

Research Article

# Genetic Variability and Character Association Analysis for Yield and Its Related Traits in Rain Fed Lowland Rice (*Oryza sativa* L.) Genotypes at Teppi and Fogera, Ethiopia

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## Abstract

In Ethiopia, rice variety development started very recently and is mainly dependent on the introduction breeding materials in which characterization and understanding of the genetic variability of genotypes is the critical step. Knowledge of the extent of genetic variability and interrelationships of yield and yield components is pre-request for designing an effective selection-based rice improvement programs for evolving high yielding rice genotypes. Therefore, this study was carried out with all objectives of assessing genetic variation for yield and yield related traits in lowland rice genotypes. Thirty-six selected lowland rice genotypes were evaluated in simple lattice design with two replications during 2017 cropping season and data on 15 quantitative morphological traits were collected and subjected to various statistical analysis. Combined analysis of variance across location revealed significant location, genotype and genotype  $\times$  location interaction effects for the traits evaluated at  $p \leq 0.01$ . The phenotypic coefficient of variation was high for un fertile tiller per plant (88.16%), followed by infertile grain per panicle (50.66%), and grain yield (21.57%), and the genotypic coefficient of variation was high for un fertile tiller per plant (50.38%), followed by infertile grain per panicle (27.22%), and culm length (17.7%). The estimate of broad sense heritability ranges from 15.2% for biological yield to 91.5% for plant height. The expected genetic advance as present of mean varied from 5.42% for biological yield to 59.3% for unfertile tiller per plant. Phenotypic and genotypic correlation revealed grain yield had a significant and positive association with primary branches per panicle ( $r_p=0.4$ ,  $r_g=0.7$ ), fertile grain per panicle ( $r_p=0.5$ ,  $r_g=0.72$ ) and harvest index ( $r_p=0.76$ ,  $r_g=0.73$ ) at both genotypic and phenotypic. Path coefficient analysis of grain yield revealed that harvest index, total tiller per plant and thousand grain weights showed positive phenotypic direct effect. A Positive direct effect was found for total tiller per plant, harvest index and biological yield at genotypic level. The present study indicated sufficient genetic variability for the characters studied in rain fed low land rice genotype, which will create opportunity for future improvement. To have full scale data, further study at various locations and years with the help of molecular techniques should be done.

## Keywords

Heritability, Path Coefficient Analysis, Genetic Variability, Trait Association

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## 1. Introduction

The total world rice production for 2022 was 776,461,457 tones. The top 10 rice-producing countries in the world are China, India, Bangladesh, Indonesia, Vietnam, Thailand, Myanmar, Philippines, Pakistan and Brazil. China is the world's largest producer of rice with 147.691 million tonnes of rice production in the year 2022-2023.

In Ethiopia, rice cultivation is recent history, however, its use as food crop, income source, employment opportunity and animal feed has been well recognized. The government of Ethiopia considers rice as the most strategic food security crop that has received special attention in the promotion of agricultural production and as such it is named as the “millennium crop” expected to contribute in ensuring food security in Ethiopia [29].

The total cultivated area at the national level has increased from 48,418.09 in 2016/2017 to 53,106.79 hectares in 2017/2018. The cultivated area has increased in 2017/18 as compared to 2016/2017 by about 9.68% nationally with considerable differences across regions. Accordingly, rice production has increased from a total of 1,360,007.26 tons, in 2016/17 to 1,510,183.30 tons in 2017/18. Similarly, productivity in ton per hectare has increased from 2.8 in 2016/17 to 2.84 in 2017/18 [8].

Even though, rice has been recognized by the government as “the new millennium crop of Ethiopia” to attain food security, lack of improved varieties, lack of recommended crop management, lack of pre and postharvest management, biotic and abiotic stresses limit the production and productivity of the crop in the country [29]. Cognizant of the stated importance, and existing potentials for its increased productivity to meet the fastest growing demand of rice crop, development of high yielding varieties with other desirable agronomic traits for diverse ecosystem through breeding programs is therefore a necessity. Although several research activities have been done by rice scientists in different rice growing regions of Ethiopia [33]. However, particularly in south western Ethiopia, only a few research works were done on rice and each of these activities was mainly focused on the identification of production and productivity constraints, assessment of disease and crop management practices the research of Mishu et al and Moosavi et al [22, 23].

Those studies mainly depend on rain fed up land rice but, study on genetic variability for yield and yield related traits for rain fed low land rice were limited.

For further improvement of the crop knowledge of the status of the genetic variability of the varieties is essential. [37] and [3]. Genetic improvement mainly relies on the amount of genetic variability present in the population which is a universal property of all species in nature [10]. In the same way heritability and genetic advancement is a useful

tool for breeders in determining the direction and magnitude of selection. Most effective yield component breeding to increase grain yield could be achieved, if the components traits are highly heritable and positively and significantly correlated with grain yield. Moreover, knowledge of heritability is essential for selection-based improvement as it indicates the extent of transmissibility of a character into future generations. However, information on the genetic variability and character association among grain yield and yield contributing traits for low land rice ecology is not sufficiently available. Given the above gaps, the present study was undertaken to investigate the association between grain yield and yield related traits as a basis for the selection of high yielding rice genotypes in low land ecology. Hence, this research was conducted with the following objectives.

1. To estimate variability, heritability and the genetic advance of lowland rice genotypes.
2. To determine the extent of association of characters among themselves and yield and there by comparing the direct and indirect effects of the characters.

## 2. Materials and Methods

The experiment was conducted at Tepi Agricultural Research Centre and Fogera National Rice Research and Training Center. Tepi Agricultural Research Centre is located 611 km from Addis Ababa in the South-western part of Ethiopia. The experimental site is situated at an altitude of 1200 meter above sea level, latitude of 7°3' N and longitude of 35°18' E and the center receives average annual rainfall 1678 mm and the mean monthly minimum and maximum temperatures of 15.4 °C and 29.5 °C, respectively. The soil type is clay with fine textured 30 to 80% with pH of 6.9-8 (neutral to moderately alkaline) [14].

Fogera National Rice Research and Training Center is located 607 km from Addis Ababa (capital of Ethiopia) in the North-western part of Ethiopia. The site is located at 11°58' N latitude, 37°41' E longitude and at an elevation of 1810 m above sea level. Based on ten years' average meteorological data, the annual rainfall, and mean annual minimum and maximum temperatures are 1300 mm, 11.5 °C and 27.9 °C, respectively. The soil type is black (Vertisol) with pH of 5.90.

The experimental materials consisted of 36 lowland rice genotypes obtained from Fogera National Rice Research and Training Center, formerly introduced by International Rice Research Institute (IRRI) and Africa Rice Center (WARDA). The list, origin, seed source and genotypes used in the experiment were given below in the table 1.

**Table 1.** Description of experimental materials (lowland rice genotypes).

S/NO	Genotype	Seed Source	Origin
1	Aromatic	2016/17 PVT	Africa Rice
2	Edirne	2016/17 PVT	Africa Rice
3	Halilbey	2016/17 PVT	Africa Rice
4	Osmancik-97	2016/17 PVT	Africa Rice
5	Trakya	2016/17 PVT	Africa Rice
6	Tunca	2016/17 PVT	Africa Rice
7	SuitouChuukanbohonNou 11	2016/17 PVT	Africa Rice
8	Condai	2016/17 PVT	Africa Rice
9	Pepita	2016/17 PVT	Africa Rice
10	Saegyejinmi	2016/17 PVT	Africa Rice
11	Lunyuki	2016/17 PVT	Africa Rice
12	Hangamchal	2016/17 PVT	Africa Rice
13	Hawaghaelo-2	2016/17 PVT	Africa Rice
14	Namcheobyeo	2016/17 PVT	Africa Rice
15	Samgangbyeo	2016/17 PVT	Africa Rice
16	SCRID091-10-1-3-2-5	2016/17 PVT	Africa Rice
17	SCRID091-15-2-2-1-1	2016/17 PVT	Africa Rice
18	SCRID091-18-1-5-4-4	2016/17 PVT	Africa Rice
19	SCRID091-20-2-2-4-4	2016/17 PVT	Africa Rice
20	SCRID091-24-3-2-2-3	2016/17 PVT	Africa Rice
21	SCRID091-38-3-1-3-1	2016/17 PVT	Africa Rice
22	SCRID090-60-1-1-2-4	2016/17 PVT	Africa Rice
23	SCRID090-72-3-1-3-5	2016/17 PVT	Africa Rice
24	SCRID090-164-2-1-2-1	2016/17 PVT	Africa Rice
25	SCRID090-177-2-4-3-4	2016/17 PVT	Africa Rice
26	SCRID090-18-1-2-2-1	2016/17 PVT	Africa Rice
27	SCRID091-20-3-1-3-4	2016/17 PVT	Africa Rice
28	SCRID122-5-2-1-1-3	2016/17 PVT	Africa Rice
29	SCRID122-13-1-1-4-3	2016/17 PVT	Africa Rice
30	SCRID186-72-1-1-2	2016/17 PVT	Africa Rice
31	SCRID198-73-5-1-3	2016/17 PVT	Africa Rice
32	GSR IR1-17-Y16-Y3-Y2	2016/17NVT	IRRI
33	GSR IR1-15-D4-D1-Y1	2016/17 NVT	IRRI

S/NO	Genotype	Seed Source	Origin
34	Ediget (Check1)	Breeder Seed	Released
35	X-Jigna (Check2)	Breeder Seed	Local
36	Hiber	2016/17 NVT	WARDA

IRRI= International Rice Research Institutes, WARDA=West Africa Rice Development Association PVT=Preliminary Variety Trial, NVT= National Variety Trail

## 2.1. Experimental Design and Procedures

The field experiment was laid out in a 6 x 6 simple lattice design. The genotypes were grown under rain fed conditions. The plot size was 4 m long and 1.75 m wide (7 m<sup>2</sup>) with 0.25 m and 0.35 m inter row and between plots spacing, respectively. Each incomplete block and replication was spaced 0.6 meter and 1.5 meter, respectively. There were seven rows per plot, out of which data were collected from the middle five rows of each plot. As per the national recommendation, seed rate of 60 Kg/ha i. e. 42 g per plot was used. Fertilizer in the forms of Urea and DAP was applied at a rate of 100/100 Kg/ha (i. e. 70/70 g/plot urea and DAP). All the DAP (70 g/plot) was applied at sowing while, Urea was applied in three splits, the first half was applied at planting, second half at tillering and third half was applied at panicle initiation stage of the crop. During the growing stage of the crop, all agronomic practices were uniformly undertaken and the required data were collected.

## 2.2. Data Collections

Data were collected on both plant (average of 5 randomly taken plants) and plot basis from the central five rows (4 x 1.25 m=5 m<sup>2</sup>) of each plot following the Standard Evaluation System for Rice (SES) [16].

*Plant height (PH, cm)*: Height of the plant in centimeters from the base of the main stem to the tip of the panicle was recorded as the average of five randomly taken plants in the middle five rows of each plot.

*Panicle length (PL, cm)*: Length of the panicle in centimeter was measured from the node, where the first panicle branch starts, to the tip of the panicle as the average of five randomly taken plants in the middle five rows of each plot.

*Culm length (CL, cm)*: The culm length was measured in centimeters from ground level to the base of the panicle or neck node (panicle base node) from five randomly taken plants in the middle five rows of each plot.

*Number of fertile grains per panicle (FGPP, No.)*: Taken by counting the number of fertile grains from the main panicle at harvest maturity from five randomly taken plants and averaged.

*Number of infertile grains per panicle (IGPP, No.)*: Taken

by counting the number of infertile grains from the main panicle at harvest maturity from five randomly taken plants and averaged to find the character.

*Number of fertile tillers per plant (FTTP, No.)*: The average number of fertile tillers from five randomly taken sample plants in the middle five rows of each plot was recorded.

*Number of total tillers per plant (TTPP, No.)*: Number of total tillers per plant was recorded from five randomly taken plants in the middle five rows of each plot.

*Number of unfertile tillers per plant (UTPP, No.)*: Number of non-fertile tillers per plant was recorded from five randomly taken plants in the middle five rows of each plot.

*Number of primary branches per panicle (PBPP, No.)*: Taken by counting the number of all primary branches produced on main panicle axis at harvest maturity from five randomly taken panicles and averaged.

*Days to heading (HD, days)*: Number of days from days to sowing to the date when the tips of the panicles first emerged from the main shoots on 50% of the plant in a plot.

*Days to maturity (MD, days)*: Number of days from the date of sowing to the date when 85% of grain on panicle are matured.

*Harvest index (HI, %)*: The ratio of grain yield per plot to biological yield per plot was expressed in percent at harvest maturity.

*Thousand grain weight (TGW, g)*: The weight of 1000 grains in gram from bulked grains, which were collected from five central rows of each plot were measured and adjusted at 14% moisture content.

*Biological yield (BY, g)*: At harvest maturity, an area of 0.25 m<sup>2</sup> (0.5 m x 0.5 m) biomass within each plot was harvested, and oven-dried for 72 hours at 70 °C and weighed, then converted into biological yield per plot.

*Grain yield per hectare (GY, kg)*: Grain yield in grams obtained from each plot of the middle five rows at physiological maturity was converted into kilogram per hectare, after cleaning and adjusting to 14% moisture content level.

## 2.3. Data Analysis

Tests of homogeneity of error variance are often of interest as a preliminary for pooling data from different source to yield improved estimated variance [7]. Consequently, homogeneity of error variance was tested using F-max test method of

Hartley [15], which is based on the ratio of the larger mean square of error (MSE) to the smaller mean square of error from the separate analysis of variance given by the formula:

$$F_{\text{-max}} = \frac{\text{Largest MSE}}{\text{Smallest MSE}}$$

Accordingly, the computed F-max was less than three; this implied that variances in each of the separate ANOVA are homogenous. Thus possible to proceed combined analysis of variance (Gomez and Gomez, 1984). Then pooled analysis of variance over locations was done using

$$\text{Genotype variance } (\sigma_g^2) = [(\sigma_e^2 + R\sigma_l^2 + RL\sigma_g^2) - (\sigma_e^2 + R\sigma_l^2)]/RL = (MS4 - MS5)/RL$$

$$\text{Genotype x location interaction variance } (\sigma_{gl}^2) = [(\sigma_e^2 + R\sigma_l^2) - (\sigma_e^2)]/R = (MS5 - MS6)/R$$

$$\text{Environmental variance } (\sigma_e^2) = \sigma_e^2 = MS6$$

Phenotypic and genotypic coefficients of variation: was expressed as percentage of the corresponding phenotypic and genotypic standard deviations as described by Burton [5] and Johnson *et al.* (1955). and will expressed as follows:

$$\text{Phenotypic coefficient of variation (PCV\%)} = \frac{\sigma_p}{\bar{x}} \times 100$$

$$\text{Genotypic coefficient of variation (GCV\%)} = \frac{\sigma_g}{\bar{x}} \times 100$$

Where,  $\sigma_p$ =phenotypic standard deviation,  $\sigma_g$ =genotypic standard deviation, and  $\bar{x}$ =grand mean for the character x.

Heritability in broad sense for all characters was computed as the percentage of genotypic to phenotypic variance (Fehr, 1987).  $h = [\sigma_g^2 / \sigma_p^2] \times 100$  where,  $\sigma_g^2$ =genotypic variance and  $\sigma_p^2$ =phenotypic variance. Genetic advance (GA) and genetic advance as percent of the mean (GAM) were estimated using the methods stated by Fehr [12] assuming a selection intensity of 5% will estimated as  $GA = k\sigma_p$

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

Where, k = the selection differential at 5% selection intensity (k = 2.06),  $\sigma_p$  = phenotypic standard deviation, h=heritability in broad sense ratio, and  $\bar{x}$ =grand mean of the respective traits.

Phenotypic and genotypic correlation coefficient analysis was performed using SAS statistical package [32]. To estimate the phenotypic and genotypic correlation coefficient, first covariance estimates between all pairs of the traits will calculated as:

$$\text{Genotypic covariance} = \text{COV}_{gxy} = \frac{MSPg - MSPe}{r}$$

SAS statistical package [32]. Mean separation was done using LSD (least significant difference) at 5% probability level.

Phenotypic variance for the pooled data analysis across the two locations was estimated as per the formula provided by Hallauer and Miranda (1988).

$\sigma_{ph}^2 = \sigma_g^2 + \sigma_{ge}^2/e + \sigma_e^2/re$  where:  $\sigma_p^2$ =phenotypic variance,  $\sigma_g^2$ =genotypic variance,  $\sigma_{ge}^2$ =variance of genotype X environment interaction,  $\sigma_e^2$ =environmental variance, r=number of replication and e=number of environments.

$$\text{Phenotypic covariance} = \text{COV}_{pxy} = \text{COV}_{gxy} + \text{COV}_{exy}$$

Where,  $MSP_e$  =mean sum of cross product for error,  $MSP_g$ = mean sum of cross products for genotypes and r=number of replications.

Phenotypic correlation and genotypic correlation coefficient will be estimated using the procedure suggested by Miller *et al.*, (1958) from the corresponding variance and covariance components as:

$$\text{Phenotypic correlation coefficient} = \frac{PCOV_{xy}}{\sqrt{\delta^2_{px} \times \delta^2_{py}}}$$

$$\text{Genotypic correlation coefficient} = \frac{GCov_{xy}}{\sqrt{\delta^2_{gx} \times \delta^2_{gy}}}$$

Where,  $r_{pxy}$  =phenotypic correlation coefficient between characters x and y,  $r_{gxy}$  =genotypic correlation between x and y. The level of significance of correlation coefficients will be determined from r-table using an appropriate degree of freedom and probability level (Gomez and Gomez, 1984).

Path coefficient analysis was performed using the formula developed by Dewey and Lu [10] using phenotypic and genotypic correlation coefficient were applied to determine the direct and indirect effect of yield components on grain yield. as:  $r_{ij} = P_{ij} + \sum r_{ik}P_{kj}$  where;  $r_{ij}$  is mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficient  $P_{ij}$  is component of direct effects of the independent trait (i) on the dependent variable (j);  $\sum r_{ik}P_{kj}$  is summation of components of indirect effect of a given independent traits via all other independent traits. After computing the direct and indirect effect of the traits, residual effect (R) will be calculated using the formula provided below (Singh and Chaudhary, [35].  $R = 1 - \sum P_{iy} \cdot r_{iy}$  where, R=residual effect,  $P_{iy}$ =direct effect of the traits on yield,  $r_{iy}$ =correlation of the traits on grain yield.

### 3. Results and Discussions

#### 3.1. Analysis of Variance

Separate analysis for each of the two-test sites showed the presence of significant difference among the rice genotypes for all the traits studied. This indicates that the locations had significant effects on the performance of rice genotypes (table 2).

The mean square from the pooled analysis of variance showed statistically significance location ( $p \leq 0.01$ ), effects for most traits except days to 85% maturity and primary branches per panicle. These results indicated the distinct agro-climatic conditions of the two test locations for these traits.

The mean square from the pooled analysis of variance over the two locations showed a statistically significant ( $p \leq 0.01$ ) effect of genotype for all traits. This might be due to the dissimilarity in the genetic composition of genotypes or the large occurrence of genotype by location interactions or both, for that fact characters might differ in their genetic properties. In line with this result, Singh *et al* [34]. reported significant difference among genotypes for most of rice yield

related traits. Mulugeta *et al.* [26] also reported difference among genotypes across location for days to 85% maturity, plant height, panicle length and grain yield per hectares [33] (table 2).

The mean square due to genotype\* location interactions was statistically significant ( $p \leq 0.01$ ) among genotypes for the studied traits, which indicates factors present in the environment as well as genetic constitutions of genotypes affect the phenotypic expression of traits. In such circumstance, genotypes performed well in one location might not consistently perform in other location; this indicates the importance of spatial replication trails, so that separate breeding program might be developed for rice improvement programs over locations. To effectively examine genotypic performance for significant traits it's essential to consider wide location interaction effects and identify traits performance about location effect. In line with the current finding, Machunde *et al* [20] reported significant genotype by location interactions among genotypes for a few of the traits such as grain yield and plant height [21]. Tefera *et al.* also observed significance genotype\*location interaction effects for days to 85% maturity, panicle length and grain yield per hectare in low land rice genotypes. [36]

**Table 2.** Mean squares from the combined analysis of variance on 15 traits of 36 genotypes tested in 2017 main cropping season over two locations.

Traits	Mean	MSL (1)	MSG (35)	MSGL (35)	MSE	CV (%)
HD	91.45	2475.06**	148.70**	40.20**	12.11	3.8
MD	128.95	5.44ns	283.90**	140.90*	59.25	5.96
PH	90.39	1481.97**	876.26**	73.97**	9.38	3.38
PL	17.98	196.23**	7.98**	2.65*	1.15	5.97
CL	72.96	12125.68**	743.46**	76.20**	10.42	4.42
PBPP	9.21	0.25ns	2.74**	0.98*	0.54	8
TTPP	7.62	954.86**	8.96**	4.52**	1.13	13.96
FTPP	7.25	836.17**	7.15**	3.73**	0.92	13.23
UFTPP	0.4	3.24**	0.49**	0.33**	0.01	25
FGPP	80.81	326.4**	501.79**	385.82**	5.85	2.99
IFGP	5.49	23.52**	30.94**	22.01**	1.34	21.03
TGW	25.98	3018.6**	41.88**	32.27**	2.21	5.71
HI	0.4	0.32**	0.01**	0.01**	0.00056	5.96
BY	5352.46	180863497.1**	3437044.10**	2914716.80**	130623	6.75
GY	2896.38	46189806.9**	1561350.37**	1158850.75**	23019	5.23

\*, \*\*significance at  $p \leq 0.05$ , and  $p \leq 0.01$  probability level respectively and ns-non significance MSL=mean square of location, MSG=mean square of genotypes, MSGL=mean square of genotypes \*location, MSE=mean square of error and CV=coefficient of variance.

### 3.2. Range and Mean of Different Characters

The range and mean of the 15 studied characters were presented in (Tables 2 and 3). Accordingly, a wide range was obtained from days to 50% heading, days to 85% maturity, biological yield, grain yield, plant height, culm length, fertile grains per panicle and infertile grains per panicle. Mulugeta *et al.* also reported the same result for days to 50% heading, days to 85% maturity, biological yield and grain yield. [33].

Grain yield/ha exhibited highly significant ( $P \leq 0.01$ ) variation among genotypes with a range from 1199.5 to 2980.7 kilogram per hectare. Highest grain yield (2980 kg/ha) was harvested from genotype SCRID 091-10-1-3-2-5 (2980.7 kg/ha) closely followed by SCRID 090-177-2-4-4 (2904 kg/ha) and SCRID 090-164-2-1-2-1 (2902.5 kg/ha). Lowest grain yield was obtained from genotype SCRID 091-38-3-1-3-1 (1199.5 kg/ha). Wide variability displayed by grain yield might be due to diverse genetic variation of tested materials as well influence of genotype location interaction. This significance variation in yield and yield related traits supported by the report of Lafarge *et al* [19] on rice study under irrigation and rain fed condition. [20]. Akinwal *et al.* [2] and Ekka *et al.* (2015) evaluated 20 and 96 rice in Philippines and India respectively, reported the presence of significant variations among genotypes for grain yield.

Days to 50% heading ranged from 76 to 112.75 days. The genotypes SCRID 122-13-1-1-4-3, EDIRNE and SCRID 090-60-1-1-2-4 headed earlier in 76-82 days. Namcheobyeo completed 50% heading in 112.75 days and it was very late among the others genotypes. The observed significant variation among genotypes for days to heading was due to G×L interaction and due to the significant difference among the tested materials. Tefera *et al.* and Mulugeta *et al.* reported significant variation among genotypes for days to 50% heading ranging from 82.5 to 110 days and 67.3 to 87.3 days respectively [27].

Days to 85% maturity ranged from 122.25-148.25 and the genotypes, EDIRINE and TRAKYA matured early in 122.5 and 117.5 days respectively. NAMCHEOBYEO matured in 148.25 days which is very late. Genotypes which mature earlier are very important for climate mitigation as drought escape mechanisms for areas with marginal rainfall. Variations in days to maturity in different genotypes have been reported by Demewez *et al* [9].

Plant height ranged from 55.9-140.97 cm. Maximum height was recorded in genotype SCRID 091-18-1-5-4-4 (140.97 cm). The genotypes NAMCHEOBYEO, Saegyjinmi and GSRIR1-15-D4-D1-Y1 showed short stature with 55.9 cm, 64.2 cm and 73.6 cm plant height respectively Sabouri *et al.* [31] reported the significant importance of plant height in rice yield improvement program. Consequently, the wider range of plant height among the currently studied genotypes will create an opportunity for breeders to improve the yield of rice through selection or via other breeding strategies [26].

Panicle length ranged from 14.6 to 22.6 cm. Maximum panicle length (22.6 cm) was recorded in SCRID 091-18-1-5-4-4 followed by GSRIR1-15-D4-D1-Y1 (20.3 cm) and SCRID122-5-2-1-1-3 (19.8 cm). The observed numeric difference in panicle length among genotypes was due to the influence of genotype and genotype x location interaction from the current study. It was observed that genotypes that had longer plant height also had longer panicles, this might be due to the positive association between plant height and panicle length. Osman *et al.* [30] reported significant variation among genotypes for panicle length with range of 18 cm to 22 cm. [38]

Culm length ranged from 41-119.52 cm. Maximum culm lengths (119.52 cm) were recorded in SCRID091-18-1-5-4-4 followed by SCRID090-164-2-1-2-1 (97.6 cm) and SCRID 122-5-2-1-1-3 (96.15 cm). The Minimum culm length was recorded in genotype Namcheobyeo which had 41 cm length. Likewise, the number of primary branches per panicle produced varied from 9.05-10.9 among genotypes. The highest number of primary branches per panicle was produced from the genotype SCRID 091-20-3-1-3-4 (10.9) and the lowest number of primary branches per panicle was obtained from genotype SCRID 122-13-1-1-4-3 (6.75).

Number of tiller affect total yield by determining the production of panicle. The genotypes which had higher number of effective tillers showed higher grain yield in rice (Dutta *et al.* [11]. Total number of tillers per plant had significance difference with range of 5.55-12.35 Maximum total number of tillers (12.35) was recorded in genotype Namcheobyeo followed by Halilbey which had (11) number of total tiller per plant and the minimum number of total tiller per plant was observed in genotypes Condai and SCRID 091-20-3-1-3-4 which had (5.55) number of total tiller per plant.

Significance variation in number of fertile tillers range from 5.35 to 11.55 per plant was observed among the genotype. Maximum number of tillers (11.55) per plant was produced by genotype Namcheobyeo followed by Halilbey (9.95), Edirne (9.8). Minimum number of tillers per plant were recorded in genotype SCRID091-20-3-13-4 (5.35) followed by Candai (5.45).

Fertile grain per panicle ranged from 55.75 to 104.75. Maximum number of fertile grains per panicle obtained from the genotype Condai (104.75) followed by SICRID 186-72-1-1-2 (104) and SCRID 091-24-3-2-2-3 (99.95). Minimum fertile grain per panicle obtained from genotype SCRID 122-13-1-1-4-3 (55.75) followed by SCRID 091-15-2-2-1-1 (59.9) and Hiber (60.1).

Thousand grain weight had significance difference in rice which ranges from 25.9 to 34.8 g. Maximum grain weight was recorded in genotype Osmancik-97 followed by genotype SCRID 090-164-2-1-2-1 (31.07 g) and SCRID 091-38-3-1-3-1 (30.37) were better than the rest of the genotype (Mulugeta *et al.* have reported significance differences in 1000-grain weight in rice the genotypes. [33] Likewise,

biomass yield showed significance difference due to genotype difference. The mean value ranged from 3689 to 7973 gm.

Harvest index ranged from 0.255-0.475 g. Maximum harvest index was obtained from genotype Suitou,

chuukanbohon Nou 11 (0.475) followed by Tunca (0.4675) and SCRID 186-72-1-1-2 (0.4675). Minimum harvest index was obtained from genotype SCRID 091-38-3-1-3-1 (0.255) followed by Trakya (0.275), SCRID 091-15-2-2-1-1 (0.285) and SCRID 090-72-3-1-3-5 (0.295).

**Table 3.** Estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variations, broad sense heritability ( $H^2b$ ), genetic advance (GA) and GA as percent of mean (GAM) for 15 traits of 36 rice varieties based on analysis of variance over two locations.

Trait	Range	$\sigma^2p$	$\sigma^2g$	GCV	PCV	$H^2b$ (%)	GA	GAM
HD	76-91.25	37.18	27.13	5.7	6.67	72.97	9.16	10.02
MD	129.5-148.25	70.98	35.75	4.64	6.53	50.37	8.74	6.78
PH (cm)	91.9-140.97	219.07	200.57	15.67	16.37	91.56	27.92	30.88
PL (cm)	18.47-22.6	2	1.33	6.42	7.86	66.79	1.94	10.81
CL	74.7-119.52	185.87	166.82	17.7	18.69	89.75	25.21	34.55
PBPP	9.6-10.9	0.69	0.44	7.21	8.99	64.38	1.1	11.92
TTPP	7.9-12.35	2.24	1.11	13.83	19.64	49.55	1.53	20.05
FTPP	7.1-11.55	1.79	0.86	12.76	18.45	47.86	1.32	18.19
UFTPP	0-1.32	0.12	0.04	50.38	88.16	32.65	0.24	59.3
FGPP	55.75-84.55	125.45	28.99	6.66	13.86	23.11	5.33	6.6
INFGP	5-14.45	7.74	2.23	27.22	50.66	28.87	1.65	30.13
TGW	25.96-34.85	10.47	2.4	5.97	12.45	22.95	1.53	5.89
HI	0.255-0.475	0.002	0.0002	6.85	14.25	23.08	0.03	6.78
BY	3689-5448.1	859261	130581.8	6.75	17.32	15.2	290.19	5.42
GY (kg/h)	1199.5-2980.7	390337.6	100624.9	10.95	21.57	25.78	331.78	11.46

### 3.3. Estimates of Variance Components

#### 3.3.1. Genotypic and Phenotypic Coefficients of Variation

In the present study, phenotypic variance was higher than genotypic variance in most characters, except total tiller per plant indicating the influence of environment on the trait. (Table 3). The extent of the environmental influence on any trait has been determined 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. Mulugeta *et al.* report some result for plant height, days to 50% heading, days to 85% maturity and biological yield, which indicate the influence of the environment on the traits. [32] Panicle length, primary branches per panicle, total tiller per plant, fertile tiller per plant and infertile tiller per plant had very close genotypic and phenotypic variance which indi-

cates the stable nature of these characters and the presence of sufficient genetic variability for the traits which may facilitate selection. Mulugeta *et al.* [26] and Fukrei *et al.* [13] reported similar findings in panicle length and fertile tiller per plant. [32, 17] Phenotypic coefficients of variation were higher than the genotypic coefficients of variation for all the traits studied. This indicates the presence of environmental influence on the phenotypic expression of the characters. Similar results were earlier reported by Konate *et al.* [18] Pandy *et al.* and Tefera *et al.* [36].

According to Sivasubramaniah and Menon (1973), PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered low and values between 10% and 20% are medium. Considering this, infertile tiller per plant, and infertile grain per panicle had high PCV and GCV values, which is an implication of the prevailing variability that opens up chance for carrying out improvement through simple selection [35]. The PCV and GCV value for plant height, culm length, total tiller per plant and fertile tiller per plant were medium hence is consider to have moderate

amount of variability and hence could be improved through selection in later generation. Mulugeta *et al.* [26] reported medium PCV estimates for number of filled grains per panicle [32] and Mishu *et al.* [24] for plant height. Thousand grain weight, Harvest index and biological yield showed medium PCV value, but they had lower GCV value. [30]. Osekita *et al.* [29] reported medium PCV value for thousand grain weight. [37]. Days to 50% heading, days to 85% maturity, panicle length and primary branches per panicle had low PCV and GCV values, it indicate the presence of narrow genetic base for such traits and hence for their improvement, methods like hybridization and induced mutagenesis can be used to widen the genetic base, followed by pedigree selection in the advanced generations [35]. Similar results have been reported by Demewez *et al.* for days to 85% maturity, panicle length [9].

### 3.3.2. Estimation of Broad Sense Heritability

In this study the broad sense heritability values of the different traits ranged from 9% for harvest index to 91.56% for plant height. Considering this range, low heritability was found on harvest index (9%), thousand grain weight (22.95%), grain yield (21.75%), fertile grain per panicle (23.11%), infertile grain per panicle (28.86%). low heritability indicates greater role of environment in the expression of the trait and therefore, direct selection for these traits will be ineffective. Therefore, creating variability by hybridization or mutation for these traits for selection. Medium heritability estimate was obtained in unfertile tiller per plant, (32.65%) fertile tiller per plant (47.83), total tiller per plant (49.55%) and days to 85% maturity (50.37%) which indicates the possibility of using for rice improvement program but their expression could be influenced by the environment in which they are grown. High heritability was found to days to 50% heading, (72.97%), plant height (91.56%), panicle length (66.79%), culm length (89.75%) and primary branches per panicle (64.6%). High values of heritability indicated that it was predominantly governed by additive gene effect. Such traits can be improved by mass selection and adapting several other breeding strategies based on progeny selection. It suggests high component of heritable portion of variation that can be exploited by breeders in selection of superior genotypes based on phenotypic performance. Similar results have been reported by Vanisree *et al.* [37] for panicle length and Akinwale *et al.* [1], Osman *et al.* [30] Tefera *et al.* [36] and Mishu *et al.* for plant height. [2, 38, 30]. In opposite of this Sathya reported low heritability for panicle length. [33]. (Table 3)

### 3.3.3. Genetic Advance

The genetic advance is an indicator of the progress that can be expected as the result of applying selection to the pertinent population. Heritability in relation to genetic advances would give a more reliable index of selection value. [17]. The genetic advance as the percentage of the mean (GAM) at 5% selection intensity is presented in (Table 5). It ranges from 2.46% for harvest index to about (59.3%) for unfertile tiller per plant.

Relatively high genetic advance estimates as the percent of the mean were recorded for unfertile tiller per plant (59.3%), infertile grain per panicle (30.12%), total tiller per plant (20.05%), culm length (34.55%) and plant height (30.88%). Tefera *et al.* reported similar finding for number of infertile grain per panicle. [36] Moderate genetic advance value as the percent of mean obtained for primary branches per panicle (11.96%), days to 50% heading (10.02%), panicle length (10.81%), fertile tiller per plant (18.17%) and grain yield/ha (11.46%). Mulugeta *et al.* reported similar finding for grain yield/ha. [27]. Low estimate of genetic advance as percent of mean was also found to harvest index (2.46%), biological yield (5.42%), fertile grain per panicle (6.6%) and days to 85% maturity (6.782%). A low GCV and GAM observed for harvest index indicate that the trait had under high environmental influence, and that selection based on these traits would be ineffective. Similar result was reported by Bhave *et al.* for days to 85% maturity which had low genetic advance. [4]. High heritability with high genetic advance as percentage of mean was recorded in plant height and culm length regarded as an indication of additive gene action and the consequent high expected genetic gain from selection for these characters. This finding agreed with (Mulugeta *et al.* for plant height. [26]. Low heritability combined with low genetic advance as percentage of mean estimates observed for harvest index which explains the dominance of non-additive gene action and genotype x environment interaction played significant role in the expression of these traits. High estimate of heritability coupled with moderate genetic advance as percentage of mean value was recorded for panicle length, indicating both additive and non-additive genes governed the expression of this character. Hence, simple direct selection could be effective in improving this trait. Relatively high estimate of GCV, PCV, broad sense heritability and genetic advance obtained for plant height and culm length imply these characters should be transmitted to the progeny when hybridization is conducted and phenotypic based selection is effective.

## 3.4. Character Associations

### 3.4.1. Relation of Grain Yield with Other Traits

Grain yield, being a quantitative trait, is a complex character of any crop. Various morphological and physiological plant traits contribute to yield. These yield contributing components are interrelated with each other showing a complex chain of relationship and highly influenced by the environmental conditions. Breeding strategy in rice mainly depends upon the degree of associated traits as well (Prasad *et al.*, 2001) (Table 4).

Grain yield had highly significant and positive phenotypic associations with days to 50% heading ( $r_p=0.39$ ), primary branches per panicle ( $r_p=0.41$ ), fertile grains per panicle ( $r_p=0.5$ ), thousand grain weight ( $r_p=0.5$ ), fertile tiller per plant and harvest index ( $r_p=0.76$ ). This implies that grain yield could be increased by increased those traits. Mishu *et al.* re-

ported positive association of days to 50% heading to grain yield. [24]. Ogunbayo *et al.* [28] observed that primary branches per panicle had positive association with grain yield. [36].

Days to 85% maturity had positive association with grain yield at phenotypic level, but not significantly correlate. At phenotypic level, total tiller per plant and infertile grain per panicle had non-significance negative correlation with grain yield.

Plant height also had negative correlation with grain yield. Negative correlation coefficient plant height with grain yield indicates that tallness in rice reduce yield due to maximum accumulation of photo synthetics in vegetative parts as compared to reproductive parts (i. e. seed formation and grain filling and lodging susceptibility). In line with this result Ukaoma *et al.* reported negative association of plant height with grain yields. On the contrary Sravan *et al.* (2012) and Mulugeta *et al.* reported positive correlation of grain yield with plant height. [26]. Positive and significance correlation of primary branches per panicle, fertile grain per panicle, fertile tiller per plant, thousand grain weight and harvest index with grain yield indicate the importance of these traits for determining grain yield, selecting those traits in rice breeding would result in increment of grain yield.

At genotypic level, panicle length, primary branches per panicle, fertile grain per panicle, fertile tiller per plant, harvest index and biological yield had positive and highly significant ( $p \leq 0.01$ ) correlation with grain yield. Days to 50% heading, days to 85% maturity, plant height and thousand grain weights had positive and non-significance correlation with grain yield. Were as, total tiller per plant, unfertile tiller per plant and infertile grain per panicle had non-significance negative correlation with grain yield. Ogunbayo *et al.* observed significant and positive association of grain yield ha<sup>-1</sup> with number of primary branches per panicle at genotypic level. [28] Positive correlated result showed that increase of one traits will lead to increase of the correlated traits and negative association of traits indicates that increase one characters will decrease the negatively correlated characters. Therefore, selection would be effective with simultaneous consideration of primary branches per panicle, fertile grain per panicle, harvest index, fertile tiller per plant, panicle length and biological yield. Pervious report also indicated that harvest index, days to 85% maturity; thousand grain weight and panicle length should be given attention on the selection criteria for genetic improvement of rice yield.

### 3.4.2. Correlation Among Yield Related Traits

Visible association was observed among yield and related traits (table 4). At phenotypic level days to 50% heading showed positive and highly significance association with days to 85% maturity, primary branches per panicle, harvest index, thousand grain weights and fertile grain per panicle and had negative significance correlation with plant height, culm length, total tiller per plant and fertile tiller per plant. Venkata *et al.* [38] and Mulugeta *et al.* reported similar

findings for days to 85% maturity. [26]. Similarly, days to 50% heading had negative but none significance correlation with panicle length ( $r_p = -0.12$ ), unfertile tiller per plant ( $r_p = -0.18$ ) and biological yield ( $r_p = -0.07$ ).

Days to 85% maturity had significance positive correlation with panicle length, primary branches per panicle, fertile grain per panicle, biological yield and harvest index. However, it had positive and non-significance correlation with total tiller per plant thousand grain weights, fertile tiller per plant and grain yield. Plant height had positive and highly significance correlation with panicle length, culm length, total tiller per plant, fertile tiller per plant, fertile grain per panicle and biological yield. However, it had negative significance correlation with infertile grain per panicle and thousand grain weight. Mulugeta *et al.* reported similar finding for plant height which had positive association with fertile tiller per plant. [27]. Mishu *et al.* also reported positive significant association of plant height with panicle length. [24] Significant positive correlation between panicle length and days to maturity was also reported by Karim *et al.* (2014).

Panicle length had positive and highly significance correlation with culm length ( $r_p = 0.65$ ), primary branches per panicle ( $r_p = 0.33$ ), fertile grain per panicle ( $r_p = 0.43$ ) total tiller per plant ( $r_p = 0.29$ ), fertile tiller per plant ( $r_p = 0.33$ ) and biological yield ( $r_p = 0.49$ ) at phenotypic level, revealing that with increasing of Panicle length, culm length, primary branches per panicle, fertile grain per panicle total tiller per plant, fertile tiller per plant and biological yield will also increase proportionately. Mulugeta *et al.* reported significant and positive association of panicle length with number of total tiller per plant. [27]. Primary branches per panicle had positive and highly significance correlation with fertile grain per panicle, fertile tiller per plant, total tiller per plant and biological yield. However, it had negative significance correlation with infertile grain per panicle.

Total tiller per plant had positive and highly significance correlation with unfertile tiller per plant at phenotypic level. However total tiller per plant had negative and highly significance correlation with harvest index and thousand grain weights. Fertile tiller per plant positively correlated with days to 85% maturity, plant height, panicle length and culm length were positively correlated with fertile tiller per plant at phenotypic level. Days to 50% heading harvest index and thousand grain weights had significance negative association with fertile tiller per plant at phenotypic level. Mulugeta *et al.* reported fertile tiller per plant had positive correlation with days to 50% heading. [27].

Fertile grain per panicle had positive and highly significance correlation with harvest index and biological yield. However, it had negative and highly significance correlation with infertile grain per panicle at phenotypic level. Harvest index had negative and non-significance correlation with biological yield.

At genotypic level days to 85% maturity had positive and

significant association with days to 50% heading (0.82\*\*), total tiller per plant (0.35\*), fertile tiller per plant (0.37\*) and biological yield (0.42\*). Chang *et al* [6] reported significant correlation of days to maturity with days to heading.

Plant height exhibited significance and positive correlation with panicle length ( $r=0.66^{**}$ ), culm length ( $r=0.99^{**}$ ). These characteristics indicated that increasing of plant height would lead to increase in the panicle length and culm length. Panicle length had positive and highly significance correlation with culm length, primary branches per panicle, unfertile tiller per plant, fertile grain per panicle and harvest index. However, it had significance negative correlation with unfilled grain per panicle.

Primary branches per panicle had positive significance correlation with filled grain per panicle ( $r=0.82^{**}$ ), harvest index ( $r=0.47^{**}$ ) and biological yield ( $r=0.34^*$ ). However, it had negative and high significance association with total tiller per plant, fertile tiller per plant and unfertile tiller per plant.

Association between number of total tiller per plant and

number of fertile tiller per plant and unfertile tiller per plant ( $r=0.98^{**}$ ), ( $r=0.63^{**}$ ) respectively were highly significance and positive, but it was highly significant and negative with grain yield per plant ( $r=-0.36^*$ ). Number of fertile tiller per plant showed significant and positive association with unfertile tiller per plant and it showed significant and negative association with thousand grain weight ( $r=-0.38^*$ ) and with grain yield ( $r=-0.34^*$ ). The trend of relationship between unfilled grains per panicle with harvest index was high and significantly negative with value of ( $r=-0.56^{**}$ ) at genotypic level.

Newall and Eberhart (1961) suggested that characters having negative phenotypic and genotypic correlation with grain yield would be difficult to apply simultaneous selection in crop improvement programs. Therefore, from the current studies for the traits which correlated negatively with grain yield the selection that we followed should be strictly seen for improvement of such important yield component characters.

**Table 4.** Estimation of phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients between yields, and yield component characters.

Traits	HD	MD	PH	PL	CL	PBPP	TTPP	FTPP	UFTPP	FGPP	INFGP	TGW	HI	BY	GY
HD		0.61**	-0.34**	-0.12	-0.35**	0.29**	-0.27**	-0.28**	-0.18	0.28**	-0.09	0.37**	0.36**	-0.07	0.39**
MD	0.82**		-0.05	0.23**	-0.08	0.27**	0.15	0.14	-0.05	0.34**	-0.14	0.004	0.21**	0.17*	0.14
PH	-0.18	-0.15		0.70**	0.99**	0.21	0.27**	0.29**	-0.04	0.28**	-0.19**	-0.29**	-0.14	0.43**	-0.1
PL	0.07	0.15	0.66**		0.65**	0.33**	0.29**	0.33**	-0.17*	0.43**	-0.20**	-0.28**	0.11	0.49**	0.04
CL	-0.2	-0.18	0.99**	0.61**		0.18	0.27**	0.28**	-0.01	0.255**	-0.18*	-0.28**	-0.17*	0.42**	-0.11
PBPP	0.39	0.24	0.25	0.45**	0.23		-0.09	-0.08	-0.19	0.63**	-0.23**	-0.001	0.32**	0.26**	0.41**
TTPP	0.25	0.35*	-0.38*	-0.31	0.38*	-0.45**		0.97**	0.48**	-0.06	0.16*	-0.67**	-0.44**	0.51**	-0.52**
FTPP	0.25	0.37*	-0.33*	-0.23	0.33*	-0.45**	0.98**		0.36**	-0.03	0.12	-0.66**	-0.39**	0.53**	0.49**
UFTPP	-0.01	0.06	-0.38*	0.59**	0.35*	-0.36*	0.63**	0.49**		-0.28**	0.25**	-0.38**	-0.48**	0.1	-0.45**
FGPP	0.35	0.31	0.28	0.51**	0.26	0.82**	-0.40*	-0.36*	0.45**		-0.44**	-0.04	0.49**	0.36**	0.50**
INFGP	0	-0.01	-0.38*	-0.35*	0.36*	-0.29	0.23	0.22	0.12	-0.42*		-0.2	-0.52**	-0.14	-0.47**
TGW	-0.09	-0.25	0.22	0.15	0.23	-0.019	-0.40*	-0.38*	-0.28	-0.06	-0.03		0.42**	-0.38**	0.50**
HI	0.01	0.001	0.12	0.48**	0.08	0.47**	-0.17	-0.1	-0.38*	0.54**	-0.56**	0.04		-0.16*	0.76**
BY	0.519**	0.42*	0.08	0.33	0.06	0.34*	-0.11	-0.09	-0.23	0.42*	-0.32	0.15	0.16		0.04
GY	0.21	0.13	0.21	0.51**	0.18	0.70**	-0.36*	0.34*	-0.42**	0.72**	-0.51*	0.1	0.73**	0.59**	

\*,\*\*significance at  $p \leq 0.05$ , and  $p \leq 0.01$  probability level respectively. HD =days heading, MD =days to maturity, PH=plant height, PL=panicle length, CL=culm length, PBPP=primary branches per panicle, TTPP=total tiller per plant, FFTP=fertile tiller per plant, UNFTP=unfertile tiller per plant, FGPP=fertile grain per panicle, INFGP=infertile grain per panicle, TGW=thousand grain weight, HI=harvest index, BY=biological yield and GY=grain yield

### 3.5. Path Coefficient Analysis

To find out the cause and effect relationship between grain yield and its related traits, path analysis was taken up in the present investigation. Grain yield as the dependent variable and other traits as independent variables were used for path coefficient analysis. (Table 5)

#### 3.5.1. Phenotypic Direct and Indirect Effect of Various Characters on Grain Yield

The phenotypic path coefficient analysis revealed that the harvest index had the highest positive direct effect (0.449) on grain yield followed by total tiller per plant (0.302) and thousand grain weight (0.195). The favorable direct effects of these traits on grain yield indicate true relationship between these traits and importance in determining these complex characters that showed other variables kept constant, improvement of these characters will increase seed yield and also increasing traits which have positive association with these traits will improve the yield of rice indirectly passing through the directly passing associated traits with grain yield. Moosavi *et al.* [25] reported similar result for harvest index. On the other hand, the highest negative direct effect (-0.432) was exerted by fertile tiller per plant followed by unfertile tiller per plant (-0.063) and infertile grain per panicle (-0.075). In such situation direct selection for genotypes that had high unfertile tiller per plant, infertile grain per panicle and fertile tiller per plant might be ineffective for grain yield improvement. Mulugeta *et al.* found the same result for number of fertile grain per panicle. [27]. The current findings suggested that improvement of grain yield of lowland rice through selection could be achieved through direct selection for positively contributed component traits to grain yield and positively exerted indirect traits to counterbalance the negative direct effects of component traits. The residual effect was (0.54), which implied that the contribution of component traits explained 48% of total variation in grain yield by the nine characters evaluated in the path analysis, the rest 53% was the contribution of other traits that are not considered in the path analysis and environmental factors. (Table 5)

#### 3.5.2. Genotypic Direct and Indirect Effect of Various Characters on Grain Yield

Genotypic path coefficient analysis for yield and yield related components revealed, maximum and positive direct effects for total tiller per plant (0.834), harvest index (0.594) and biological yield (0.418) and on rice grain yield respectively. The High direct effect of these traits therefore, gives the impression to be the main factor for their positive and significant relationship with grain yield and should be considered as important traits for rice improvement. In line with the current result for harvest index positive and direct on rice grain yield were reported by Satheeshkumar and Saravanaa [33], Badriet *al* [2]. The indirect effect of biological yield and harvest index on grain yield via panicle length, primary branches per panicle and fertile grain per panicle were positive. Traits like harvest index, biological yield and primary branches per panicle showed positive and indirect association with grain yield passing through panicle length. In contrary fertile tiller per plant had the highest negative direct effect (-0.923) on yield followed by unfertile tiller per plant (-0.102). Number of fertile tiller per plant expressed negative indirect effect on grain yield through infertile grain per panicle (-0.202), unfertile tiller per plant (-0.455) and total tiller per plant (-0.906) respectively. Panicle length was positively and significantly correlated with grain yield but its direct effect was negative, indicating that indirect effects would be the cause of correlation. In this condition the indirect factors to be considered for selection. (Table 6)

Therefore, from the present genotypic path coefficient analysis it is found that rice yield component like biological yield, harvest index, primary branches per panicle and total tiller per plant had positive direct effect on yield which indicates considering these traits during selection of rice genotypes would be more rewarding to involve potential varieties of rice. The residual effect was (0.44), indicating that 56% of the variability in grain yield was contributed by traits considered in the path analysis and the remaining might be due to environmental factors.

**Table 5.** Phenotypic direct and indirect effects of nine component traits on grain yield in lowland rice.

Traits	FD	PBPP	TTPP	F TPP	UFTPP	FGPP	INFGP	TGW	HI	rp
HD	0.014	0.035	-0.081	0.120	0.012	0.046	0.007	0.072	0.166	0.39**
PBPP	0.004	0.120	-0.027	0.039	0.013	0.103	0.018	0.0001	0.145	0.41**
TTPP	-0.004	-0.011	0.302	-0.423	-0.031	-0.010	-0.012	-0.131	-0.197	-0.52**
F TPP	-0.004	-0.011	0.296	-0.432	-0.023	-0.005	-0.009	-0.128	-0.177	0.49**
UFTPP	-0.003	-0.024	0.146	-0.158	-0.063	-0.045	-0.019	-0.074	-0.215	-0.45**
FGPP	0.004	0.076	-0.019	0.013	0.018	0.163	0.033	-0.009	0.223	0.5**
INFGP	-0.001	-0.028	0.048	-0.052	-0.016	-0.072	-0.075	-0.040	-0.232	-0.47**

Traits	FD	PBPP	TTPP	FTPP	UFTPP	FGPP	INFGP	TGW	HI	rp
TGW	0.005	0.0001	-0.203	0.284	0.024	-0.008	0.015	0.195	0.188	0.5**
HI	0.005	0.039	-0.132	0.170	0.030	0.081	0.039	0.082	0.449	0.76**

Residual effect =0.54

**Table 6.** Genotypic direct and indirect effects of nine component traits on grain yield in lowland rice.

Traits	PL	PBPP	TTPP	FTPP	UFTPP	FGPP	INFGP	HI	BY	Rg
PL	-0.010	0.065	-0.262	0.209	0.061	0.040	-0.014	0.291	0.137	0.5**
PBPP	-0.005	0.143	-0.376	0.424	0.037	0.064	-0.012	0.285	0.146	0.7**
TTPP	0.003	-0.064	0.834	-0.906	-0.065	-0.031	0.010	-0.100	-0.048	-0.3*
FTPP	0.002	-0.066	0.818	-0.923	-0.050	-0.029	0.009	-0.061	-0.041	0.34*
UFTPP	0.006	-0.052	0.531	-0.455	-0.102	-0.035	0.005	-0.227	-0.098	-0.42**
FGP	-0.005	0.117	-0.336	0.341	0.046	0.078	-0.017	0.326	0.179	-0.72**
INFGP	0.004	-0.043	0.196	-0.202	-0.012	-0.033	0.041	-0.333	-0.137	-0.51*
HI	-0.005	0.068	-0.140	0.094	0.039	0.043	-0.023	0.594	0.066	0.73**
BY	-0.003	0.050	-0.096	0.091	0.024	0.033	-0.013	0.093	0.418	0.59**

Residual effect =0.44

## 4. Conclusions

The analysis of variance revealed significant difference between the genotypes for traits, days to 50% heading, days to 85% maturity, plant height, panicle length, culm length, primary branches per panicle, total tiller per plant, fertile tiller per plant, un fertile tiller per plant, fertile grain per panicle, infertile grain per panicle, thousand grain weight, harvest index, biological yield and grain yield, indicating the presence of considerable amount of variability among the genotypes. Phenotypic variance was greater than genotypic variance except biological yield and grain yield. Phenotypic coefficients of variation were higher than the genotypic coefficients of variation for all the traits studied. This indicates the presence of environmental influence to some degree in the phenotypic expression of the traits. High phenotypic and genotypic coefficient of variation was recorded for grain yield.

Heritability estimate in rice was found to be high for days to 50% heading, plant height, panicle length, culm length, and primary branches per panicle. High heritability of the traits indicates that the direct selection would be effective for improvement of these characters. The genetic advance as the percent of mean estimates were high for unfertile tiller per plant, culm length, plant height and infertile grain per panicle. Plant height displayed high heritability and high heritability

with high genetic advance as percent of mean indicates the predominance of additive gene action in the expression of traits.

Grain yield had significant and positive association with primary branches per panicle, fertile grain per panicle and harvest index at both genotypic and phenotypic levels. There was significant positive association of grain yield with days to 50% heading at phenotypic level. Total tiller per plant, fertile tiller per plant, unfertile tiller per plant and infertile grain per panicle had non-significance negative correlation with grain yield. Harvest index, total tiller per plant and thousand grain weights showed positive phenotypic direct effect, on the other hand total tiller per plant, harvest index, biological yield and primary branches per panicle showed positive genotypic direct effects on grain yield. This indicates considering of these traits during selection of rice genotypes would be more effective in evolving potential varieties of rice.

## Abbreviations

GA	Genetic Advance
GAM	Genetic Advance at Percent of Mean
GCV	Genetic Coefficient of Variation
PCV	Phenotypic Coefficient of Variation
IRRI	International Rice Research Institute
$\sigma^2_p$	Phenotypic Variance

$\sigma^2_g$	Genotypic Variance
$H^2_b$	Broad Sense Heritability
$\sigma^2_e$	Environmental Variance
R	Residual Effect

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## Author Contributions

**Mequannit Aklilu:** Data curation, Formal Analysis, Methodology, Validation, Writing – original draft

**Sentayehu Alameraw:** Supervision, Writing – review & editing

**Abewaw Dessie:** Supervision, Writing – review & editing

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## Conflicts of Interest

The authors declare no conflicts of interest.

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## Research Fields

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