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Genetic variability and heritability of yield and yield components in rice genotypes

Igbenedion Gideon and Ubah Dennis

Department of Plant Breeding and Seed Technology, Federal University of Agriculture (FUNAAB), P. M. B. 2240, Abeokuta, Ogun State, Nigeria.

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A study was conducted during 2008 to 2009 in 12 environments in Nigeria, Benin Republic and Togo to evaluate genetic variation and heritability of yield and related traits in 48 rice genotypes. The experiments were laid out in a randomized complete block design (RCBD) with three replications. Genotypes differed significantly at $p > 0.001$ for all the traits studied, which implies that the genotypes contain adequate genetic variability. Phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) in all the characters across the 12 environments. High heritability estimates were obtained for days to flowering (91.37), days to maturity (86.86), plant height at maturity, number of tiller per meter square, panicle shattering, panicle threshability, panicle per meter and panicle length (72.21) suggesting that the traits are primarily under genetic control. High estimates of heritability, GCV and genetic advance (GA) observed for grain yield is an indication that selection for grain yield could be achieved through phenotypic performance. Furthermore, high estimates of heritability, GA and GCV recorded in these characters could be explained by additive gene action. Low estimates of heritability, GCV and GA recorded for grain yield and number of grains per panicle could be due to non-additive gene effect suggesting that these traits were less responsive to specific environment influences. Grain yield recorded highly significant positive correlation with panicle length (0.28), leaf width (0.40), grain length (0.30), number of panicles per meter square (0.19) and 1000-grain weight (0.17). It correlated negatively with basal leaf sheath coloration (-0.33) and grain width (-0.20) in the 12 environments. The current study indicated that more number of tillers, panicles per meter square, long panicles, high number of primary and secondary branch panicles and large 1000-grain weight are important yield related traits and could be used for selection in rice breeding programs.

Key words: Correlation coefficients, heritability, phenotypic coefficients, rice, variability, yield components.

INTRODUCTION

Rice is the most rapidly growing food commodity in sub-Saharan Africa (SSA), mainly driven by urbanization. It has become a commodity of strategic significance and

the fastest-growing food source in Africa, such that its availability and price are now a major determinant of the welfare of the poorest segments of consumers who are

*Corresponding author: E-mail: dr.gideonig@gmail.com

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the least food-secure consumers in Africa. It is no longer a luxury food but has become the cereal that constitutes a major source of calories for the urban and rural poor (Ogunbayo et al., 2005; Seck et al., 2013). Rice is now grown and consumed in more than 40 African countries, where about 20 million farmers are engaged in its production and about 100 million people depend on rice directly for their livelihood (Nwanze et al., 2006). The world population is expected to reach 8 billion by 2030 and rice production must be increased by 50% in order to meet the growing demand (Khush and Brar, 2002). The demand for rice in SSA is expected to grow substantially as the population is currently growing at the rate of 3 to 4% per annum and rice consumption is growing faster than that of any major food. However, self-sufficiency in African rice production is declining as demand increases, driving the urgent need to increase and improve the continent's production of rice to satisfy the high demand (Sanni et al., 2012). To attain rice self-sufficiency and meet the future demand resulting from population growth, development of high yielding genotypes with desirable agronomic traits for diverse ecosystem is therefore, a necessity (Ogunbayo et al., 2007; Akinwale et al., 2011; Mulugeta et al., 2012).

The development of high yielding cultivars with wide adaptability is the ultimate aim of plant breeders. Therefore, by exploiting the good adaptation and stability of yield and its components in rice genotypes, it would be possible to develop/identify high yielding and well adapted varieties (Ogunbayo, 2011). Thus, effective yield component breeding to increase grain yield could be achieved, if the components traits are highly heritable and positively correlated with grain yield (Sabesan et al., 2009; Ullah et al., 2011). The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding program, heritability and genetic advance (GA) are important selection parameters.

Genetic variability is important for breeding and in selecting desirable traits. Thus, character association of component traits with yield and among themselves is very important. The relationship between rice yield and yield component traits has been studied widely at a phenotypic level. Idris et al. (2012) observed positive phenotypic and genotypic correlation coefficient between grain yield and number of filled grains per panicle, harvest index, panicle length and number of grains per panicle. Sadeghi (2011) observed positive significant association of grain yield with grains per panicle, days to maturity, number of productive tillers and days to flowering. Ullah et al. (2011) detected that grain yield was positively and significantly associated with panicle length

and grains per panicle. Hairmansis et al. (2010) also recorded a positive and significant association of grain yield with filled grains per panicle, spikelets per panicle and spikelet fertility.

Heritability estimates along with GA are normally more helpful in predicting the gain under selection than heritability estimates alone. Therefore, the estimation of heritability for any trait requires the partitioning of the observed variation between genetic effects and environmental effects (Cockerham, 1963). However, when the phenotypic variability is large, traits with high heritability values are subject to large genetic gains per generation when selection is applied (Dudley and Moll, 1969; Hesse, 1975; Hansche, 1983; Falconer, 1989; Nyquist, 1991). The broad sense heritability is the relative magnitude of genotypic variance for the traits and it gives an idea of the total variation accounted to genotypic effect (Allard, 1960).

Karthikeyan et al. (2010) recorded broad sense heritability estimates of 99.8% for days to flowering, 99.2% for days to maturity, 87.3% for plant height, 79.8% for panicle length, 93.4% for a number of branches per panicle, 88.8% for number of fertile florets per plant, 97.6% for 1000 grain weight and 73.2% for grain yield per plant. Padmaja et al. (2008) also reported 98.52% for days to flowering, 99.05% for plant height, 78.72% for total tillers per plant and 76.82% for productive tillers per plant, 81.54% for panicle length and 99.38% for grains per panicle, 99.46% for spikelet fertility, 87.21% for 100 grain weight and 94.21% for single plant yield.

The objective of this study was to assess genetic variability and heritability of yield and yield components in 48 rice genotypes.

MATERIALS AND METHODS

Forty-eight (48) rice varieties that included 37 interspecific (*Oryza glaberrima* × *Oryza sativa indica*) and 11 intraspecific (*O. sativa indica* × *O. sativa indica*) were evaluated in 2008 and 2009 wet seasons at the International Institute of Tropical Agriculture (IITA) Ibadan (Nigeria), Africa Rice Center (AfricaRice) Ouédémé (Benin Republic) and Farmers field in Kpalime (Togo). All the varieties used for the experiment were collected from the lowland breeding unit and Genebank of Africa Rice Center, Cotonou, Benin. Field evaluation was carried out under irrigated lowland, valley bottom and valley fringe conditions. Randomized complete block design (RCBD) with three replications was used in all locations and years. Each plot size was 1 × 5 m with 20 cm within and between rows. Five rows per plot and inter-plot spacing of 40 cm was used. Seeds were sown directly for valley bottom and valley fringe environments at 2 seeds per hill and later thin to one plant. Nursery beds were prepared for the irrigated plots and seedlings were transplanted at 21 days old. NPK (15-15-15) fertilizer was applied as basal application at the rate of 200 kg/ha before transplanting and top dressed with urea at the rate of 65 kg/ha at the tillering stage

*Corresponding author. E-mail: a.ogunbayo@cgiar.org

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Table 1. List of characters studied in the experiment.

Character	Abbreviation
Plant vigor	Pltvigor
Number of tiller at 60 days	NmTiller
Flowering date	Flwdays
Maturity date	Matdays
Plant height (cm)	PltHght
Panicle exertion	PanExt
Panicle shattering	PSht
Panicle threshability	Pthres
Yield (gms)	Yld
Hairnes	Hairnes
Panicle number/m ²	Pan_m
Awning	Awning
Panicle length (cm)	Panlght
Primary branch panicle	Prybrpan
Secondary branch panicle	Secbrpan
Leaf length (cm)	Lflgth
Leaf width (cm)	Lfwdth
Flag leaf angle	FlaglAng
Base tiller coloration	Bastlcol
Grain length (mm)	Grlght
Grain width (mm)	Grwidth
1000 grain weight (gms)	1000grwt

followed by 35 kg/ha at booting stage. The plots were hand-weeded regularly to minimize weed infestation.

Data collection and analysis

Morphological data were collected for 22 quantitative and qualitative characters at appropriate growth stage of rice plant following the Standard Evaluation System (IRRI, 2002). The characters that were evaluated included days to 50% flowering, days to 85% maturity, plant height, number of tiller at 60 days, number of panicles per m², grain yield, panicle length, panicle exertion, plant vigor, panicle shattering, panicle threshability, hairness, awning, primary panicles branching, secondary panicles branching, leaf length, leaf width, flag leaf angle, basal leaf sheath colour, grain length, grain width and 1000-grain weight. The characters that were evaluated are shown in Table 1. The data collected on 22 agro-botanical traits from the rice accessions were subjected to statistical analysis using SAS/PC version 9 packages (SAS Institute, 2000). Analysis of variance (ANOVA) was carried out on the data to assess the genotypic effects and their interaction using a general linear model (GLM) procedure for RCBD in SAS (9.2 version). Estimates of variance components were generated. Broad-sense heritability (h^2) was calculated as the ratio of the genotypic variance to the phenotypic variance using the formula according to Allard (1960):

$$h^2 = \sigma^2_g / \sigma^2_{ph} \times 100$$

Where h^2 = broad sense heritability (%), σ^2_g = genotypic variance and σ^2_{ph} = phenotypic variance.

GA was calculated at 20% selection intensity ($I = 1.4$). Phenotypic coefficients of correlation were computed using Pearson's linear correlation outlined by Steel and Torrie (1984).

RESULTS

Table 2 presents combined ANOVA for flowering days, maturity days, plant height, panicle/m² and yield of 48 rice genotypes at 12 environments. Significant replicate effects were observed for flowering days, maturity days, plant height, panicle/m² and yield. Also, the result indicates that the rice genotypes varied significantly with respect to all traits. The location, genotype $\times$ locations were highly significant to all traits except panicle/m². The 2 years differed significantly with respect to all traits meaning that climatic changes were observed during the study. Significant genotype $\times$ year effects were observed for flowering days and maturity days but non-significant G $\times$ E effects were observed for plant height, panicle/m² and yield meaning that the last three traits remained similar over the 2 years. Location $\times$ year interaction reported highly significant effects for all the five traits meaning that the location of experiments differed in the 2 years of the study, suggesting that rice genotypes performed differently in every location in each year. Genotype $\times$ location $\times$ year were significant with respect to flowering days and yield and non-significant effects were observed for maturity days, plant height and panicle/m².

Table 3 presents means, estimates of genotypic and phenotypic variance, genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV), broad-sense heritability and GA expressed as percentage of mean over twelve environments. Expectedly, phenotypic variances were generally higher than the genotypic variances in all the characters studied. The highest phenotypic and genotypic variances in all the characters considered were recorded in yield (1667418.63 and 743746.19), respectively. Equally, high phenotypic and genotypic variances were observed in number of panicles per meter square (89.00 and 48.72) and plant height at maturity (64.00 and 58.02), respectively. The PCV generally ranged between 2.87% for maturity date and 563.18% for awning, respectively. Similarly, the GCV ranged between 2.68% for maturity date and 563.18% for awning. Generally, heritability in the broad-sense estimate varied from 46.98% for panicle exertion and 100.00% for awning, respectively. Similarly, GA had a general range between 5.14% for maturity date and 160.16% for awning. A joint consideration of GCV, broad-sense heritability estimates and GA revealed that panicle shattering (16.28, 86.50, and 31.19%), panicle threshability (23.67, 93.60, and 47.17%), hairiness (29.49, 94.39, and 59.03%), flag leaf angle (35.89, 89.47, and 69.93%), basal leaf sheath colour (63.08, 95.75, and 127.16%) combined high GCV, heritability and high GA, whereas number of tillers per meter square (5.68, 66.22, and 9.52%), days to flowering (4.19, 91.37, and 8.24%), yield (22.32, 44.6, and 30.7%) combined high heritability with moderate, GCV and GA.

Table 4 presents phenotypic correlation coefficient between 22 characters of rice in 12 environments (6

Table 2. Mean squares of the combined analysis of variance for yield and related characters of forty-eight rice genotypes at 12 environments (6-locations by 2-seasons).

Source	DF	Flowering days	Maturity days	Plant height	Panicle/m ²	Yield (kg)
Rep	2	405.57**	320.90*	935.73*	17802.79**	3172332.00*
Genotype	47	573.99**	445.64**	2510.16**	3224.97*	4241473.00**
Location	5	3415.67**	3293.76**	16468.86**	58159.07**	478999838.00**
Genotype × location	235	39.00**	59.01**	431.84**	1640.01 ^{ns}	2045861.00**
Year	1	598.55**	987.06**	11891.26**	2518782.18**	214102592.00**
Genotype × year	47	55.59**	74.22*	60.48 ^{ns}	1076.35 ^{ns}	1323782.00 ^{ns}
Location × year	5	11053.14**	4314.64**	6147.59**	662751.43**	337035964.00**
Genotype × location × year	235	56.47**	48.14 ^{ns}	60.66 ^{ns}	1267.41 ^{ns}	1876652.00*
Error	1150	23.14	39.26	107.85	1895.73	1411702.00

*, ** Significant at 5 and 1% probability levels, respectively.

Table 3. General mean, estimate of phenotypic and genotypic variance, phenotypic and genotypic coefficient of variability (PCV and GCV), broad sense heritability and genetic advance (GA) expressed for 48 rice genotypes

Character	Grand mean	Phenotypic variance	Genotypic variance	Environmental variance	PCV	GCV	Broad-sense Heritability	GA (%)
Plant Vigor	2.98	0.17	0.12	0.02	13.94	11.86	72.41	20.79
Number of Tiller	12.16	0.72	0.48	0.14	6.98	5.68	66.22	9.52
Flowering days	89.28	15.28	13.96	0.60	4.38	4.19	91.37	8.24
Maturity days	119.07	11.72	10.18	1.10	2.87	2.68	86.86	5.14
Plant height	100.57	64.00	58.02	2.91	7.95	7.57	90.65	14.85
Panicle exertion	5.92	0.25	0.12	0.03	8.39	5.75	46.98	8.12
Panicle shattering	3.83	0.45	0.39	0.01	17.51	16.28	86.50	31.19
Panicle threshability	5.42	1.76	1.65	0.00	24.46	23.67	93.60	47.17
Yield	3864.26	1667418.63	743746.19	923672.45	33.42	22.32	44.60	30.70
Hairness	2.10	0.41	0.38	0.00	30.36	29.49	94.39	59.03
Panicle/meter square	198.51	89.00	48.72	44.12	4.75	3.52	54.74	5.36
Awning	0.13	0.54	0.54	0.00	563.18	563.18	100.00	160.16
Panicle length	25.93	2.41	1.74	0.70	5.98	5.08	72.21	8.90
Primary branch panicle	9.74	0.53	0.41	0.03	7.49	6.57	76.91	11.86
Secondary branch panicle	19.80	5.86	4.13	0.63	12.23	10.26	70.40	17.73
Leaf length	29.05	3.23	2.66	0.60	6.19	5.61	82.23	10.48
Leaf width	1.05	0.00	0.00	0.00	5.15	4.33	70.48	7.48
Flag leaf angle	1.64	0.39	0.35	0.01	37.94	35.89	89.47	69.93
Base tiller coloration	1.42	0.84	0.80	0.00	64.47	63.08	95.75	127.16
Grain length	8.84	0.10	0.10	0.00	3.65	3.49	91.39	6.87
Grain width	2.34	0.01	0.01	0.00	4.57	4.38	91.97	8.65
1000grwt	23.56	0.73	0.64	0.05	3.62	3.39	87.74	6.54

sheath coloration (-0.33) and significant to grain width (-0.20). Hairiness had highly significant positive correlation with awning (0.46), basal sheath coloration (0.23) and significant positive correlation with flag leaf angle (0.20). Similarly, highly significant negative correlation was observed with panicle length (-0.28), leaf length (-0.29), and significant with primary branch panicle (-0.16) and secondary branch panicle (-0.20).

Panicle per meter square was highly and positively significant correlated with grain length (0.27) and significant with awning (0.17). However, highly significant correlation was observed with primary branch panicle (-0.25). Awning had highly significant positive correlation with flag leaf angle (0.42), basal sheath coloration (0.24) and significant with secondary branch panicle (0.16) and negative with grain width (-0.18).

Panicle length was highly significant positively correlated with primary branch panicle (0.24), secondary branch panicle (0.36) and leaf length (0.39) and highly significant and negatively correlated with grain width (-0.22). Primary branch panicle had highly significant positive correlation with secondary branch panicle (0.73), leaf length (0.53), flag leaf angle (0.24), grain width (0.23) and highly significant negative correlation with basal sheath coloration (-0.24) and significant to 1000 grain weight (-0.24).

Secondary branch panicle was significantly and negatively correlated with leaf width (-0.22), basal sheath coloration (-0.25) and positively significantly correlated to leaf length (0.59). Leaf length was significant negatively correlated with grain width (-0.17). Leaf width also had significant negative correlation with 1000 grain weight (0.16). Leaf width had highly significant correlation with basal sheath coloration (0.34), grain width (0.22) and similarly had highly significant and negative correlation with grain length (-0.50). Basal sheath coloration had significant and negatively correlated with grain length (-0.19).

Grain length had a highly significant negative correlation with grain width (-0.22) and grain width had highly significant correlation with 1000 grain weight (-0.24).

DISCUSSION

The present study results indicated that there is adequate genetic variability present in the materials studied. The PCV was higher than the GCV in all the characters across the 12 environments. The difference between PCV and GCV is probably accounted for by the environmental effects. There was high heritability estimates for days to flowering, days to maturity, plant height at maturity, number of tiller per meter square, panicle shattering, panicle threshability, panicle per meter and panicle length suggesting that environmental factors did not affect greatly the phenotypic performance of these traits. Thus,

high estimates of heritability GCV and GA may be good predictors of seed yield in rice. Hence, selection based on the phenotypic performance of these characters will be reliable and effective.

Murtadha et al. (2004) suggested that traits with high heritability estimates, GA and GCV could be good predictors of seed yield in crops. Ibrahim and Hussein (2006) had a similar view in their report on *Hibiscus sabdarifa*. Furthermore, the moderate to high estimates of heritability, GA and GCV recorded in days to flowering, days to maturity, plant height at maturity, number of tiller per meter square, panicle shattering, panicle threshability, panicle per meter and panicle length could be explained by additive gene action and hence their improvement can be done through mass selection (Ibrahim and Hussein, 2006). However, non-additive gene effect could be the explanation for the low heritability, GCV and GA recorded for mature grain and number of seeds per panicle (Yadev, 1996; Koorse, 1987; Subramayan et al., 1995), suggesting that these traits could be improved by developing hybrid varieties, through recurrent selection method because they are less responsive to improvement by selection in specific environment, hence the need to breed for specific environment.

For inter-character association estimates to be repeatable, such character must be both significantly genotypic and phenotypically correlated for any selection based on this is reliable. The positive significant phenotypic and genotypic correlations between plant height at maturity, panicle length, primary branch panicle, secondary branch panicle, panicle per meter square in all environments is strong indication that these traits are major factors in relation to seed yield. This suggests that selection directed towards these characters will be effective in ensuring seed yield in rice. However, under phenotypic correlation, yield had highly significant positive correlation with panicle length (0.28), leaf width (0.40), grain length (0.30), and significant to panicle per meter square (0.19), primary branch panicle (0.16), secondary branch panicle (0.16), 1000 grain weight (0.17) and also had highly significant negative correlation with basal leaf sheath coloration (-0.33) and significant to grain width (-0.20) in 12 environments. Similarly, under genotypic correlation, yield was highly and positively significant correlated with panicle length (0.79), primary branch panicle (0.24), secondary branch panicle (0.26), grain length (0.37) and 1000 grain weight (0.24). These results suggest that selection to improve rice yield directed by the phenotype of these traits may be effective and negative correlation between yield and grain width may be due to the inability of the plant to feed and fill longer grain compared to shorter grains, hence making plants with longer panicle to have fewer numbers of grains and consequently having lower seed yield.

Therefore, from a present study, it can be concluded that for increasing rice grain yield, a genotype should possess more number of tillers, panicle per meter square,

panicle length, high primary and secondary branch panicle and 1000 grain weight. The results suggest that these characters are important yield contributing traits and selection on these traits would be most effective.

Conflict of Interest

The author(s) have not declared any conflict of interest.

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