Genetic Variability and Inter-relationship between Yield and Yield Components in Jhum Rice (Oryza sativa L.) Genotypes of Khagrachhari District in Bangladesh

Mohammad Zahidul Islam*, Nadia Akter, Md. Ferdous Rezwan Khan Prince, Nashirum Monir and Mohammad Khalequzzaman

Genetic Resources and Seed Division, Bangladesh Rice Research Institute (BRRI), Bangladesh

*Corresponding author and Email: zahid.grs@gmail.com

Received: 20 March 2020  Accepted: 25 June 2020

Abstract

The present investigation consists of 47 rice genotypes and the experiment was conducted during Aus season, 2016 in Randomized Block Design with three replications. The data were recorded for 13 quantitative characters to study genetic variability, heritability, genetic advance, correlation coefficient analysis and path analysis. Analysis of variance among 47 genotypes showed a significant difference for all characters studied. The highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for grain yield followed by the number of effective tillers, the number of filled grains per panicle and 1000 grain weight indicating that these characters could be used in selection for the crop improvement program. High estimates of heritability was observed for grain yield, grain length, plant height, number of filled grain per panicle, 1000 grain weight and days to 50% flowering. High genetic advance was observed for the number of filled grains per panicle and plant height, indicating predominance of additive gene effects and possibilities of effective selection for the improvement of these traits. Grain yield showed positive association with number of effective tiller and number of filled grain per panicle at genotypic in conjunction with phenotypic level. Days to maturity possessed the highest positive direct effect and significant indirect correlation with yield.

Keywords: Genetic variability, heritability, path co-efficient and rice (Oryza sativa L.)

1. Introduction

Rice is a major food source for more than half of the world’s population. Rice is also the major crop of Bangladesh. This crop plays an important role in feeding the huge population of the small country. Rice yield improvement is a priority to meet its rising demand owing to a constant increase in population. Considering this context, assessment of variability in rice crop for grain yield and yield attributes is essential for successful exploitation and improvement of yield through effective breeding.

Jhum rice is a unique kind of plant genetic resource which is cultivated through hilly areas of Bangladesh. The local farmers usually grow low yielding local landraces. More than 300 local jhum rice landraces have been collected from various hilly districts of Bangladesh and conserved in Bangladesh Rice Research Institute (BRRI) genebank (Islam et al., 2017). Further,
grain yield depends on various component characters and knowledge of correlations among yield component traits and yield is of great importance in the selection of elite genotypes for breeding program. Path analysis also helps in determining the direct and indirect causes of association and formulation of effective breeding strategies for the development of better genotypes (Sameera et al., 2016).

The existence of variability in germplasm provides the basis for selection of elite germplasm that may be used either as an end product in form of improved variety or can be used as starting material in several breeding program intended to accomplish diverse objectives (Singh et al., 2017). Genetic parameters such as GCV and PCV are the extent of genetic variation present in germplasm and the extent to which genotype is influenced by the environment. Heritability along with genetic advance reflects the reliability of the transmission of trait variation to the next generation. Genotypic correlation among grain quality trait is an indicator of stable association between traits and helps in indirect selection.

2. Materials and Methods

2.1 Plant materials, experimental site and experimental design
Forty seven jhum rice genotypes were collected from Khagrachhari district of Bangladesh were grown under during Aus season 2016. The experiment was conducted following a Randomized Complete Block design with three replicates for each treatment at the experimental field of BRRI, Gazipur. Geographically, the place is located at about 23° 59' 35.8” N latitude and E 90.24’ 27” E longitude with an elevation of 15 meters from the sea level and is characterized by subtropical climate. The soil of the experimental site was clay loam in texture.

2.2 Transplantation and management practices
Twenty days-old seedlings from each entry were transplanted using single seedling per hill in 2.4 m² plot with 25cm and 20cm space between rows and plants, respectively. Fertilizers were applied @ 80:60:40:12 kg N: P: K: S h⁻¹. However, except N, the other fertilizers were applied at final land preparation. 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 performed as and when necessary.

2.3 Data collection
Five plants were randomly selected and were evaluated for yield and its component traits. The traits studied were: Flag leaf length (cm), flag leaf width (cm), culm diameter (mm), panicle length (cm), plant height (cm), days to flowering, days to maturity, effective tiller number (ET), panicle length (cm), 1000 grain weight (g), number of filled grains per panicle, grain length (mm), grain breadth (mm), and yield per hill (g) for 47 samples collected from different areas of Khagrachari (Table 1).

2.4 Statistical analysis
Genotypic and phenotypic co-efficient of variation were calculated following the methodology delineated by Burton (1952), while the estimates of heritability and genetic advance were computed as per the procedures elaborated by Burton and Devane (1953) and Johnson et al. (1955), respectively. Normal Pearson’s correlation and path coefficient analysis was undertaken using R software (version 3.2.1). Furthermore, genotypic and phenotypic correlation co-efficients were calculated with Multi Environment Trait Analysis with R (META-R) software.

3. Results and Discussion
Information on mean, range, PCV, GCV, heritability, genetic advance and genetic, advance in percent of mean for yield and yield component traits are presented in Table 2. The relative values of genotypic and phenotypic coefficient of variation provide important information on the magnitude of variation. Higher phenotypic co-efficient of variation
compared to genotypic co-efficient of variation was recorded for all the traits studied in the present investigation, indicating the influence of the environment. Similar findings were reported earlier by Islam et al. (2016) and Aker et al. (2018a).

A wide range of phenotypic coefficient of variation (5.74% - 32.77%) and genotypic coefficient of variation (5.68% - 30.76%) was observed for the traits studied. Besides, highest (32.77%) phenotypic co-efficient of variation for grain yield in the present investigation was noticed to be closely and essentially associated with high genotypic co-efficient of variation for the trait, demonstrating the little influence of environment and presence of high genetic variability for the trait in the experimental material. Hence, selection on the basis of phenotype in these genotypes can also be effective for the improvement of grain yield. Similar results were reported earlier by Mishra and Verma (2002). However, moderate (16-30%) genotypic and phenotypic coefficients of variation were recorded in the present study for 1000 grain weight, number of filled grains per panicle and number of effective tiller. These results are in partial conformity with the findings of Bornare et al. (2014) for no. of effective tiller and 1000 grain weight. In contrast, low (<10%) estimates of genotypic and phenotypic coefficients of variation were observed in the present study for plant height, panicle length, days to 50% flowering and days to maturity indicating low variability for these characters in the present experimental material and therefore little scope for improvement of these traits.

Table 1. Information on local name and place of collection of 47 Jhum rice genotypes

| Sl. No. | Genotypes    | District   | Sl. No. | Genotypes    | District   |
|---------|--------------|------------|---------|--------------|------------|
| 1       | Kamarang (gol) | Khagrachhari | 25      | Maloty       | Khagrachhari |
| 2       | Binnidhan    | Khagrachhari | 26      | Binni Dhan   | Khagrachhari |
| 3       | Asasuri      | Khagrachhari | 27      | Kotoktara    | Khagrachhari |
| 4       | Banor binni  | Khagrachhari | 28      | Cholokka binni | Khagrachhari |
| 5       | Company (boro) | Khagrachhari | 29      | Kuttosa binni | Khagrachhari |
| 6       | Choroi (sada) | Khagrachhari | 30      | Galon (sada) | Khagrachhari |
| 7       | Suri dhan    | Khagrachhari | 31      | Ameo         | Khagrachhari |
| 8       | Company (gol) | Khagrachhari | 32      | Chamaful     | Khagrachhari |
| 9       | Bodakusum    | Khagrachhari | 33      | Churi dhan (sada) | Khagrachhari |
| 10      | Jakton binni | Khagrachhari | 34      | Binni dhan   | Khagrachhari |
| 11      | Kainchole    | Khagrachhari | 35      | Galon (Red)  | Khagrachhari |
| 12      | Binnidhan(lal) | Khagrachhari | 36      | Wasa         | Khagrachhari |
| 13      | Longapura binni | Khagrachhari | 37      | Galon (Red)  | Khagrachhari |
| 14      | Mala Dhan    | Khagrachhari | 38      | Full badam   | Khagrachhari |
| 15      | Choroi (lal) | Khagrachhari | 39      | Mashusai mokom | Khagrachhari |
| 16      | Pidi         | Khagrachhari | 40      | Solai        | Khagrachhari |
| 17      | Galon (lal)  | Khagrachhari | 41      | Nola binni   | Khagrachhari |
| 18      | Binni (sada) | Khagrachhari | 42      | Ameosori     | Khagrachhari |
| 19      | Kamarang     | Khagrachhari | 43      | Badia        | Khagrachhari |
| 20      | Galon (gol)  | Khagrachhari | 44      | Shailangma   | Khagrachhari |
| 21      | Modhu maloty | Khagrachhari | 45      | Kamarang     | Khagrachhari |
| 22      | Koborok      | Khagrachhari | 46      | Mongshe      | Khagrachhari |
| 23      | Hori binni   | Khagrachhari | 47      | Ameo dhan    | Khagrachhari |
| 24      | Company      | Khagrachhari |         |              |            |
Similar findings were reported earlier by Akter et al. (2018b) for panicle length, days to 50% flowering and days to maturity. High (>90%) estimates of heritability were recorded for all the traits studied excluding flag leaf length, culm diameter, panicle length and number of effective tiller in the present investigation (Table 2). Similar findings were reported earlier by Islam et al. (2018) and Islam et al. (2019).

These results are in conformity with the reports of Idris et al. (2013) for 1000-seed weight and plant height; Bisne et al. (2009) for ear bearing tillers per hill; Dhanwani et al. (2013) for days to 50 per cent flowering; Chakrabarty et al. (2019) for filled grains per panicle and Kundu et al. (2008) for grain yield per plant. A perusal of the results on genetic advance revealed the highest value (40.13%) on number of filled grain per panicle, moderate value (>10%) for plant height. The estimation of genetic advance in per cent of mean was also high (>20%) for number of effective tiller, number of filled grains per panicle, 1000 grain weight, grain length and grain yield. These results are in conformity with the findings of Babu et al. (2012) for the number of filled grains per panicle; and Dhanwani et al. (2013) for 1000 grain weight and grain yield per plant. Further, low (<5%) estimates of genetic advance were recorded in the present investigation for flag leaf width, culm diameter, panicle length, number of effective tiller, grain length, grain breadth and yield.

| Character | Mean | Range | V_p | V_g | PCV | GCV | h^2 | GA (5%) | GAPM |
|-----------|------|-------|-----|-----|-----|-----|-----|--------|------|
| FLL       | 41.88| 27.00-58.00 | 26.76 | 22.51 | 12.35 | 11.33 | 84.10 | 6.87 | 16.41 |
| FLW       | 1.80 | 1.20-2.40  | 0.07 | 0.05 | 13.25 | 12.65 | 90.23 | 1.34 | 19.10 |
| CD        | 4.91 | 3.38-6.10  | 0.49 | 0.37 | 13.23 | 12.47 | 88.85 | 0.91 | 18.58 |
| PL        | 28.79| 23.20-35.60| 5.75 | 4.06 | 7.57 | 7.00 | 85.43 | 2.94 | 10.22 |
| PH        | 121.44 | 94.00-147.00 | 95.91 | 94.26 | 9.02 | 7.99 | 91.31 | 15.29 | 12.59 |
| DF        | 92.22| 75.00-116.00| 45.62 | 44.84 | 7.32 | 7.26 | 93.30 | 9.49 | 11.38 |
| DM        | 118.52| 103.00-145.00 | 46.35 | 45.36 | 5.74 | 5.68 | 91.86 | 8.53 | 8.88 |
| ET        | 6.45 | 2.00-14.00  | 5.05 | 4.83 | 28.14 | 27.44 | 86.35 | 1.74 | 48.06 |
| TGW       | 22.30| 12.85-31.60 | 18.78 | 18.39 | 17.40 | 17.21 | 90.30 | 7.41 | 33.23 |
| FG        | 117.83| 47.60-189.00 | 1119.48 | 1103.88 | 28.40 | 26.20 | 94.61 | 40.13 | 37.24 |
| GL        | 8.79 | 6.45-11.68  | 1.46 | 1.35 | 14.74 | 13.70 | 95.45 | 1.90 | 21.59 |
| GB        | 3.04 | 2.32-3.84  | 0.15 | 0.12 | 11.54 | 11.16 | 93.50 | 0.52 | 17.05 |
| Y         | 5.90 | 2.19-12.30 | 6.36 | 6.23 | 32.77 | 30.76 | 91.97 | 3.98 | 47.55 |

V_p = Phenotypic variance, V_g = Genotypic variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, h^2 = Heritability (Broad sense), GA = Genetic advance, GAPM = Genetic advance in per cent of mean

(FLL= Flag leaf length, FLW= Flag leaf width, CD= Culm diameter, PL= Panicle length, PH=Plant height, DF= Days to 50% flowering, DM=Days to maturity, ET= Number of effective tiller, TGW=Thousand grain weight, FG= Number of filled grains per panicle, GL= Grain length, GB=Grain breadth, Y=Yield per hill)
Low (<15%) estimates of genetic advance in per cent of mean were also noticed for panicle length, plant height, days to 50% flowering and days to maturity in the present investigation. These results are in conformity with the findings of Seyoum et al. (2012). High heritability coupled with high genetic advance in per cent of mean was recorded for grain yield, number of filled grain per panicle, number of effective tiller and 1000 grain weight indicating that the high heritability observed due to additive gene effects and selection may be effective for these characters. Similar observations were reported by Adilakshmi and Girijarani (2012) for 1000-seed weight and Madhavilatha et al. (2005) for grain yield per plant.

Further, information on genetic variation along with heritability and genetic advance estimates has been reported to give a better idea about the efficiency of selection (Burton, 1952). In the present study, high GCV and PCV coupled with high heritability and high genetic advance in per cent of mean were observed for grain yield indicating the preponderance of additive gene action and therefore scope for improvement of the trait through selection. Similar results were reported earlier by Mohana Krishna et al. (2009).

The genotypic and phenotypic correlations for yield and yield components are showed in Table 3. Flag leaf width possessed positive association with culm diameter. Panicle length showed a highly significant and positive correlation with plant height (Rangare et al., 2012) both at genotypic and phenotypic levels. Moreover, days to 50% flowering had a highly significant positive correlation with culm diameter. Days to maturity also showed a significant positive correlation with culm diameter and days to 50% flowering. Furthermore, the number of effective tiller showed a negative association with flag leaf width, culm diameter, days to 50% flowering and days to maturity at genotypic as well as phenotypic level but showed positive association with plant height at the genotypic and phenotypic level.

Grain breadth has a negative but significant association with both days to 50% flowering and days to maturity; however, it showed a positive significant association with 1000 grain weight. In connection to that, 1000 grain weight possessed a negative correlation with the number of filled grains per panicle but had a positive significant association with grain length and grain breadth. The number of effective tiller and number of filled grain per panicle showed significant positive correlation with yield, but negatively significant association with grain length at genotypic along with phenotypic level. Hence, the number of effective tiller and filled grain per panicle should be given prior attention in rice improvement program because of their major influence on yield. This finding was in accordance with Hasan et al. (2010), Manikyaminnie et al. (2013), Sudharani et al. (2013), Idris et al. (2013) and Adilakshmi and Girijarani (2012).

Path coefficient analysis was done to partition the direct and indirect effects of different yield contributing traits on the yield of rice. Path coefficient analysis (Table 4) revealed that days to maturity possessed the highest positive direct effect on the yield that also made the indirect effect positive and significant. Grain length had a higher negative direct effect on yield, which also had negative indirect effect on total correlation. Moreover, the negative direct effect was observed for flag leaf width, days to flowering, effective tiller and plant height. On the other hand, the number of filled grains per panicle, 1000 grain weight and panicle length exhibited positive direct effect along with a positive correlation with yield.

The residual effect of the present study was 0.560 which indicated that 56% of the variability was accounted for 13 yield contributing traits included in the present investigation. The rest amount of variability might be controlled by other yield contributing traits that were not considered in the present study.
Table 3. Genotypic (rg) and phenotypic (rp) correlations among yield and yield contributing characters in Jhum rice genotypes

| Traits  | FLL  | FLW  | CD   | PL   | PH   | DF   | DM   | ET   | TGW  | FG   | GL   | GB   |
|---------|------|------|------|------|------|------|------|------|------|------|------|------|
|         | rg   | rp   | rg   | rg   | rg   | rg   | rg   | rg   | rg   | rg   | rg   | rg   |      |
|         | 0.167| 0.137| 0.247| 0.304*| 0.244*| 0.244*| 0.037| 0.007| -0.165|      |      |      |      |
| FLW     |      |      |      |      |      |      |      |      |      |      |      |      |      |
|         |      |      |      |      |      |      |      |      |      |      |      |      |      |
| CD      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| PL      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| PH      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| DF      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| DM      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| ET      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| TGW     |      |      |      |      |      |      |      |      |      |      |      |      |      |
| FG      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| GL      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| GB      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| Y       |      |      |      |      |      |      |      |      |      |      |      |      |      |

*, **Significant at 5% and 1% levels, respectively

(FLL= Flag leaf length, FLW= Flag leaf width, CD= Culm diameter, PL= Panicle length, PH=Plant height, DF= Days to 50% flowering, DM=Days to maturity, ET= Number of effective tiller, TGW=Thousand grain weight, FG= Number of filled grains per panicle, GL= Grain length, GB=Grain breadth, Y= Yield per hill)
Table 4. Partitioning of genotypic correlation into direct (bold phase) and indirect components of 47 genotypes of jhum rice

|       | FLL  | FLW  | CD   | PL   | PH   | DF   | DM   | ET   | TGW  | FG   | GL   | GB   | Y    |
|-------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| FLL   | 0.074| -    | -    | 0.002| 0.006| -    | 0.067| -    | 0.088| 0.009| 0.027| 0.003| 0.063| 0.009| -0.029|
| FLW   | 0.010| -    | 0.226| 0.010| 0.002| 0.003| -    | 0.009| -    | 0.013| 0.025| 0.043| -    | 0.072| 0.030| -0.260|
| CD    | 0.017| -    | 0.035| -    | -    | 0.009| -    | -    | 0.155| -    | 0.170| 0.020| -    | 0.043| 0.038| -0.087|
| PL    | 0.001| -    | 0.045| 0.127| 0.040| 0.007| -    | 0.009| -    | 0.010| 0.004| -    | 0.056| 0.078| 0.009| 0.200|
| PH    | 0.006| 0.009| 0.004| 0.075| -    | 0.068| -    | -    | 0.005| 0.023| 0.060| 0.064| 0.143| -    | 0.011| 0.109|
| DF    | 0.011| -    | 0.004| 0.045| -    | 0.004| -    | -    | 0.552| 0.022| 0.053| 0.065| -    | 0.023| 0.054| 0.050|
| DM    | 0.011| 0.005| 0.010| 0.002| -    | 0.001| 0.438| -    | 0.568| 0.022| 0.055| 0.055| -    | 0.027| 0.054| 0.740**
| ET    | 0.010| 0.085| 0.010| 0.019| -    | 0.023| 0.145| -    | 0.187| 0.068| 0.040| 0.015| 0.116| 0.003| 0.060|
| TGW   | 0.010| 0.048| 0.006| 0.003| 0.021| 0.121| -    | 0.155| 0.014| 0.200| -    | 0.091| 0.275| 0.059| 0.163|
| FG    | 0.001| 0.041| 0.006| 0.029| 0.018| 0.120| -    | 0.128| -    | 0.004| 0.075| 0.243| 0.242| 0.022| 0.436*|
| GL    | 0.009| 0.031| 0.002| 0.019| 0.019| 0.020| 0.234| 0.303| 0.015| 0.105| 0.112| 0.522| -    | 0.008| 0.522**
| GB    | 0.006| 0.066| 0.002| 0.011| 0.007| 0.234| 0.298| 0.002| 0.113| 0.051| 0.041| 0.103| 0.010| -    | -    |

Residual Effect = 0.560

* **Significant at 5% and 1% levels, respectively

(FLL= Flag leaf length, FLW= Flag leaf width, CD= Culm diameter, PL= Panicle length, PH=Plant height, DF= Days to 50% flowering, DM=Days to maturity, ET= Number of effective tiller, TGW=Thousand grain weight, FG= Number of filled grains per panicle, GL= Grain length, GB=Grain breadth, Y= Yield per hill)
4. Conclusions

The presence of genetic variability in a crop is an utmost prerequisite for the improvement of economically important traits like yield in rice. From this study, we conclude that the jhum rice possessed sufficient amounts of variability for yield and its associated traits. The traits number of filled grains per panicle, 1000 grain weight and panicle length had a positive correlation with grain yield (GYD) and hence can be used as selection indices for improving grain yield in rice. Moreover, the presence of high heritability and significant positive correlation between yield and its component traits in Jhum rice genotypes, confirm its suitability for pre-breeding materials.

References

Adilakshmi D., Girijarani M. 2012. Variability, character association and path analysis in rice under submergence. Crop Research, 44 (1 and 2): 146-151.

Akter N., Islam MZ., Chakrabarty T., Khalequzzaman M. 2018a. Variability, heritability and diversity analysis for some morphological traits in basmati rice (Oryza sativa L.) genotypes. The Agriculturists, 16(2): 01-14.

Akter N., Khalequzzaman M., Islam MZ., Mamun MAA., Chowdhury MAZ.2018b. Genetic variability and character association of quantitative traits in jhum rice genotypes. SAARC Journal of Agriculture, 16(1): 193-203.

Babu VR., Shreya K., Dangi KS., Usharani G., Nagesh P. 2012. Genetic variability studies for qualitative and quantitative traits in popular rice (Oryza sativa L.) hybrids of India. International Journal of Scientific and Research Publications, 2(6): 1-5.

Bisne R., Sarawgi AK.,Verulkar SB. 2009. Study of heritability, genetic advance and variability for yield contributing characters in rice. Bangladesh Journal of Agricultural Research, 34(2); 175-179.

Bornare SS., SK Mittra, Mehta AK. 2014. Genetic variability, correlation and path analysis of floral, yield and its component traits in CMS and restorer lines of rice (Oryza sativa L.). Bangladesh Journal of Botany, 43(1): 45-52.

Burton GW. 1952. Proceedings of Intercropping Grassland Congress: Quantities inheritance in grasses. 1(6): 277-283.

Burton G., Devane EH. 1953. Estimating heritability in tall fescue (Festuca arundinaceae) from replicated clonal material. Agronomy Journal, 45(10): 478-481.

Chakrabarty T., Islam M.Z., Akter N., Khalequzzaman M.2019. Variability, traits association and pathcoefficient of yield and yield contributing traits of selected boro rice (Oryza sativa L.) germplasm SAARC Journal of Agriculture, 17(2): 103-115. DOI: https://doi.org/10.3329/sja.v17i2.45298

Dhanwani R K., Sarwgi A. K., Akashsolanki., Jitendrakumartiwari. 2013. Geneticvariability analysis for various yield attributing and quality traits in rice (Oryza sativa L.). The Bioscan. 8(4):1403-1407.

Hasan MJ., Kulsum MU., Hoque N., Miah M.A., Azam FAMS. 2010. Genetic variability, correlation and path coefficient analysis in some restorer lines of hybrid rice (Oryza sativa L.). Eco-friendly Agriculture Journal, 3(5): 222-226.

Idris AE., Mohamed KA. 2013. Estimation of genetic variability and correlation for grain yield components in rice (Oryza sativa L.). Global Journal of Plant Ecophysiology, 3(1):1-6.

Islam MZ., Khalequzzaman M., Siddique, MA., Akter N., Ahmed MS., Chowdhury

Islam et al. /The Agriculturists 18(1): 1-9 (2020)
Genetic variability of jhum rice genotypes

MAZ. 2017. Phenotypic characterization of Jhum rice (Oryza sativa L.) landraces collected from Rangamati district in Bangladesh. Bangladesh Rice Journal, 21 (1): 47-57.

Islam MZ., Chakrabarty T., Akter N., Rashid ES M H., Khalequzzaman M., Chowdhury MAZ. 2018. Genetic variability, character association and path analysis in boro rice (Oryza sativa L.) germplasm from Bangladesh. Bangladesh Rice Journal. 22 (1): 35-43.

Islam MZ., Khalequzzaman M., Bashar MK., Ivy NA., Haque MM., Mian MAK. 2016. Variability assessment of aromatic and fine rice germplasm in Bangladesh based on quantitative traits. The Scientific World Journal, 2016:1-14.

Islam MZ., Mian M A K., Ivy NA., Akter N., Rahman MM. 2019. Genetic variability, correlation and path analysis for yield and its component traits in restorer lines of rice. Bangladesh Journal of Agricultural Research. 44(2): 291-301.

Johnson HW., Robinson HF., Comstock RE. 1955. Estimates of genetic and implications in selection. Agronomy Journal, 50: 126-131.

Kundu A., Senapati B K., Bakshi A., Mandal GS. 2008. Genetic variability of panicle characters in tall indica aman rice. Oryza. 45(4): 320-323.

Madhavilatha L., Sekhar RM., Suneetha Y., Srinivas T. 2005. Genetic variability, correlation and path analysis for yield and quality traits in rice (Oryza sativa L.). Research on Crops. 6 (3): 527-534.

Manikyaminie C., Reddy T D., Raju CS. 2013. Correlation and path analysis for yield and its components in rice (Oryza sativa L.).The Journal of Research ANGRAU. 41(1): 132-134.

Mishra L K., Verma RK. 2002. Genetic variability for quality and yield traits in non segregating populations of rice (Oryza sativa L.). Plant Archives. 2(2): 251-256.

Mohana K D., Reddy DM., Reddy KHP., Sudhakar P. 2009. Character association and interrelationship of yield and quality attributes in rice (Oryza sativa L.). The Andhra Agricultural Journal, 56(3): 298-301.

Rangare NR., Krupakar A., Ravichandra K., Shukla AK., Mishra AK. 2012. Estimation of characters association and direct and indirect effects of yield contributing traits on grain yield in exotic and Indian rice (Oryza sativa L.) germplasm. International Journal of Agricultural Science, 2(1): 54-61.

Sameera SK., Srinivas T., Rajesh AP., Jayalakshmi V., Nirmala P J. 2016. Variability and path co-efficient for yield and yield components in rice. Bangladesh Journal of Agricultural Research, 41(2): 259-271.

Seyoum M., Bantte S. 2012. Genetic variability, heritability correlation coefficient and path analysis for yield and yield related traits in upland rice (Oryza sativa L.). Journal of Plant Sciences, 7(1): 13-22.

Singh MK., Singh S., Nautiyal MK., Pandey ID., Gaur AK. 2017. Variability, heritability and correlation among grain quality traits in basmati rice (Oryza sativa L.). International Journal of Chemical Studies, 5(5): 309-312.

Sudharani M., Raghavareddy P., Reddy G H., Raju CS. 2013. Correlation and path coefficient analysis for yield and physiological attributes in rice (Oryza sativa L.) hybrids under saline soil conditions The Journal of Research ANGRAU, 41(1): 105-108.