Genetic Variability and Traits Association Study in Rainfed Lowland Rice (*Oryza sativa* L.) Genotypes in Southwestern Ethiopia

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Abstract: Background and Objective: Complete knowledge on the extent of genetic variability and interrelationships of yield and components traits is pre-request for designing an effective and efficient selection based rice improvement programs for generating high yielding rainfed lowland rice genotypes. The objective of this study was in order to determine the extent of genetic variability and association of characters with grain yield and among themselves. Materials and Methods: Twenty-five rainfed lowland rice genotypes were evaluated during the 2016 main cropping season at two rainfed lowland agro-ecologies of Southwestern Ethiopia. The experiment was laid out in a simple lattice design and data on 14 yield and yield component traits were collected and subjected to various statistical analyses. Results: Combined analysis of variance across locations revealed significant location, genotype and genotype x location interaction effects for several traits evaluated at p ≤ 0.01. The phenotypic coefficient of variation (PCV) ranged from 2.14% for days to 85% maturity to 18.09% for grain yield, while the genotypic coefficient of variation (GCV) ranged from 0.71% for days 85% to maturity to 10.48% for grain yield. Heritability estimate in broad sense was high for plant height (74.15) and low for days to 85% maturity (11.06) and harvest index (23.47). Plant height displayed high heritability along with moderate genetic advance as percent of mean value and days to 85% maturity and harvest index exhibited low GCV, heritability and genetic advance as percentage of mean estimates. Correlation coefficient analysis of grain yield showed positive and significant association with number of primary branches per panicle at both phenotypic and genotypic levels. Separation of correlation coefficients into direct and indirect effects of component traits on grain yield revealed that number of primary branches per panicle exerted the maximum positive direct effect on grain yield at both genotypic and phenotypic levels. Conclusion: The present study indicated sufficient amount of genetic variability for the majority of the characters studied in rainfed lowland rice genotype for future exploitation in selection based improvement programs.

Keywords: Lowland Rice, Genetic Variability, Traits Association, Heritability, Phenotypic Correlation, Genotypic Correlation

1. Introduction

The government of Ethiopia considered rice as the most strategic food security crop that has received special attention in promotion of agricultural production and as such it is named as the "millennium crop" expected to contribute in ensuring food security in Ethiopia [1]. The country expected to find export market in near future for other African countries and thus, the crop is one of the main trust areas of attracting for domestic consumption or international trade purposes [2].

In Ethiopia rainfed rice is cultivated in Amhara, Tigray, Oromia, South Nation Nationalities and Peoples Region (SNNPR), Gambella and Benshangul Gumuz Regions of

Ethiopia [1]. SNNPR is the third largest producer of lowland rice next to Gambella and Tigray in Ethiopia in terms of estimated area coverage and it was principally cultivated in Kaffa (Gimbo District), Benchi Maji (Guraferda, Menit Goldia and Menit Shasha Districts) and Sheka zones [3, 4]. The total cultivated area at national level has increased from 33,819.65 in 2013/2014 to 45, 454.2 hectares in 2015/2016. Accordingly, production has increased from a total of 92,362.7 tons, in 2013/14 to 1,268,064.47 tons in 2015/16. Similarly, productivity in ton per hectare has increased from 2.7 in 2013/14 to 2.8 in 2015/16. Out of the total rice produced in the country in 2015/16, 4,940.67 tons were produced in SNNPR and of these; 4,854.79 tons were produced in Keffa, Benchi Maji and Sheka zones [5].

Despite the country has immense potential for growing this crop, production, productivity and expansion of the rice has been challenged by lack of improved varieties, lack of recommended crop management practices for different rice ecosystems, lack of pre and post-harvest management technologies and lack of awareness on its utilization [6-8]. As a result, rice yield remains progressively low with average national productivity of 2.8 tons/ha[5], which is very much lower than the average yield of rice in the world that accounts 4.54 tons per hectare according to FAOSTAT, 2015 [9]. Among the production constraints, lack of improved varieties is one of the most pressing constraint in rice production and productivity in the country [10].

Although, genetic variability and performance evaluation studies were also done at southwestern Ethiopia on rainfed upland rice genotypes, there has been no studies done on rainfed lowland rice genotypes at south western Ethiopia in order to determine the extent of genetic variability and character association in rainfed lowland rice genotypes [7, 11].

Among the existing options to overcome the low rice production and productivity in order to meet the fastest growing demand, exploiting genetic variability which exists among rice genotypes for grain yield and yield components receives due emphasis. Since grain yield is a complex polygenic quantitative trait, selection for high yielding genotypes usually possible through by using various component traits associated with grain yield in a population [12]. This is important because the success of any selection program depends on the degree of inherent variability present in the population and direct or indirect selection of positively contributed component traits towards grain yield.

The present study was carried out with an objective to understand the genetic background and inheritance of the different traits in rainfed lowland rice genotypes. Furthermore, the specific objective of this study is to estimate genetic variability, heritability and correlation among the various quantitative traits of rice grown under rainfed lowland environments in order to aid the effective selection for successful breeding program. The findings of this study would help to identify the highly suitable genetic material and assist to design the subsequent breeding program to foster the varietal improvement programs.

2. Materials and Methods

Description of the Experimental Site

The Trial was conducted during the main cropping season in July 2016 in two locations of Gimbo and Yeki districts of Southwestern Ethiopia (Table 1).

Table 1. Detail Description of the Study Area.

Districts	Trial station	Altitude (m)	Longitude (°E)	Latitude (°N)	Temperature (Mean Monthly °C)		Mean Annual rainfall (mm)
					Minimum	Maximum	
Gimbo	Shomba Kichib	1235	36° 0′ 0″	7° 15′ 0″	16.7	24.0	1710
Yeki	Tepi	1200	35° 18' 0″	7° 3' 0″	15.4	29.5	1678

Experimental Materials

The experimental materials consisted of 25 rainfed lowland rice genotypes (Advanced lines) obtained from Fogera National Rice Research and Training Center (FNRRTC) and Bonga Agricultural Research Center (Table 2).

Table 2. Description of the experimental materials.

No	Genotypes/pedigree	Origin	Seed Source	Ecotype
1	WAB189-B-B-B-HB	WARDA	2014 LRNVT-FNRRTC	Rainfed Lowland
2	IAC-164	WARDA	2014 LRNVT-FNRRTC	Rainfed Lowland
3	DEMOZE	-	2014 LRNVT-FNRRTC	Rainfed Lowland
4	ROJOMENA271/10	-	2014 LRNVT-FNRRTC	Rainfed Lowland
5	IRGA370-38-1-1F-B1-1	IRRI	2014 LRNVT-FNRRTC	Rainfed Lowland
6	scrid113-3-5-3-5-4	Madagascar	2014 LRNVT-FNRRTC	Rainfed Lowland
7	scrid037-4-2-2-5-2	Madagascar	2014 LRNVT-FNRRTC	Rainfed Lowland
8	scrid017-1-4-4-4-1	Madagascar	2014 LRNVT-FNRRTC	Rainfed Lowland
9	scrid014-1-1-1-1	Madagascar	2014 LRNVT-FNRRTC	Rainfed Lowland
10	scrid006-3-2-3-2	Madagascar	2014 LRNVT-FNRRTC	Rainfed Lowland
11	WAB95-B-B-40-HB (Hiber)	WARDA	2014 LRNVT-FNRRTC	Rainfed Lowland
12	RPBIO4919-117	India	2015 LRRVT-BARC	Rainfed Lowland
13	IR82912-B-B-5	IRRI	2015 LRRVT –BARC	Rainfed Lowland
14	IR88628-B-B-30	IRRI	2015 LRRVT- BARC	Rainfed Lowland
15	IR83106-B-B-6	IRRI	2015 LRRVT –BARC	Rainfed Lowland

No	Genotypes/pedigree	Origin	Seed Source	Ecotype
16	scrid006-2-4-3-4-5	Madagascar	2014 LRNVT-FNRRTC	Rainfed Lowland
17	WAB-4507	WARDA	2014 LRNVT-FNRRTC	Rainfed Lowland
18	FOFIFA172	Madagascar	2014 LRNVT-FNRRTC	Rainfed Lowland
19	FOFIFA171	Madagascar	2014 LRNVT-FNRRTC	Rainfed Lowland
20	FOFIFA161	Madagascar	2014 LRNVT-FNRRTC	Rainfed Lowland
21	WAB502-8-5-1	WARDA	2014 LRNVT-FNRRTC	Rainfed Lowland
22	WABC165	WARDA	2014 LRNVT-FNRRTC	Rainfed Lowland
23	scrid079-1-5-4-2	Madagascar	2014 LRNVT-FNRRTC	Rainfed Lowland
24	NERICA-18	WARDA	2014 LRNVT-FNRRTC	Rainfed Lowland
25	FOFIFA 165	Madagascar	2014 LRNVT-FNRRTC	Rainfed Lowland

Source: Fogera National Rice Research and Training Center (FNRRTC) and Bonga Agricultural Research Center (BARC) Where, WARDA = West Africa Rice Development Association, IRRI = International Rice Research Institute., LRNVT = Lowland Rice National Variety Trial, LRRVT = Lowland Rice Regional Variety Trial

Experimental Design and Data Collection

The experiment was laid out in a 5x5 simple lattice design and five genotypes were assigned into each incomplete blocks. Standard evaluation system developed by IRRI [13] was followed in order to collect yield and yield component data. Days to 50% heading and days to 85% maturity, biomass yield, harvest index, thousand seed weight and grain yield per hectare were computed from plot basis. Five representative plants for each genotype in each replication were randomly taken to record observations on plant height (cm), panicle length (cm), total tillers per plant, fertile or productive tillers per plant, filled grains per panicle, unfilled grains per panicle, and primary branches per panicle grain yield per plant. Grain yield obtained on plot base was converted into Kg ha^{-1} and adjusted to 14% grain moisture content.

Statistical Analysis

For combined analysis of variance across locations, the homogeneity of error variance was tested by using F-$_{max}$ test developed by Hartley [14], 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 of each location given by the formula:

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

Error variances were homogenies for all traits evaluated and then pooled analysis of variance over locations was done using SAS [15]. Mean separation was done by using ANOVA protected LSD (least significant difference) at 1% and 5% probability levels Gomez and Gomez [16].

Estimation of genetic parameters

Estimates of variance components were computed using the formula suggested by Burton and De Vane [17] as follows.

1) Genotype variance

$$(\sigma^2 g) = (MSG\text{-}MSGXL)/RL$$

2) Genotype x location interaction variance

$$(\sigma^2 gl) = (MSGXL\text{-}MSE)/R$$

3) Environmental variance (mean square error)

$$(\sigma^2 e) = (MSE/R)$$

4) Phenotypic variance

$$(\sigma^2 p) = \sigma^2 g + \sigma^2 gl\ /L + \sigma^2 e\ /LR = MSG\ /\ RL$$

Where, $\sigma^2 p$ = Phenotypic variance
$\sigma^2 g$ = Genotypic variance
$\sigma^2 e$ = Environmental variance (mean square of error), then by using the methods suggested by Dewey and Lu [18], phenotypic and genotypic coefficient of variation was calculated as follows:

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma2p}}{\bar{x}} x100$$

$$\text{Genotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma2g}}{\bar{x}} x100$$

Where: $\sigma^2 p$ = Phenotypic variation; $\sigma^2 g$ = Genotypic variation and $\bar{x}$ = Grand mean of the trait under consideration. According to Sivasubramanian and Menon [19], PCV and GCV values more than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be moderate.

Estimation of broad sense heritability, genetic advance and genetic advance as percentage of mean.

Heritability in broad sense estimate for all parameters (h_b^2) was computed as the percentage of genotypic to phenotypic variances and classified as low (below 30%), medium (30-60%) and high (above 60%) according to reference points suggested by Johnson et al. [20].

$$h_b^2 = [\sigma^2 g/\sigma^2 p]*100$$

Where, H_b^2 = heritability in broad sense
$\sigma^2 g$ = Genotypic variance and
$\sigma^2 p$= Phenotypic variance, $\sigma^2 p = \sigma^2 g + \sigma^2 gl\ /L + \sigma^2 e\ /LR$
The expected response to selection was computed by using the method illustrated by Allard [21] assuming selection intensity of 5% given as follows:

$$GA= \sqrt{\sigma2ph}\ *k\ *\ h_b^2\ \text{or}\ k\ *\ \sigma_{ph}\ *\ h_b^2$$

Where, GA= Expected genetic advance, h_b^2 = Heritability in broad sense, $\sigma^2 ph$= Phenotypic variance, σph= phenotypic standard deviation, k = the standardized selection differential at 5% selection intensity (k = 2.063).

The genetic advance as percentage of population mean (GAM) was estimated with the method suggested by Johnson

et al. [20] and classified as low (<10%), moderate (10-20%) and high (>20%).

$$GAM = \frac{GA}{\bar{x}} \; X \; 100$$

Where, GAM = Genetic advance as percent of mean, GA = Genetic advance under selection and x̄= Grand mean of the trait under consideration.

Phenotypic and genotypic correction coefficient analysis

Phenotypic and genotypic correlation coefficients were computed from variance and covariance components based on the method described by Chaudhury and Singh [22] (1996). The correlation analysis was performed using SAS statistical package SAS [15].

$$Phenotypic\ correlation\ coefficients\ (rp_{xy}) = pcov\ (x,y)/\sqrt{(\sigma2px * \sigma2py)},$$

$$Genotypic\ correlation\ coefficients\ (rg_{xy}) = gcov\ (x,y)/\sqrt{(\sigma2gx * \sigma2g\ y)}$$

Where, pcovx.y and gcovx.y are phenotypic and genotypic covariance between variables x and y, respectively; $\sigma^2 px$ and $\sigma^2 gx$ are phenotypic and genotypic, variances for variable x; and $\sigma^2 py$ and $\sigma^2 g$ yare phenotypic and genotypic variances for the variable y, respectively.

Phenotypic and genotypic path coefficient analysis

The direct and indirect effect of yield related traits on yield and among themselves were estimated following the method suggested by Dewey and Lu [18] given as follows.

$$r_{ij} = P_{ij} + \Sigma r_{ik} p_{kj}$$

Where: rij = Mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficient.

Pij = Component of direct effects of the independent trait (i) on the dependent variable (j) as measured by the path coefficient and,

Σrikpkj = Summation of components of indirect effect of a given independent trait (i) on the given dependent trait (j) via all other independent traits (k).

Residual effect estimated by the formula

$$\sqrt{1 - R^2};\ Where:\ -R^2 = \Sigma p_{ij}\ r_{ij}$$

Where, R^2 is the residual factor, P_{ij} is the direct effect of yield by i^{th} trait, and r_{ij} is the correlation of yield with the ith trait.

3. Results

Analysis of Variance (ANOVA)

The mean square from the pooled analysis of variance over the two test locations showed significant location effects (P≤ 0.01) for evaluated parameters of days 50% heading, number of total tillers per plant, number of fertile tillers per plant, number of primary branches per plant, biomass yield, harvest index and grain yield per hectare. Combined analysis of variance across locations revealed statistically significant genotype effects (P≤0.01) for investigated traits of days to 85% maturity, plant height, panicle length, number of filled grains per panicle, number of primary branches per panicle, harvest index and grain yield per hectare (Table 3). The mean squares due to genotype x location interaction effects were statistically significant (P≤ 0.01) for days to 85% maturity, panicle length, grain yield per plant, thousand seed weight and grain yield per hectare. Days to heading, plant height, number of total tiller per plant, number of fertile tiller per plant, number of filled grains per panicle, number of unfilled grains per panicle, number of primary branches per panicle, biomass yield and harvest index showed non-significant genotype x location interaction effects.

Table 3. *Mean squares of combined analysis of variance for 14 traits of 25 rainfed lowland rice genotypes evaluated in 2016/17 main cropping season across two locations.*

Traits	MSL (1)	MSG (24)	MSGxL (24)	MSE (40)	CV (%)
DH	0.49**	0.09 ns	0.088ns	0.06	2.59
DM	0.36 ns	29.1*	25.88*	12.70	2.83
PH	0.0009 ns	148.1**	38.27 ns	36.43	7.70
PL	0.028 ns	5.24**	2.74*	1.53	6.17
TTPP	1.68**	0.31 ns	0.31 ns	0.18	13.78
FTPP	109.41**	7.74 ns	6.41 ns	4.92	31.43
FGPP	1.59 ns	3.01**	1.55 ns	0.97	12.61
UGPP	0.000289ns	2.1 ns	1.35 ns	1.23	22.40
PBPP	4.41*	2.09*	1.42 ns	1.03	10.69
£GYPP	0.07 ns	0.04 ns	0.05*	0.02	5.06
BY	53130.25**	4998.26ns	2197.96 ns	3349.48	25.37
HI	0.15**	0.01*	0.0078 ns	0.0053	18.92
TSW	28.9 ns	18.2 ns	24.47*	11.37	14.32
GY	3890097.46**	963568.41**	640318.3**	258769.50	18.75

Where, * = significant at (P≤0.05), and ** = significant at (P≤ 0.01), MSL = mean Squares of locations, MSG = mean squares of genotypes, MSGxL = mean square of genotype x location interaction, MSE = mean squares of error, CV = coefficient of variation. DH = days to heading, DM = days to maturity, PH = plant height, PL = panicle length, TTPP = number of total tiller per plant, FTPP = number of fertile tiller per plant, FGPP = number of filled grains per panicle, UGPP = number of unfilled grains per panicle, PBPP = number of primary branches per panicle, GYPP = grain yield per plant, BY = biological yield, HI = harvest index, TSW = thousand seed weight, GY = grain yield per hectare.

Estimation of Genetic Parameters

Phenotypic and genotypic coefficients of variation

The current study revealed that phenotypic variance ($\sigma^2 p$) and phenotypic coefficient variation (PCV) were generally higher than that of their corresponding genotypic variance ($\sigma^2 g$) and genotypic coefficient of variation (GCV), respectively for all the characters evaluated. Phenotypic coefficient of variation (PCV) values varied from 2.14 to 18.09% (Table 4). The PCV values for number of filled grains per panicle, harvest index and grain yield ha^{-1} were medium. Days to 85% maturity, plant height, panicle length and number of primary branches per panicle had low PCV values.

Genotypic coefficient of variability (GCV) values were low for days to 85% maturity, plant height, panicle length, number of filled grains per panicle, number of primary branches per panicle and harvest index. Moderate GCV estimate was observed for grain yield ha^{-1} (10.48%). The magnitude of the difference between the PCV and GCV were relatively large for number of filled grains per panicle, harvest index and grain yield ha^{-1}. However, extent of this difference was comparatively small for days to 85% maturity, plant height, panicle length and number of primary branches per panicle.

Estimates of broad sense heritability, genetic advance (GA) and genetic advance as percentage of mean (GAM)

The estimates of broad sense heritability were varied from 11.06 % for days to maturity to 74.15% for plant height (Table 4). In the present study, plant height exhibited high heritability estimate moderate heritability estimates were registered for panicle length, number of filled grains per panicle, number of primary branches per panicle and grain yield ha^{-1}. Low estimates of heritability were obtained for days to 85% maturity and harvest index.

The highest value of genetic advance was recorded with grain yield (339.68) and the lowest with harvest index (0.02). Genetic advance as percent of mean had a general range between 0.49 % for days to 85% maturity and 12.52 % for grain yield. Among the characters moderate values of GAM (10 to 20%) were recorded for plant height, number of filled grains per panicle and grain yield ha^{-1} and low (<10%) for days to 85% maturity, panicle length, number of primary branches per panicle and harvest index. High estimate of heritability coupled with moderate genetic advance as percentage of mean value was recorded for plant height. Low heritability combined with low genetic advance as percentage of mean estimates was obtained for days to 85% maturity and harvest index.

Table 4. *Estimates of range mean and variance components of different traits in rainfed lowland rice genotypes over the two locations.*

Traits	Range	Mean ±SD	$\sigma^2 p$	$\sigma^2 g$	PCV	GCV	h^2_b (%)	GA	GAM (%)
DM	122-131	126.14±3.56	7.28	0.80	2.14	0.71	11.06	0.62	0.49
PH	63.85-89.5	78.39±6.04	37.02	27.45	7.76	6.68	74.15	9.31	11.87
PL	17.3-22.25	20.05±1.24	1.31	0.63	5.71	3.94	47.72	1.13	5.62
FGPP	38.7- 95.8	60.9±0.98	0.75	0.36	11.11	7.74	48.45	0.87	11.11
PBPP	8.4-11.2	9.47±1.01	0.52	0.17	7.63	4.29	31.65	0.47	4.98
HI	0.25-0.48	0.38±0.07	0.003	0.001	13.08	6.33	23.47	0.02	6.33
GY	1926.4-4015.3	2712.61±508.69	240892.1	80812.53	18.09	10.48	33.55	339.68	12.52

Where, SD = standard deviation, DM = days to maturity, PH = plant height, PL = panicle length, FGPP = number of filled grains per panicle, PBPP = number of primary branches per panicle, HI = harvest index, GY = grain yield per hectare

Correlation of grain yield and yield related traits at phenotypic and genotypic levels

At phenotypic level, except days to heading, plant height, number of filled grains per panicle and number of primary branches per panicle all other traits exhibited non-significant association with grain yield ha^{-1}. Number of primary branches per panicle displayed the highest significant and positive correlation with grain yield ha^{-1} (r = 0.47**). In addition to positive and significant correlation, high to moderate heritability estimate is necessary for the indirect selection to enhance grain yield. Significant and negative associations were obtained for grain yield with days to 50% heading (r = -0.41**), plant height (r = -0.27*) and number of filled grains per panicle (r = - 0.31*) indicated in the Table 5.

Similarly at genotypic level, number of primary branches per panicle (r = 0.52**) depicted significant and positive association with grain yield. Days to 50 % heading (r = -0.45**) and number of total tiller per plant (r = -0.43*) displayed significant and negative correlation with grain yield (Table 5).

Table 5. *Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients of 14 yield and yield component traits on 25 rainfed lowland rice genotypes.*

Traits	DH	DM	PH	PL	TTPP	FTPP	FGPP
DH		0.21	0.10	-0.03	0.15	0.12	0.13
DM	0.18		-0.05	-0.06	0.02	0.01	0.01
PH	0.07	-0.11		0.46**	0.52**	0.48**	0.23
PL	-0.03	-0.30	0.50*		0.34*	0.26	-0.01
TTPP	0.20	0.05	0.62**	0.28		0.77**	-0.04
FTPP	0.08	0.02	0.43*	0.16	0.76**		0.12
FGPP	0.14	-0.09	0.26	-0.10	0.01	0.19	
UGPP	-0.32	0.01	0.28	0.20	-0.14	-0.24	0.13
PBPP	-0.32	-0.14	0.10	0.21	-0.27	-0.06	0.10

Traits	DH	DM	PH	PL	TTPP	FTPP	FGPP
GYPP	-0.31	-0.02	-0.32	-0.10	-0.51**	-0.40**	-0.19
BY	-0.20	-0.33	0.15	0.27	0.12	0.24	0.02
HI	0.35	0.09	-0.11	-0.19	0.19	0.46*	0.38
TSW	0.02	-0.22	-0.14	0.10	0.22	0.18	-0.17
GY	-0.45 **	-0.31	-0.30	0.22	-0.43*	-0.09	-0.37

***Table 5.** Continued.*

Traits	UGPP	PBPP	GYPP	BY	HI	TSW	GY
DH	-0.16	-0.28*	-0.09	-0.08	0.36*	0.06	-0.41**
DM	-0.06	0.06	0.04	-0.06	0.10	-0.06	-0.14
PH	-0.01	0.09	-0.11	0.18	0.07	-0.12	-0.27*
PL	-0.01	0.18	-0.03	0.30*	-0.08	-0.09	0.21
TTPP	-0.01	-0.03	-0.29*	0.14	0.17	-0.07	-0.22
FTPP	-0.19	0.09	-0.12	0.17	0.48**	0.02	-0.10
FGPP	-0.01	0.05	-0.07	0.09	0.37**	-0.14	-0.31*
UGPP		0.15	-0.13	0.08	-0.48**	-0.05	0.13
PBPP	-0.02		0.09	0.06	0.03	0.07	0.47 **
GYPP	0.01	0.34		0.14	0.17	-0.01	0.07
BY	0.12	-0.09	0.00		-0.19	-0.03	0.09
HI	-0.62**	0.06	-0.08	-0.12		0.04	-0.21
TSW	-0.19	-0.04	-0.08	0.15	-0.004		0.08
GY	-0.03	0.52**	0.32	0.04	-0.099	0.15	

* = significant at P<0.05; ** = significant at P<0.01; ns = non-significant., DH = days to heading, DM = days to maturity, PH = plant height, PL = panicle length, TTPP = number of total tiller per plant, FTPP = number of fertile tiller number per plant, FGPP = number of filled grains per panicle, UGPP = number of unfilled grains per panicle, PBPP = number of primary branches per panicle, GYPP = grain yield per plant, BY = biological yield, HI = harvest index, TSW = thousand seed weight, GY = grain yield per hectare

Path coefficient analysis at phenotypic and Genotypic level

In the current study, traits that showed significant correlation with grain yield ha^{-1} were advanced to path coefficient analysis at both phenotypic and genotypic levels. Phenotypic path coefficient analysis revealed that number of primary branches per panicle (0.44) exerted the highest positive direct effect on grain yield ha^{-1}. The indirect exertion of number of primary branches per panicle on grain yield was positive for days to 50% heading (0.06) and negative for plant height (-0.02) and number of filled grains per panicle (-0.01).

Days to 50% heading (-0.23), plant height (-0.23) and number of filled grains per panicle (-0.25) exerted negative direct effect on grain yield ha^{-1}. Days to 50% heading displayed negative indirect effect on grain yield ha^{-1} through plant height, number of filled grains per panicle and number of primary branches per panicle. The indirect exertion of plant height on grain yield ha^{-1} was negative for days to 50% heading, number of filled grains per panicle and positive for number of primary branches per panicle. Number of filled grains per panicle exerted negative indirect effect on grain yield along with days to 50% heading plant height and positive via number of primary branches per panicle. The residual effect was (0.75), indicating that 25% of the variability in grain yield was contributed by traits considered in the path analysis.

***Table 6.** Phenotypic and genotypic direct (bolded along diagonal) and indirect effects of some component traits on grain yield of 25 rainfed lowland rice genotypes.*

Phenotypic path coefficient analysis					Genotypic path coefficient analysis				
Traits	DH	PH	FGPP	PBPP	r^{ph}	Traits	DH	TTPP	PBPP	r^{g}
DH	-0.23	-0.023	-0.033	-0.12	-0.41**	DH	-0.28	-0.06	-0.11	-0.45**
PH	-0.023	-0.23	-0.058	0.04	-0.27*	TTPP	-0.02	-0.32	-0.09	-0.43*
FGPP	-0.032	-0.054	-0.25	0.023	-0.31*	PBPP	0.09	0.08	0.35	0.52**
PBP	0.065	-0.022	-0.013	0.44	0.47**	Residual effect		0.75		
Residual effect		0.75								

DH = days to heading, PH = plant height, TTPP = number of total tiller per plant, FGPP= number filled grains per panicle, PBPP = number primary branches per panicle, r^{ph} = phenotypic correlation with grain yield, r^{g} = genotypic correlation with grain yield.

Genotypic path coefficient analysis indicated that number of primary branches per panicle showed the maximum positive direct effect (0.36) and significant genotypic correlation (0.52**) with grain yield. The positive direct effect of number of primary branches per panicle with grain yield was assisted by days to 50% heading (0.09) and total number of tillers per plant (0.08). The direct effects of days to 50% heading (-0.28) and number of total tiller number per plant (-0.32) on grain yield were negative. It displayed the negative casual factors via number of total tiller number per plant (-0.06) and number of primary branches per panicle (-0.11). Number of total tiller per plant expressed negative indirect effect on grain yield through days to 50% heading (-0.02) and number of primary branches per panicle (-0.09),

respectively. The residual effect was (0.75), explaining that the contribution of component traits on grain yield was 25% by the three characters evaluated in the path analysis, the rest 75% was the contribution of other traits that are not considered in the path analysis and environmental factors.

4. Discussion

The presence of significant location and genotype effects across the tested locations indicated their distinct differences agro-climatic conditions of the two test locations and presence of considerable amount genetic variability among the tested breeding materials. The possible cause for these significant difference between genotypes for traits imparted due to diverse source of materials tested that differ in their genetic constitution or genetic background as well as influence of environments on which they are raised. Differences among genotypes across locations have been reported by Mulugeta *et al*. [7] in upland rice genotypes at Southwest Ethiopia. When traits display significant genotype x location interaction effects, the differences among genotypes were not stable across the two test locations and genotypes show differential performance for these traits. Therefore, location specific breeding strategy might be adopted for each location for these traits. Similar to the current findings, Tefera *et al*. [23] found differential performance of lowland rice genotypes in Ethiopia. Addis [11] examined unstable performance of upland rice genotypes at southwestern Ethiopia, particularly at Guraferda and Gojeb. Similarly, when traits show non-significant genotype x location interaction effects, it suggests consistent performance of the genotypes across the two test locations with regard to those traits, hence it is expected that genotypes selected for those traits at one location may exhibit a similar relative performance at other location. In line with the current findings, stable performance of genotypes across locations were reported for number of fertile tiller per plant and unfilled grains per panicle by Sewagegne and Taddesse [10] and Tefera *et al*.[23]. Estimation of phenotypic and genotypic coefficients of variation values indicated greater influence of environment in the expression of the characters investigated. High heritability combined with moderate genetic advance as percent of mean estimate was obtained for plant height, suggesting simple direct selection of semi dwarf genotypes could be effective to improve this trait or it may be also improved by adapting recurrent selection method by breeders for future grain yield improvement. Plant height exhibited high heritability estimate, indicating the predominance of additive gene effects in the inheritance of this trait and it creates an opportunity for breeders to exploit this trait by selection on the basis of phenotypic performance. High heritability estimate in broad sense for plant height have been reported by Tefera *et al*. [23] in lowland rice genotypes at Pawe and Fogera Districts in Amhara Regional State in Ethiopia. Low estimates of heritability were obtained for days to 85% maturity and harvest index which indicates greater role of environment on the expression of these traits

and therefore, direct selection for these traits will be ineffective. Therefore, selection might be effective after creating variability by hybridization or mutation for these traits. High heritability coupled with moderate genetic advance record was also reported earlier in rice for plant height by Mulugeta *et al* [7]. Days to 85% maturity and harvest index displayed low GCV, heritability and genetic advance estimates. Therefore, selection for these traits may be ineffective for further grain yield improvement of lowland rice genotypes. Number of primary branches per panicle influenced grain yield of rainfed lowland rice genotypes at both phenotypic and genotypic levels and displayed significant and positive association with grain yield and hence, more emphasis should be placed on increasing the magnitude of number of primary branches per panicle. Number of primary branches per panicle exerted maximum positive direct effect on grain yield at both genotypic and phenotypic levels. The current findings were supported by Ogunbayo *et al*. [24] that observed increase in number of primary branches per panicle resulted in an increase in grain yield of rice genotypes. Days to 50% heading at both phenotypic and genotypic levels and number of total tiller per plant at genotypic level supported the direct contribution of number of primary branches per panicle with grain yield. Therefore, along with number of primary branches per panicle, indirect selection for genotypes having medium to late heading time and medium to good tillering ability might be considered simultaneously in order to increase grain yield of lowland rice genotypes in the study areas. This result was in harmony with the findings of Hossian *et al*. [25] but, in contrary to the finding of Moosavi *et al*. [26] that found negative direct contribution of number of primary branches per panicle on grain yield ha^{-1}. The present study indicated that there is adequate genetic variability for most of yield and yield component traits evaluated in rainfed lowland rice genotypes for future. However, it is recommended that the experiment should be repeated at more locations with more number of genotypes to effectively predict genotypic performance across several locations and to validate the obtained current results.

5. Conclusions

The tested materials differ in their genetic constitution and showed differential performance across the locations. Phenotypic coefficient of variation (PCV) was found slightly higher than the genotypic coefficient of variation (GCV), higher heritability combined with moderate genetic advance as percentage of mean (GAM) and phenotypic correlation coefficients were higher than their genotypic correlation coefficients reflected that there is presence of non-additive genetic control and revealed influence of environmental effects in phenotypic expression of the traits evaluated.

Significance of the study

This study results showed the existence of adequate genetic variability among the evaluated rainfed lowland rice genotypes of the region, on which so far in the study areas

little where known about the genetic background of those breeding materials. Hence the current findings will create an opportunity to breeders to improve the rice yield and other desirable traits.

Authors Contribution

This manuscript is one of my thesis work (first author) and it seriously advised and coordinated by Wosene Gebreselassie (second author) and Techale Birhan (second author also) as major and co-adivisor for this activity. Each of the authors (both major and minor advisors) has contributed very much from starting of proposal writing up to final completion of the thesis. They seriously evaluated field works, models, formulas and software's I adopted, grammar sessions, and spelling errors.

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