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Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.)

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The objectives of this study were to estimate the phenotypic and genotypic coefficients of variation, broad sense heritability, genetic gain and correlations in rice (*Oryza sativa* L.). The experiment was laid out in a randomized complete block design (RCBD) with three replications in the International Institute of Tropical Agriculture, Ibadan, Nigeria during 2008/2009 cropping season. Genotypes differed significantly at (p>0.001) for all the traits studied, which implies that the genotypes constitute a pool of germplasm with adequate genetic variability. Genotypic coefficients of variation were lower than the corresponding phenotypic coefficients in all the traits studied, indicating considerable influence of the environment on the expression of the traits. High to medium broad sense heritability estimates observed on days to heading, days to maturity, plant height, grain yield and number of grains per panicle, panicle weight, number of panicles per m^2 and panicle length suggests high component of heritable portion of variation, which is the portion exploited by breeder and that selection for these traits can be achieved directly based on their phenotypic performance. The low broad sense heritability observed for the number of tillers per plant and 1000 grain weight is indicative of the influence of the environment on these traits. Low heritability of these traits indicates the ineffectiveness of direct selection for these traits. High to medium heritability and genetic advance were recorded for the number of grains per panicle, grain yield, panicle weight and the number of panicles per plant. This suggests that these traits are primarily under genetic control and selection for them can be achieved through their phenotypic performance. Grain yield exhibited significantly positive correlation with the number of tillers per plant (r = 0.58**), panicle weight (r =0.60*) and number of grains per panicle (r= 0.52*). Therefore, the results suggest that these traits can be used for grain yield selection.

Key words: Broad sense heritability, rice, genotypic coefficient of variation, phenotypic coefficient of variation, genetic gain, rice yield, yield components.

INTRODUCTION

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). Hence, rice breeders are interested in developing cultivars with improved yield and other desirable agronomic characters. Genetic variability for agronomic traits is the key component of breeding programmes for broadening the gene pool of rice. Plant breeders commonly select for yield components which indirectly increase yield. Heritability (h^2) 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. El-Malky et al. (2003) observed high broad sense heritability estimate of 98.89% for days to maturity, 75.20% for the number of tillers per plant, 41.74% for the number of panicles per plant, 98.97% for 1000 grain weight and 90.87% for

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panicle weight. Babar et al. (2007) also reported high heritability of 0.74 for panicle length, 0.75 for plant height, 0.63 for the number of panicles per plant, 0.64 for days to heading and 0.81 for grain yield. On the other hand, Kato (1997) estimated low broad sense heritability of 0.16 for the number of panicles per plant and 0.20 to 0.33 for number of spikelet per panicle. Sürek and Korkut (1998) estimated high narrow sense heritability for grain weight, moderate for the number of spikelets per panicle and low for the number of panicles per plant.

The relationship between rice yield and yield components has been studied extensively at phenotypic level; Sharma and Choubey (1985) and Dhanraj and Jagadish (1987) reported that yield per plant was positively correlated with the number of productive tillers per plant, the number of panicles per plant and spikelets per plant and 1000 grain weight while Prasad et al. (1988) observed positive correlations between grain yield per plant and the number of spikelets per panicle, the number of fertile grains per panicle and 1000 grain weight. Bai et al. (1992) reported that grain yield is positively correlated with the number of productive tillers per plant, and the number of grains per panicle. Sürek and korkut (1998) reported that grain yield per plant was significantly correlated with the number of panicles per plant and 1000 grain weight.

Yield component breeding to increase grain yield would be most effective, if the components involved are highly heritable and genetically independent or positively correlated with grain yield. However, it is very difficult to judge whether observed variability is highly heritable or not. Moreover, knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character into future generations (Sabesan et al., 2009). Therefore, the objectives of this study were (i) to estimate the heritability of yield and yield components, and (ii) to compute the correlation of grain yield with yield components among the rice genotypes.

MATERIALS AND METHODS

Twenty rice genotypes were laid out in a randomized complete block design with three replications in the International Institute of Tropical Agriculture, Ibadan, Nigeria during 2008/2009 cropping season. Seeds sown in the wet nursery were transplanted to the puddled field after 21 days. Two seedlings were transplanted per each hill at a spacing of 20 cm between rows and between hills in 12 rows of 6 m^2. Inorganic fertilizer (NPK 15 15 15) was applied in three split applications, a basal of 200 kg/ha before transplanting and top dressed with urea at the rate of 65 kg/ha at the tillering stage and at the rate of 35 kg/ha at booting stage. Approximately 5 cm of standing water was maintained in the field until drainage before harvest. Weeds were controlled by application of post-emergence herbicide (Oritzoplus) 14 days after transplanting (DAT) and hand weeding.

Data collection

In all the plots, Data were collected for plants for days to 50% flowering, days to maturity, plant height, number of tillers per plant, number of panicles per plant, panicle length, 1000 grain weight, panicle weight, number of grains per panicle, and grain yield.

Statistical analysis

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 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):

$$h^2 = \sigma^2g / \sigma^2ph \times 100$$

where h^2 = broad sense heritability (%), σ^2g = genotypic variance and σ^2ph = phenotypic variance.

Genetic advance 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 AND DISCUSSION

The analysis of variance revealed significant variations among the genotypes for all the character examined (Table 1). The phenotypic variance was partitioned into genotypic and environmental variances for a clear understanding of the pattern of variation. Number of grains per panicle exhibited the highest genotypic variance (322) and also the highest environmental variance (139). However, panicle weight had the lowest magnitude of genotypic, environmental and phenotypic variance of 0.15, 0.1 and 0.2 respectively. 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. 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 characters. Iftekharuddeula et al. (2001) observed similar result.

Moderate to low genotypic and phenotypic coefficients of variation obtained for days to heading, days to maturity, plant height and panicle length may be due to the presence of both positive and negative alleles in the population. The findings were supported by Iftekharuddeula et al. (2001). They obtained moderate genotypic and phenotypic coefficients of variation for plant height, days to maturity and panicle length when nineteen rice hybrids were evaluated. The small differences observed between genotypic and phenotypic

Table 1. Genetic parameters of variation for agronomic characters.

Traits	Mean square	$\Delta^2 g$	$S^2 e$	$S^2 P$	GCV%	PCV%	$h^2 B$	GA
Days to heading	43.98***	14.4	0.7	15	4.46	4.56	95.1	8.97
Days to maturity	46.12***	14.9	1.3	16	3.36	3.51	92.1	6.63
Plant height (cm)	134.11***	39.6	15	55	6.54	7.69	72.4	11.45
No of panicles/ plant	11.63***	3.14	2.2	5.4	16.74	21.84	59.4	26.44
Panicle length(cm)	6.13***	1.58	1.4	3.0	5.20	7.12	53.6	7.81
No of tillers /plant	3.08*	0.42	1.8	2.2	5.95	13.71	19.2	5.38
Panicle weight(gm)	0.52*	0.15	0.1	0.2	16.95	20.58	68.1	28.78
No of Grains/panicle.	1106.19***	322	139	461	14.33	17.15	70.5	24.68
1000-grain weight	16.51*	2.43	9.2	12	5.52	12.09	21.7	5.2
Yield(t/ha)	0.85*	0.25	0.1	0.4	12.51	21.91	72.1	21.91

Genetic variance($S^2 g$), error variance($S^2 e$), phenotypic variance ($S^2 P$),genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability(h2B) and genetic advance (GA)*, ** and *** significant P= 0.05, P=0.01, and P= 0.001 respectively.

coefficients of variation on days to heading, days to maturity, plant height and panicle length indicate the presence of sufficient genetic variability for the traits which may facilitate selection (Yadav, 2000). The high to moderate differences between genotypic and phenotypic coefficients of variation observed in number of panicles per square meter, number of tillers per plant, panicle weight, number of grains per panicle, 1000 grain weight and grain yield indicate high influence of the environment on the traits.

The broad sense heritability is the relative magnitude of genotypic and phenotypic variances for the traits and it is used as a predictive role in selection procedures (Allard, 1960). This gives an idea of the total variation ascribable to genotypic effects, which are exploitable portion of variation. The heritability estimates obtained for the traits studied ranged between 19.2 to 95.1% (Table 1). High to medium broad sense heritability estimates observed for days to heading, days to maturity, plant height, grain yield and the number of grains per panicle, panicle weight, the number of panicles per square meter and panicle length. It suggests high component of heritable portion of variation, it is the portion which is exploited by breeders. On the other hand, Bhatti et al. (1998) reported high heritability for the number of spikelets per panicle, 1000 grain weight and the number of panicles per plant in rice. The low broad sense heritability observed for the number of tillers per plant and 1000 grain weight indicates the influence of the environment on these traits.

The low heritability recorded for these traits indicates that direct selection for these traits will be ineffective. Since high heritability do 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). High to medium heritability and genetic advance were recorded for the number of grains per panicle, grain yield, panicle weight and the number of panicles per plant. This suggests that these traits are primarily under genetic

control and selection for them can be achieved through their phenotypic performance. High heritability estimates with low genetic advance observed for days to heading, days to maturity, plant height and panicle length indicates non additive type of gene action and that genotype x environment interaction plays a significant role in the expression of the traits.

The results further revealed that most of the characters exhibited wide range of Variability (Table 2). Days to 50% flowering shows significant differences among genotypes at (p < 0.001) with genotype IR 79971-B-93-B-3 taking the shortest time (74.33 days) to attained 50% flowering while genotype PSBRC 14 took the longest period (91.66 days). Days to maturity follows the same trend with days to 50% flowering which ranges between 104 and120.33 days with genotype IR 79971-B-93-B-3 taking the shortest period (104 days) to mature while genotype PSBRC 14 takes the longest period (120.33 days) to mature. Plant height shows significant difference (p<0.001) among the genotypes at maturity. Genotype NERICA -L-40 is significantly taller with a height of 107.66 cm while genotype IR7851-12-3-2-2 is the shortest (86.06 cm). Number of tillers per plant varied significantly among the genotypes. The number of tillers per plant ranges between 9.50 and 12.25 with genotypes IR7851-12-3-2-2, IR 77674-3B-8-3-1-10-2, IR 77674-3B-63-3-3-7-3 and NERICA -L-2 recording the highest number (12.25). The number of panicles per m2 is significantly affected by genotypes. It varies from 6.06 in IR 80431-B-44-4 to 14.70 in genotype IR7851-12-3-2-2. Number of grains per panicle is one of the most important components of yield and probably this character will be helpful in breaking the yield plateau. Number of grains per panicle differs significantly among the tested genotypes. The highest grain number (164.88) is recorded in genotype IR7851-12-3-2-2 followed by FARO 37 (ITA 306) (154.66). The highest grain yield (5.16t/ha) is observed in IR7851-12-3-2-2 (p<0.001) while the lowest grain yield (2.83 t/ha) is observed in genotype

Table 2. Mean performance of 20 rice genotypes for 10 agronomic traits.

Designation	Days to Heading	Days to maturity	Plant height(cm)	No of tillers/plant	No of panicles/ plant	Panicle length(cm)	Panicle weight (g)	No of grains/pa nicle	1000grain weight (g)	Grain yield at 14% t/ha
FARO 35 (ITA 212)	88.33dc	119.67ab	101.33abcdef	9.58defg	10.66bcdef	26.26ab	1.76fgh	116.55def	25.67bc	2.93f
FARO 37 (ITA 306)	87.00de	117.33cde	95.33fghij	11.25def	9.16efg	24.90abcde	2.92ab	154.66ab	25.93bc	4.20bcde
IR 77384-12-17-3-18-2-B	87.66d	118bcd	91.83ghijkl	9.58defg	12.25abcd	24.23bcdef	2.91ab	119.44ed	29.86abc	3.97cde
IR 77645-3B-21-2-3-17-5	85.33fg	115.33efg	97.2defghi	10.25gh	12.32abc	23.10defg	2.29cde	149.33abc	31.66ab	4.42bc
IR 77645-3B-21-2-3-9-4	85.00fgh	114.33fgh	90.83ijkl	11.42ab	12.50abc	24.10bcdef	2.76abc	104.77fg	25.00c	4.70ab
IR 77674-3B-63-3-3-7-3	85.33fg	116def	104.03abcd	12.25a	10.90bcdef	23.60dcef	2.06defg	106.55f	34.66a	4.05cde
IR 77674-3B-8-2-2-14-4	83.33i	114fgh	103.00abcde	11.33ab	9.25efg	24.96abc	2.46abcd	110.33ef	28.33bc	4.02cde
IR 77674-3B-8-2-2-8-1	84.00ghi	113.67gh	99.26bcdefg	10.58ab	8.91fg	26.66a	2.03defg	130.33cde	28.33bc	4.11cde
IR 77674-3B-8-3-1-10-2	82.66ij	112.67hi	93.96fghij	12.25a	11.91bcde	22.23fg	2.37cde	123.80def	29.66abc	3.84cde
IR 77674-B-20-1-2-1-3-12	81.66j	111i	94.30fghij	9.67def	11.17bcdef	26.06ab	2.16def	131cde	29.33abc	3.92cde
IR7851-12-3-2-2	91.00ab	120.67a	90.33ijkl	12.25a	10.11bcdefg	24.33bcdef	2.23def	135.88bcd	27.00bc	4.39bc
IR 79971-B-93-B-3	74.33k	104j	106.20ab	9.75abc	9.75cdefg	21.10g	1.43h	85.67g	26.00bc	2.83f
IR 80431-B-44-4	87.00de	117cde	105.36abcde	9.50abcd	6.08h	24.00bcdef	2.43bcde	130.55cde	25.66bc	3.65de
IR 80463-B-39-1	85.66ef	116def	98.26cdefgh	10.25ab	10.66bcdef	23.66dcef	2.49abcd	149.22abc	26.33bc	4.24bcd
IR 82873-9	85.66ef	114.33fgh	88.20jkl	10.91ab	10.25bcdef	24.43abcdef	2.44bcde	122.00def	28.66bc	3.86cde
IR76926-5-1-1-4	81.66j	111i	96.06efhhij	10.67ab	11.58bcdef	22.43fg	2.95a	108.33ef	27.00bc	3.68de
IR7851-12-3-2-2	89.66bc	119abc	86.06l	12.00a	14.70a	25.63abc	2.96a	164.88a	29.33abc	5.16a
NERICA -L-2	83.33i	112.33hi	90.23ijkl	12.25a	12.75ab	24.23bcdef	2.39cde	112.77ef	28.67bc	4.29bc
NERICA -L-40	83.66hi	113hi	107.66hi	11.75ab	9.36defg	22.73efg	2.28cde	117.66edf	27.66bc	4.34bc
PSBRC 14	91.66a	120.33a	86.63a	10.25ab	7.41h	25.26bcda	2.29cde	131.22cde	30.00abc	3.60e
Means	85.20	114.98	96.31	10.89	10.59	24.20	2.38	125.26	28.23	4.01
SE	0.86	0.88	1.50	0.23	0.44	0.32	0.09	4.29	0.52	0.12
CV	0.98	1.01	4.04	12.33	14.03	4.87	11.68	9.41	10.75	7.73
R2	0.96	0.94	0.82	0.54	0.74	0.73	0.78	0.82	0.47	0.81
Pr > F	* * *	* * *	* * *	*	* * *	* * *	* * *	* * *	*	* * *

* = significant at P<0.05; ** = significant at P<0.01; *** = significant at P<0.001; ns = non significant.

IR 79971-B-93-B-3. The high grain yield performance of genotype IR7851-12-3-2-2 could be attributed to the high number of grains per panicle, high panicle weight and large number of panicles per plant.

Correlation

The degree of correlation among the characters is an important factor especially in economic and complex character as yield. Steel and Torrie (1984) stated that correlations are measures of the intensity of association between traits. The selection for one trait results in progress for all characters that are positively correlated and retrogress for traits that are negatively correlated.

Table 3. The phenotypic correlations among the traits.

Traits	Days to heading	Days to maturity	Plant height (cm)	No of panicles/plant	Panicle length	No of tillers/plant	Panicle weight	No of grains/panicle	1000 grain weight	Grain yield at 14% t/ha
Days to heading	1									
Days to maturity	0.98***	1								
Plant Height (cm)	-0.49*	-0.38ns	1							
No of Panicles/plant	-0.06ns	-0.06ns	-0.44*	1						
Panicle length(cm)	0.55*	0.55*	-0.32ns	-0.07ns	1					
No. of tillers/plant	0.12ns	0.08ns	-0.23ns	0.35ns	0.13ns	1				
Panicle weight(gm)	0.38*	0.34ns	-0.50*	0.32ns	0.01ns	0.23ns	1			
No of grains/panicle.	0.60**	0.58**	-0.39ns	0.1ns	0.41ns	0.05ns	0.53*	1		
1000-Gwt	0.10ns	0.10ns	-0.11ns	0.26ns	0.01ns	0.26ns	0.25ns	0.07ns	1	
Yield(t/ha)	0.37ns	0.32ns	-0.42ns	0.47ns	0.18ns	0.58**	0.60*	0.52*	0.20ns	1

* = significant at P<0.05; ** = significant at P<0.01; *** = significant at P<0.001; ns = non significant.

The result of correlation analysis as shown by their coefficients of correlation (Table 3) reveals that grain yield exhibits significantly positive correlation with the number of tillers per plant (r = 0.58**), panicle weight (r =0.60*) and the number of grains per panicle (r= 0.52*). The results are in conformity with Mohammed.et al. (2007) for the number of panicles per plant and Ramakrishman et al. (2006) for number of grains per panicle. The number of grains per panicle shows significantly positive correlation with days to 50% heading (r=o.60**), days to maturity (r=0.58**) and panicle weight (0.53*). Panicle weight correlated positively with days to heading (r=0.38*) and negatively correlated with plan height (r=0.50*).

Conclusion

The overall results indicated that there is adequate genetic variability present in the material studied. The broad sense heritability, genetic

advance and correlation analysis of the study revealed that the number of panicles per plant, panicle weight and the number of grains per panicle were the most important yield components. These characters also showed moderate to high heritability and genetic advance in percentage of mean. Therefore, the results suggest that the number of panicles per plant, panicle weight and the number of grains per panicle are important yield contributing traits and selection based on these traits would be most effective.

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