Genetic Variability, Heritability and Correlation Coefficient Analysis for Yield and Yield Component Traits in Upland Rice (*Oryza sativa L.*)

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Abstract:Rice (*Oryza sativa L.*) is one of the most important staple crops consumed by more than half of the world's population. To assess the range of genetic variability, heritability and association between yield and yield component traits of upland rice, a field experiment was conducted using twelve upland rice genotypes during 2013 main cropping season. The experiment was laid out in a randomized complete block design, with three replications under rain-fed condition. The analyses of variances (ANOVA) showed significant differences nearly for all traits tested, except panicle length and number of fertile tillers per plant. Grain yield ranged from 2340 kg/ha for genotype FOFIFA-3737 to 3400 kg/ha for genotype AD-48, with a mean value of 2868 kg/ha. High to medium phenotypic and genotypic coefficients of variability were observed for thousand grain weight, biomass yield and grain yield. High broad sense heritability estimates were observed for thousand seed weight, days to 75% maturity, days to 50% heading and biomass yield kg/ha. High to medium heritability and genetic advance were observed for plant height, thousand grain weight, biomass yield and grain yield. Days to 75% maturity, panicle length, plant height, number of fertile tillers per plant, number of spikelet per panicle, number of filled grains per panicle and biomass yield had a positive and significant correlation with grain yield. Generally from this study, plant height, number of spikelet per panicle, number of filled grains per panicle, and biomass yield were found to be important yield component traits.

Keywords: Broad Sense Heritability; Genetic Advance; Genotype; Grain Yield; GCV; PCV

1. Introduction

There is high potential for rice (*Oryza sativa L.*) production in Ethiopia. However, the crop has been introduced recently to the country. The finding of wild rice in the Fogera Plain in the early 1970s was the foundation for rice introduction in the area as well as in the Amhara region (Astewel, 2010). The number of farmers, who are growing rice, the area covered with rice and its production has been increasing from time to time (Tilahun *et al.,* 2013).

The development of rice cultivars which have high yielding potential is the most important aim in breeding programs (Jing and Jianchang, 2011). The genetic variation for the traits under selection process and high heritability and genetic advance are necessary factors to develop the high yielding cultivars in the breeding program (Ulloa, 2006). Heritability estimates provide information on the proportion of variation that is transmissible to the progenies in subsequent generations (Satheeshkumar and Saravanan, 2012). However, the estimates of heritability alone are not indicative of the genetic progress that would result from selecting the best plants (Chaghakaboodi *et al.,* 2012). Genetic advance has also a considerable importance because it indicates the extent of the expected genetic gain from one cycle of selection (Hamdi *et al.,* 2003). Grain yield is a complex character, quantitative in nature and anintegrated functionof a

number of component traits. Therefore, selection for yield may not be much satisfying unless other yield attributing traits are taken into consideration (Akinwale *et al.,* 2011). There is no clear information regarding range of the genetic variability and yield attributing traits of upland rice in the study area. Hence, the objectives of this study were to estimate the genetic variability of upland rice genotypes using morphological traits and to assess the association between yield and yield related traits.

2. Materials and Method
2.1. Experimental Materials, Design, and Procedures

Twelve upland rice genotypes collected from Adet Agricultural Research Center: NERICA-3, NERICA-10, NERICA-12, NERICA-13, NERICA-14, Hidasie, Kokit, Superica-1, Getachew, Andasa, Tana and Kallafo-1 were used as experimental material. The experiment was laid out in a randomized complete block design (RCBD) with three replications and was conducted under rain fed situations in the 2013 main cropping season at Wereta rice research center. Each entry was sown with the seed rate of 60 kg per hectare by hand drilling in five row plots of 5 m length and 1 m width with 20 cm inter row space with three replications. There was 1m space between replications and 50 cm between varietal plots. DAP and Urea

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fertilizers were applied at the rate of 100 kg per hectare. DAP was applied once at the time of planting, whereas Urea was applied in three splits equally at planting, tillering and panicle initiation. All other management practices were uniformly applied to all experimental plots as per recommendations.

2.2. Data Collection

Data were collected on plot and plant basis according to standard evaluation systems for rice (IRRI, 1988). Plant height (cm), panicle length (cm), number of effective tillers per plant, number of spikelet per panicle and number of filled grains per panicle were measured from ten randomly selected plants in the middle three rows of each plot. Data for days to 50% heading and days to 75% physiological maturity were collected from plot basis. However, thousand grain weight (g), biomass yield (kg/ha), and grain yield were collected on the three central rows.

2.3. Data Analysis

Analysis of variance (ANOVA) and correlation coefficient were conducted using the procedure for randomized complete block design in SAS (9.1 version). The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and De Vane (1953). Broad sense heritability (H²) expressed as the percentage of the ratio of the genotypic variance ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 p$) as described by Allard (1960):

$$H^2 = \left[\frac{\sigma^2{}_g}{\sigma^2{}_p} \right] x100 \text{ Where,}$$

$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance

Genetic advance under selection (GA) refers to the improvement of traits in genotypic value for the new population as compared with the base population under one cycle of selection at a given selection intensity (Singh, 2001). Genetic advance in absolute unit (GA) and Genetic advance in percent of the mean (GAM), was estimated in accordance with the methods illustrated by Johnson *et al.* (1955):

$$GA = K \, \sigma_p H^2$$

GAM = (GA/$\bar{x}$) x 100 Where, k = the standardized selection differential at 5% selection intensity (K = 2.063).

σ_p = Phenotypic standard deviation
H² = Broad sense heritability

$\bar{x}$ = grand mean of a character

3. Results and Discussion

The analyses of variances revealed significant variations among the genotypes for all the characters examined with the exception of effective tiller per plant and panicle length (Table 1). The results show the presence of adequate variability which can be important for selection of the preferred genotype in rice breeding programme. Similar results were accounted by Surek and Beser (2003); Osman *et al.* (2012) and Mulugeta *et al.* (2012).

The maximum yield was obtained from the genotype AD-48 (3399.5 kg/ha) followed by AD-01 (3396 kg/ha) and AD-12 (3277.9 kg/ha) (Table 2). The highest grain yield performance of the genotypes could be attributed to plant height, number of fertile tillers per plant, spikelet per panicle, filled grain per panicle and biomass yield.

3.1. Phenotypic and Genotypic Coefficients of Variation

The phenotypic variance was separated into genotypic and environmental variances to estimate the contribution of each to the total variation. The minimum (3.34) and maximum (19.31) values of phenotypic coefficient of variation (PCV) were observed on biomass yield and days to maturity, respectively (Table.3).

Table 1. Analysis of variance (ANOVA).

Source of Variation	df	DH	DM	PL	PH	FTPP	SPP	FGPP	TSW	BY	GY
Replication	2	3.08	0.58	0.22	5.84	0.01	2.89	1.33	0.002	743361.83	84527.24
Genotype	11	44.09**	64.91**	2.41NS	95.51**	0.56NS	59.48*	33.76*	24.02**	3523820.64**	366650.02**
Error	22	5.63	0.79	1.73	22.31	0.49	24.58	12.58	0.23	535134.09	100109.56
CV		2.36	0.63	8.54	6.56	12.08	6.29	5.03	1.81	11.42	11.03

* = significant at P<0.05; ** = significant at P<0.01; NS = non significant. DH = Days to 50% heading, DM = Days to 75% maturity, PL = panicle length (cm), PH = Plant height (cm), FTPP = Number of fertile tiller per plant, SPP = Number of spikelet per panicle, FGPP = Number of filled grains per panicle, BY = Biomass yield (kg/ha), TGW = 1000 grain weight (g), GY = grain yield (kg/ha).

Table 2. Agronomic performance of the tested upland rice genotypes.

Genotype	DH	D M	PL	PH	FTPP	SPP	FGPP	TSW	BY	GY
Kokit	94.33	138.33	14.97	65.37	5.67	72.07	67.03	30.33	5600.00	2895.82
Hedase	96.33	138.00	16.30	64.40	5.53	80.53	72.87	26.00	6000.00	2667.29
Superica-1	102.67	139.33	14.90	70.70	6.00	78.63	68.80	23.00	6511.11	2620.11
NERICA-12	104.00	140.00	14.50	73.73	5.77	76.60	68.33	28.67	5000.00	2447.46
Getachew (AD01)	106.67	147.67	16.73	78.00	6.50	91.80	80.53	25.00	8222.22	3396.15
NERICA-13	98.00d	137.67	16.00	77.87	5.37	77.83	70.80	31.00	6000.00c	2928.33
Andasa (AD012)	103.67	148.67	16.10	78.03	6.20	83.53	72.90	23.73	7666.67	3277.86
NERICA- 4	99.33	137.33	13.97	67.07	5.93	78.10b	69.23	25.00	6266.67	2691.98
FOFIFA-3737	101.00	139.33	14.57	69.90	5.63	77.30	69.60	30.00	5888.89	2339.67
NERICA-3	99.33	138.33	14.63	65.73	5.43	83.20	74.93	25.00	5555.55	2769.02
Tana (AD-048)	104.33	149.67	15.67	80.30	6.43	83.67	73.73	23.67	8333.33	3399.53
NERICA-10	96.33	138.67	16.27	71.57	5.07	76.17	67.87	27.67	5822.17	2977.62
P level	**	**	NS	**	NS	*	*	**	**	**
LSD value	4.0174	1.5102	2.226	7.9977	1.1855	8.3968	6.008	0.8146	1238.70	535.76
CV	2.36	0.63	8.54	6.53	12.08	6.29	5.03	1.81	11.42	11.03
SE±	0.69	0.76	0.22	1.11	0.11	0.97	0.71	0.46	203.19	71.29

* = significant at P<0.05; ** = significant at P<0.01; NS = non significant, CV = coefficient of variation, SE = standard error, P = probability level, LSD = least significance difference, DH = Days to 50% heading, DM = Days to maturity, PL = panicle length, PH = Plant height (cm), FTPP = Number of fertile tiller per plant, SPP = Number of spikelet per panicle, FGPP = Number of filled grains per panicle, BY = Biomass yield (kg/ha), TGW = 1000 grain weight (g), GY = grain yield (kg/ha).

The PCV values for number of fertile tillers per plant, thousand grain weight, biomass yield and grain yield were medium. It indicated the phenotypic difference between the tested rice genotypes with the above traits is moderate. In agreement with the present results, Akinwale *et al.* (2011) also reported medium PCV for thousand grain weight and number of fertile tillers per plant.

Days to 50% heading, days to 75% maturity, panicle length, plant height, number of spikelet per panicle and number of filled grains per panicle had low PCV values. This result is in conformity with the finding of Akinwale *et al.* (2011), who observed low PCV for days to 50% heading, days to maturity, plant height and panicle length. Selvaraj *et al.* (2011) also observed low PCV for days to 75% maturity and panicle length.

Genotypic coefficient of variation measures the variability of any character. The extent of the environmental influence on any character is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation. Large differences reflect high environmental influence, while small differences reveal high genetic influence (Akinwale *et al.,* 2011)

Genotypic coefficient of variability (GCV) values were low for days to 50% heading, days to 75% maturity, panicle length, plant height, number of fertile tillers per plant, and number of spikelet per panicle. Similar results have been reported by Chakraborty and Chakraborty (2010) for days to 50% heading and panicle length. Likewise Selvaraj *et al.* (2011) for panicle length and days to maturity and Akinwale *et al.* (2011) for days to 50% heading, days to 75% maturity, panicle length, plant height and number of fertile tillers per plant. In contrast to the present study, Akinwale *et al.* (2011) reported low GCV for thousand grain weight and Selvaraj *et al.* (2011) observed high GCV for number of fertile tillers per plant. The difference between this finding and the previous findings may be related to environmental factors in which experiments conducted and genotypes used are quite different.

Medium GCV was observed for thousand grain weight, biomass yield and grain yield. It pointed out the possibility of yield improvement through selection of these traits. Similar results have been reported for thousand grain weight by Kumar and Saravanan (2012) and for grain yield by Akinwale *et al.* (2011). On the other hand Selvaraj *et al.* (2011) observed high GCV for grain yield.

The difference between PCV with the corresponding GCV values was relatively higher for number of fertile tillers per plant, panicle length, grain yield, biomass yield and number of spikelet per panicle, indicating the higher influence of the environment on the traits. However, this difference was comparatively low for days to 75% maturity, thousand grains weight, days to 50% heading, filled grains per panicle, and plant height. The small difference indicating that there is a minimal influence of environment on the expression of these traits. In addition, it indicates the presence of sufficient genetic variability for observed traits may facilitate the selection process (Yadav *et al.*, 2011). Therefore, selection based on phenotypic performance of the traits would be effective to bring considerable improvement in these traits.

3.2. Heritability and Genetic Advance

Broad sense heritability estimates ranged from 5.04 for number of fertile tillers per plant to 97.17% for thousand grain weight (Table 3). High broad sense heritability estimates observed for thousand seed weight, days to 75% maturity, days to 50% heading and biomass yield (kg/ha). Similar results have been reported by Yadav *et* al. (2011) for days to maturity; Akinwale *et al.* (2011) for days to 50% heading and days to maturity; Osman *et al.* (2012) for thousand grain weight. Whereas, Yadav *et al.* (2011) found low heritability for thousand grain weight, Akinwale *et al.* (2011) and Osman *et al.* (2012) found high heritability for plant height quite the opposite of the present result. High heritability values pointed out that the traits under study are less influenced by the environment in their expression (Babu *et al.,* 2012). Therefore, selection can be effective on the basis of phenotypic expression of these traits in the individual plant by implementing simple selection methods.

Medium broad sense heritability estimates were observed for plant height, grain yield (kg/ha), number of filled grains per panicle and number of spikelet per panicle, which indicates the possibility of using these traits in rice improvement programs, but the expressions could be influenced by the environment. A similar result has been observed by Mulugeta *et al.* (2012) for grain yield. The moderate heritability estimate for grain yield could be attributed to the fact that yield is a complex trait and is controlled by many genes (Osman *et al.*, 2012).

Table 3. Estimates of range, mean, phenotypic and genotypic variances, broad sense heritability, and genetic advance in 12 upland rice genotypes.

Trait	Range	Mean	σ2p	σ2g	σ2e	PCV (%)	GCV (%)	H² (%)	GA	GA (%)
DH	94.33_106.67	100.50	18.45	12.82	5.63	4.27	3.56	69.49	6.16	6.13
DM	137.33_149.67	141.08	22.17	21.37	0.80	3.34	3.28	96.41	9.36	6.64
PL	13.97_16.73	15.38	1.96	0.23	1.73	9.09	3.11	11.75	0.33	2.15
PH	64.40_80.30	71.89	46.71	24.40	22.31	9.51	6.87	52.24	7.37	10.25
FTPP	5.07_6.50	5.79	0.52	0.03	0.49	12.39	2.78	5.04	0.07	1.21
SPP	72.07_91.80	78.83	36.22	11.63	24.59	7.63	4.33	32.11	3.99	5.06
FGPP	67.03_80.53	70.48	19.65	7.06	12.59	6.29	3.77	35.93	3.29	4.66
TSW	23.00_31.00	26.59	8.16	7.93	0.23	10.74	10.59	97.17	5.73	21.53
BY	5000.00_8333.33	6405.55	1531363.00	996228.85	535134.09	19.31	15.58	65.06	1660.81	25.93
GY	2339.67_3399.53	2867.57	188956.42	88846.82	100109.56	15.16	10.39	47.02	424.65	14.81

DH = Days to 50% heading, DM = Days to maturity, PL = panicle length, PH = Plant height (cm), FTPP = Number of fertile tiller per plant, SPP = Number of spikelet per panicle, FGPP = Number of filled grains per panicle, BY = Biomass yield (kg/ha), TGW = 1000 grain weight (g), GY = grain yield (kg/ha), phenotypic (σ^2p) genotypic (σ^2g) and environmental (σ^2e) variances, phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad sense heritability (H²), expected genetic advance (GA) and genetic advance as percent of the mean (GA%).

Low broad sense heritability was observed for number of fertile tillers per plant and panicle length, which indicates high influence of the environment on these traits. Similar results have been reported by Akhtar *et al.* (2011) and Akinwale *et al.* (2011) for number of fertile tillers per plant. The low heritability recorded for these traits indicates that direct selection for these traits will be ineffective.

Estimation of GA for grain yield was 424.68 kg/ha, indicating that when ever we select the best 5% high yielding genotypes as parents, mean grain yield of progenies could be improved by 424.68 kg/ha for the first cycle, that is, the mean genotypic value of the new population for grain yield will be improved from 2867.57 kg/ha to 3292.25 kg/ha.

The Genetic advance as percent of the mean (GAM) at 5% selection intensity was high for biomass yield per hectare followed by thousand grain weight. A similar result has been reported by Singh *et al.* (2011) for biomass yield. However, the authors observed high genetic advance for plant height and number of spikelet per panicle in contrast to the results of this study. Genetic advance as per cent of the mean (GAM) at 5% selection intensity was medium for plant height and grain yield. This result agrees with the finding of Akinwale *et al.* (2011); Babu *et al.* (2012) and Mulugeta *et al.* (2012).

Genetic advance as percent of the mean (GAM) at 5% selection intensity was low for number of fertile tillers per plant, panicle length, number of filled grains per panicle, number of spikelet per panicle, days to 50% heading and days to 75% maturity. Similar results have been reported by Akinwale *et al.* (2011) for number of fertile tillers per plant; Babu *et al.* (2012) forpanicle length and Mulugeta *et al.* (2012) for days to 75% maturity, panicle length, number of fertile tillers per plant and number of spikelet per panicle. However, this result is quite different comapare to the results of Nandan *et al.* (2010) for number of fertile tillers per plant and number of spikelet per panicle.

In view of the fact that, high heritability does not always indicate a high genetic gain, heritability should be used together with genetic advance in predicting the ultimate effect for selecting superior varieties (Ali *et al.*, 2002). In this study, high heritability and high genetic advance were recorded for thousand grain weight and biomass yield which could be considered as an essential traits for upland rice improvement by selection. Similar results have been reported by Shukla *et al.* (2005); Nandan *et al.* (2010); Sravan *et al.* (2011) and Toshimenla and Sapuchangkija (2013).

Moderate heritability with moderate genetic advance was recorded for the traits like plant height and grain yield. On the other hand, high heritability estimates with low genetic advance observed for days to heading and days to maturity. Similar results have been reported for days to maturity by Karim *et al.* (2007) and Akinwale *et al.* (2011).

Low heritability with low genetic advance was observed in the traits like panicle length and number of fertile tillers per panicle, this result agrees with the work of Chakraborty and Chakraborty (2010) for panicle length and Mulugeta *et al.* (2012) for number of fertile tillers per panicle.

3.3. Correlation

Among the tested parameters days to 75 % maturity (r = 0. 59**), plant height (r = 0.56**) and biomass yield (r = 0.76**) had a positive and highly significant correlation with grain yield. Panicle length (r = 0.39*), number of fertile tillers per plant (r = 0.34*), number of spikelet per panicle (r = 0.35*) and number of filled grains per panicle (r = 0. 39*) had a positive and significant correlation with grain yield. The positive and significant correlation indicates a strong association of these traits with grain yield. In addition to positive and significant correlation, high to moderate heritability is necessary for the indirect selection to enhance grain yield. Days to 75% maturity, plant height, number of spikelet per panicle number of filled grains per panicle and biomass yield reviled positive and significant correlation with high to moderate heritability. Therefore, a selection of these traits is very important in improving grain yield for upland rice. This result is in agreement with the result of Akhtar *et al.* (2011) and Akinwale *et al.* (2011). In contrast to present result, Hairmansis *et al.* (2010) reported a negative correlation between plant height and grain yield.

Table 3. Phenotypic correlation coefficients between pairs of traits studied in 12 upland rice genotypes.

TRAIT	DH	D M	PL	PH	FTPP	SPP	FGPP	TSW	BY	GY
DH	1.00									
DM	0.67**	1.00								
PL	0.043	0.29	1.00							
PH	0.39*	0.62**	0.16	1.00						
NFT	0.32	0.46**	0.28	0.27	1.00					
SPP	0.52**	0.55**	0.24	0.31	0.21	1.00				
FGPP	0.33*	0.41	0.12	0.17	0.11	0.88**	1.00			
TSW	-0.46**	-0.51**	-0.07	-0.14	-0.35*	-0.35*	-0.22	1.00		
BY	0.43**	0.74**	0.34*	0.63**	0.49**	0.47**	0.36*	-0.55**	1.00	
GY	0.18	0.59**	0.39*	0.56**	0.34*	0.35*	0.39*	-0.31	0.76**	1.00

* = significant at P<0.05 and ** = significant at P<0.01. DH = Days to 50% heading, DM = Days to maturity, PL = panicle length, PH = Plant height (cm), FTPP = Number of fertile tiller per plant, SPP = Number of spikelet per panicle, FGPP = Number of filled grains per panicle, BY = Biomass yield (kg/ha), TGW = 1000 grain weight (g), GY = Grain yield (kg/ha).

4. Conclusion

In general, the study showed variation for almost all the traits studied among the tested rice genotypes, which is an indication of the presence of sufficient variability that can be exploited through selection. In the broad sense heritability, genetic advance and correlation analysis of the study revealed that plant height, number of spikelet per panicle, number of filled grains per panicle, and biomass yield were the most important yield component traits. From this result, genotypes AD-048, AD-01 and AD-012 can be suggested for commercial production in the upland ecosystem of Fogera district and other similar areas in the region.

5. Acknowledgements

6.References

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