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ORIGINAL ARTICLES

Estimation of Genetic Variability and Correlation for Grain Yield Components in Rice (*Oryza sativa* L.)

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ABSTRACT

Eighteen rice (*Oryza sativa* L.) genotypes were evaluated at the Faculty Agriculture and Natural resources, Ed-duim, Sudan during 2011/2012 cropping season, to estimate the phenotypic and genotypic coefficients of variation, broad sense heritability, genetic advance and correlations. The experiment was laid out in a randomized complete block design (RCBD) with three replications. Eleven different traits were measured including yield and yield components. The genotypes differed significantly at ($p>0.001$) for most of the traits, 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 studied traits, indicating considerable influence of the environment on the expression of the traits. High to medium broad sense heritability estimates observed for days to 50% flowering, days to 50% maturity,1000-grain weight, number of filled grains per panicle, number of panicles per m^2 and panicle length suggests high component of heritable portion and selection for these traits can be achieved directly based on their phenotypic performance. The low broad sense heritability observed for the plant height, number of tillers per plant and grain yield 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, number of filled grain per panicle, days to 50% flowering, days to 50% maturity and number of panicles/m^2. 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 =0.49***), plant height (r =0.44***) and the number of filled grains per panicle (r= 0.36***). Therefore, these results suggest that the trait (number of filled grains per panicle) can be used for grain yield selection.

Key words: Rice genotypes, Genetic Variability, Heritability, Genetic advance, Correlation.

Introduction

Rice (*Oryza sativa* L.) belongs to family Poaceae (Gramineae). Morphologically, rice is an annual grass and one of the most important crops. Globally it is grown extensively in tropical and sub-tropical regions of the world. More than half of the people on the globe depend on rice as their basic diet and it is generally extensively consumed in the producing countries (FAO,2004). Sudan has a total estimated potential rice area for more than 300.000 hectares, if this area properly utilized it would suffice the local consumption demand to fill the gap for non-course food grain. Rice production in the Sudan has been practiced mainly in the southern states since it was introduced. In the northern states, particularly in the Gezira State the crop was introduced by the technical assistance from China in 1973 through 1980. (Mohamed,2010). During this period 12.000 hectares were cultivated as irrigated system attaining 3.5 to 7.6 ha^{-1}. In the White Nile State the crop had been cultivated as irrigated and is being cultivated as a flood ecosystem. Low yields of (0.98-1.2) t ha^{-1} were produced using traditional varieties with low inputs that are not adequate to enhance productivity.(Mohamed *et al*. 2012).

Development of high yielding varieties requires the knowledge of existing genetic variability. Hence, rice breeders are interested in developing varieties with improved yield and other desirable agronomic characters. Genetic variability for agronomic traits is the key component of breeding programs for broadening the gene pool of rice. Plant breeders commonly select for yield components which indirectly increase yield. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm.(Idris *et al*. 2012).

Heritability coupled with high genetic advance would be more useful tool in

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Predicting the resultant effect in selection of the best genotypes for yield and its attributing traits. It helps in determining the influence of environment on the expression the genotypic and reliability of characters. The relationship between rice yield and yield components has been studied extensively at phenotypic level. Zahid *et al*. (2006) studied correlation and path analysis in 14 genotype of Basmati rice. They found that number of grains per panicle had the highest positive direct effect (0.1486) on grain yield followed by 1000 grain weight (0.1064). 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 to estimate the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability in broad sense and to compute the correlation of grain yield with yield components among the rice genotypes.

Materials And Methods

The study was conducted in the summer season of 2011 at the Faculty of Agriculture and Natural Resources, University of Bakht ALruda , Ed-duim, Sudan (Long. 32˚20′E), (Lat. 13˚ 39′ N) and 380 msl ,. The experimental material composed of Eighteen rice genotypes (Table, 1), introduced by ARC from West African Rice Development Association (WARDA), International Rice Research Institute (IRRI) and China.

The seeds were sown directly in field on 15 of June 2011. The experiment was laid out in a randomized complete block design with three replications. The row to row and plant to plant distance was 25 x 25 cm. Phosphorus fertilizer in form of triple super phosphate (P_2O_5) was applied as basal dose before sowing at the rate of 43 Kg ha^{-1}. Nitrogen, in the form of urea (46% N), was applied in two equal split doses one after three weeks from sowing and the second after one month from the first one at the rate of 86 Kg ha^{-1} of N.

Data were recorded for days to 50% flowering and days to 50% maturity at each plot. At the time of harvesting the data on five plants from each plot were recorded for plant height (cm), panicle length (cm), number of tillers per plant, number of grains/panicle, number of filled grains/panicle, percentage of unfilled grains/panicle, 1000-grain weight, number of panicles/m^2 and grain yield t/ha.

Analysis of variance for the data was carried out by using computer program Statistical Analysis System (SAS. 1997). DMRT was used as mean separation method. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability in broad sense(h^{2}B) and genetic advance (GA) as per cent of means were estimated by the formula as suggested by Johanson *et al* (1955). Simple linear correlation coefficient between the eleven pairs of traits was calculated by using Minitab computer program version 16.

Table 1: Rice genotypes evaluated for yield and yield components at Ed-duim-Sudan season 2011.

Genotype	Origin
NERICA 2	WARDA.
NERICA 4	WARDA.
NERICA 5	WARDA.
NERICA 12	WARDA.
NERICA 14	WARDA.
NERICA 15	WARDA.
NERICA 17	WARDA.
YUNLU 22	CHINA.
YUNLU 24	CHINA.
YUNLU 26	CHINA.
YUNLU 30	CHINA.
YUNLU 33	CHINA.
WAB-1-38-19-14-P2-HB	IRRI.
WAB880-1-38-19-8	IRRI.
WAB891SG12	IRRI.
HANDAO 221	CHINA.
HANDAO 502	CHINA.
ZhONG HAN 3	CHINA.

WARDA=West African Rice Development Association.
IRRI=International Rice Research Institute.

Results And Discussion

The analysis of variance revealed significant variations among the genotypes for all the examined traits except number of tillers per plant and grain yield (Table, 2), indicating that these genotypes are highly variable especially for the traits that are significant, thus genetic improvement through selection could be promising. Number of panicle/m^2 exhibited the highest genotypic variance (3223.78) and also the highest environmental variance (1516.04). However, grain yield had the lowest magnitude of genotypic, environmental and phenotypic variance of 0.08, 0.76 and 0.84, respectively.

Genotypic coefficient of variation (GCV) measures the variability of any trait. The extent of the environmental influence on any trait 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 (Allard,2000). In this study phenotypic coefficients of variation were slightly higher than the genotypic coefficients of variation for all the studied traits(Table,3). This indicates the presence of environmental influence to some degree in the phenotypic expression of the characters. Iftekharuddeula *et al*. (2001) and Idris *et al* (2012) observed similar results. Moderate to low genotypic and phenotypic coefficients of variation were obtained for plant height, panicle length, days to 50% flowering, days to 50% maturity and 1000-grain weight. These findings were supported by Iftekharuddeula *et al*. (2001). The small differences observed between genotypic and phenotypic coefficients of variation for days to flowering, days to maturity, plant height and panicle length indicate the presence of sufficient genetic variability for these traits which may facilitate selection (Yadav, 2000). The high to moderate differences between genotypic and phenotypic coefficients of variation observed for number of tillers/plant, number of grains/panicle, number of filled grains/panicle, percentage of unfilled grains/panicle, number of panicles/m^2 and grain yield indicate the high influence of the environment on these 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,2000). This gives an idea of the total variation ascribable to genotypic effects, which are exploitable portion of variation. The heritability estimates obtained for the studied traits ranged between 0.84 to 89.68% (Table 2). High to medium broad sense heritability estimates observed for days to 50% maturity, days to 50% flowering, 1000-grain weight, number of panicles/m^2, number of filled grains/panicle, panicle length and percentage of unfilled grains/panicle. 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 number of panicles per plant in rice. The low broad sense heritability observed for the plant height, number of tillers per plant and grain yield 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 genotypes (Ali *et al*., 2002). High to medium heritability and genetic advance were recorded for the number of grains per panicle, number of filled grain per panicle, days to 50% flowering, days to 50% maturity and number of panicles/m^2 (Table,3). 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 panicle length and 1000-grain weight 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 traits exhibited wide range of Variability (Table 3). Plant height shows significant difference ($p<0.001$) among the genotypes at maturity. Genotype YUNLU 30 is significantly taller with a height of 93.3 cm while genotype WAB880-1-38-19-8 is the shortest (68.3 cm). Number of tillers per plant showed non significant differences among the genotypes. The number of tillers per plant ranges between 8.3 and 14.0 with genotype YUNLU 26 recording the highest number (14.0).

Number of grains per panicle is one of the most important components of yield and probably this trait will be helpful in breaking the yield plateau. Number of grains per panicle differs significantly among the tested genotypes. The highest grain number (132.0) is recorded for genotype HANDAO 502 followed by WAB891SG12 (100.0). Days to 50% flowering shows significant differences among genotypes at ($p < 0.001$) with genotype NERICA 5 taking the shortest time (62.0 days) to attained 50% flowering while genotype HANDAO 221 took the longest period (82.0 days). Days to maturity follows the same trend with days to 50% flowering which ranges between 86.0 and 110.0 days with genotype ZHONG HAN 3 taking the shortest period (86.0 days) to mature while genotype HANDAO 502 takes the longest period (110.0 days) to mature. The number of panicles per m^2 is significantly affected by genotypes. It varies from124.0 in ZHONG HAN 3 to 384.0 in genotype HANDAO 221. The highest grain yield (3.40t/ha) is observed in YUNLU 26 while the lowest grain yield (1.16 t/ha) is observed in genotype YUNLU 24. The high grain yield performance of genotype YUNLU 26 could be attributed to the high number of tillers per plant, low percentage of unfilled grains per panicle and high number of panicles/m^2.

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. The result of correlation analysis as shown by their coefficients of correlation. Table (4) reveals that grain yield exhibits significantly positive correlation with the number of tillers per plant ($r = 0.49$***), plant height ($r = 0.44$***) and the number of filled grains per panicle (r=

0.36***). The results are inconformity with Muhammed.*et al*. (2007) for the number of panicles per plant, Ramakrishman *et al*. (2006) for number of grains per panicle and Idris *et al*(2102). for number of filled grains per panicle. A negative and significant correlation was present between grain yield and percentage of unfilled grains per panicle. The negative association between grain yield and percentage of unfilled grains/panicle was expected since filled grains/panicle has a high significant correlation with grain yield, similar findings were obtained by (Luzikihupi, 1998) and Idris *et al*(2102). The number of grains per panicle shows significantly positive correlation with panicle length (r=o.45***), but positively and not significant with number of tillers per plant (r= 0.07) and plant height (r= 0.17). A positive and significant correlation was present between number of filled grains per panicle and plant height, panicle length, and number of grain per panicle with correlation coefficients of (0.42***, 0.52***, and 0.69***) respectively.

Table 2: Genetic parameters of variation for agronomic characters

Traits	Mean square	∂^2g	∂^2e	∂^2ph	GCV	PCV	h^{2}B	GA
Plant height	137.29***	31.1	43.99	75.09	6.97	10.87	7.39	41.41
Number of tillers/plant	8.82^{ns}	1.06	5.63	6.69	9.03	22.68	0.84	15.84
Panicle length (cm)	5.18***	1.22	1.41	2.73	5.84	8.74	44.68	1.52
Number of grains/panicle	728.89***	200.14	128.47	328.61	16.14	20.69	60.90	22.74
Number of filled grains/panicle	362.37***	89.87	92.76	182.63	16.09	22.94	49.20	13.69
Percentage of unfilled grains/panicle	194.04*	36.27	85.25	121.52	18.93	34.66	29.82	6.77
Days to 50% flowering	153.38***	48.06	9.18	57.24	9.41	10.27	83.96	13.08
Days to 50% maturity	117.06***	37.58	4.32	41.9	6.51	6.87	89.68	11.95
1000 grains weight (gm)	15.14***	4.68	1.10	5.78	12.65	14.05	80.96	6.95
Number of panicles/m^2	11187.57***	3223.78	1516.04	4739.82	28.85	34.97	68.01	96.46
Grain yield (ta/ha)	1.01^{ns}	0.08	0.76	0.84	12.97	42.04	9.52	0.17

∂^2g = genetic variance, ∂^2e= Error variance, ∂^2ph = Phenotypic variance, GCV= Genetic coefficient of variation, PCV= Phenotypic coefficient of variation, h^{2}B= Broad sense heritability, GA= Genetic advance, *, ** and *** significant P=0.05, P=0.01 and P=0.001 respectively, ns= not significant.

Table 4: Phenotypic correlation among the traits.

Traits	PH	PL	NT/P	NG/P	NFG/P	PUG/P	NT/m^2	DTF	DTM	TSW	GY
PH	-										
PL	0.18^{ns}	-									
NT/P	-0.02^{ns}	0.21^{ns}	-								
NG/P	0.17^{ns}	0.45***	0.07^{ns}	-							
NFG/P	0.42***	0.52***	0.09^{ns}	0.69***	-						
PUG/P	-0.35*	-0.22^{ns}	-0.08^{ns}	0.19^{ns}	-0.56***	-					
NT/m^2	-0.08^{ns}	-0.004^{ns}	0.43***	-0.07^{ns}	-0.12^{ns}	0.08^{ns}	-				
DTF	0.09^{ns}	-0.45***	0.06^{ns}	-0.33*	-0.34*	0.11^{ns}	0.32*	-			
DTM	-0.17^{ns}	-0.08^{ns}	0.06^{ns}	0.45***	0.12^{ns}	0.27*	0.20^{ns}	-0.007^{ns}	-		
TSW	0.17^{ns}	-0.08^{ns}	-0.19^{ns}	-0.19^{ns}	-0.10^{ns}	-0.02^{ns}	-0.38***	0.03^{ns}	-0.53***	-	
GY	0.44***	0.21	0.49***	0.66^{ns}	0.36***	-0.42***	0.22^{ns}	-0.009^{ns}	-0.05^{ns}	-0.007^{ns}	-

PH= Plant height, NT/P= Number of tillers/plant, PL= Panicle length, NG/P= Number of grains/panicle, NFG/P= Number of filled grains/panicle, PUG/P= Percentage of unfilled grains/panicle, DTF= Days to 50% flowering, DTM= Days to 50% maturity, TSW= 1000-seed weight, NP/m^2= Number of panicles/m^2 and GY= Grain yield.

Table 3: Mean performance of 18 rice genotypes for 12 agronomic traits

Designation	PH/cm	NT/P	PL/cm	NG/P	NFG/P
NERICA 2	78.6 BCDE	13.3 A	20.0 ABC	80.6 BCDE	59.0 ABCDE
NERICA 4	85.0ABC	11.0 AB	19.6 ABCD	99.0 B	70.6 ABC
NERICA 5	80.3 BCDE	10.3 AB	20.3 ABC	94.3 BC	63.0 ABCD
NERICA 12	82.0 ABCD	13.6 A	20.6 AB	97.3 B	76.3 A
NERICA 14	70.3 DE	10.6 AB	19.3 ABCD	71.6 DE	48.6 DE
NERICA 15	79.0 BCDE	10.0 AB	18.0 CDE	86.6 BCDE	49.0 DE
NERICA 17	85.0 ABC	12.0 AB	18.6 ABCD	73.0 CDE	50.0 DE
YUNLU 22	85.6 ABC	9.3 AB	16.0 E	86.3 BCDE	50.6 DE
YUNLU 24	80.3 BCDE	9.3 AB	18.3 BCDE	69.3 E	47.0 DE
YUNLU 26	88.0 AB	14.0 A	18.6 ABCD	69.0E	57.6 BCDE
YUNLU 30	93.3 A	10.3 AB	17.3 DE	99.3 B	74.6 AB

YUNLU 33	80.6 ABCDE	12.0 AB	19.3 ABCD	84.6 BCDE	56.6 BCDE
WAB880-1-38-19-8	68.3 E	13.3 A	18.0 CDE	90.6 BCDE	54.6 CDE
WAB891SG12	74.0 CDE	12.6 AB	18.0 CDE	100.0 B	56.6 BCDE
WAB-1-38-19-14-P2HB	77.0 BCDE	11.0 AB	19.0 ABCD	79.0 BCDE	56.0 CDE
HANDAO 221	71.6 DE	13.6 A	18.0 CDE	71.0 E	41.0 E
HANDAO 502	71.3 DE	11.0 AB	21.0 A	132.0 A	76.6 A
ZhONG HAN 3	85.3 ABC	8.3 B	20.6 AB	93.3 BCD	72.3 ABC
Means	79.7	11.4	18.9	87.6	58.9
SE	3.8	1.3	0.7	6.5	5.5
CV %	8.31	20.7	6.5	12.9	16.3
R^2	0.61	0.44	0.63	0.73	0.66
Pr□ F	***	Ns	***	***	***

PH= Plant height, NT/P= Number of tillers/plant, PL= Panicle length, NG/P= Number of grains/panicle, NFG/P= Number of filled grains/panicle, PU/P= Percentage of unfilled grains/panicle, DTF= Days to 50% flowering, DTM= Days to 50% maturity, TSW= 1000-seed weight, NP/m^2= Number of panicles/m^2 and GY= Grain yield.

*, ** and *** significant P=0.05, P=0.01 and P=0.001 respectively, ns= not significant.

Table 3: Continue

Designation	PU/P	DTF	DTM	TSW	NP/m^2	GY
NERICA 2	26.6 ABCD	68.6 FG	91.6 DEF	17.3 CDE	166.0 DE	2.66 AB
NERICA 4	28.3 ABCD	70.6 DEFG	88.0 FGH	18.3 BCD	208.0 CD	2.50 AB
NERICA 5	31.6 ABCD	62.0 H	93.0 CD	20.0 AB	179.6 DE	2.25 AB
NERICA 12	21.0 CD	75.3 BCDE	91.0 DEFG	18.6 ABCD	162.3 DE	2.83 AB
NERICA 14	31.6 ABCD	73.0 CDEF	87.3 GH	19.0 ABC	190.0 CDE	2.26 AB
NERICA 15	42.3 A	75.6 BCDE	96.0 BC	18.6 ABCD	153.6 DE	1.56 B
NERICA 17	30.6 ABCD	70.0 EFG	92.0 DE	15.3 FG	206.6 CD	2.50 AB
YUNLU 22	40.6 AB	81.0 B	96.0 BC	18.0 BCDE	193.0 CDE	2.33 AB
YUNLU 24	32.0 ABCD	77.0 BC	107.3 A	18.0 BCDE	142.6 DE	1.16 B
YUNLU 26	16.3 D	79.6 B	96.0 BC	16.6 DEF	262.0 BC	3.40 A
YUNLU 30	32.6 BCD	80.6 B	96.0 BC	16.3 EFG	180.3 DE	2.66 AB
YUNLU 33	33.3 ABCD	76.0 BCD	93.0 CD	18.6 ABCD	190.6 CDE	2.63 AB
WAB880-1-38-19-8	38.6 ABC	63.0 H	98.0 B	14.6 G	280.0 B	1.70 AB
WAB891SG12	42.6 A	72.0 CDEFG	91.3 DEF	20.3 A	137.0 DE	2.23 AB
WAB-1-38-19-14-P2HB	28.3 ABCD	72.6 CDEFG	89.0 EFGH	14.6 G	176.6 DE	1.90 AB
HANDAO 221	42.6 A	82.0 A	109.0 A	15.3 FG	384.0 A	1.60 B
HANDAO 502	40.0 AB	67.0 GH	110.0 A	11.3 H	206.0 CD	1.60 B
ZHONG HAN 3	22.6 BCD	68.6 FG	86.0 H	18.0 BCDE	124.0 E	1.46 B
Means	31.8	73.6	94.1	17.1	196.8	2.18
SE	5.3	1.7	1.2	0.6	22.4	0.5
CV %	28.9	4.1	2.2	6.1	19.7	40.1
R^2	0.53	0.89	0.93	0.87	0.79	0.45
Pr□ F	*	***	***	***	***	Ns

PH= Plant height, NT/P= Number of tillers/plant, PL= Panicle length, NG/P= Number of grains/panicle, NFG/P= Number of filled grains/panicle, PU/P= Percentage of unfilled grains/panicle, DTF= Days to 50% flowering, DTM= Days to 50% maturity, TSW= 1000-seed weight, NP/m^2= Number of panicles/m^2 and GY= Grain yield.

*, ** and *** significant P=0.05, P=0.01 and P=0.001 respectively, ns= not significant.

Conclusions:

The overall results indicated that there is adequate genetic variability present in the material studied. This variation in the evaluated rice genotypes could be effectively manipulated with appropriate breeding methods and programs at the Sudan to develop improved varieties and hybrids for use by farmers. The broad sense heritability, genetic advance and correlation analysis of the study revealed that the number of filled grains per panicle was the most important yield components. This trait also showed moderate to high heritability and genetic advance in percentage of mean. Therefore, the results suggest that the number of filled grains per panicles is important yield contributing trait and selection based on this trait would be most effective.

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