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Genetic variability for yield and related attributes of upland rice genotypes in semi arid zone (Sudan)

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Thirteen genotypes of upland rice were evaluated at White Nile Research Station Farm, Kosti, of the Agricultural Research Corporation (ARC), Wad Medani Sudan for two consecutive years (2008 and 2009). The objectives of this study were to estimate the genotypic and phenotypic variability, broad sense heritability for maturity, morphological and yield associated traits. The highest genotypic coefficient of variation and genetic advance were recorded for number of tillersplant⁻¹ and plant height in both seasons. High heritability estimates (>85%) were recorded for plant height, number of tillersplant⁻¹ and 1000 grain weight in both years and high heritability estimates with low genetic advance observed for days to 50% flowering and days to maturity in both years. The high yielding genotypes were WAB891 SG14, WAB981 SG33 and Yunlu No.30 with grain yields of 3.6, 3.5 and 3.4 tha⁻¹, respectively. Grain yield tha⁻¹ was significantly and negatively correlated with percent of unfilled grains/panicle. However, it was highly significantly and positively correlated with panicle length, number of tillersplant⁻¹, number of filled grainspanicle⁻¹ and 1000 grain weight in both seasons. Path coefficient analysis indicated that number of tillersplant⁻¹, 1000 grain weight, panicle length and number of filled grainspanicle⁻¹ were most directly related traits to grain yield tha⁻¹. Traits such as panicle length, number of tillersplant⁻¹, number of filled grainspanicle⁻¹ and 1000 grain weight could be useful as index traits for improving the total grain yield. Furthermore, our results suggest that selection for plant height, number of tillersplant⁻¹ and 1000 grain weight would be more effective as compared to other traits in boosting yield performance of upland rice genotypes.

Key words: Upland rice, yield component, genotypic and phenotypic variability, path coefficient analysis, broad sense heritability.

INTRODUCTION

Rice (*Oryza sativa* L.) is the world leading cereal crop for human utilization, with cultivated area of almost 150 million ha and a total production of almost 600 million mega grams annually (Khush, 2005). 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 for the world (Khush and Brar, 2002). Sub Saharan Africa produced about 21.6 million

tons of rice in 2006 and accounted for 32% of rice import in the global international market to meet its demand (Africa Rice Center, 2008; FAO, 2005). This was the result of population growth (about 4% per annum) and the increased consumer preference in favor of rice in urban area (Africa Rice Center, 2008; Kijima et al., 2006; Atera et al., 2011). In Sudan rice has been grown since 1905 on an area of almost 5.5 thousand hectares and the total production is almost 8 thousand tones far below the requirement of the country's food requirements. Rice yield potentials have almost leveled off at 10 tha⁻¹ for the high-yielding inbred cultivars while the theoretical potential has been estimated at 15.9 t ha⁻¹ in tropical

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environments (Morgan et al., 2002). Sudan produces an average of 1.5 t ha⁻¹, therefore the breeders are interested in developing cultivars with improved yield and other desirable agronomic characters to overcome the global problem of hunger and starvation especially in African countries. Genetic variability for agronomic traits is the key component of breeding programs for broadening the gene pool of rice and would require reliable estimates of heritability in order to plan an efficient breeding program. (Akinwale et al., 2011). 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). The process of breeding is primarily conditioned by the magnitude and nature of interactions of genotypic and environmental variations in plant characters. It becomes necessary to partition the observed variability into its heritable and non-heritable components and to have an understanding of parameters such as genotypic coefficient of variation, heritability and genetic advance. The advantage of path analysis is that it permits the partitioning of the correlation coefficient into its components, one component being the path coefficient that measures the direct effect of a predictor variable upon its response variable; the second component being the indirect effect(s) of a predictor variable on the response variable through another predictor variable. In agriculture, path analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Dewey and Lu, 1959; Milligan et al., 1990).

The utilization of heritability and genetic advance of yield traits and inferences from significant genotypic correlation between yield and its components should permit selection of predictable rice genotypes for upland ecosystem. Keeping in view the afore said problems and advantages of selection the present study was conducted to improve the yield through direct selection and by enhancing the yield related attributes for upland rice genotypes in wet and dry seasons. Furthermore, to establish suitable selection criteria to provide basis for selection and yield improvement in upland rice and identify high yielding cultivars that can resist the harsh climatic conditions of semi arid zone Sudan.

MATERIALS AND METHODS

Study site and experimental design

The study was laid out in a randomized complete block design with four replications in the White Nile Research Station Farm (latitude 14° 24'N and longitude 33° 29'E), (Kosti) of the Agricultural Research Corporation (ARC), Wad Medani, Sudan, during 2008

and 2009 cropping seasons. The soil of the experimental plots was classified as vertisol with high clay content (40 to 65%), less than 1% organic carbon, low in available nitrogen (0.03% total nitrogen) and medium in available P₂O₅ (406 to 700 ppm total phosphorus), pH values ranging from 7 to 8.2. The climate was semi-arid.

Eleven rice genotypes were selected for 82 aerobic rice varieties and lines and two New Rice for Africa (NERICA) varieties (NERICA4 and the aromatic NERICA1) were introduced from the International Rice Research Institute (IRRI), and Africa Rice Center (WARDA), respectively. In preliminary yield tests selection was based on yield components, early maturity and general performance. The description and details of the genotypes used in this study are listed in Table 2. The trial plot size was 5 × 5 m and consisted of 25 rows spaced 20 cm apart. The seed were drilled on July the 7th and 2nd of 2008 and 2009, respectively using a seed rate of 120 kg/ha. Fertilizers were applied at the rate of 86 and 43 kg/ha of nitrogen and P₂O₅, respectively, in the form of urea and triple super phosphate. P₂O₅ was applied as basal dose during final land preparation. Nitrogen was top dressed in two equal split doses one at 21 days after sowing and the other before panicle initiation. Hand weeding was performed three times per season. All plots were irrigated at sowing and then at weekly intervals until it reached maturity.

Data collection

Data were collected on days to 50% flowering (days from sowing to time when 50% of the plants start to flower) and days to maturity (days from sowing to time when panicles reached full maturity). Then at harvest, plant height (cm), panicle length (cm), number of tillersplant⁻¹, number of filled grainspanicle⁻¹, percent of unfilled grainspanicle⁻¹, 1000 grain weight (g) and grain yield (t/ha) based on grain yield per plot were recorded. The data were collected according to standard evaluation systems for rice standard evaluation system (SES), IRRI (1988). Ten randomly selected plants in the middle of the row of each plot were used for data collection.

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 (version 8). Estimates of variance components were generated and combined analysis of variance was done for the traits in which the mean squares were homogenous. The phenotypic and genotypic variances and their coefficients, heritability in the broad sense and genetic advance were computed according to the formula described by Singh and Chaudhary (1985). Means for each season were used to compute simple linear correlation coefficients. Path coefficient analysis was used to partition the simple linear correlation coefficients, combined over seasons, between grain yields/ha and four other traits; namely number of tillersplant⁻¹, 1000 grain weight, panicle length and number of filled grainspanicle⁻¹, into the direct and indirect effects.

RESULTS AND DISCUSSION

The results revealed a wide range of variability among the genotypes for most of the traits studied in both seasons (Table 1).

In this study the range and analysis of variance indicated potential genetic variability and diversity in the

Table 1. Estimates of phenotypic variability, heritability in broad sense (h^2_B), genotypic (GCV) and phenotypic (PCV) Coefficients of variation, genetic advance as percentage of the mean for 10 traits in 13 rice genotypes grown at the WNRS Farm, seasons 2008 and 2009.

Trait	Range	General mean	F value	h^2_B (%)	GCV (%)	PCV (%)	GA as % of mean
Days to 50% flowering	64-79	71.7	5.0***	79.9	5.8	6.1	10.7
Days to maturity	88-110	98.6	4.3***	75.2	7.0	8.1	12.5
Plant height (cm)	71-102	85.0	10.2***	90.1	11.7	12.3	22.3
Panicle length (cm)	18-22	20.0	2.5*	60.0	5.2	6.7	8.5
Number of panicle/m ²	211-266	243.0	1.9*	46.6	5.1	7.4	7.1
Number of tillers/plant	3-6	4.0	12.0***	92.0	19.5	20.4	38.6
Number of filled grains/panicle	60-70	64.0	4.2***	76.0	4.1	4.6	7.3
Percent of unfilled grains/panicle	18-27	23.0	1.3 ^{ns}	20.8	4.6	10.0	4.3
1000 grain weight (g)	28-35	32.0	16.9***	94.0	6.9	7.1	13.8
Grain yield (t/ha)	2.5-3.5	2.9	10.6**	90.0	10.6	11.2	21.6
Season 2009							
Days to 50% flowering	66-77	71.1	7.5***	86.6	4.8	5.2	9.1
Days to maturity	84-102	95.7	3.8**	73.4	5.7	6.7	10.4
Plant height (cm)	69-100	86.2	12.3***	91.9	9.6	10.0	19.7
Panicle length (cm)	19-24	21.2	3.5**	71.0	7.2	8.3	12.6
Number of panicle/m ²	232-291	267.1	0.8 ^{ns}	18.6	6.6	7.6	2.5
Number of tillers/plant	3-6	4.6	8.3***	88.0	18.5	19.7	35.8
Number of filled grains/panicle	89-74	64.7	12.1***	92.0	7.0	7.3	13.9
Percent of unfilled grains/panicle	16-26	20.9	3.1**	67.6	6.5	10.3	17.7
1000 grain weight (g)	28-35	31.4	6.7***	85.0	6.4	6.9	12.0
Grain yield (t/ha)	2.4-3.7	3.1	16.6***	93.0	12.2	12.6	23.4

*. *****. Significant at 0.05, 0.01 and 0.001 probability levels, respectively.

material under consideration. These results indicated better scope for genetic improvement through conventional breeding.

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. This gives an idea of the total variation ascribable to genotypic effects, which are exploitable portion of variation. Higher heritability estimates in broad sense (h^2_B) (>85%) were exhibited by plant height, number of tillers/plant¹ and 1000 grain weight in both seasons. Nuruzzaman et al. (2002) reported similar results. This indicated that selection of these traits would be more effective as compared to others. Low heritability estimate were exhibited by number of panicle/m² and percent of unfilled grains/panicle¹ in both seasons. This result might be due to the variation of environmental component involved in this trait. The moderate heritability estimate for grain yield was attributed to the fact that yield is a complex trait and is controlled by many genes. Since high heritability does 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 heritability and genetic

advance were recorded for the plant height, number of tillers/plant¹ and 1000 grain weight in both seasons. These results suggested that these traits were primarily under genetic control and selection for these traits can be achieved through their phenotypic performance. High heritability estimates with low genetic advance observed for days to 50% flowering days to maturity indicated non additive type of gene action and that genotype × environment interaction played a significant role in the expression of the traits.

Genotypic coefficient of variation 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. Phenotypic coefficients of variation were slightly higher than the genotypic coefficients of variation for all the traits studied. This indicated the presence of environmental influence to some degree in the phenotypic expression of the characters, similar results were observed by Iftikharuddaula et al. (2002) and Akinwale et al. (2011). The excepted genetic advance expressed as percentage

Table 2. Mean performance of 13 rice genotypes grown at the (WNRS) farm Sudan (combined over two seasons, 2008 and 2009).

Designation	DTF	DTM	PH(cm)	PL(cm)	NPPM
WAB891 SG14	73.4 ^{ABC}	105.5 ^A	94.8 ^{BC}	23.0 ^A	273.3 ^A
WAB981 SG33	72.1 ^{BC}	102.3 ^A	85.5 ^{DE}	23.0 ^A	271.4 ^A
Yunlu No.30	72.7 ^{BC}	100.2 ^{AB}	79.4 ^{EF}	22.4 ^{AB}	271.0 ^A
Yunlu No. 34	76.8 ^A	100.9 ^{AB}	101.1 ^A	21.1 ^{ABCD}	252.4 ^{AB}
WAB880-1-38-19-8	71.2 ^{CD}	97.5 ^{ABC}	89.8 ^{CD}	18.9 ^E	257.8 ^{AB}
Yunlu No. 24	75.8 ^{AB}	105.2 ^A	97.8 ^{AB}	19.5 ^{DE}	252.9 ^{AB}
NERICA 4	67.1 ^E	94.2 ^{BCD}	87.4 ^D	18.8 ^E	221.8 ^B
WAB891SG12	67.1 ^E	88.3 ^D	77.1 ^F	20.0 ^{CD E}	269.4 ^A
WAB880SG49	67.5 ^{DE}	91.4 ^{CD}	80.1 ^{EF}	20.5 ^{BCDE}	242.9 ^{AB}
WAB891SG9	76.8 ^A	101.6 ^{AB}	90.9 ^{CD}	19.3 ^{DE}	242.4 ^{AB}
WAB450-5-1-BL1-DR2	67.7 ^{DE}	87.0 ^D	73.9 ^{FG}	20.1 ^{CDE}	240.3 ^{AB}
WAB880-1-38-19-14-P2-HB	74.0 ^{ABC}	103.6 ^A	85.5 ^{DE}	19.1 ^{DE}	268.3 ^A
NERICA 1 (Aromatic)	66.2 ^E	87.3 ^D	70.5 ^G	21.6 ^{ABC}	251.1 ^{AB}
CV%	5.1	7.5	6.8	8.5	12.9
SE	2.8	4.87	6.5	1.1	11.0
Pr > F	**	***	***	***	*

Means followed by the same letter(s) within a column are not significantly different at 0.05 probability level according to the Duncan's multiple range test, days to 50% flowering (DTF), days to maturity (DTM), plant height (PHT), panicle length (PL) and number of panicles/m² (NPPM).

of mean, varied from 4.3 to 38.6% in the first season, and from 2.5 to 35.8% in the second season. In this study, traits that exhibited high genotypic coefficient of variation like plant height, number of tillers/plant⁻¹ also gave high genetic advance as percentage of mean (GA %), in both seasons (Table 1). This specified the possibility of their use as selection criteria for high grain yield.

The results further revealed that most of the traits exhibited wide range of variability (Table 2). The late flowering and maturing genotypes were Yunlu No. 34 and WAB891SG9, while the early flowering and maturing genotypes were NERICA 1 and WAB891SG12. The range for plant height was 70 to 101 cm with genotype Yunlu No. 34 as the tallest and genotypes NERICA 1 and WAB450-5-1-BL1-DR2 as the shortest. The range for number of filled grains per panicle was 60 to 72 for genotypes WAB880-1-38-19-14-P2-HB and WAB891 SG14, respectively. The range of percentage of unfilled grains/panicle⁻¹ was 17 to 27 for genotypes WAB981 SG33 and, NERICA 4 respectively (Table 3). Adequate number of fertile grains/panicle and heavy grains are important traits, which should be considered in selection for high yield (Prasad et al., 2001; Sürek and Beser, 2003).

These results showed that increasing the number of spikelets/panicle⁻¹ does not always result in higher grain yield, but with increased filled grains percentage it increases yield. The highest yielding genotypes were; WAB891 SG14, WAB981 SG33 and Yunlu No. 30 with grain yields of 3.6, 3.5 and 3.4 t/ha, respectively.

Grain yield was positively and significantly ($P \leq 0.01$)

correlated with panicle length (cm) number of tillers/plant, number of filled grains/panicle⁻¹ and 1000 grain weights in both seasons (Table 4), indicating the importance of these components in rice yield. These results were in agreement with that of Süerk (2003) and Kato et al. (2008). The results were in conformity with Ramakrishnan et al. (2006) for number of filled grains/panicle⁻¹. Grain yield was significantly and negatively correlated with percent of unfilled grains/panicle⁻¹. The negative association between yield and percent of unfilled grains/panicle was expected since filled grains/panicle⁻¹ had a high significant correlation with grain yield (Luzikihupi, 1998). There was a negative relationship between number of filled grains/panicle⁻¹ and number of unfilled grains/panicle. Days to maturity were positively and significantly correlated with days to 50% flowering, similar results were reported by Mehetre et al. (1996).

The result of path coefficient analysis based on combined data was presented in Table 5 and will be very useful when deciding upon selection criterion in upland rice genotypes. The direct effect of number of tillers/plant⁻¹ on grain yield/ha⁻¹ was the positive and of greater magnitude than direct effects of other three traits (0.291). It had positive indirect effect on grain yield through 1000 grain weight (0.164), panicle length (0.115) and number of filled grains/panicle⁻¹ (0.134). These results were congruent with that reported by Prasad et al. (2001) and Agbo and Obi (2005) and this indicate that for increasing effective tillers/plant, other causal factors must be considered simultaneously.

Table 3. Mean performance of 13 rice genotypes grown at the WNRS Farm (combined over two seasons, 2008 and 2009).

Genotype	NTPP	NFGPP	PUGPP	T GW	GY(t/ha)
WAB891 SG14	5.9 ^A	72.3 ^A	18.8 ^{ED}	34.6 ^A	3.6 ^A
WAB981 SG33	5.5 ^{AB}	68.8 ^B	17.4 ^E	34.8 ^A	3.5 ^A
Yunlu No.30	5.0 ^{BC}	67.5 ^{BC}	20.6 ^{CDE}	33.0 ^B	3.4 ^A
Yunlu No. 34	4.9 ^{CD}	65.8 ^{BC}	22.5 ^{BCD}	32.4 ^{BC}	3.2 ^B
WAB880-1-38-19-8	3.8 ^{EF}	61.5 ^E	21.1 ^{BCD}	29.3 ^{FG}	2.8 ^{DEF}
Yunlu No. 24	4.5 ^{CD}	62.5 ^{DE}	21.0 ^{CD}	31.1 ^{CDE}	2.9 ^{CDE}
NERICA 4	3.0 ^G	60.1 ^E	26.9 ^A	29.4 ^{FG}	2.5 ^G
WAB891SG12	4.5 ^{CD}	62.1 ^E	21.5 ^{BCD}	30.3 ^{EF}	2.9 ^{CDE}
WAB880SG49	4.5 ^{CD}	66.0 ^{BC}	22.0 ^{BCD}	31.9 ^{BCD}	3.1 ^{BC}
WAB891SG9	4.3 ^{DE}	65.3 ^{CD}	21.9 ^{BCD}	30.8 ^{DEF}	3.0 ^{CDE}
WAB450-5-1-BL1-DR2	3.5 ^{FG}	60.5 ^E	21.9 ^{BCD}	29.4 ^{FG}	2.7 ^{EF}
WAB880-1-38-19-14-P2-HB	3.3 ^{FG}	60.0 ^E	23.3 ^{BC}	27.9 ^G	2.7 ^{FG}
NERICA 1 (Aromatic)	4.3 ^{DE}	62.5 ^{DE}	24.9 ^{AB}	29.9 ^{EF}	3.0 ^D
CV%	12.9	4.5	15.1	4.6	6.8
SE	0.6	2.6	1.6	1.5	0.2
Pr > F	***	***	***	***	***

Means followed by the same letter(s) within a column are not significantly different at 0.05 probability level According to Duncan multiple range test. number of tillers/plant (NTPP), number of filled grains/panicle (NFGPP), percent of unfilled grains/panicle (PUGPP), 1000 grain weight (TGW) and grain yield (t/ha).

Table 4. Simple linear correlation coefficients between 10 pairs of traits in rice using season 2008 (above the diagonal) and season 2009 (below the diagonal).

Genotype	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀
X ₁		0.58***	0.50***	0.09	-0.07	0.04	0.16	-0.19	0.27*	0.19
X ₂	0.41**		0.54***	0.22	0.11	0.26*	0.31*	-0.27*	0.29*	0.28*
X ₃	0.55***	0.57***		0.06	-0.17	0.15	0.06	.001	0.27*	0.08
X ₄	0.07	-0.07	-0.08		0.02	0.47***	0.40**	-0.27*	0.48***	0.58***
X ₅	0.05	0.19	0.07	0.13		0.22	0.09	0.07	-0.02	0.15
X ₆	0.29*	0.22	0.25*	0.38**	0.42**		0.64**	-0.32*	0.64***	0.72***
X ₇	0.39**	0.29*	0.35*	0.47***	0.22	0.67***		-0.12	0.63***	0.58***
X ₈	-0.17	-0.24*	-0.23*	-0.36**	-0.26*	-0.61**	-0.53***		-0.27*	-0.27*
X ₉	0.18	0.14	0.15	0.47***	0.43**	0.63***	0.71***	-0.49**		0.69***
X ₁₀	0.30*	0.24*	0.25*	0.55***	0.31*	0.65***	0.75***	-0.49**	0.71***	

* ** *** Significant at 0.05, 0.01 and 0.001 probability levels, respectively. N = 52; X₁: Days to 50% flowering; X₂: Days to maturity; X₃: Plant height (cm); X₄: Panicle length (cm); X₅: No. of panicles/m²; X₆: No. of tillers/plant; X₇: No. of filled grains/panicle; X₈: unfilled grains/panicle (%); X₉: 1000 grain weight (g); X₁₀: yield t/ha.

The direct effect of 1000 grain weight on grain yieldha⁻¹ was the second largest (0.258) and also had positive indirect effect on grain yieldha⁻¹ through panicle length (0.121) and number of filled grains/panicle (0.138). These results indicated that the significant positive correlation between 1000 grain weight and grain yieldha⁻¹ resulted mainly from the direct effect of 1000 grain weight. The panicle length had positive direct effect on grain yieldha⁻¹ (0.247) and positive indirect effect on grain yieldha⁻¹ through number of filled grainspanicle⁻¹ (0.092). Number

of filled grainspanicle⁻¹ had the fourth direct positive contribution (0.204) to the grain yieldha⁻¹. Positive correlation of number of filled grainspanicle⁻¹ with grain yieldha⁻¹ resulted in a positive direct effect. Many research workers reported similar findings (Prasad et al., 2001; Iftekharrudaula et al., 2002; Sürek and Beser, 2003).

The present study showed that number of tillersplant⁻¹, 1000 grain weight, panicle length and number of filled grains⁻¹panicle were the most important traits that directly

Table 5. Path coefficient analysis of the direct and indirect effects of the different yield components and their simple correlation coefficients with grain yield /ha.

Traits	Effect via				Simple correlation with grain yield/ha
	NTPP	TGW	PL	NFGPP	
NTPP	0.291	0.164	0.115	0.134	0.704**
TGW	0.185	0.258	0.121	0.138	0.702**
PL	0.135	0.126	0.247	0.092	0.601**
NFGPP	0.191	0.174	0.112	0.204	0.681*

***** Significant at 0.05, 0.01 and 0.001 probability levels respectively. The direct effects are underlined. NTPP number of tillers/plant, TGW 1000 grains weight, PL panicle length, NFGPP number of filled grains/panicle.

contributed to the grain yield ha^{-1} . Similar results were reported by Luzikihupi (1998). The path coefficient analysis showed that number of tillers $plant^{-1}$, 1000 grain weight, panicle length and number of filled grains $panicle^{-1}$ were the most important traits related to grain yield. These results agreed with the conclusion from correlation analysis that number of tillers $plant^{-1}$, 1000 grain weight, panicle length and number of filled grains/panicle are important grain yield traits. These traits would offer a prime scope for the development and selection of high yielding upland rice genotypes.

Conclusion

The overall results divulged that there is adequate genetic variability present in the material studied. The broad sense heritability, genetic advance, correlation and path coefficient analysis revealed that the selection for plant height, number of tillers $plant^{-1}$, 1000 grain weight panicle length and number of filled grains/panicle would be more effective as compared to other traits in boosting yield performance of upland rice genotypes. Among the evaluated, the high yielding genotypes were WAB891 SG14, WAB981 SG33 and Yunlu No.30 with grain yields of 3.6, 3.5 and 3.4 tha^{-1} , respectively and have the greatest potential to adapt in semi arid zone climatic conditions and to enhance rice production in upland rice areas in the Sudan.

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REFERENCES

Africa Rice Center (WARDA)/FAO/SAA (2008). NERICA: The New Rice for Africa – a Compendium. Somado EA, Guei RG and Keya SO

- (eds.). Cotonou, Benin: Africa Rice Center (WARDA); Rome, Italy: FAO; Tokyo, Japan: Sasakawa African Association. p. 210.
- Agbo CU, Obi IU (2005). Yield and Yield Component Analysis of Twelve Upland Rice Genotypes. *J. Agric. Food, Environ. Ext.* 4:29-33.
- Akinwale M, Gregorio G, Nwilene F, Akinyele B, Ogunbayo SA, Odiyi AC (2011). Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *Afr. J. Plant Sci.* 5:207-212.
- Ali A, Khan S, Asad MA (2002). Drought tolerance in wheat: Genetic variation and heritability for growth and ion relations. *Asian J. Plant Sci.* 1:420-422.
- Atera EA, Onyango JC, Azuma T, Asanuma S, Itoh K (2011). Field evaluation of selected NERICA rice cultivars in Western Kenya. *Afr. J. Agric. Res.* 6(1):60-66.
- Dewey DR, Lu KH (1959). A correlation and path co-efficient analysis of components of crested wheat grass and seed production. *Agron. J.* 51:515-518.
- FAO (2005). Production Yearbook Food and Agricultural Organization of The United Nation (FAO), Rome Italy. p. 56.
- Iftekharruddaula KM, Akler K, Hassan MS, Falema K, Badshah A (2002). Genetic divergence, character association and selection criteria in irrigated rice. *Online J. Biol. Sci.* 2(4):243-246.
- IRRI (1988). International Rice Research Institute. Standard Evaluation System for Rice (SES). Revised edition, Manila Philippines. pp. 10-35.
- Kato Y, Kamoshita A, Yamagishi J (2008). Preflowering abortion reduces spikelet number in upland rice (*Oryza sativa* L.) under water stress. *Crop Sci.* 48:2389-2395.
- Khush GS (2005). What it will take to feed 5.0 billion rice consumers by 2030. *Plant Mol. Biol.* 59:1-6.
- Khush GS, Brar DS (2002). Biotechnology for rice breeding: progress and impact. In: Sustainable rice production for food security. Proceed. 20th Session Int. Rice Comm. pp. 23-26.
- Kijima Y, Sserunkuuma D, Otsuka K (2006). How revolutionary is the "NERICA revolution"? Evidence from Uganda. *Dev. Econ.* 44:252-267.
- Luzikihupi A (1998). Interrelationship between yield and some selected agronomic characters in rice. *Afr. Crop Sci. J.* 6(3):323-328.
- Mehetre SS, Mahajan CR, Patil PA, Dhumal PM (1996). Variability, heritability, correlation, path analysis and genetic divergence studies in F2 generation of gamma-irradiated upland rice. *Int. Rice Res. Notes* 21(3):56-58.
- Milligan SB, Gravois KA, Bischoff KB, Martin FA (1990). Crop effects on genetic relationships among sugarcane traits. *Crop Sci.* 30:927-931.
- Morgan PW, Finlayson SA, Childs KL, Mullet JE, Rooney WL (2002). Opportunities to improve adaptability and yield in grasses. *Crop Sci.* 42(6):1-18.
- Nuruzzaman M, Alam MF, Ahamed MG, Shohacl AM, Biswas MK, Amin MR, Hassain MM (2002). Studies on parental variability and heterosis in rice. *Pak. J. Biol. Sci.* 5(10):1006-1009.
- Prasad B, Atwary AP, Biswas PS (2001). Genetic variability and selection criteria in fine rice (*Oryza Sativa* L.). *Pak. J. Biol. Sci.* 4(10):1188-1190.
- Ramakrishnan SH, Amandakumar CR, Saravanan S, Malini N (2006). Association Analysis of some Yield traits in Rice (*Oryza sativa* L.). J.

- App. Sci. Res. 2(7):402-404.
- Sabesan T, Suresh R, Saravanan K (2009). Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline lowland of Tamiluadu. *Electr. J. Plant Breed* 1:56-59.
- Singh RK, Chaudhary BD (1985). *Biometrical Methods in Quantitative Genetic Analysis*. Third edition. Kalyani Publisher, New Delhi. pp. 165-167.
- Sürek H, Beser N (2003). Correlation and path coefficient analysis for some yield related traits in rice (*Oryza sativa* L.) under Thrace. *Turk. J. Agric. Sci.* 27:77-83.