

Traits Interrelationships in Lowland Rice Genotypes under Rain-fed Condition of Fogera, North Western Ethiopia

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ABSTRACT

Rice (*Oryza sativa* L.) is one of the most important staple crops consumed by more than half of the world's population. To estimate the level of genetic variability, association of grain yield with other traits as well as direct and indirect effects of yield attributing traits on lowland rice genotypes. A field experiment was conducted using thirty-six low land rice genotypes during 2017 main rainy season. The experiment was laid out in a simple lattice design under rain-fed condition. The analyses of variances showed significant differences nearly for all traits tested, except harvest index. Maximum genotypic coefficient of variation was observed for number of panicles per plant (19.85) and maximum phenotypic coefficient of variation was reported for number of panicles per plant (23.43) and number of grains per panicle (19.50). High broad sense heritability was observed for plant height (93), biomass yield (89), grain yield (89.5), number of panicles per plant (71.69), panicle length (73), number of spikelets per panicle (62.62) and thousand-seed weight (64.4). The genetic advance as percent of the mean at 5% selection intensity was high for plant height (30.66), number of panicles per plant (35), number of grains per panicle (21.89), biomass yield (27.35) and grain yield (30.89). Genotypic path coefficients evoke that plant height (0.3862), number of panicles per plant (0.2246), number of spikelets per panicle (0.3331), number of grains per panicle (0.2265) and biomass yield (0.3574) exerts comparatively higher positive genotypic direct effects on grain yield.

Keywords: Correlation, Genetic advance, Heritability, Path coefficient, Rice, Variability

INTRODUCTION

Rice is the most important staple food crop in the world, and used by more than half of the world population [1]. On global basis, it is planted on area of 159 million hectares with production of 481.04 million tons. China is the leading country in production (145 million tons), followed by India (106 million tons), Indonesia (37 million tons), Bangladesh (34 million tons), Vietnam (28 million tons) and Thailand (19.5 million tons).

In Sub-Saharan Africa (SSA), consumption is increasing at a rate of 6% per annum, the highest in the world. The rate of increase in the consumption of rice in Africa has not been matched by corresponding increases in production and the demand-supply gap is widening. The continent currently imports about US \$5 billion worth of rice every year. However, self-sufficiency in Africa rice production is declining as demand increases, driving urgent need to increase and improve the continent's production of rice to satisfy the high demand [2]. Ethiopia is one of the rice producing countries in Africa. However, the crop has been introduced in recent times to the country. The finding of wild rice in the Fogera plain in the early 1970s was the basis for rice introduction in the area [3]. The number of farmers growing rice, the area covered with rice and its production has been increasing from time to time.

Heritability of a trait is important to determine its response to selection. It was found out earlier that genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program. The broad sense heritability is the relative magnitude of genotypic and phenotypic variance for the traits and it gives an idea of the total variation accounted to genotypic effect [4].

According to Falconer and Mackay, heritability is the measure of relative between breeding values and phenotypic values [5]. Thus, heritability plays a predictive role in breeding, expressing the heritability of phenotype as a guide to its breeding value [6]. There is a direct relationship between heritability and response to selection, which means that genetic advance with high heritability estimates offer the most effective condition for selection [7]. Genetic advance refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity [8].

Path coefficient analysis partitions the genetic correlation between yield and yield related traits into direct and indirect effects and hence has effectively been used in identifying useful traits as selection criteria to improve grain yield in rice [9,10].

Information on variability and association of grain yield and yield related traits for lowland rice of Ethiopian agro-ecology is not well addressed. Thus, there is a need to investigate genetic variability, heritability and genetic advance for yield related traits as a basis for selection of high yielding rice genotypes. Hence, the present study was undertaken with the objectives to assess genetic variability, heritability and genetic advance and to estimate the extent of correlation and path coefficients among traits in lowland rice.

MATERIALS AND METHODS

Description of the study area

The field experiment was conducted at Fogera National Rice Research and Training Center (FNRRTC), Woreta, Ethiopia. It is located in at 11°46' to 11°59' latitude north and 37°33' to 37°52' longitude east at an altitude of 1800 mean above sea level. The center is 55 km far from Bahir Dar and 607 km from Addis Ababa. It has an annual average rainfall of 1216 mm with unimodal rainfall pattern where most of the rain usually falls in the period from June to September. It has mean maximum and minimum temperatures of 27.3°C and 10.7°C, respectively.

Planting materials

A total of thirty-six rice (*Oryza sativa L.*) genotypes that introduced from Asian and African rice were included in this study. The genotypes were obtained kindly from Fogera National Rice Research and Training Center, Ethiopia (Table 1).

Table 1. List of the thirty- six lowland rice genotypes tested at Fogera in 2017, Ethiopia.

| G.N. | Genotype Name | G.N. | Genotype Name |
|------|-------------------------|------|----------------------|
| 1 | Aromatic-1 | 19 | SCRID091-20-2-2-4-4 |
| 2 | Edirne | 20 | SCRID091-24-3-2-2-3 |
| 3 | Halilbey | 21 | SCRID091-38-3-1-3-1 |
| 4 | Osmancik-97 | 22 | SCRID090-60-1-1-2-4 |
| 5 | Trakya | 23 | SCRID090-72-3-3-5 |
| 6 | Tunka | 24 | SCRID090-164-2-1-2-1 |
| 7 | Suitouchuukanbohonou 11 | 25 | SCRID090-177-2-4-3-4 |
| 8 | Condai | 26 | SCRID090-18-1-2-2-1 |
| 9 | Pepita | 27 | SCRID091-20-3-1-3-4 |
| 10 | Saegyjinmi | 28 | SCRID122-5-2-1-1-3 |
| 11 | Lunyuki | 29 | SCRID122-13-1-1-4-3 |
| 12 | Hangamchal | 30 | SCRID122-72-1-1-2 |
| 13 | Hawaghaelo-2 | 31 | SCRID198-73-5-1-3 |
| 14 | Namcheobyeo | 32 | Ediget |
| 15 | Samgangbyeo | 33 | X-jigna |
| 16 | SCRID091-10-1-3-2-5 | 34 | Abay |
| 17 | SCRID091-15-2-2-1-1 | 35 | Erib |
| 18 | SCRID091-18-1-5-4-4 | 36 | Shaga |

G. N=genotypic number

Experimental design and trial management

The experiment was laid out in 6 × 6 lattice design with two replications. The dimension of an individual plot area was 1.2 m width × 2.5 m length (3 m²) with six rows for each entry. The spacing between blocks, plots and rows were

1 m, 0.5 m and 0.2 m, respectively. The experimental field was well tilled and planting rows were prepared using hand-pulled row-maker. Planting was done by direct sowing with the seed rate of 64 kg/ha (19.2 g/plot) and 3.2 g/row. Both UREA (46-0-0) and DAP (18-46-0) were applied at the rate of 100 kg/ha. Urea was applied in three splits of the total dose: $\frac{1}{3}$ at planting, $\frac{1}{3}$ mid tillering and $\frac{1}{3}$ at panicle initiation stages. All cultural practices were applied as recommended. Weeds were removed manually when needed.

Data were collected on plot and plant basis according to standard evaluation systems for rice [11]. Plant height (cm), panicle length (cm), number of panicles per plant, number of spikelet per panicle and number of grains per panicle were measured from ten randomly selected plants in the middle four rows of each plot. Data for days to 50% heading, Grain-filling period and days to 85% physiological maturity were collected from plot basis. However, Thousand-seed weight (g), biomass yield (kg/ha) and grain yield were collected on the four central rows.

Statistical analysis

Analysis of variance: Analysis of variance (ANOVA) was computed to test the presence of significant differences among genotypes for different traits. The data collected for each quantitative trait were subjected to analysis using Proc lattice and Proc GLM procedures of SAS version 9.2. Then after testing the ANOVA assumptions, Fisher's Least Significant Difference (LSD) test at 1% or 5% level of significance was used for mean comparisons. The model for lattice design was:

$$Y_{il}(j) = \mu + t_i + r_j + \left(\frac{b}{r}\right)l(j) + e_{il}(j)$$

Where,

$Y_{il}(j)$ is the observation of the treatment i ($i=1, \dots, v=k^2$)

in the block l ($l=1, \dots, k$) of the replication j ($j=1, \dots, m$)

μ is a constant common to all observations, t_i is the effect of the treatment i .

r_j is the effect of the replication j , $(b/r)l(j)$ is the effect of the block l of the replication j .

$e_{il}(j)$ is the error associated to the observation $Y_{il}(j)$, where $e_{il}(j) \sim N(0, s)$, independent.

Estimation of genetic parameters: Different genetic parameters including genotypic variance (σ^2_g), phenotypic variance (σ^2_p), Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were estimated by using below formula:

$$\text{Genotypic variance: } (\sigma^2_g) = \frac{MSg - MSe}{r}$$

Where,

σ^2_g =Genotypic variance, MSg=Mean square due to genotypes.

MSe=Environmental variance (error mean square), r = Number of replications

Phenotypic variance (σ^2_p)= $\sigma^2_g + \sigma^2_e$

Where σ^2_p =Phenotypic variance, σ^2_e =Error variance

Coefficients of variation at phenotypic and genotypic levels were estimated using the following formula:

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{X}} * 100$$

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{X}} * 100$$

Where,

GCV=Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation

\bar{x} =Grand mean of the characters under study.

Heritability: Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance

in the total population. Heritability (H^2) in the broad sense was calculated according to the formula given by Allard [4].

$$H^2 = \left[\frac{\sigma^2_g}{\sigma^2_p} \right] \times 100$$

Where,

H^2 =heritability in broad sense, σ^2_g =genotypic variance

σ^2_p =phenotypic variance (σ^2_g) + (σ^2_e), σ^2_e =environmental variance

Genetic advance: Genetic advance (GA) was calculated with the method suggested by Allard [4]:

$$GA = K \cdot \sigma^2_p \cdot H^2$$

Where,

GA= genetic advance, K=constant=2.06 at 5% selection intensity.

σ^2_p = phenotypic standard deviation, H^2 =Heritability in broad sense.

Genetic advance as percent of mean: Genetic advance as percent of the mean (GAM) was calculated to compare the extent of predicted advance of different traits under selection, using the following formula:

$$GAM = GA \times 100 / \bar{x}$$

Where GA=Genetic advance under selection, \bar{x} =Grand mean of the trait.

Correlation analysis: Phenotypic and genotypic correlations were estimated using the standard procedure from the corresponding variance and covariance components.

$$r_g = \frac{g\text{cov}_{x,y}}{\sqrt{\sigma^2_{gx} \cdot \sigma^2_{gy}}}$$

$$r_p = \frac{p\text{cov}_{x,y}}{\sqrt{\sigma^2_{px} \cdot \sigma^2_{py}}}$$

Where:

r_g = Genotypic correlation coefficient

r_p = Phenotypic correlation coefficient

$G\text{cov}_{xy}$ = Genotypic covariance between variables x and y

$P\text{cov}_{xy}$ = Phenotypic covariance between variables x and y

σ^2_{gx} = Genotypic variance for variables x

σ^2_{gy} = Genotypic variance for variables y

σ^2_{px} = Phenotypic variance for variables x

σ^2_{py} = Phenotypic variance for variables y

To test the significance of correlation coefficients, the following formula was used:

$$t = r / SE(r)$$

$$SE(r) = \sqrt{1 - r^2}$$

Where,

r is correlation coefficient, n is number of genotypes. Then, calculated 't' values were compared with standard values at n-2 degrees of freedom.

Path coefficient analysis

The analysis was done following the method given below:

$$r_{ij} = p_{ij} + \sum r_{ik} + p_{kj}$$

Where,

r_{ij} = mutual association between the dependent character,

i = (yield-related trait) and independent character,

j = (grain yield) as measured by the correlation coefficients,

P_{ij} = is the components of direct effects of the independent character (i),

$\sum r_{ik} + p_{kj}$ = summation of components of indirect effect of a given independent character (i) on the given dependent character (j) via all other independent characters (k). Whereas the contribution of the remaining unknown characters is measured as the residual effect (R^2) which is calculated as: $\sqrt{1-R^2}$.

Where,

$$R^2 = \sum p_{ij} + r_{ij}$$

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance showed that genotypes were highly significant ($p < 0.01$) for number of grains per panicle, days to heading, grain-filling period, days to maturity, thousand-seed weight, plant height, panicle length, number of spikelets per panicle, number of grains per panicle, biomass yield and grain yield indicating the existence of variability among the tested genotypes. But harvest index showed non-significant variation on the tested genotypes (Table 2).

Table 2. The mean squares for different sources of variation for 12 Traits of thirty-six genotypes evaluated under rainfed condition and the corresponding CV.

| Traits | Mean Squares | | | | | |
|--------|---------------------|---------------------|-------|--------|----------------|------|
| | Genotypes (36) | Blocks (6) | Error | CV (%) | R ² | LSD |
| DH | 124.54** | 62.8* | 21.25 | 4.57 | 0.9 | 3.56 |
| GFP | 67.96** | 25.65* | 26.71 | 4.81 | 0.85 | 3.39 |
| DM | 83.37** | 11.75 ^{ns} | 24.46 | 3.67 | 0.85 | 3.25 |
| PH | 294.15** | 17.95 ^{ns} | 10.33 | 4.17 | 0.98 | 2.11 |
| NPP | 2.86** | 0.41 ^{ns} | 0.45 | 12.48 | 0.91 | 0.44 |
| PL | 4.49** | 0.9 ^{ns} | 1.39 | 6.98 | 0.86 | 0.77 |
| NSPP | 1.73** | 1.16* | 0.4 | 7.64 | 0.88 | 0.41 |
| NGP | 280.58** | 263.76** | 83.1 | 13.23 | 0.87 | 5.99 |
| TSW | 3.6** | 0.54 ^{ns} | 0.78 | 5.4 | 0.9 | 0.58 |
| BY | 0.22** | 0.01 ^{ns} | 0.013 | 5 | 0.96 | 0.07 |
| GY | 85.94** | 4.64 ^{ns} | 4.75 | 5.4 | 0.96 | 1.43 |
| HI | 84.15 ^{ns} | 25.85 ^{ns} | 46.08 | 20.17 | 0.77 | - |

*, ** Indicate significance at 0.05, 0.01 probability levels. NS = Non-significant Where: GY=grain yield, DH=number of days to heading, DM=number of days to mature, GFP=grain filling period, PL=panicle length, PH=plant height, NPP=number of panicles per plant, NSPP=number of spikelets per panicle, NGP=number of grains per panicle, BY=biomass yield, HI=harvest index, TSW=thousand-seed weight.

Genotypic and phenotypic coefficients of variation

The phenotypic variance was separated into genotypic and environmental variances to estimate the contribution of each to the total variation. In this study the genotypic coefficient of variation ranged from 4.14% for maturity date to 19.85% for number of panicles per plant and phenotypic coefficient of variation (PCV) ranged from 5.54% for maturity date to 23.98% for harvest index. The phenotypic coefficient of variation values for number of panicles per plant (23.43%), number of grains per panicles (19.50%) and number of panicles per plant (23.43%) were higher. Plant height (16.00%), panicle length (10.15%), number of spikelets per panicle (12.50%), biomass yield (15%), grain yield (16.75%) were medium. Whereas, heading to days (8.37%), grain-filling period (7.17%), days to maturity (5.54%) and thousand-seed weight (9.06%) had low PCV values. This result is in conformity with the finding of, who observed low PCV for, days to maturity and also observed low PCV for days to 75% maturity [9,12,13]. Similar result has been reported by for maturity days. The extent of the environmental influence on any character is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients

of variation. Large differences reflect high environmental influence, while small differences reveal high genetic influence [9] (Table 3).

Genotypic coefficient of variation measures the variability of any character. The extent of the environmental influence on any character is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation. Large differences reflect high environmental influence, while small differences reveal high genetic influence [9]. Genotypic coefficient of variation (GCV) values were low for days to 50% heading (6.39), days to 85% maturity (4.14), panicle length (7.36), number of spikelet per panicle (9.92) and thousand-seed weight (7.27). Similar results have been reported by Chakraborty *et al.* for days to 50% heading [14]. Likewise, Selvaraj *et al.* for days to maturity and Akinwale *et al.* for days to 50% heading, days to 75% maturity by Demewez *et al.* for days to 50% heading, days to 75% maturity, panicle length and number of spikelets per panicle [9,12,13]. The difference between this finding and the previous findings may be related to environmental factors in which experiments conducted and genotypes used are quite different. Medium GCV was observed for plant height (15.40), number of grains per panicle (14.41), grain yield (15.84), biomass yield (14.11) and number of panicles per plant (23.43). Similar results have been reported for grain yield by Akinwale *et al.* [9]. On the other hand, Selvaraj *et al.* observed high genotypic coefficient of variation for grain yield and Demewez *et al.* was observed medium genotypic coefficient of variation for grain yield and biomass yield [9,13]. The traits like number of panicles per plant (19.85), gave comparatively higher value for genotypic coefficient of variation. The higher values clearly indicated a high degree of variability in these quantitative characters and suggest the possibility of yield improvement through selection of this trait. Similar findings were reported by Rangare *et al.* and Mulugeta *et al.* also observed high genotypic coefficient of variation for number of panicles per plant [15,16].

Table 3. Estimates of mean, standard deviation, range, variance components and coefficients of variability, heritability and genetic advance of the 12 characters studied at Fogera.

| Traits | Mean | σ^2_g | σ^2_p | σ^2_e | GCV | PCV | H ² | GA | GAM |
|--------|--------|--------------|--------------|--------------|-------|-------|----------------|-------|-------|
| HD | 100.65 | 41.2 | 70.7 | 29.5 | 6.39 | 8.37 | 58 | 10.04 | 10 |
| GFP | 34.09 | 32.59 | 59.3 | 26.71 | 5.31 | 7.17 | 55 | 8.72 | 8.12 |
| DM | 134.75 | 31.02 | 55.48 | 24.46 | 4.14 | 5.54 | 56 | 8.59 | 6.39 |
| PH | 77.1 | 141.91 | 152.24 | 10.33 | 15.4 | 16 | 93 | 23.63 | 30.66 |
| NPP | 5.4 | 1.14 | 1.59 | 0.45 | 19.85 | 23.43 | 71.69 | 1.87 | 35 |
| PL | 16.9 | 1.55 | 2.94 | 1.39 | 7.36 | 10.15 | 73 | 2.58 | 15.25 |
| NSPP | 8.25 | 0.67 | 1.07 | 0.4 | 9.92 | 12.5 | 62.62 | 1.33 | 16.16 |
| NGP | 68.9 | 98.74 | 181.84 | 83.1 | 14.41 | 19.5 | 54.3 | 15.08 | 21.89 |
| TSW | 16.34 | 1.41 | 2.19 | 0.78 | 7.27 | 9.06 | 64.4 | 1.96 | 12.01 |
| BY | 2.24 | 0.1 | 0.113 | 0.013 | 14.11 | 15 | 89 | 0.613 | 27.35 |
| GY | 40.2 | 40.59 | 45.35 | 4.75 | 15.84 | 16.75 | 89.5 | 12.42 | 30.89 |

σ^2_g =Genotypic variance, σ^2_e =Environmental variance, σ^2_p =Phenotypic variance, GCV=Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation, H²=Broad sense heritability, GA=Genetic Advance, GAM=Genetic advance as percent of mean, GY=grain yield, DH=number of days to heading, DM=number of days to mature, GFP=grain filling period, PL=panicle length, PH=plant height, NPP=number of panicles per plant, NSPP=number of spikelets per panicle, NGP=number of grains per panicle, BY=biomass yield, TSW=thousand-seed weight.

HERITABILITY AND GENETIC ADVANCE

Heritability estimate for characters under study is indicated in. In this study heritability in broad sense ranged from 54.3% for number of grains per panicle to 93% for plant height. Estimates are categorized as low (0-30%), medium (30-60%) and high (above 60%). High broad sense heritability estimates observed for plant height (93%), biomass yield (89%), grain yield (89.5%), number of panicles per plant (71.69%), panicle length (73%), number of spikelets per panicle (62.62%) and thousand-seed weight (64.4%), suggested that high component of heritable portion of variation that can be exploited by breeders in the selection of superior genotypes on the bases of phenotypic performance [17]. Similar results were observed for biomass yield, days to 50% heading, plant height, number of panicle per plant and grain yield, Hasan *et al.* for plant height, days to 50% heading, panicle length, thousand seed weight and grain yield and Mulugeta *et al.* for days to 50% heading, plant height, panicle length, number of spikelet per panicle and thousand-seed weight in lowland rice genotypes [16,18]. Medium broad sense heritability were observed for days to heading (58%), grain-filling period (55%), days to maturity (56%) and number of grains

per panicle (54.3%), indicates the possibility of using for rice improvement program, but their expression can be affected by the environment.

The genetic advance as percent of the mean at 5% selection intensity was high for plant height (30.66), number of panicles per plant (35), number of grains per panicle (21.89), biomass yield (27.35) and grain yield (30.89) and moderate for number of spikelets per panicle (16.16), thousand-seed weight (12.01). These result were supported by Akinwale *et al.*, Sadeghi *et al.* and Demewez *et al.* [9,10,13]. In this study high to medium heritability and high genetic advance were obtained for plant height, number of grains per panicle and grain yield which suggests these traits could be considered as favourable attributes for low land rice improvement through selection. Similarly, high heritability combined with high genetic advance could be regarded as an indication of additive gene action. High heritability and high genetic advance records were reported for plant height and for number of grains per panicle and grain yield [10]. High heritability with low genetic advance observed for biomass yield, number of panicle per plant and panicle length indicates non additive type of gene action and the genotype by environment interaction plays a significant role in the expression of the traits. In agreement with the present findings high heritability with low genetic advance for panicle length [9].

CORRELATIONS ANALYSIS OF QUANTITATIVE TRAITS

Genotypic and phenotypic correlations of all possible combinations for traits under study are presented in Table 4. A positive value of correlation shows that the changes of two variables are in the same direction, that is, high values of one variable are associated with high values of other and vice versa. Very close values for genotypic and phenotypic correlations might be due to reduction in error (environmental) variance to minor proportions. When value of r_p is greater than r_g , it shows apparent association of two traits is not only due to genes but also due to favorable influence of environment. By contrast, if value of r is zero or insignificant, this shows that the two traits are independent (Table 4).

Table 4. Genotypic correlation coefficient (r_g) (upper diagonal) and phenotypic correlation coefficient (r_p) (below diagonal) of 11 traits of thirty-six lowland rice genotypes.

| | HD | GFP | MD | PH | NPP | PL | NSPP | NGP | TSW | BY | GY |
|------|---------------------|---------------------|---------------------|---------------------|-----------------------|--------------------|---------------------|--------------------|---------------------|---------------------|---------------------|
| HD | | 0.86** | 0.75** | -0.08 ^{ns} | 0.06 ^{ns} | 0.05 ^{ns} | 0.22 ^{ns} | 0.14 ^{ns} | -0.3 ^{ns} | 0.47* | -0.08 ^{ns} |
| GFP | 0.88** | | 0.67** | 0.02 ^{ns} | 0.00004 ^{ns} | 0.11 ^{ns} | 0.31 ^{ns} | 0.23 ^{ns} | -0.32 ^{ns} | 0.62** | 0.04 ^{ns} |
| MD | 0.7** | 0.6** | | -0.1 ^{ns} | -0.02 ^{ns} | 0.06 ^{ns} | 0.3* | 0.4* | -0.13 ^{ns} | 0.38* | 0.004 ^{ns} |
| PH | -0.06 ^{ns} | 0.02 ^{ns} | -0.09 ^{ns} | | -0.42* | 0.68** | 0.11 ^{ns} | 0.4* | 0.07 ^{ns} | 0.09 ^{ns} | 0.4** |
| NPP | 0.09 ^{ns} | 0.07 ^{ns} | -0.02 ^{ns} | -0.4** | | -0.3 ^{ns} | -0.4* | -0.5* | -0.1 ^{ns} | -0.07 ^{ns} | 0.2 ^{ns} |
| PL | -0.05 ^{ns} | 0.007 ^{ns} | 0.008 ^{ns} | 0.6** | -0.2 ^{ns} | | 0.3 ^{ns} | 0.5* | -0.2 ^{ns} | 0.2 ^{ns} | 0.4* |
| NSPP | 0.13 ^{ns} | 0.3* | 0.2* | 0.14 ^{ns} | -0.3* | 0.2 ^{ns} | | 0.7** | -0.1 ^{ns} | 0.3 ^{ns} | 0.4* |
| NGP | 0.2 ^{ns} | 0.2 ^{ns} | 0.3** | 0.4** | -0.3** | 0.4** | 0.7** | | 0.03 ^{ns} | 0.2 ^{ns} | 0.5** |
| TSW | -0.2 ^{ns} | -0.2 ^{ns} | -0.11 ^{ns} | 0.07 ^{ns} | -0.1 ^{ns} | -0.2 ^{ns} | -0.08 ^{ns} | 0.04 ^{ns} | | -0.2 ^{ns} | 0.02 ^{ns} |
| BY | 0.4** | 0.5** | 0.4** | 0.09 ^{ns} | -0.04 ^{ns} | 0.2 ^{ns} | 0.2 ^{ns} | 0.2 ^{ns} | -0.2 ^{ns} | | 0.3 ^{ns} |
| GY | -0.07 ^{ns} | 0.04 ^{ns} | 0.009 ^{ns} | 0.04** | 0.2 ^{ns} | 0.4** | 0.4** | 0.4** | 0.03 ^{ns} | 0.3* | |

*, **=significant at 5 % and 1% probability level, respectively, GY=grain yield, HD=number of days to heading, MD=number of days to mature, GFP=grain-filling period, PL=panicle length, PH=plant height, NPP=number of panicles per plant, NSPP=number of spikelets per panicle, NGP=number of grains per panicle, BY=biomass yield, TSW=thousand-seed weight.

Days to heading showed negative non-significant association at genotypic and at phenotypic levels ($r_g = -0.08$, $r_p = -0.07$) with grain yield per hectare. Yadav *et al.* reported negative associations between days to heading and grain yield per hectare at genotypic and phenotypic levels [19]. While Fiyaz *et al.* reported positive and significant association between days to heading and grain yield per hectare [20]. Days to heading had highly significant positive association at genotypic and phenotypic levels with maturity date ($r_g = 0.75$ **, $r = 0.7$ **) and biomass yield ($r_g = 0.47$ *, $r_p = 0.44$ **).

Grain-filling period was positively and very highly significantly associated with biomass yield per plot ($r_g = 0.5$, $r_p = 0.62$) and days to maturity ($r_g = 0.6$, $r_p = 0.67$) at genotypic and phenotypic levels. Days to maturity showed positive and weak non-significant association at genotypic ($r_g = 0.004$) and at phenotypic ($r_p = 0.009$) levels with grain yield per hectare. This finding is contradicted with the findings of Aditya and Anuradha *et al.* which showed positive significant association at genotypic and phenotypic levels [21]. Days to maturity showed positive highly significant association

with number of spikelets per panicle ($r_g=0.3^*$, $r_p=0.2^*$), number of grains per panicle ($r_g=0.23_{ns}$, $r_p=0.3^*$) and biomass yield plant ($r_g=0.38^*$, $r_p=0.4^{**}$) at both levels.

The correlation between plant height and grain yield per hectare was positive and significant at both genotypic and phenotypic levels ($r_g=0.4^*$, $r_p=0.04^{**}$) which indicates that an increase in plant height leads to an increased grain yield. Similar to the present results, Karim *et al.*, Ramanjaneyul *et al.*, Aditya and Anuradha, Singh *et al.*, Patel *et al.*, reported significant and positive correlation between plant height and grain yield at genotypic and phenotypic levels [21-25]. Plant height showed negative significant association at genotypic and phenotypic levels with number of panicles per plant. However, it was positively and highly significantly associated with panicle length ($r_g=0.68^{**}$, $r_p=0.6^{**}$) and number of grains per panicle ($r_g=0.4$, $r_p=0.4^{**}$) at both correlation types.

The correlation between number of panicles per plant and grain yield per hectare was positive and non-significant at both genotypic and phenotypic levels ($r_g=0.2$, $r_p=0.2$). This finding agrees with the reports of Rangare *et al.*, Babu *et al.*, Yadav *et al.*, Karim *et al.*, Patel *et al.*, Bagheri *et al.*, Naseem *et al.* [15,17,19,22,25-27]. Number of panicles per plant was negatively and significantly associated with number of spikelets per panicle and number of grains per plant at genotypic and phenotypic levels, indicating that increase in number of panicles per plant reduces number of spikelets per panicle and number of grains per panicle. Panicle length had positively significant relationship at genotypic and phenotypic levels with grain yield per hectare ($r_g=0.4^*$, $r_p=0.4^{**}$). Similar results have been observed by Yadav *et al.*, Rangare *et al.*, Aditya and Anuradha, Singh *et al.* and Patel *et al.* [15,19,21,24,25]. Panicle length had positively significant relationship at genotypic and phenotypic levels with number of grains per panicle ($r_g=0.5^*$, $r_p=0.4^{**}$).

Number of spikelets per panicle was in positive significant relationship at genotypic level ($r_g=0.4^*$) and positive highly significant relationship at phenotypic level ($r_p=0.4^{**}$) with grain yield per hectare. This result agrees with a number of works in rice [15,17,19,26-28]. A highly significant and positive genotypic and phenotypic correlation was observed with number of grains per panicle ($r_g=0.7^{**}$, $r_p=0.7^{**}$). It had positive highly significant association with grain yield per hectare at genotypic ($r_g=0.5^{**}$) and phenotypic ($r_p=0.4^{**}$) levels. Many workers reported similar findings with this result [21,23,25,27,29]. Thousand-seed weight showed positive and non-significant association at genotypic and phenotypic levels with grain yield per hectare ($r_g=0.02$, $r_p=0.03$). This result agrees with Karad *et al.* [30].

Biomass yield was in positive and non-significant relationship at genotypic level and positive and significant relationship at phenotypic level with grain yield per hectare ($r_g=0.3$, $r_p=0.3^*$). These results are supported by the findings of Rangare *et al.* and Rathor *et al.* [15,28].

PATH COEFFICIENT ANALYSIS

Path coefficient analysis of yield and its components revealed that plant height (0.38), number of spikelets per panicle (0.33) and biomass yield (0.35) had the highest positive direct effect on grain yield. High positive direct effect of this character was nullified by the negative indirect effect of panicle length (-0.0074), however its indirect effect *via* the number of grains per panicle, number of spikelets per panicle and plant height were very high, bringing the total correlation to $r=0.500$ with grain yield. Similar results were reported by Dilruba *et al.*, Jambhulkar *et al.*, Karim *et al.*, Naseem *et al.* [22,27,31,32]. The biomass yield was the second most important traits, it showed high positive direct effect (0.35) on grain yield. Its indirect effect *via* plant height, number of spikelets per panicle and number of grains per panicle was high. The number of spikelets per panicle was the third most important traits, it showed high positive direct effect (0.33) on grain yield. Its indirect effect *via* days to heading, days to maturity, grain filling period, number of panicle per plant, panicle length and thousand- seed weight was negative (Table 5).

Negative genotypic direct effects of studied traits on grain yield were in the range between from -0.2439 to -0.0986. Negative direct effect contributing traits to grain yield were days to heading (-0.0986), grain-filling period (-0.2439), maturity days (-0.0354) and panicle length (-0.0347). The negative direct effects of these traits should not be neglected as the effects of these traits were towards declining grain yield. These results are supported by the findings of Kole *et al.* for panicle length and Yadav *et al.* for days to heading, and contradicted with other workers for number of spikelets per panicle, plant height, number of panicles per plant, thousand-seed weight and plant height (Table 5) [19,15,30,31,33].

Table 5. Genotypic path coefficients of direct (bold diagonal) and indirect effects of 36 lowland rice genotypes.

| | HD | GFP | MD | PH | NPP | PL | NSPP | NGP | TSW | BY | r _g |
|------|----------------|----------------|----------------|---------------|---------------|----------------|---------------|---------------|---------------|---------------|----------------------------|
| HD | -0.0986 | -0.2088 | -0.0288 | -0.0305 | 0.0129 | -0.0016 | 0.0728 | 0.0311 | -0.0011 | 0.1682 | -0.080^{ns} |
| GFP | -0.0844 | -0.2439 | -0.0258 | 0.0074 | 0 | -0.0038 | 0.1032 | 0.051 | -0.0011 | 0.2204 | 0.040^{ns} |
| MD | -0.074 | -0.1636 | -0.0384 | -0.0393 | -0.005 | -0.0019 | 0.1108 | 0.079 | -0.0005 | 0.1373 | 0.004^{ns} |
| PH | 0.0078 | -0.0047 | 0.0004 | 0.3862 | -0.0936 | -0.0236 | 0.0376 | 0.0917 | 0.0003 | 0.0337 | 0.400^{**} |
| NPP | -0.0056 | 0 | 0.0009 | -0.161 | 0.2246 | 0.0088 | -0.1304 | -0.1043 | -0.0004 | -0.0263 | 0.200^{ns} |
| PL | -0.0044 | -0.0267 | -0.0021 | 0.262 | -0.057 | -0.0347 | 0.1036 | 0.1092 | -0.0007 | 0.0758 | 0.400[*] |
| NSPP | -0.0216 | -0.0756 | -0.0128 | 0.0436 | -0.0879 | -0.0108 | 0.3331 | 0.1641 | -0.0004 | 0.0906 | 0.400[*] |
| NGP | -0.0135 | -0.0549 | -0.0134 | 0.1564 | -0.1035 | -0.0167 | 0.2414 | 0.2265 | 0.0001 | 0.0798 | 0.500^{**} |
| TSW | 0.03 | 0.0786 | 0.005 | 0.0282 | -0.0234 | 0.0066 | -0.0412 | 0.0061 | 0.0035 | -0.078 | 0.020^{ns} |
| BY | -0.0464 | -0.1504 | -0.0148 | 0.0364 | -0.0165 | -0.0074 | 0.0844 | 0.0506 | -0.0008 | 0.3574 | 0.300^{ns} |

Residual effect=0.2373, GY=grain yield, HD=number of days to heading, MD=number of days to mature, GFP=grain-filling period, PL=panicle length, PH=plant height, NPP=number of panicles per plant, NSPP=number of spikelets per panicle, NGP=number of grains per panicle, BY=biomass yield, TSW=thousand-seed weight.

CONCLUSION

The results suggest that the plant height, number of spikelete per panicle and biomass yield can be used as reliable selection criteria for improving grain yield in rice. The presence of higher heritability and genetic advance estimates for plant height, grain yield and number of grains per panicle indicates that these characters can be exploited more efficiently through selection in further generations.

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