



Estimation of Genetic Parameters, Heritability and Genetic Advance for Yield Related Traits in Upland Rice (*Oryza sativa* L. and *Oryza glaberrima* Steud) Genotypes in Northwestern Ethiopia

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ABSTRACT

This study was carried out to assess the extent of genetic variability for yield and yield related traits and to estimate heritability and genetic advance in rainfed upland rice genotypes. Twenty-two selected upland rice varieties were evaluated in randomized complete block design with three replications during 2014 cropping season. The analysis of variance showed highly significant differences ($p \leq 0.01$) for days to flowering, days to maturity, hundred seed weight, plant height and panicle length and differed significantly ($p < 0.05$) for fertile tiller per plant, filled grains per panicle, unfilled grains per panicle, biomass yield and grain yield per plot except harvest index, indicating the existence of variability. The higher phenotypic and genotypic variance were obtained from number of filled grains, plant height, days for 50% heading, days for 85% maturity and biomass yield indicating high influence of the environment on the traits. The high level of genotypic and phenotypic coefficients of variation was recorded for traits like biomass yield, grain yield, number of fertile tillers per plant and unfilled grains per panicle. Heritability estimates were moderately high for days to maturity (66.01%), and thousand-grain weight (66.80%). High genetic advance as percent of means was observed for biomass yield per plot, unfilled grains per panicle, grain yield per plot, and fertile tiller per plant. Thousand-grain weight showed moderately high heritability coupled with high genetic advance as percent of mean. Therefore, selection based on this character might be effective for increasing grain yield.

Keywords: Genetic advance; Heritability; upland Rice; Variability

1. INTRODUCTION

Rice; *Oryza sativa* (Asian rice) or *Oryza glaberrima* (African rice) is the most important food crop and a major food grain for more than a third of the world's population (Zhao *et al.*, 2011). It is the second highest produced grain in the world after corn. However, since a large portion of corn is produced for purposes other than human consumption. Rice is the most important grain with regard to human nutrition and calorific intake, providing more than one fifth of the calories consumed worldwide by the human species (Smith, 1998). Rice provides 21% of global human per capita energy and 15% of per capita protein and Calories. Rice is particularly important in Asia, especially among the poor, where it accounts for 50-80% of daily caloric intake (IRRI, 2001).

Throughout history, rice has been one of the most important food crops for humans. This unique grain is the lifeline for nearly two-thirds of the world's population. It is deeply embedded in the cultural and economic heritage of their societies. About four-fifths of the world's rice is produced on small-scale by farmers and is consumed locally. Rice cultivation is the principal activity and source of income for about 100 million households in Asia and Africa (Chakraborty, 2011).

It is among the important cereal crops grown in different parts of Ethiopia as food crop. Wide production of rice in the country is believed to make a great contribution to food security. Considering the importance and potential of the crop, it has been recognized by the Government as "the new millennium crop of Ethiopia" to attain food security (MoA, 2010). However, the production, productivity, and expansion of rice have been limited (Tesfaye *et al.*, 2005). In order to meet the fastest growing demand for rice grain, developing high yielding genotypes with desirable agronomic traits for diverse ecosystem is, therefore, a requisite.

A successful breeding program depends on the genetic diversity of a crop for achieving the goals of improving the crop and producing high yielding varieties (Padulosi, 1993). Grain yield is a complex polygenic quantitative trait, greatly affected by environment and determined by the magnitude and nature of their genetic variability (Singh *et al.*, 2000). Genetic variability, which is due to the genetic differences among individuals within a population, is the core of plant breeding because proper management of diversity can produce permanent gain in the performance of plant and can buffer against seasonal fluctuations (Sharma, 1998) Genetic variability among traits is important for breeding and in selecting desirable types. The low heritability of grain yield characters made selection for high yielding varieties possible usually using various components traits associated with yield (Atlin, 2003).

Heritability of a trait is important in determining its response to selection. It was found out earlier that genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program (Akinwale *et al.*, 2011). Heritability, a measure of the phenotypic variance attributable to genetic causes, has predictive function of breeding crops (Songsri *et al.*, 2008). Generally, heritability indicates the effectiveness with which selection of genotypes could be based on phenotypic performance.

Genetic advance expected from selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Singh, 2001). Since high heritability does not always indicate high genetic gain, heritability with genetic advance considered together should be used in predicting the ultimate effect for selecting superior varieties (Ali *et al.*, 2002).

Genetic advance gives clear picture and precise view of segregating generations for possible selection. Estimates of heritability and genetic advance will help in knowing the nature of gene action affecting the concerned traits (Sravan, 2012). Higher estimates of heritability coupled with better genetic advance confirms the scope of selection in developing new genotypes with desirable characteristics (Ajmal *et al.*, 2009).

However, information on relationship of grain yield and yield contributing traits for upland rice of Ethiopian agro-ecology is not sufficiently available. In view of the above gaps, the present study was undertaken to investigate the genetic variability, heritability and genetic advance for yield related traits as a basis for selection of high yielding rice genotypes in upland ecology. Hence, the present study was undertaken with the objectives of; - To assess the extent of genetic variability for yield and yield related traits and to estimate heritability and genetic advance in upland rice genotypes

2. MATERIALS AND METHODS

2. 1. Experimental Materials

The experimental materials were 22 promising and released upland rice genotypes. They were introduced from IRRI, WARDA and EMBRAPA. Some of them were evaluated at different locations of the country, and released in different years.

Table 1. Description of experimental materials (upland rice genotypes).

Genotype	Status	Year of release	Seed source	Origin
Hiwassee (WAB515-B-16A1-2)	Released variety	2012	FNRRTC	IRRI
Getachew (AD01)	Released variety	2007	FNRRTC	IRRI
Andassa (AD012)	Released variety	2007	FNRRTC	IRRI
Tana (AD048)	Released variety	2007	FNRRTC	IRRI
NERICA-3 (WAB-450-IB-P-28-HB)	Released variety	2006	PARC	WARDA
NERICA-4 (49WAB-450-IB-P-9/1)	Released variety	2006	PARC	WARDA
SUPERICA-1 (WAB-4507)	Released variety	2006	PARC	WARDA
Kokit (IRAT-209)	Released variety	2000	FNRRTC	IRRI
NERICA-12	Released variety	2013	FNRRTC	WARDA
NERICA-13	Released variety	2014	FNRRTC	WARDA
Upland NERICA-14	Released variety	2010	FNRRTC	IRRI

Upland NERICA – 15	Released variety	2011	FNRRTC	WARDA
Upland NERICA – 18	Experimental materials		FNRRTC	WARDA
FOFIFA-4129	Experimental materials		FNRRTC	IRRI
FOFIFA-3737	Released variety	2010	FNRRTC	IRRI
FOFIFA-3730	Experimental materials		FNRRTC	IRRI
ARCCUFfa11-L1P1-B-B-1	Experimental material		FNRRTC	IRRI
WAB450-1-B-P-462-HB	Released variety	2014	FNRRTC	WARDA
Variety-1	Experimental materials		PAR	Brazil (EMBRAPA)
Variety -2	Experimental materials		PARC	Brazil (EMBRAPA)
Variety-3	Experimental materials		PARC	Brazil (EMBRAPA)
Pawe-1	Released variety	1999	PARC	WARDA

FNRRTC = Fogera national rice research and training center, PARC = Pawe agricultural research center

2. 2. Experimental Design and Procedure

A field experiment was conducted using 22 rainfed upland rice genotypes in the Northwestern part of Ethiopia at Pawe agricultural research center during 2014 main cropping season. Randomized complete block design with three replications was used. Each experimental plot had a total area of 6 m² (1.2 m x 5 m) and six rows at 0.2 m interval. Seeds were sown in rows with manual drilling at a rate of 60 kg % ha. Fertilizer was applied at a rate of 100 kg DAP and 100 kg Urea per ha. Nitrogen was applied three times in the form of urea. All DAP was applied during planting while urea was applied in three splits at planting tillering and at panicle initiation stages.

2. 3. Data collection and analysis

Data like; number of fertile tillers per plant, plant height, panicle length, number of filled grains per panicle and number of unfilled grains per panicle were collected on plant base and days to heading ,days to maturity, harvest index, thousand-grain weight, biological yield and grain yield were collected on plot base.

Analysis of variance (ANOVA) was carried out on the data to assess the genotypic effects and their interaction using general linear model (GLM) procedure for randomized complete blocks design (RCBD) using SAS (2004) version 9.1.3. Mean comparisons among treatment means were conducted by the least significant difference (LSD) test at 5% levels of significance. The analysis of variance for RCBD design was used to derive variance components as structured in Table 1 (Cochran and Cox, 1957).

Table 2. ANOVA table for RCBD

Source of Variation	d f	Mean square	Expected mean square
Genotypes	g-1	Msg	$\sigma_e^2 + g\sigma_r^2$
Replication	r-1	Msr	$\sigma_e^2 + r\sigma_g^2$
Error	(r-1)(g-1)	Mse	σ_e^2

2. 4. Estimation of Genetic Parameters

Different genetic parameters including genotypic variance (σ^2g), phenotypic variance (σ^2p), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated by using the formula, adopted from Burton and De vane (1953) and Johnson *et al.*, 1955a and 1955b.

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

where:

σ^2_g = genotypic variance

MSg = mean square due to genotypes.

MSe = environmental variance (error mean square)

r = number of replication

Phenotypic variance (σ^2_{ph}) = $\sigma^2_g + \sigma^2_e$

Where:

σ^2_p = phenotypic variance

σ^2_e = error variance

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

Phenotypic Coefficient of Variation PCV = (σ^2_p / grand mean) * 100

Genotypic Coefficient of Variation GCV = (σ^2_g / grand mean) * 100

2. 5. Estimation of broad sense heritability

Heritability (H): in broad sense for all characters was computed using the formula given by Falconer (1989).

$$H^2 = \sigma^2_g / \sigma^2_p * 100$$

where:

- σ_p^2 = phenotypic variance
- σ_g^2 = Genotypic variance
- $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$
- σ_e^2 = Environmental (error) variance

2. 6. Estimation of Expected Genetic Advance from Selection

The genetic advance for selection intensity (k) at 5% (2.06) was estimated by the following formula (Johnson *et al.*, 1955):

$$EGA = k * \sigma_{ph} * H_b^2$$

where, EGA represents the expected genetic advance under selection; σ_{ph} is the phenotypic standard deviation; h_b^2 is heritability in broad sense and k is selection intensity

The genetic advance as percent of population mean was also estimated following the procedure of Johnson *et al.*, (1955). Genetic advance per population mean = (EGA / grand mean) *100

3. RESULT AND DISCUSSIONS

The analysis of variance showed the presence of significant differences among the tested genotypes for all characters considered, indicating the existence of variability among the tested genotypes. The analysis of variance showed that the genotypes differed significantly ($p < 0.05$) for fertile tiller per plant, filled grains per panicle, unfilled grains per panicle, biomass yield and grain yield per plot. and highly significant ($p < 0.001$) for days to flowering, days to maturity, hundred seed weight, plant height and panicle length .But harvest index showed non-significant variation on the tested genotypes (Table 1).

Table 3. The mean squares for different sources of variation for 11 Traits of 22 genotypes evaluated under rainfed upland condition and the corresponding CV in percentage.

Traits	Mean Squares			CV%
	Replication (2)	Genotype (21)	Error (42)	
DH	10.92	61.74**	25.15	6.75
DM	1.7	20.58**	3.01	1.6
PL	6.28	6.31**	2.35	7.1
PH	115.44	140.06**	40.87	6.39
FTPP	4.8	2.25*	0.96	14.64

GF	43.45	215.98*	121.96	10.61
UFGPP	1.46	2.69*	1.27	19.43
HI	0.0003	0.005NS	0.006	20.46
BY	271867	1446863.28*	575738	19.21
TGW	3.61	11.40***	1.62	4.27
GY	2326975	717166.85*	317754	15.5

“*, ** Indicate significance at 0.05 and 0.01 probability levels”.

NS = Non Significant

Where: GY = grain yield, DH = number of days to heading, DM = number of days to mature, PL = panicle length, PH = plant height, GF = filled grains per panicle, BY = biomass yield, HI = harvest index, TGW = thousand grain weight, UFGPP = unfilled grains per panicle and FPHP = fertile tiller per plant.

3. 1. Estimation of Genetic Parameters

Phenotypic variance was higher than the genotypic variances for all the characters indicating the influence of the environmental factors on these traits. The higher phenotypic and genotypic variance were obtained from number of filled grains, plant height, days for 50% heading, days for 85% maturity and biomass yield indicating high influence of the environment on the traits . Biomass yield per plot, grain yield and number of unfilled grains per panicle had high phenotypic coefficient of variation (PCV) values. The PCV values for number of fertile tiller per plant, filled grains per panicle and grain yield were medium. Days for 50% heading, days to maturity, plant height, panicle length and thousand seed weight had low values.

The characters as biological yield, number of fertile tiller per plant and unfilled grains per panicle gave comparatively higher value of genotypic coefficient of variation. The high level of genotypic and phenotypic coefficients of variation was recorded for traits like biomass yield, grain yield, number of fertile tillers per plant and unfilled grains per panicle. However, moderate estimates were observed for panicle length, plant height, filled grains per panicle, and thousand-grain weight. The rest of the traits showed low estimates of genotypic and phenotypic coefficients of variation.

In the present study, phenotypic coefficients of variation were slightly higher than the genotypic coefficients of variation for all the traits studied. This indicates the presence of slight environmental influence to some degree in the phenotypic expression of the characters. Pandey *et al* (2010) and Mulugeta *et al.* (2012) also observed similar findings.

3. 2. Estimation of Broad-sense Heritability and Genetic advance as percent of mean

In this study estimate of heritability in broad sense ranged from 20.44 % for filled grains per panicle to 66.80 % for thousand-grain weight. Heritability estimate was moderately high for days to 85% maturity and thousand-grain weight, Mulugeta *et al.* (2012) observed similar

findings. It was low < 40%) for the remaining quantitative characters in this study. Very low heritability indicates greater role of environment on the expression of the trait.

Genetic advance as percent of mean ranged from 3.74 for days to maturity to 16.80 for biomass yield per plot. Relatively higher genetic advance was observed for biomass yield, unfilled grains per panicle, grain yield per plot and fertile tiller per plant. Likewise, estimates of genetic advance (as percent of the mean) for thousand grain weight, days to 50% heading, plant height, and panicle length were also considerably high. Thousand-grain weight showed moderately high heritability (66.80) with high genetic advance in percent of mean (10.22). Ullah *et al.* (2011) also reported earlier in rice the existence of high heritability and high genetic advance records for thousand-grain weight. Therefore, selection based on this character might be effective for increasing grain yield.

Medium heritability and genetic advance were recorded for fertile tiller per plant, plant height and biomass yield. This suggests that these traits are primarily under genetic control and selection for them can be achieved through their phenotypic performance. Very low heritability and genetic advance for filled grains per panicle was observed due to non-additive gene action and great influence of the environment on the trait as reported by Akinwale *et al.* (2011).

Table 4. Estimates of mean, standard deviation, range, variance components and coefficients of variability, heritability and genetic advance of the 10 characters studied at pawe.

Traits	Means ± SD	Range	σ_g^2	σ_p^2	σ_e^2	GCV (%)	PCV (%)	h_b^2 (%)	EGA, (k = 5%)	GAM (K = 5%)
DH	74.26 ±6.04	67.3 -87.33	12.199	37.346	25.15	4.70	8.23	32.67	4.12	5.55
DM	108.42 ±2.94	104 -115	5.854	8.869	3.01	2.23	2.75	66.01	4.06	3.74
PL	21.6 ±1.93	18.27 -24.07	1.320	3.672	2.35	5.32	8.87	35.95	1.42	6.58
PH	99.92 ±8.67	90.27 -110.8	33.065	73.931	40.87	5.75	8.61	44.72	7.93	7.94
FTPP	6.72 ±1.22	5.53 -8.4	0.430	1.390	0.96	9.75	17.53	30.92	0.75	11.19

GF	104.06 ±12.24	88.73 -121.7	31.340	153.300	121.96	5.38	11.90	20.44	5.22	5.02
UFGPP	5.55 ±1.31	4.27 -6.93	0.473	1.743	1.27	11.86	22.76	27.15	0.74	12.75
BY	4002.27 ±960.79	2966.67 -5533.33	290375.183	866112.913	575737.7	13.67	23.61	33.53	643.68	16.30
TGW	29.8 ±2.20	27.00 -32.17	3.260	4.880	1.62	6.06	7.41	66.80	3.04	10.22
Gy	3624.81 ±713.17	2755 -4538.33	133137.770	450891.310	317753.5	10.07	18.52	29.53	409.04	11.28

SD = standard deviation, σ_g^2 = Genotypic variance, σ_e^2 = Environmental variance, σ_{ph}^2 = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, h_b^2 = Broad sense heritability, EGA = Expected Genetic Advance, GAM = Genetic advance as percent of mean and K = Selection intensity.

GY = grain yield, DH = number of days to head, DM = number of days to mature, PL = panicle length, PH= plant height, GF = filled grains per panicle, BY = biomass yield, TGW = thousand grain weight, UFGPP = unfilled grains per panicle, FTTP = fertile tillers per plant.

4. CONCLUSION

The analysis of variance showed the presence of significant differences among the tested genotypes for all characters considered, indicating the existence of variability among the tested genotypes. Phenotypic variance was higher than the genotypic variances for all the characters indicating the influence of the environmental factors on these traits. Phenotypic coefficients of variation were slightly 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 coefficient of variation was recorded for biomass yield per plot, grain yield per plot and unfilled grains per panicle. Heritability estimate was moderately high for days to 85% maturity and thousand-grain weight. It was low for the remaining quantitative characters in this study. Very low heritability indicates greater role of environment on the expression of the trait. Relatively higher genetic advance was

observed for biomass yield, unfilled grains per panicle, grain yield per plot and fertile tiller per plant. Likewise, estimates of genetic advance (as percent of the mean) for thousand grain weight, days to 50% heading, plant height, and panicle length were also considerably high. In this study, thousand-grain weight showed moderately high heritability coupled with high genetic advance as percent of mean. This condition indicates that there is good opportunity to improve this trait using the tested genotypes.

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