Generation using Multivariate Analysis. *International Journal of Advanced Biological and Biomedical Research,* 1(6): 572-577. DOI: 10.26655/ijabbr.2017.9.1

Girma, B T, M A Kitil, D G Banje, H M Biru, and T B Serbessa. 2018. Genetic variability study of yield and yield-related traits in rice (*Oryza sativa* L.) genotypes. *Advances in Crop Science and Technology,* 6(4): 381. DOI: 10.4172/2329-8863.1000381

Govintharaj, P, T Shalini, S Manonmani and S Robin. 2016. Estimates of genetic variability, heritability and genetic advance for blast resistance gene introgressed segregating population in rice. *International Journal of Current Microbiology and Applied Sciences,* 5(12): 672-677. DOI: http://dx.doi.org/10.20546/ijcmas.2016.512.075

Gupta, R, M Faruquee and M J Sarkar. 2022. Performance of high yielding boro rice varieties in Khagrachhari district of Bangladesh. *International Journal of Agricultural Technology,* 18(5):1961-1972. Available at: http://www.ijat-aatsea.com/pdf/v18_n5_2022_September/6_IJAT_18(5)_2022_Gupta,%20R..pdf

HIES (Household Income and Expenditure Survey). 2016. Bangladesh Bureau of Statistics. Government of Bangladesh, Dhaka. Available at: http://bbs.portal.gov.bd/sites/default/files/files/bbs.portal.gov.bd/page/b343a8b4_956b_45ca_872f_4cf9b2f1a6e0/HIES%20Preliminary%20Report%202016.pdf

Hossain, S, M Haque and J Rahman. 2015. Genetic variability, correlation and path coefficient analysis of morphological traits in some extinct local Aman rice (*Oryza sativa* L). *Rice Research: Open Access,* 3(158): 2. DOI: 10.4172/2375-4338.1000158

Islam, M Z, M A Siddique, E S M H Rashid, M S Ahmed and M Khalequzzaman. 2014. Genetic diversity in Sadajira rice (*Oryza sativa* L.) germplasm. *The Agriculturists* 12(1): 26-32. DOI: https://www.cabidigitallibrary.org/doi/pdf/10.5555/20143294021

Islam, M Z, M A Siddique, N Akter, M F R K Prince, M R Islam, M Anisuzzaman and M A K Mian. 2019. Morpho-molecular divergence of restorer lines for hybrid rice (*Oryza sativa* L.) development. *Cereal Research Communications,* 47(3): 531–540. DOI: https://doi.org/10.1556/0806.47.2019.29

Islam, M Z, M Khalequzzaman, M A Siddique, N Akter, M S Ahmed and M A Z Chowdhury. 2017. Phenotypic characterization of jhum rice (*Oryza sativa* L.) germplasm collected from Rangamati district in Bangladesh. *Bangladesh Rice Journal,* 21(1): 47-57. DOI: https://doi.org/10.3329/brj.v21i1.37382

Islam, M Z, N Akter, T Chakrabarty, A Bhuiya, M A Siddique and M Khalequzzaman. 2018. Agro-morphological characterization and genetic diversity of similar named Aromatic rice (*Oryza sativa* L.) landraces of Bangladesh. *Bangladesh Rice Journal,* 22(1): 45-56. DOI: https://doi.org/10.3329/brj.v22i1.41836

Karad, S R and K M Pol. 2008. Character association, genetic variability and path coefficient analysis in rice (Oryza sativa L.). *International Journal of Agricultural Sciences,* 4(2): 663-666.

Karim, D, U Sarkar, M N A Siddique, M K Miah and M Z Hasnat. 2007. Variability and genetic parameter analysis in aromatic rice. *International Journal of Sustainable Crop Production,* 2(5): 15-18. Available at:

https://ggfjournals.com/assets/uploads/4.15-18_.pdf

Khalequzzaman, M, M A Siddique and M K Bashar. 2012. Rice genetic resources conservation and utilization in Bangladesh. *Genetic Resources and Seed Division*, Gazipur, Bangladesh, 50-60.

Khalequzzaman, M, T Chakrabarty, M Z Islam, E S M H Rashid, M F R K Prince and M A Siddique. 2022. Assessment of mean performance, variability, traits association and path coefficient in transplanted Aman rice (*Oryza sativa* L.) landraces. *Asian Journal of Biology*, 16 (4): 27-39. DOI: 10.9734/ajob/2022/v16i4308

Khalequzzaman, M, T Chakrabarty, M Z Islam, E S M H Rashid, M F R K Prince and M A Siddique. 2023. Deciphering genetic variability, traits association, correlation and path coefficient in selected Boro rice (*Oryza sativa* L.) landraces. *Asian Journal of Biology*, 19(2): 33-45. DOI: 10.9734/ajob/2023/v19i2361

Kishore, N S, N A Ansari, V R Babu, N S Rani, L V Rao and R Subba. 2007. Correlation and path analysis in aromatic and non-aromatic rice genotypes. *Agricultural Science Digest,* 27:2.

Kulsum, M U, M J Hasan, M A Siddique, F Begum and Z Akond. 2015. Genetic diversity in selected rice genotypes (*Oryza sativa* L.). *Bangladesh Journal of Agriculture,* 38-40: 63-72.

Lingaiah, N, V Venkanna and C Cheralu. 2014. Genetic variability analysis in rice (*Oryza sativa* L.). *International Journal of Pure & Applied Bioscience,* 2(5): 203-204. Available at: https://www.ijpab.com/form/2014%20Volume%202,%20issue%205/IJPAB-2014-2-5-203-204.pdf

Makwana, B P, G C Jadeja, C G Patel, R M Patel and R A Gami. 2010. Path analysis of qualitative and quantitative characters in slender grain rice (*Oryza sativa* L.) *International Journal of Plant Sciences,* 5(1):294-296. Available at: http://researchjournal.co.in/upload/assignments/5_294-296.pdf

Manohara, K K, Morajkar S and Shanbagh, Y. 2020. Genetic analysis of grain yield and its associated traits in diverse salt-tolerant rice genotypes under coastal salinity conditions. *Journal of Cereal Research,* 12(3):290–296. Available at: https://epubs.icar.org.in/index.php/JWR/article/view/105442

Milligan, S B, K A Gravois, K P Bischoff and F A Martin. 1990. Crop effects on genetic relationships among sugarcane traits. *Crop Science,* 30(4): 927-931. DOI: https://doi.org/10.2135/cropsci1990.0011183X003000040034x

Mottaleb, K A, A Hossain and M I Hossain. 2020. Agriculture on the rise in Bangladesh: The future role of value chains. *In. Transforming Agriculture in South Asia*, Routledge, 30-48.

Muthayya, S, J D Sugimoto, S Montgomery and G F Maberly. 2014. An overview of global rice production, supply, trade, and consumption. *Annals of the New York Academy of Sciences*, 1324(1): 7-14. DOI: https://doi.org/10.1111/nyas.12540

Muti, S A A, M I Hoque, M M Islam, M A Siddique and M S Islam. 2020. Morpho-molecular characterization and screening of rice (*Oryza sativa* L.) genotypes for salinity tolerance at seedling stage. *SAARC Journal of Agriculture,* 18(2): 1-15. DOI: https://doi.org/10.3329/sja.v18i2.51104

Neeru N K, R Avtar and A Singh. 2016. Evaluation and classification of Indian mustard (Brassica juncea L.) genotypes using principal component analysis. *Journal of Oilseed Brassica.* 1(1):167-174. DOI: https://www.cabidigitallibrary.org/doi/pdf/10.5555/20153179334

Rahangdale, S, Singh Y, Upadhyay P and Koutu G. 2021. Principal component analysis of JNPT lines of rice for the important traits responsible for yield and quality. *Indian*

Journal of Genetics and Plant Breeding, 81(1):127-131. DOI: 10.31742/IJGPB.81.1.14.

Roy, B. 2001. Genetic variability in yield components of rice (*Oryza sativa)*. *Environment and Ecology,* 19(1): 186-189.

Sahu, H, Saxena R R, Verulkar S B and Rawte S. 2016. Association, principal component and genetic divergence study in recombinant inbred lines (RIL's) population of rice. *International Journal of Bio-resource and Stress Management,* 7(4): 673–681. Available at: https://ojs.pphouse.org/index.php/IJBSM/article/view/948

Satheeshkumar, P. and K. Saravanan (2012). Genetic variability, correlation and path analysis in rice (Oryza sativa L.). *International Journal of Current Research,* 4(9): 82-85.

Shivani, D, Neeraja C N, Cheralu C and Shankar V G. 2021. Multivariate analysis and character association studies for yield and nutritional characters in Swarna and type 3 RIL population of rice (*Oryza sativa* L.). *Journal of Cereal Research,* 13(2): 180–187. Available at: https://epubs.icar.org.in/index.php/JWR/article/view/113440

Siddique, M A, M Khalequzzaman, M Z Islam, M H K Baktiar and M S Ahmed. 2016. Genetic diversity assessment of quantitative traits in landraces of Aus rice. *Bangladesh Journal of Plant Breeding and Genetics,* 29(2): 17-24.

Siddique, M A, M Khalequzzaman, M Z Islam, M S Ahmed and E S M H Rashid. 2013. Genetic diversity in local Boro rice (*Oryza sativa* L.) genotypes of Bangladesh. *Bangladesh Journal of Plant Breeding and Genetics,* 26(1): 19-24.

Siddique, M A, M Z Islam, M Khalequzzaman and A Bhuiya. 2018. Agro-Morphological characterization of geographical indication rice cultivars grown in Bangladesh. *The Experiment,* 45(4): 2598-2610.

Siddique, M A, M Z Islam, M Khalequzzaman and M S Ahmed. 2011. Genetic diversity in rice (*Oryza sativa* L.) landraces of hilly areas in Bangladesh. *Bangladesh Journal of Plant Breeding and Genetics,* 24(2): 25-30.

Singh, B D. 2015. Plant breeding: principles and methods. Kalyani Publishers, India.

Sravan, T, N R Rangare, B G Suresh and S R Kumar. 2012. Genetic variability and character association in rainfed upland rice (*Oryza sativa* L.). *Journal of Rice Research,* 5(1): 2.

Team, R. 2017. R Studio: Integrated Development for R. http://www.rstudio.com/.

Thirumala, R V, M Y Chandra, D Bhadru, D Bharathi and V Venkanna. 2014. Genetic Variability and Association Analysis in Rice. *International Journal of Applied Biology and Pharmaceutical Technology,* 5(2): 63-65.

Vaithiyalingan, M and N Nadarajan. 2006. Genetic variability, heritability and GA in F2 population of inter sub-specific crosses of rice. *Crop Research,* 31(3): 476-477.

Yadav, S, B Suresh, P Pandey and B Kumar. 2011. Assessment of genetic variability, correlation and path association in rice (*Oryza sativa* L.). *Journal of Bio-Science,* 18: 1–8. DOI: 10.3329/jbs.v18i0.8767