Estimation of Genetic Variability, Hertability and Genetic Advance in Upland Rice (Oryza Sativa L.*)* Genotypes at Guraferda, South West Ethiopia

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Abstract

A field experiment was executed using fifteen rain fed upland rice genotypes for two consecutive years (2014 and 2015) during the main cropping season in South Western Ethiopia, to estimate the extent of genetic variability, heritability and genetic advance. The experiment was laid down in a randomized complete block design with three replications and data on seven quantitative phenotypic traits were collected and subjected to various statistical analysis. Combined analysis of variance across years revealed significant ($P \leq 0.05$) difference of year, genotype and genotype x year interaction effects for most of the traits evaluated. The phenotypic coefficient of variation ranged from 2.76% for days 85% to maturity to 15.21% for grain yieldha^{-1}, while the genotypic coefficient of variation ranged from 1.52% for days 85% to maturity to 9.67% for plant height. Heritability estimates in broad sense were high for days to 50% heading (89.98%), plant height (84.49%), thousand seed weight (77.00%) and panicle length (65.10%) and moderate and low for days to 85% maturity (30.38%) and grain yield ha^{-1} (8.40%), respectively. Days to 50% heading, plant height and thousand seed weight displayed high heritability along with moderate genetic advance as percent of mean estimates and days to 85% maturity and grain yield exhibited low GCV, heritability and genetic advance estimates. The present study revealed reasonable amount of genetic variability for the majority of the considered quantitative traits in rain fed upland rice genotype, indicating that it could be used in future rice breeding programs. However, it is recommended that the experiment could be replicated at more locations with more number of genotypes to assure the obtained results. In addition, it is better if more number of quantitative and qualitative traits included for widening the scope inference.

Keywords: Genetic advance, Genetic variability, Heritability, Upland Rice

1. INTRODUCTION

Rice (*Oryza sativa* L. and *Oryza glaberrima* Steud) belongs to the family Poaceae, is the most significant food crops of the world and assists as a chief food basis for more than 50% of the world population (Wang *et al.,* 2014). According to FAO (2017), globally its production has risen to 758.8 million tons of paddy rice. Rather than its contribution for consumption it is a good opportunity for domestic and international market for economic development in China, India Indonesia and USA (Hegde and Hegde, 2013).

In Ethiopia, the cultivation of rice is of a recent history, however, its use as a food crop, income source, employment opportunity and animal feed have been well recognized (Nigusse and Alemu, 2011). Currently it is considered as a strategic food security crop that has received due emphasis in promotion of agricultural production and as such it is considered as the “millennium crop” expected to contribute in ensuring food security in Ethiopia. Volume of rice production in Ethiopia is also on moving with the national average productivity rise of 1.8 tons per hectare (CSA, 2005) to 2.8 ton per hectare (CSA, 2015) at on-farm level. According to Seck *et al.* (2013) and Kebede (2011), the number of participant farmers and the demand for improved rice technologies is also highly increasing from time to time. The country has planned to meet the projected average productivity increase of 5.1ton/ha in 2019.

Rain fed rice is cultivated in Amhara, Tigray, Oromia, SNNPR (Southern Nations Nationalities and Peoples Region), Gambella and Benshangul Gumuz Regions of Ethiopia (MoA, 2010). SNNPR is the third largest producer of upland rice next to Gambella and Tigray in terms of estimated area coverage. In the region, rice is principally cultivated in Keffa (Gimbo), Bench Maji (Guraferda, Menit Goldia and Menit Shasha) and Sheka (Yeki) zones (EIAR/ FRG II; 2012; Asfaha *et al.* 2015). Out of the total rice produced in the country in 2014/15, 2,802.02 tons were produced in SNNPR and of these; 2,753.316 tons were produced in Keffa, Benchi Maji and Sheka zones (CSA, 2015).

Recognizing the stated importance and existing potentials to boost rice production and productivity to cope up with the fastest growing demand, utilization of genetic variability which exists among rice genotypes for grain yield will provide the basis for selection to improve productivity of rice in Ethiopia. Hence, breeding for yield component to increase grain yield would be more efficient if the components involved are highly heritable and genetically independent (Akinwale *et al*., 2011). In addition, the knowledge of heritability in the selection based improvement programs indicates the extent of transmissibility of a character in future generations

(Sabesan *et al*., 2009). It is also pertinent to note that high heritability alone does not guarantee large gain from selection unless sufficient genetic advance (GA) attributed to additive gene action is present (Tiawari *et al*., 2011; Akinwale *et al*., 2011).

Genetic variability studies have been done in upland rice genotypes in different parts of the country; however, no studies were done by using currently used upland rice genotypes in south western Ethiopia in order to determine the extent of genetic variability, heritability and genetic advance. In view of above gaps, the present study was undertaken to determine the extent of genetic variability, heritability and genetic advance for the agronomic traits as a basis for selection of high yielding genotypes in rain fed upland rice ecology in the area.

2. MATERIALS AND METHODS

2.1. Description of the Experimental Site, Materials and Procedures

The experiment was conducted at Guraferda in Bonga Agricultural Research Center experimental station for two consecutive years (2014 and 2015). The site is located at an altitude of 1235 meters above sea level, 7° 26' N and 36° 22' E latitude and longitude, respectively. It receives an annual rainfall of 1710mm and mean monthly minimum and maximum temperature of 16.7^0C and 24.0^0C, respectively (Asfaha *et al.,* 2015). The experimental materials consisted of 15 upland rice genotypes (Advanced lines) obtained from Fogera National Rice Research and Training Center (FNRRTC) and Bonga Agricultural Research Center: Hidassie (WAB515-B-16A1-2), Getachew (AD01), Andassa (AD012), Tana (AD048), NERICA-3(WAB-450-IB-P-28-HB), SUPERICA-1(WAB-4507), Koki(IRAT-209), NERICA-12, NERICA-13, NERICA-14, NERICA-15, NERICA-18, FOFIFA-4129, FOFIFA-3737, FOFIFA-3730 were used as experimental materials. The experiment was laid out in randomized complete block design in three replications. The spacing between replications, plots and rows was 1, 0.3 and 0.2m, respectively. Seeds were drilled in rows with a rate of 60kg per hectare. The gross and net harvestable plot size of the experiment were $6m^2$ (six rows of 5m of long and 1.2m wide) and $4m^2$ (four rows of 5m long and 0.8m wide), respectively, and four inner most central rows were used for data collection. Fertilizer was applied at a rate of 100kg DAP and 100kg Urea ha^{-1}. All DAP was applied during sowing whereas urea was applied in three equal splits at sowing, tillering and at panicle initiation stages. Weeding was done three times manually during the whole experimental period as required.

2.2. Data Collection and Analysis

Based on the Standard Evaluation System for Rice developed by the International Rice Research Institute (IRRI, 2002) seven quantitative agro morphological data were taken on plot basis and from randomly taken five plants from the inner most central rows of each plot. Days to 50% flowering and days to 85% maturity were computed on plot basis. Five representative plants for each genotype in each replication were randomly taken to record observations on plant height (cm), panicle length (cm), fertile or productive tillers per plant. Grain yield obtained on plot bases was converted into Kg ha^{-1} and adjusted to 14% grain moisture content.

The analysis of variance for different traits was statistically analyzed using the SAS statistical package version 9.2 (SAS, 2002) and means were separated by employing least significant difference (LSD) method according to (Gomez and Gomez, 1984). Before undertaking individual location statistical analysis, data were checked for the normality assumption and all data met the normality assumption; and for combined analysis of variance of across locations, the homogeneity of error variance was tested using $F\text{-}_{max}$ test method of Hartley (1950). Based on the result of this test, equality of error variance was satisfied and data were pooled across years.

2.3. Estimation of Variance Components

Estimates of variance components were computed using the formula suggested by Burton and De Vane (1953).

1) Genotype variance (σ^2g) = (MSG-MGxY)/RY
2) Genotype x location interaction variance (σ^2gy) = (MGxY– MSE)/R
3) Environmental variance (error mean square) (σ^2e) = M6
4) Phenotypic variance (σ^2p) = $\sigma^2g+\sigma^2gy/Y+\sigma^2e/YR$

Where, σ^2p = Phenotypic variance
σ^2g = Genotypic variance
σ^2e = Environmental variance (error mean square), then by using the methods suggested by Dewey and Lu (1959) phenotypic and genotypic coefficient of variations were calculated as follows:

Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma 2p}}{\bar{x}} x100$

Genotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma 2g}}{\bar{x}} x100$

Where: σ^2p =Phenotypic variation; σ^2g= Genotypic variation and $\bar{x}$= Grand mean of the trait under consideration. According to Siva Subramanian and Menon (1973), 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.

2.4. Estimation of Broad Sense Heritability

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.* (1955).

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

Where, H_b^2 =heritability in broad sense

$\sigma^2 g$ = Genotypic variance and

$\sigma^2 p$= Phenotypic variance

$\sigma^2 p = \sigma^2 g + \sigma^2 e$

Where, $\sigma^2 e$ Environmental (error) variance

2.5. Genetic advance (GA) and Genetic Advance as Percentage of Mean (GAM)

The expected response to selection was computed by using the method illustrated by Allard (1960) assuming selection intensity of 5% given as follows:

$GA= \sqrt{\sigma 2ph} *k * H_b^2 \text{or } k * \sigma_{ph} * H_b^2$

Where, GA= Expected genetic advance, H_b^2 = Heritability in broad sense, $\sigma^2 ph$= phenotypic variance, σ_{ph}= 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*. (1955) 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.

3. RESULT AND DISCUSSION

3.1. Analysis of Variance (ANOVA)

The mean square of the pooled analysis of variance over the two test years revealed statistically significant ($P \leq 0.05$) year effects for most of the traits evaluated except, thousand seed weight and grain yield. These results showed that difference in environmental conditions might have contributed to the differences observed in the two test years. Similar results were reported by Lakew *et al.* (2014) for days to 85% maturity and number of fertile tillers per plant.

The mean square from the pooled analysis of variance across the two test years displayed statistically significant ($P \leq 0.05$) genotype effects for all of the traits evaluated except, number fertile tiller per plant (Table 1), indicating the presence of considerable amount genetic variability among the tested breeding materials. The possible reason for this significant difference between genotypes of those traits imparted due to differences in their genetic constitution or genetic background and differences in environmental factors in two years. Similar significant genotype effects across years were reported by Ogunbayo *et al.* (2014) days to 85% maturity, plant height, panicle length and grain yield ha^{-1}, Seyoum *et al.* (2012) and Ullah *et al.* (2011) for days to 85% maturity, plant height and panicle length and grain yield ha^{-1}.

The mean squares due to genotype x year interaction were statistically highly significant ($P \leq 0.01$) for days to 50% heading, days to 85% maturity, number of fertile tillers per plant, and grain yield per hectare. Similar to the current findings, Lakew *et al.* (2014) found significant genotype x year interaction effects for days to maturity, thousand seed weight and grain yield ha^{-1}. When genotypes display significant genotype x year interaction on different traits, the differences among genotypes were not stable across the two test years or genotypes showed differential performance with regard to these significant traits. In the present experiment, plant height, panicle length and thousand seed weight displayed a non- significant genotype x year interaction effects. These results suggested consistent performance of the genotypes across the two test years with regard to these traits. If varieties perform consistently for those traits over the years, breeders may be able to reduce the cost of extensive varietal evaluation by eliminating unnecessary testing years and by modifying the breeding programs. To effectively assess varietal performance for significant traits it’s essential to consider several year interaction effects and identify traits performance in relation to years’ effect

Table 1. Mean squares from the combined analysis of variance for seven traits of seven rice genotypes evaluated across two years.

Traits	MSY(1)	MSG(15)	MSGxY(15)	MSE(60)	CV (%)
DH	634.68**	180.52**	18.08*	7.92	3.29
DM	1102.5**	65.56**	45.64**	11.22	2.80
PL	8.96**	5.53**	1.93 ns	1.32	5.58
PH	248.00*	670.14**	103.97ns	60.57	7.75
NFTPP	238.77**	4.98 ns	6.58*	3.52	28.8
TSW	0.00 ns	44.95**	0.00 ns	6.89	8.65
GYLD	31859.05ns	2389785.26*	2188945.27*	992402.1	24.01

*= significant at ($P \leq 0.05$), and ** = significant at ($P \leq 0.01$), MSY= Mean Squares of Years, MSG= Mean squares of Genotypes, MG x Y = Mean Square of Genotype x Year interaction, MSE = Mean Squares of Error, CV = Coefficient of Variation, DH = Days to 50% Heading DM = Days to85% Maturity, PL=Panicle Length, PH=Plant Height, NFTPP= Number of Fertile Tiller Per Plant, TSW= Thousand Seed Weight and GYLD=Grain Yield per hectare (kg/ha).

3.2. Range and Mean of Parameters

Based on the combined analysis result, most of the traits exhibited sufficient amount of variability that can be reflected by high values of range and analysis of variance among genotypes for traits considered. Highly significant variation was noted among genotypes for days to 50% heading that ranged from 75.83 to 94.67 days. Early heading was noted in NERICA-15 (76.83 days) succeeded by FOFIFA-4129 (79.5 days) while, late heading was recorded on Andassa (AD012) (94.67 days) followed by Tana (AD048) (93.83 days). Genotypes displayed a highly significant difference in days to maturity that varied from 112.5 to 125.67 days. NERICA-15 (112.5 days) and FOFIFA-4129 (117 days) were matured early, while genotypes FOFIFA-3730 (125.67 days) and Andassa (AD012) (124.17 days) were late (Table 2).

Genotypes showed significant difference in plant height measurement that ranged from 81.63 to 116.60cm. Maximum height was noted in FOFIFA-3730 (116.60cm) which was statistically at par with Getachew (AD01) (116.07cm), Andassa (AD012) (112.53cm) and Tana (AD048) (110.77cm). Kokit (IRAT-209) had displayed the shortest plant height (81.63cm) but it was statistically at par with NERICA-3 (WAB-450-IB-P-28-HB) and Hidassie (WAB515-B-16A1-2) which displayed 87.47 and 87.97cm, respectively. Similar experimental result was reported by Bitew *et al.* (2016) who have found a highly significant variation in plant height measurement in rain fed upland rice genotypes. Generally, in the present experiment, genotypes that have scored the highest and lowest plant height measurements gave the lowest grain yield ha^{-1}. Aa research result showed that, there is a negative correlation of plant height and lodging with paddy yield and a significant positive relationship of plant height and lodging (Unan *et al*., 2013). In addition, the susceptibility of tall genotypes for lodging and less light penetration and serious shading within plant because leaves are very closely spaced on short culm in short genotypes (Setter *et al*., 1997).

Table 2. Mean separation of combined analysis of variance for upland rice genotypes

Genotypes	Traits						
	Days to 50% Heading	Days to 85% Maturity	Plant Height (cm)	Panicle Length (cm)	Number of Fertile Tillers Per Plant	Thousand Seed Weight (g)	Paddy yield (kg/ha)
Hidassie (WAB515-B-16A1-2)	85.5^{ef}	119.33^{cd}	87.97^{fg}	19.47^{fg}	6.53^{abcd}	27.67^{ef}	4523.2^{ab}
Getachew (AD01)	91.50^{ab}	122.50^{abc}	116.07^{a}	21.92^{ab}	5.13^{d}	28.67^{def}	4340.1^{ab}
Andassa (AD012)	94.67^{a}	124.17^{ab}	112.53^{ab}	20.70^{bcdef}	6.8^{abcd}	29.33^{cdef}	3749.9^{bc}
Tana (AD048)	93.83^{ab}	123.67^{ab}	110.77^{abc}	21.03^{abcde}	6.57^{abcd}	27.33^{f}	4179.1^{abc}
NERICA-3 (WAB-450-IB-P-28-HB)	83.00^{efg}	117.33^{d}	87.47^{fg}	19.58^{fg}	7.33^{abcd}	26.33^{f}	5320.1^{a}
SUPERICA-1(WAB-4507)	86.17^{de}	119.17^{cd}	98.87^{de}	20.00^{defg}	6.43^{abcd}	33.67^{ab}	4532.7^{ab}
Kokit (IRAT-209)-	88.00^{dc}	119.39^{cd}	81.63^{g}	19.63^{fg}	7.03^{abcd}	33.67^{ab}	3172.7^{c}
NERICA-12	81.50^{fgh}	118.00^{d}	101.53^{d}	21.27^{abcd}	5.30^{d}	30.67^{bcde}	4427.8^{ab}
NERICA-13	85.50^{de}	118.00^{d}	91.50^{ef}	21.32^{abc}	6.47^{abcd}	33.33^{ab}	3495.1^{bc}
UPLAND NERICA-14	81.83^{fgh}	118.5^{d}	95.57^{def}	19.75^{efg}	5.77^{bcd}	31.33^{abcd}	5301.0^{a}
UPLAND NERICA-15	75.83^{i}	112.5^{d}	99.17^{de}	21.23$_{abcd}$	8.27^{a}	28.67^{def}	3514.7^{bc}
UPLAND NERICA-18	80.33^{gh}	118.67^{cd}	100.13^{de}	21.07^{abcde}	7.30^{abcd}	26.67^{f}	4106.4^{bc}
FOFIFA-4129	79.50^{h}	117.00^{d}	104.03^{bcd}	20.50^{cdef}	7.93^{ab}	32.33^{abc}	3853.3^{bc}
FOFIFA-3737	85.17^{de}	120.33^{bcd}	102.87^{cd}	19.10^{g}	7.53^{abc}	34.33^{a}	3486.1^{bc}
FOFIFA-3730	91.17^{bc}	125.67^{a}	116.60^{a}	22.25^{a}	5.63^{cd}	31.00^{bcd}	4253.5^{abc}
Mean	85.5	119.6	100.45	20.59	6.67	30.33	4149.78
LSD	3.25	3.89	9.00	1.33	2.22	3.03	1152.2

Means with the same letter in a column are not significantly different at p=0.05.

Panicle length also varied highly significantly in different genotypes with a range of 19.10- 22.25cm. Maximum panicle length (22.25cm) was found in FOFIFA-3730 followed by Getachew (AD01), NERICA-13 and NERICA-12. Generally, it was observed that genotypes showing short plant height had also shown short panicles and vice versa. This might be attributed due to the positive association between plant height and panicle length. Likewise, genotypes differed highly significantly in thousand seed weight measurements that ranged from 26.33 to 34.33g. Highest thousand seed weight value was noted in FOFIFA-3737(34.33), followed by Kokit (IRAT-209) (33.67g) and SUPERICA-1(WAB-4507) (33.67g), while the lowest value was exhibited in NERICA-3 (WAB-450-IB-P-28-HB (26.33g) succeeded by NERICA-18 (26.67g) and Tana (AD048) (27.33g).

In this study, grain yield per hectare varied from 3172.7 to 5320.10kg ha^{-1} and revealed a statistically significant difference among genotypes. Highest grain yield (5320.10 kg ha^{-1}) was obtained from NERICA-3 (WAB-450-IB-P-28-HB, nearly succeeded by NERICA-14 (5301.0kg ha^{-1}) and SUPERICA-1 (WAB-4507) (4523.7kg ha^{-1}) Abebe *et al.* (2017), Bitew *et al.* (2016) and Ogunbayo *et al.* (2014); reported a significant variation of grain yield (kg ha^{-1}) between rice genotypes grown under rain fed conditions.

3.3. Estimation of Genetic Parameters

3.3.1. Phenotypic and genotypic coefficients of variation

The current study suggests that phenotypic variance (σ^2p) and phenotypic coefficient variation estimates (PCV) were slightly higher than that of their corresponding genotypic variance (σ^2g) and genotypic coefficient of variation (GCV), respectively for all the characters studied except grain yield per hectare. The magnitude of the difference between the PCV and GCV was relatively high for grain yield ha^{-1}. This large difference between PCV and GCV value reflects greater environmental influence on the expression of this trait. However, these differences were comparatively small for days to 50% heading, days to 85% maturity, plant height, panicle length and thousand seed weight. These small differences might suggest a minimal influence of environment on the expression of these traits. In addition, it indicates the presence of sufficient genetic variability for observed traits and may facilitate the success of the selection process. Therefore, selection based on phenotypic performance of these traits would be effective to bring considerable improvement in grain yield of upland rice genotypes. Similar results were earlier reported by Konate *et al.* (2016), Singh *et al.* (2013) and Dutta and Borua (2013) in rice.

Phenotypic coefficients of variation (PCV) values ranged from 2.76% (for days to 85% maturity) to 15.21% (grain yield ha^{-1}) (Table 2). PCV values for plant height, thousand seed weight and grain yield ha^{-1} were medium.

Bitew *et al.* (2016) have reported medium PCV estimates for plant height, thousand seed weight and grain yield ha^{-1}. Similarly, Hassan *et al.* (2013) have obtained the same result on grain yield ha^{-1}. Based on the obtained result there is a possibility of yield improvement through selection of these traits. But it must be reminded that their expression can be influenced very much by environment. Days to 50% heading, days to 85% maturity and panicle length had low PCV values. These low values indicated a need for creation of variability by hybridization or mutation followed by selection. These results are in conformity with the findings of Bagati *et al.* (2016) and Fentie *et al.* (2014) who reported low PCV values on panicle length and thousand seed weight. Similarly, Selvaraj *et al.* (2011) also observed low PCV estimates for days to 85% maturity and panicle length.

Genotypic coefficients of variability (GCV) values were low (<10) for all traits considered in this study. Similar results have been reported by Fentie *et al.* (2014) for days to 75% maturity, plant height, panicle length, number of filled grains per panicle and harvest index; similarly, Hassan *et al.* (2013) also found low estimates on days to 85% maturity and plant height.

Table 3. Estimates of genetic parameters of different traits in upland rice genotypes

Traits	Range	Mean ±SD	$\sigma^2 p$	$\sigma^2 g$	PCV	GCV	h^2_b(%)	GA	GAM (%)
DH	75.83-94.67	85.50±2.81	30.09	27.07	6.42	6.09	89.98	10.18	11.91
DM	112.5-125.67	119.61±3.35	10.93	3.32	2.76	1.52	30.39	2.07	1.73
PL	19.00-22.25	20.59±1.15	0.92	0.60	4.66	3.76	65.10	1.29	6.54
PH	81.63-116.6	100.45±7.78	111.69	94.36	10.52	9.67	84.49	18.42	18.34
TSW	26.33-34.33	30.33±2.62	9.73	7.49	10.29	9.02	77.00	4.95	16.34
GYLD	3172.7-5320.1	4149.78±996.36	398297.54	33473.33	15.21	4.41	8.40	109.42	2.64

SD = Standard Deviation, DH = Days to 50% Heading DM = Days to 85% Maturity, PL= Panicle Length, PH = Plant Height, TSW = Thousand Seed Weight and GYLD = Grain Yield per hectare (kg/ha)

3.3.2. Estimates of broad sense heritability

Estimates of broad sense heritability varied from 8.40% (grain yield) to 89.98% (days to 50% heading) (Table 2). High heritability estimates (>60%) were obtained for days to 50% heading, panicle length, plant height and thousand seed weight. Similar results were reported by Mishu *et al.* (2016), Khare *et al.* (2014) and Selvaraj *et al.* (2011). The present experimental result indicated that the major role of additive gene action in the inheritance of these traits; and it would help breeders to select genotypes based on these phenotypic performances.

Moderate heritability estimate (between 30- 60%) was registered for days to 85% maturity and low estimate was exhibited by grain yield ha^{-1} which indicates the possibility of using for rice improvement program, but their expression could be highly influenced by the environment in which they grown. Similar results have been reported by Fentie *et al.* (2014) and Seyoum *et al.* (2012) for grain yieldha^{-1}. This low heritability estimate for grain yield could be attributed due to the fact that yield is a complex trait and controlled by many genes (Osman *et al.*, 2012).

3.3.3. Estimates of genetic advance (GA) and genetic advance as percentage of mean (GAM)

The high value of genetic advance was recorded on grain yield (109.42) and the low on panicle length (1.29). Based on the estimate of genetic advance of grain yield we could improve the grain yield of progenies by 109.42kg ha^{-1} whenever we select the best 5% high yielding genotypes as parents. Fentie *et al.* (2014) reported 424.68kg ha^{-1}mean grain yield improvement of progenies from the first cycle of selection in rain fed upland rice genotypes.

Genetic advance as percent mean expected (GAM) had a general range between 1.73% (days to 85% maturity) and 18.34% (plant height). Among the characters, moderate estimates of GAM (10 to 20%) were recorded for days to 50% heading, plant height, and thousand seed weight and low (<10%) for days to 85% maturity, panicle length and grain yield ha^{-1}. High estimate of heritability coupled with moderate genetic advance as percentage of mean values was exhibited for days to 50% heading, plant height and thousand seed weight indicating both additive and non-additive genes governed the expression of these characters. Hence, simple direct selection could be effective to improve these traits or they could also be improved by adapting recurrent selection method. High heritability coupled with moderate genetic advance as percentage of the mean record was also reported earlier in rice for plant height and thousand seed weight by Mishu*et al.* (2016). Similarly, Fentie *et al.* (2014) also found high heritability combined with moderate genetic advance estimate as percentage of mean for thousand seed weight. High heritability along with low genetic advance as percentage of mean estimate was obtained for panicle length which explains the dominance of non-additive gene action; and genotype x environment interaction played a significant role in the expression of this trait. Expression of low GCV, low heritability and genetic advance values were obtained from days to 85% maturity and grain yield ha^{-1} suggested that these characters could be governed by non-additive genes and highly influenced by the environment in which genotypes were raised.

4. CONCLUSION AND SUMMURY

Exploitation of genetic variability which exists among rice genotypes and transmissibility of important characters will provide the basis for selection to improve productivity of upland rice. Therefore, the present study was executed in order to determine the extent of genetic variability, heritability and genetic advance estimates in upland rice genotypes in South West Ethiopia. Based on the combined analysis of variance across years displayed significant year, genotype and genotype x year interaction effects for most traits considered. Hence it indicated a wide range of differences between years, genetic constitution of genotypes and differential performances of genotypes across the two tested years, respectively.

Estimation of phenotypic and genotypic coefficients of variation ranged from low to moderate for the traits evaluated, indicating greater influence of environment on the expression of the characters. Heritability estimate in a broad sense was high for days to 50% heading, plant height, panicle length and thousand seed weight suggesting the governance of additive gene action and low environmental influence for phenotypic expression of these traits. Days to 85% maturity and grain yield exhibited low heritability estimates, indicating greater influence environment and non-additive gene effects for the phenotypic expression of these traits and therefore, selection devised on these traits could be ineffective. Days to heading, plant height and thousand seed weight exhibited high heritability along with moderate genetic advance as percent of mean values and simple direct selection could be effective to improve this trait or, it may be also improved by adapting recurrent selection method. Days to 85% maturity and grain yield ha^{-1} displayed low GCV, heritability and genetic advance estimates. Therefore, selection for these traits may be ineffective for further grain yield improvement of upland rice genotypes, because of governance of non-additive gene actions and greater influence of environment on the expression of the characters.

Generally, the present study indicated adequate genetic variability on most of the quantitative characters evaluated in rain fed upland rice genotypes. However, it is recommended that the experiment should be repeated at more locations with more genotypes to validate the obtained results. In addition, it is better to support future rice research works with modern biotechnology approaches, and inclusion of more number qualitative and quantitative morphological traits to confirm the outcome of the current findings.

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