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# GENETIC VARIABILITY, HERITABILITY, GENETIC ADVANCE AND PATH COEFFICIENT IN BC$_2$F$_2$ POPULATION OF RICE

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## ABSTRACT

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A total of fifty-two BC$_2$F$_2$ rice genotypes derived from crossing between salt tolerant rice variety Binadhan-10 and bacterial leaf blight resistant rice line IRBB60 followed by backcrossing were studied in field condition for genetic variability, heritability, genetic advance, correlation and path coefficients of yield and yield contributing traits along with parents. The quantitative agronomic data of these traits were collected from three plants of each genotype. A wide range of significant variation was observed among the genotypes for yield contributing traits namely days to flowering, days to maturity, plant height, total tillers plant[-1], effective tillers plant[-1], panicle length, filled grains panicle[-1], unfilled grains panicle[-1], 1000 seeds weight as well as on grains yield plant[-1]. The phenotypic variability was higher than the genotypic variability for all traits, indicated these traits were influenced with environmental factors. The highest phenotypic and genotypic variances were observed in filled grains panicle[-1], while the highest phenotypic and genotypic coefficients of variation were observed in unfilled grains panicle[-1]. These two traits also showed high heritability in conjunction with high percentage of genetic advance over mean indicated the significant role of additive gene actions on these traits and therefore an accountable scope of selection utilizing their phenotypic performance is pertinent. The correlation and path coefficient analysis also revealed that filled grains panicle[-1] showed strong positive association with grains yield plant[-1] along with their direct effect on grains yield plant[-1] both at phenotypic and genotypic level. Considering estimation of phenotypic and genotypic variability, heritability and genetic advance along with correlation and path coefficients it could be concluded that filled grain panicle[-1] would be the useful selection trait for improvement of the rice yield among the studied rice genotypes.

*Key words:* rice, genotype, phenotype, correlation coefficient, path coefficient, backcrossing

## INTRODUCTION

Rice (*Oryza sativa* L.) is one of the important cereal crops providing staple food to more than half of the world's population (Maraseni *et al.* 2018). Different biotic and abiotic stresses reduce its production. Among the biotic stresses, bacterial leaf blight (BLB) of rice, caused by *Xanthomonas oryzae* pv. *Oryzae (Xoo)*, is a major pathogen that negatively impacts rice production, especially in irrigated and rainfed lowland agricultural production systems, and resulting in annual yield loss by 20-30% worldwide (Nguyen *et al.* 2018). In a very severe condition, the production loss may be as high as 80% and even 100% (Agarwal *et al.* 2005). However, rice production is required to be increased 42% by 2050 to fulfill the demand of an increased human population worldwide (Seck *et al.* 2012; Ray *et al.* 2013). Increasing the crop land by introducing climate smart as well as host resistance rice variety has been shown to be the only reliable, economical and environment-friendly method to meet up increasing demand of rice globally (Rashid and Nasrin, 2014; Peng *et al.* 2015; Huang *et al.* 2016; Balachiranjeevi *et al.* 2018; Sultana *et al.* 2019).

Binadhan-10, which is a popular salt tolerant rice variety in Bangladesh, can tolerate up to 12 dS m^{-1} of salinity, has been released by Bangladesh Institute of Nuclear Agriculture (BINA) in 2012 (Sultana *et al.* 2019). This is an early maturing variety and capable of producing higher grain yield both in saline and non-saline condition compared to other salt tolerant varieties (Rashid and Nasrin, 2014; Prodhan *et al.* 2019; Sultana *et al.* 2019). Unfortunately, this variety is not resistant to bacterial leaf blight disease (Mubassir *et al.* 2016). In contrast, IRBB60 is a near isogenic line possessing BLB resistant genes, which are capable of preventing bacterial leaf blight infection (Swamy *et al.* 2006; Bharani *et al.* 2010). This BLB resistant line has been used in backcross breeding program to develop new lines or varieties, which could prevent such disease (Huang *et al.* 1997; Bharani *et al.* 2010; Weerasinghe *et al.* 2017). Therefore, crossing of Binadhan-10 with IRBB60 could be an option to develop a variety, which could be both salt tolerant and resistant to the bacterial leaf blight pathogen. The quantitative genetics of the agronomic traits is important tool to evaluate the agronomic performances of the backcross derived rice genotypes (Kumar *et al.* 2012; Dilruba *et al.* 2014; Adhikari *et al.* 2018). The measurement of coefficient of variation is useful in measuring the variability among the traits, while heritability along with genetic advance is important for selection procedures in plant breeding (Johnson *et al.* 1955; Rasel *et al.* 2018). Correlation coefficients and path coefficients are also important to see the association between agronomic traits and impact of different agronomic traits on the yield in plant breeding (Saha *et al.* 2019). The main interest of rice cultivation is grain yield, which could be influenced with many other yield contributing traits. Direct and indirect effects of such traits on the grain yield are estimated with correlation and path

coefficients, which has also been established as important criteria for trait selection breeding (Rashid *et al.* 2010; Rasel *et al.* 2018). However, no information is available on the agronomic performances of backcross-derived population of Binadhan-10×IRBB60. Therefore, the objective of the present study was to evaluate the quantitative genetic parameters of backcross derived $BC_2F_2$ population of Binadhan-10×IRBB60 on different agronomic traits.

## MATERIALS AND METHODS

### Experimental period and location

The experiment was carried out in the Plant Breeding Division of BINA, Mymensingh during the period of December 2016 to May 2019. BINA is situated at 24°55′ 23.1″ North latitude and 90°25′54.1″ east longitude with an elevation of 19 m above the sea level. The experimental soil was highland under the soil series of Agro Ecological Zone 8.

### Plant materials and crossing schemes

IRBB60, a near isogenic line (NIL) was used as donor parent. The Binadhan-10 was used as the recurrent parent. Binadhan-10 was crossed with IRBB60 to produce 34 $F_1$ plants. The $F_1$ plants were backcrossed with Binadhan-10 to produce 52 $BC_1F_1$ plants. Each $BC_1F_1$ plant was considered as individual genotype. Each genotype was again backcrossed with Binadhan-10 to get $BC_2F_1$ populations. Sixty-six $BC_2F_1$ plants of each genotype were transplanted, maintaining 15cm × 20cm spacing from plant to plant and row to row, into individual plot measuring 1m×2m = 2 $m^2$ and $BC_2F_2$ populations were generated after selfing. Sixty-six $BC_2F_2$ plants of each genotype were transplanted similarly into individual plot measuring 1m×2m = 2 $m^2$, and were subjected to agronomic data collection.

### Data collection

Three plants of each genotype, donor parent and recurrent parent from the middle row of the plot were randomly selected for days to flowering, days to maturity, plant height, total tillers plant[-1], effective tillers plant[-1], panicle length, filled grain panicle[-1], unfilled grain panicle[-1], 1000 seeds weight and yield plant[-1].

### Statistics and quantitative genetic parameters

The one-way analysis of variance (ANOVA), correlation coefficients and regression coefficients were calculated using statistical program SPSS version 17.

The phenotypic and genotypic variances were estimated according to the formula given by Johnson *et al.* (1955).

Genotypic variance $(\sigma_g^2) = \frac{GMS - EMS}{r}$

Phenotypic variance $(\sigma_p^2) = \sigma_g^2 + EMS$

> Where,
> > GMS = Genotypic mean square
> > EMS = Error mean square
> > r = Number of plants per genotype

The phenotypic and genotypic coefficients of variation were calculated by the formula suggested by Burton (1952).

Phenotypic coefficient of variation (PCV) $= \frac{\sigma_p}{\overline{X}} \ x \ 100$

Genotypic coefficient of variation (GCV) $= \frac{\sigma_g}{\overline{X}} \ x \ 100$

> Where,
> > $\sigma_p$ = Phenotypic standard deviation
> > $\sigma_g$ = Genotypic standard deviation
> > $\overline{X}$ = Population mean

The estimation of broad sense heritability was define by Lush (1949) calculated by the formula suggested by Johnson *et al.* (1955) and Hanson *et al.* (1956).

Heritability in broad sense $(H^2) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$

> Where,
> > $\sigma_g^2$ = Genotypic variance
> > $\sigma_p^2$ = Phenotypic variance

The genetic advance was calculated following the formula given by Johnson *et al.* (1955) and Allard (1960).

Genetic advance (GA) = H$^2$.K.$\sigma_p$

Where,

H$^2$ = Heritability in broad sense

K = Selection differential, the value of which is 2.06 at 5% selection intensity

$\sigma_p$ = Phenotypic standard deviation

The genetic advance in percentage of mean was calculated from the formula given by Comstock and Robinson (1952).

Genetic advance in percentage of mean (GA %) $= \frac{GA}{\overline{X}} \times 100$

Where,

GA = Genetic advance

$\overline{X}$ = Population mean

The phenotypic and genotypic correlation coefficients were estimated following the formula suggested by Miller *et al*. (1958), Hanson *et al*. (1956) and Johnson *et al*. (1955).

Phenotypic correlation coefficient (r$_p$) $= \frac{Cov_p\ 1.2}{\sqrt{\sigma_p^2\ 1 \times \sigma_p^2\ 2}}$

Genotypic correlation coefficient (r$_g$) $= \frac{Cov_g\ 1.2}{\sqrt{\sigma_g^2\ 1 \times \sigma_g^2\ 2}}$

Where,

Cov$_p$ 1.2 = Phenotypic covariance of traits 1 and 2

$\sigma_p^2$ 1 = Phenotypic variance of trait 1

$\sigma_p^2$ 2 = Phenotypic variance of trait 2

Cov$_g$ 1.2 = Genotypic covariance of traits 1 and 2

$\sigma_g^2$ 1 = Genotypic variance of trait 1

$\sigma_g^2$ 2 = Genotypic variance of trait 2

For path coefficient analysis, yield plant$^{-1}$ was considered as dependent variable while days to flowering (DF), days to maturity (DM), plant height (PH), total tillers plant$^{-1}$ (TP), effective tillers plant$^{-1}$, panicle length (PL), filled grain panicle$^{-1}$ (FG), unfilled grain panicle$^{-1}$ (UFG) and 1000 seeds weight (TGW) were considered as the independent variables or predictors. The direct and indirect impacts of the predictors on the yield plant$^{-1}$ were estimated using the formula described by Deway and Lu (1959).

Path coefficient (r$_{ij}$) $= p_{ij} + \sum r_{ik} p_{kj}$

Where,

P$_{ij}$ = Components of direct effects of the i$^{th}$ independent characters on the j$^{th}$ independent characters as measured by correlation coefficients

$\sum r_{ik} p_{kj}$ = Summation of components of indirect effects of a given i$^{th}$ independent characters on given j$^{th}$ dependent character via all other k independent characters.

**RESULTS AND DISCUSSION**

The analysis of variance (ANOVA) of the quantitative traits is presented in Table 1. Each rice genotype was considered as the treatments.

Table 1. Analysis of variance (ANOVA) for different morphological plant characters of recipient parent Binadhan-10, donor parent IRBB60 and their backcross derived BC$_2$F$_2$ population of fifty-two genotypes

| Traits | MS between treatments | MS within treatments | F | LSD$_{0.05}$ | CV% | P value |
|--------|----------------------|---------------------|-------|--------------|-------|---------|
| DF | 10.07 | 1.00 | 10.07 | 1.62 | 1.75 | <0.001 |
| DM | 3.09 | 0.22 | 13.90 | 0.76 | 0.77 | <0.001 |
| PH | 191.60 | 8.51 | 22.53 | 4.72 | 7.66 | <0.001 |
| TP | 5.94 | 0.81 | 7.40 | 1.45 | 11.95 | <0.001 |
| ETP | 4.88 | 0.63 | 7.75 | 1.28 | 11.19 | <0.001 |
| PL | 7.75 | 1.43 | 5.43 | 1.93 | 6.75 | <0.001 |
| FG | 444.37 | 6.78 | 65.50 | 4.22 | 11.76 | <0.001 |
| UFG | 23.73 | 2.53 | 9.38 | 2.57 | 26.15 | <0.001 |
| TGW | 9.24 | 0.47 | 19.61 | 1.11 | 6.64 | <0.001 |
| YP | 24.63 | 1.79 | 13.73 | 2.17 | 9.34 | <0.001 |

**Note:** MS = Mean square value, DF = Days to flowering, DM = Days to maturity, PH = Plant height (cm), TP = Total tillers plant$^{-1}$, ETP = Effective tillers plant$^{-1}$, PL = Panicle length (cm), FG = Filled grains panicle$^{-1}$, UFG = Unfilled grain panicle$^{-1}$, TGW = 1000 seeds weight (g), YP = Grain yield plant$^{-1}$ (g). Degrees of freedom between treatments and within treatments were 53 and 108 respectively.

The yield and yield contributing traits namely days to flowering (DF), days to maturity (DM), plant height (PH), total tillers plant[-1] (TP), effective tillers plant[-1] (ETP), panicle length (PL), filled grain panicle[-1] (FG), unfilled grains panicle[-1] (UFG), 1000 seeds weight (TGW) and grains yield plant[-1] (YP)were highly significant between treatments (P≤0.001). Significant differences of the quantitative agronomic traits between genotypes indicated that these traits were inherently different among the genotypes studied. The current results are in agreement with recently published results (Dhanwani *et al.* 2013; Abebe *et al.* 2017; Rashid *et al.* 2017; Sumanth *et al.* 2017; Bandi *et al.* 2018 and Gyawali *et al.* 2018). Adhikari *et al.* (2018) also found significant differences between genotypes on plant height, panicle length, seeds weight and grain yield, while they found insignificant differences on number of effective tillers, filled grains and grain yield.

### Phenotypic and genotypic variability, heritability and genetic advance

The range of the yield and yield contributing traits along with mean and standard deviation, phenotypic and genotypic variability, heritability and genetic advance are presented in Table 2.

Table 2. Mean, standard deviation (SD), range, phenotypic ($\delta^2_p$) and genotypic variance ($\delta^2_g$), phenotypic coefficient (PCV) and genotypic coefficient of variance (GCV), broad sense heritability ($H^2$%), genetic advance (GA) and genetic advance as percent over mean (GA%) for yield and yield contributing morphological traits

| Traits | Mean | SD | Range | $\delta^2_p$ | $\delta^2_g$ | PCV (%) | GCV (%) | $H^2$ (%) | GA | GA (%) |
|--------|------|------|-------------|--------|--------|---------|---------|-----------|-------|--------|
| DF | 114.27 | 2.00 | 104-117 | 4.02 | 3.02 | 1.75 | 1.52 | 75.12 | 3.09 | 2.70 |
| DM | 140.86 | 1.08 | 135-142 | 1.18 | 0.96 | 0.77 | 0.69 | 81.13 | 1.82 | 1.29 |
| PH | 108.24 | 8.29 | 85-131 | 69.54 | 61.03 | 7.70 | 7.22 | 87.77 | 15.08 | 13.93 |
| TP | 13.22 | 1.58 | 9-16 | 2.52 | 1.71 | 12.00 | 9.90 | 67.98 | 2.22 | 16.80 |
| ETP | 12.72 | 1.42 | 9-16 | 2.05 | 1.42 | 11.24 | 9.35 | 69.20 | 2.04 | 16.03 |
| PL | 27.75 | 1.87 | 23-31 | 3.53 | 2.11 | 6.77 | 5.23 | 59.64 | 2.31 | 8.33 |
| FG | 104.46 | 12.28 | 73-132 | 152.65 | 145.86 | 11.83 | 11.56 | 95.56 | 24.32 | 23.28 |
| UFG | 11.79 | 3.08 | 5-20 | 9.60 | 7.07 | 26.27 | 22.54 | 73.63 | 4.7 | 39.86 |
| TGW | 27.60 | 1.83 | 23.96-32.80 | 3.39 | 2.92 | 6.67 | 6.19 | 86.12 | 3.27 | 11.85 |
| YP | 32.66 | 3.05 | 24.64-39.51 | 9.41 | 7.61 | 9.39 | 8.45 | 80.92 | 5.11 | 15.65 |

**Note:** SD = Standard deviation, DF = Days to flowering, DM = Days to maturity, PH = Plant height (cm), TP = Total tillers plant[-1], ETP = Effective tillers plant[-1], PL = Panicle length (cm), FG = Filled grains panicle[-1], UFG = Unfilled grain panicle[-1], TGW = 1000 seeds weight (g), YP = Grain yield plant[-1].

The phenotypic and genotypic variances along with their coefficient of variations among the studied yield and yield contributing traits were higher at phenotypic level than the genotypic level. These differences indicated that environmental factors influenced the measured traits. Similar findings were reported by other authors (Abdul Fiyaz *et al.* 2011; Islam *et al.* 2015; Rasel *et al.* 2018). The highest phenotypic and genotypic variances (152.65 and 145.86 respectively) were observed in FG, while these were observed lowest (1.18 and 0.96 respectively) in DM. The phenotypic and genotypic variances were similarly observed highest for FG in case of advanced rice lines (Islam *et al.* 2015), was in agreement with the current investigation. Rashid *et al.* (2017) reported that the phenotypic and genotypic variances of filled grain panicle[-1] showed second highest after the plant height. The phenotypic and genotypic variances of the YP were estimated 9.41 and 7.61, respectively in the present investigation. The highest phenotypic coefficient of variation (PCV) was observed for UFG (26.27%) followed by TP (12.00%) and FG (11.83%). Similar PCV of unfilled grain panicle[-1], tillers plant[-1] and filled grain panicle[-1] were observed by other authors (Rashied *et al.* 2017; Dhanwani *et al.* 2013; Mallimar *et al.* 2015, respectively). The PCV for ETP and YP were estimated 11.24% and 9.39%, respectively, which was in agreement with the results published by others (Rashid *et al.* 2017). The other traits namely DF, DM, PH, PL and TGW showed low PCV ranged from 0.77% for DM to 7.70% for PH. Relatively low PCV for these traits were also reported by other authors (Aditya and Bhartiya, 2013; Ogunbayo *et al.* 2014; Islam *et al.* 2015; Adhikari *et al.* 2018). The genotypic coefficient of variation (GCV) for all these traits were low compared to PCV, indicated an impact of environment on the phenotypic expression of the traits, which are in agreement with recently published results (Adhikari *et al.* 2018; Gyawali *et al.* 2018; Rasel *et al.* 2018).

The estimation of heritability in broad sense ($H^2$) was classified as three different categories as suggested by Johnson *et al.* (1955). The estimation of <30% heritability was considered as low while heritability calculated 30-60% and >60% were considered as medium and high respectively. In the present study high heritability was calculated in case of all traits except panicle length which has been estimated as 59.64% and fall into medium heritability. Broad sense heritability for DF and DM have been estimated 75.12% and 81.13%, respectively in the present investigation, which were similar with other reports (Ogunbayo *et al.* 2014; Islam *et al.* 2015; Adhikari *et al.* 2018; Bandi *et al.* 2018). However, Abede *et al.* (2017) reported less than moderate $H^2$ for these two traits. Saha *et al.* (2019) also reported moderate $H^2$ for DM. PH showed high heritability (87.77%), which was similar to the results published by others (Dhanwani *et al.* 2013; Rashid *et al.* 2017; Saha *et al.* 2019).

However, Islam *et al*. (2015) reported that the heritability of plant height was low. The TP and ETP had high H$^2$ (67.98 and 69.20%, respectively) that were similar with other published findings (Bekele *et al*. 2013; Dhanwani *et al*. 2013; Saha *et al*. 2019). The current estimation of H$^2$ for PL was moderate (59.64%), which was similar to the findings published by others (Adhikari *et al*. 2018; Bandi *et al*. 2018). However, high H$^2$ of the trait was reported by others (Saha *et al*. 2019) and low H$^2$ of the trait was reported by Gyawali *et al*. (2018). FG and UFG showed very high estimation of H$^2$ (95.56 and 73.63%, respectively), which were in agreement with other published results (Dhanwani *et al*. 2013; Rashid *et al*. 2017; Saha *et al*. 2019). In contrast to the current results H2 was very low for filled grain panicle$^{-1}$ reported by Adhikari *et al*. (2018). Estimated H$^2$ for TGW was high (86.12%), which was similar to other studies (Pandey *et al*. 2012; Islam *et al*. 2015; Rashid *et al*. 2017). Conversely, Adhikari *et al*. (2018) found moderate H$^2$ for thousand seeds weight. The YP was estimated 80.92% in the present study which was similar with other published findings (Pandey *et al*. 2012; Rashid *et al*. 2017; Saha *et al*. 2019). Estimation of heritability is important for selective breeding technique as high estimation of H$^2$ for a particular trait indicates it could be improved by selection. In the present investigation it is revealed that most of the traits investigated could be improved by selection.

Estimation of heritability includes additive and non-additive genes. Therefore estimation of genetic advance along with heritability could be used to find out accurate results on the particular trait after selection from the population while percentage of genetic advance over mean produce more precise result (Johnson *et al*. 1955). The prediction of gain of a trait under selection is suitable when high heritability is estimates along with high genetic advance while high heritability itself alone is less useful. The percentage of genetic advance over mean was categorized as low (0 to 10%), moderate (10-20%) and high (≥20%) according to Adhikari *et al*. (2018). In the present study FG and UFG showed high H$^2$ with high percentage of genetic advance over mean (GA%) (23.28% and 39.86%, respectively), while, PH, TP, ETP and YP estimated high H$^2$ with moderate GA% (13.93, 16.80, 16.03 and 15.65% respectively) indicating that these traits could be used as effective selection instruments. The FG and UFG were also estimated high H$^2$ with high GA% by other authors (Dhanwani *et al*. 2013; Rashid *et al*. 2017; Saha *et al*. 2019), which were in agreement with the current investigation. However, Adhikari *et al*. (2018) reported filled grain panicle$^{-1}$ had low H$^2$ along with low percentage of GA over mean. The high H$^2$ of PH in conjunction with moderate percentage of GA over mean in the current investigation was estimated, which were in agreement with the results published by Aditya and Bhartiya (2013) and Saha *et al*. (2019). Besides, many authors published plant height with high H$^2$ and GA% (Dhanwani *et al*. 2013; Rashid *et al*. 2017; Gyawali *et al*. 2018), while others found it had moderate to low H$^2$ with low percentage of GA over mean (Fiyaz *et al*. 2011; Islam *et al*. 2015). The high H$^2$ with moderate GA% of TP and ETP of the present study were in agreement with the results published by Rashid *et al*. (2017), while others found high H$^2$ with high (Bekele *et al*. 2013; Dhanwani *et al*. 2013; Saha *et al*. 2019) or low (Singh *et al*. 2011) percentage of GA over mean. However, Aditya and Bhartiya (2013) reported that TP and ETP had low H$^2$ in conjunction with low GA%. For TGW, the current estimation of GA% (11.85%) was moderate along with high H$^2$, which was in agreement with the results published by others (Aditya and Bhartiya, 2013; Islam *et al*. 2015; Gyawali *et al*. 2018). Furthermore, moderate to high H$^2$ with low GA% for the trait had also been reported by other authors (Abebe *et al*. 2017; Adhikari *et al*. 2018). The current investigation revealed that YP had high H$^2$ along with moderate percentage of GA over mean (15.65%), which was in agreement with the results reported by Singh *et al*. (2011). However, high GA% for the trait has been reported by many authors (Dhanwani *et al*. 2013; Islam *et al*. 2015). The results of the current investigation indicated that FG and UFG along with PH, TP, ETP, TGW and YP could be used as selection tools for the rice genotypes.

**Phenotypic and genotypic correlation coefficients**

Correlation coefficient is the association between two characters while it is useful to find out the indirect effect of predicting characters on the dependent characters in plant breeding. The phenotypic and genotypic correlation coefficients of yield and yield attributing characters for BC$_2$F$_2$ populations of fifty-two genotypes along with parents are presented in Tables 3. The YP showed significant positive correlation at both phenotypic and genotypic level with TP ($r_p$=0.457**, $r_g$=0.472**), ETP ($r_p$=0.409**, $r_g$=0.418**), PL ($r_p$=0.235**, $r_g$=0.289*) and with FG ($r_p$=0.481**, $r_g$=0.510**). In addition, YP showed significant positive correlations with DM and PH at phenotypic level ($r_p$= 0.174* and 0.155* respectively), while correlations were insignificant at genotypic level ($r_g$= 0.209 and 0.167, respectively). Kishore *et al*. (2015) reported that effective tillers and filled grains panicle$^{-1}$ had positive significant correlation with grain yield at phenotypic and genotypic level. The positive significant correlation of days to flowering, days to maturity, total tillers, effective tillers and filled grains panicle$^{-1}$ with grain yield plant$^{-1}$ were reported at phenotypic and genotypic level by Saha *et al*. (2019). Pandey *et al*. (2012) found negative correlation of grain yield with plant height. Adhikari *et al*. (2018) found positive correlation of grains yield with effective tillers, while he found negative correlation with plant height. Dilruba *et al*. (2014) reported positive correlation of grains yield hill$^{-1}$ with plant height while negative correlation was found with filled grains panicle$^{-1}$.

Table 3. Phenotypic ($r_p$) and genotypic correlation coefficient ($r_g$) among yield and yield contributing traits of recipient parent Binadhan-10, donor parent IRBB60 and their backcross derived $BC_2F_2$ population of fifty-two genotypes

| Traits | $r_p/r_g$ | DM | PH | TP | ETP | PL | FG | UFG | TGW | YP |
|--------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| DF | $r_p$ | .376** | 0.004 | .202* | .198* | -0.137 | .191* | 0.028 | -0.146 | 0.137 |
| | $r_g$ | .403** | -0.011 | 0.225 | 0.222 | -0.16 | 0.206 | 0.038 | -0.163 | 0.152 |
| DM | $r_p$ | | -0.043 | -0.091 | -0.103 | 0.059 | .256** | -.186* | -.174* | .174* |
| | $r_g$ | | -0.058 | -0.081 | -0.099 | 0.095 | 0.265 | -0.199 | -0.179 | 0.209 |
| PH | $r_p$ | | | -0.077 | -0.079 | .331** | .239** | 0.11 | -0.09 | .155* |
| | $r_g$ | | | -0.101 | -0.105 | .409** | 0.258 | 0.118 | -0.101 | 0.167 |
| TP | $r_p$ | | | | .944** | -0.053 | 0.000 | -0.132 | -0.039 | .457** |
| | $r_g$ | | | | .976** | -0.058 | -0.006 | -0.142 | -0.046 | .472** |
| ETP | $r_p$ | | | | | -0.061 | -0.049 | -.156* | -0.075 | .409** |
| | $r_g$ | | | | | -0.073 | -0.062 | -0.183 | -0.081 | .418** |
| PL | $r_p$ | | | | | | .261** | -0.038 | -0.121 | .235** |
| | $r_g$ | | | | | | .316* | -0.072 | -0.132 | .289* |
| FG | $r_p$ | | | | | | | 0.091 | -.199* | .481** |
| | $r_g$ | | | | | | | 0.097 | -0.213 | .510** |
| UFG | $r_p$ | | | | | | | | -0.133 | -0.066 |
| | $r_g$ | | | | | | | | -0.157 | -0.091 |
| TGW | $r_p$ | | | | | | | | | 0.142 |
| | $r_g$ | | | | | | | | | 0.136 |

**Note:** DF = Days to flowering, DM = Days to maturity, PH = Plant height (cm), TP = Total tillers plant[-1], ETP = Effective tillers plant[-1], PL = Panicle length (cm), FG = Filled grains panicle[-1], UFG = Unfilled grain panicle[-1], TGW = 1000 seeds weight (g), YP = Grain yield plant[-1].
**. Correlation is significant at the 0.01 level (2-tailed)
*. Correlation is significant at the 0.05 level (2-tailed)

The TGW showed significant negative correlation at phenotypic level with DM ($r_p$=-0.174*) and FG ($r_p$=0.199*), while correlations between TGW with other traits were insignificantly negative at both phenotypic and genotypic level. The present results were in agreement with the results published by Saha *et al*. (2019), who reported negative correlation of 100 seeds weight with days to flowering, days to maturity, panicle length, and filled grains panicle[-1]. The correlation coefficient of TGW with days to flowering and maturity is also in agreement with the results published by other authors (Pandey *et al*. 2012; Adhikari *et al*. 2018). The correlation coefficient between thousand seeds weight and panicle length was reported both positive (Pandey *et al*. 2012; Dilruba *et al*. 2014) and negative (Adhikari *et al*. 2018; Saha *et al*. 2019). The association between thousand seeds weight and filled grains panicle[-1] was also reported both positive (Adhikari *et al*. 2018) and negative (Dilruba *et al*. 2014; Saha *et al*. 2019).

The FG had significant positive correlations at phenotypic level with DF ($r_p$=0.191*), DM ($r_p$=0.256**) and with PH ($r_p$=0.239**), while correlation between them was insignificant at genotypic level. It had also significant positive correlation with PL both at phenotypic and genotypic level ($r_p$=0.261**, $r_g$=0.316*). Saha *et al*. (2019) reported that significant positive correlations of DF, DM and PH with FG were found at phenotypic and genotypic level. They found negative correlation between FG and effective tillers, which was in agreement with the current investigation. However, other authors reported negative correlations between FG and DM (Dilruba *et al*. 2014; Adhikari *et al*. 2018). The correlations between FG and PL were reported positive by others (Adhikari *et al*. 2018), which were in agreement with the present investigation. However, Dilruba *et al*. (2014) found negative correlation between FG and PL. The PL also showed significant positive correlation with plant height both at phenotypic and genotypic level ($r_p$=0.331**, $r_g$=0.409**), which was in agreement with the results published by others (Kishore *et al*. 2015; Saha *et al*. 2019).

The significant strong positive correlation coefficients were found between TP and ETP both at phenotypic and genotypic level ($r_p$=0.944**, $r_g$=0.976**). The present investigation was in agreement with other authors (Saha *et al*. 2019), who found very similar results. The correlation coefficient between DF and DM revealed significantly positive both at phenotypic and genotypic level ($r_p$=0.376**, $r_g$=0.403**) indicates early flowering are associated with the early maturity for all rice genotypes. This result is in agreement with the results published by other authors (Pandey *et al*. 2012; Ogunbayo *et al*. 2014; Adhikari *et al*. 2018; Saha *et al*. 2019).

The analysis of correlation coefficient between yield and yield contributing components revealed that total tillers plant[-1], effective tillers plant[-1] and filled grains panicle[-1] had moderate to strong correlation with the grains yield plant[-1]. Therefore, selection of these yield contributing characters could be helpful to increase the yield.

**Phenotypic and genotypic path coefficients**

The partitioning of the direct and indirect effects of yield contributing traits on the YP both at phenotypic and genotypic levels is presented in Table 4. Yield contributing traits FG and TGW showed positive significant effect both at phenotypic (r$_{ij}$=0.482*** and 0.141*** respectively) and genotypic (r$_{ij}$=0.510*** and 0.136** respectively) level on the grains yield plant$^{-1}$ (YP) in the present study. The DM, TP and PL showed positive significant effect on the YP at phenotypic level (r$_{ij}$=0.174**, 0.457* and 0.235* respectively), while positive insignificant effect at genotypic level (r$_{ij}$=0.209, 0.473 and 0.289 respectively). All the nine traits showed positive effect on the YP except UFG, which showed insignificant negative phenotypic and genotypic effect (r$_{ij}$=-0.065 and -0.091 respectively). Saha *et al.* (2019) reported similar positive effect of yield contributing traits except seed weight on the YP and was in agreement with the present study. The FG showed highest positive phenotypic and genotypic effects on the YP followed by TP (r$_{ij}$=0.457* and 0.473 respectively) and ETP (r$_{ij}$=0.409 and 0.418 respectively). Similar effects of filled grain on the YP were reported by Aditya and Bhartiya (2013) and Saha *et al.* (2019). But, Kishore *et al.* (2015) reported comparatively low positive effect of FG on the YP. Moreover, Dilruba *et al.* (2014) found negative phenotypic effect of FG on the YP.

Table 4. Partitioning of phenotypic (P) and genotypic (G) correlation coefficient into direct (bold phase) and indirect effects of yield contributing morphological traits on total yield plant$^{-1}$ (YP)

| Traits | P/G | DF | DM | PH | TP | ETP | PL | FG | UFG | TGW | YP (r$_{ij}$) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| DF | P | **-0.063** | 0.070 | 0.000 | 0.071 | 0.034 | -0.019 | 0.088 | 0.001 | -0.046 | 0.137 |
| | G | **-0.080** | 0.088 | -0.001 | 0.102 | 0.022 | -0.025 | 0.098 | 0.002 | -0.053 | 0.153 |
| DM | P | -0.024 | **0.187** | -0.003 | -0.032 | -0.018 | 0.008 | 0.118 | -0.008 | -0.054 | 0.174** |
| | G | -0.032 | **0.219** | -0.004 | -0.037 | -0.010 | 0.015 | 0.126 | -0.009 | -0.059 | 0.209 |
| PH | P | 0.000 | -0.008 | **0.072** | -0.027 | -0.014 | 0.046 | 0.110 | 0.005 | -0.028 | 0.155 |
| | G | 0.001 | -0.013 | **0.077** | -0.046 | -0.011 | 0.063 | 0.122 | 0.005 | -0.033 | 0.167 |
| TP | P | -0.013 | -0.017 | -0.006 | **0.353** | 0.164 | -0.007 | 0.000 | -0.006 | -0.012 | 0.457* |
| | G | -0.018 | -0.018 | -0.008 | **0.452** | 0.098 | -0.009 | -0.003 | -0.006 | -0.015 | 0.473 |
| ETP | P | -0.012 | -0.019 | -0.006 | 0.333 | **0.174** | -0.009 | -0.022 | -0.007 | -0.023 | 0.409 |
| | G | -0.018 | -0.022 | -0.008 | 0.441 | **0.100** | -0.011 | -0.029 | -0.008 | -0.026 | 0.418 |
| PL | P | 0.009 | 0.011 | 0.024 | -0.019 | -0.011 | **0.140** | 0.120 | -0.002 | -0.038 | 0.235* |
| | G | 0.013 | 0.021 | 0.031 | -0.026 | -0.007 | **0.154** | 0.150 | -0.003 | -0.043 | 0.289 |
| FG | P | -0.012 | 0.048 | 0.017 | 0.000 | -0.009 | 0.037 | **0.459** | 0.004 | -0.062 | 0.482*** |
| | G | -0.016 | 0.058 | 0.020 | -0.003 | -0.006 | 0.049 | **0.474** | 0.004 | -0.070 | 0.510*** |
| UFG | P | -0.002 | -0.035 | 0.008 | -0.047 | -0.027 | -0.005 | 0.042 | **0.042** | -0.041 | -0.065 |
| | G | -0.003 | -0.044 | 0.009 | -0.064 | -0.018 | -0.011 | 0.046 | **0.045** | -0.051 | -0.091 |
| TGW | P | 0.009 | -0.033 | -0.006 | -0.014 | -0.013 | -0.017 | -0.091 | -0.006 | **0.312** | 0.141*** |
| | G | 0.013 | -0.039 | -0.008 | -0.021 | -0.008 | -0.020 | -0.101 | -0.007 | **0.327** | 0.136** |

**Note:** DF = Days to flowering, DM = Days to maturity, PH = Plant height (cm), TP = Total tillers plant$^{-1}$, ETP = Effective tillers plant$^{-1}$, PL = Panicle length (cm), FG = Filled grains panicle$^{-1}$, UFG = Unfilled grain panicle$^{-1}$, TGW = 1000 seeds weight (g), YP = Grain yield plant$^{-1}$.
Residual effect at phenotypic level = 0.680, Residual effect at genotypic level = 0.670.
*. Indicates significant at P<0.05 level
**. Indicates significant at P<0.01 level
***. Indicates significant at P<0.001 level

The partitioning of direct and indirect effects revealed that highest positive direct effect was found for FG both at phenotypic and genotypic levels (r$_{ij}$=0.459 and 0.474 respectively) followed by TP (r$_{ij}$=0.353 and 0.45 respectively) and TGW (r$_{ij}$=0.312 and 0.327 respectively). The highest positive direct effect of FG followed by TP on the YP was similarly reported by Aditya and Bhartiya (2013). The positive effect of FG on the grain yield was reported second highest by Kishore *et al.* (2015). The direct effect of TGW on the YP reported by Kishore *et al.* (2015) was in agreement with the current investigation. The highest positive direct effect of TGW on the grain yield was reported by Dilruba *et al.* (2014). However, negative direct effects of KSW on the grain yield were reported by others (Aditya and Bhartiya, 2013). The indirect positive effects of yield contributing traits on the YP were negligible at phenotypic and genotypic level except for DF (r$_{ij}$=0.200 and 0.233 respectively), TP (r$_{ij}$=0.104 and 0.021 respectively), ETP (r$_{ij}$=0.235 and 0.318 respectively) and PL (r$_{ij}$=0.235 and 0.135 respectively). The indirect negative effects of UFG and TGW on the YP were estimated at phenotypic level (r$_{ij}$=-0.107 and -0.171 respectively) and at genotypic level (r$_{ij}$=-0.136 and -0.191 respectively). Dilruba *et al.* (2014) reported negligible indirect of yield contributing traits on the grain yield. Saha *et al.* (2019) reported that DF, DM, TP and FG had large positive indirect effect on the YP compared to others traits.

High direct effects of the predictor traits (yield contributing traits) are accounted for the main factors for their association with the dependable variable (YP). The yield contributing traits FG, TP and TGW exhibited high scores of positive direct effects on the YP both at phenotypic and genotypic level. Among these traits, FG and TGW showed significant positive effect on the YP. Therefore, FG and TGW might be used as major selection

criteria for improvement of the grains yield plant$^{-1}$, while TP can also be used as a selection criteria with lower extend.

**CONCLUSION**

The study of BC$_2$F$_2$ populations of 52 backcross derived rice genotypes (Binadhan-10×IRBB60), recipient parent Binadhan-10 and donor parent IRBB60 were studied for genetic parameters of yield and yield contributing traits. High estimation of PCV, GCV, heritability and percent of genetic advance over mean in addition with high degree of positive correlation and direct positive effect of filled grains panicle$^{-1}$ with the grains yield plant$^{-1}$ indicated that this yield contributing trait could be a selection criterion for yield improvement of the studied rice genotypes. In addition, effective tillers plant$^{-1}$ and 1000 seeds weight could also be effective in selection criteria.

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