



Assessment Of Variability, Heritability And Correlation In Some Lowland Rice (*Oryza sativa* L.) Genotypes Evaluated For Tolerance To Flooding In Anwai, Delta State

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ABSTRACT

As the Nigerian population keeps increasing and urbanization taking over available arable land for food production, coupled with the effect of climate change on this agricultural land, the need to channel research efforts towards developing materials that would tolerate some of the effects, particularly that of flood posed by climate change cannot be overemphasized. In 2019, fifty-one (51) lowland rice genotypes were obtained from the National cereal research institute (NCRI), Badeggi, Niger State, and Africa Rice Centre (Africa Rice), Nigeria. The rice genotypes were screened in a Completely Randomized Block design with three replications and thereafter reduced to 21 genotypes and planted in the field under Randomized Completely Block Design for the determination of their genetic variability. This research was conducted in Asaba, Delta State. The result showed significant differences among the evaluated genotypes for plant height (cm), panicle length (cm), number of tillers/plants, 1000 grain weight (g), and grain yield (t/ha). The highest values of genotypic coefficient of variation (GCV: 28.89%), phenotypic coefficient of variation (PCV: 25.64%), and genetic advance as percent of mean (GA: 38.43 %) were recorded for the grain yield. Grain yield showed very good correlation with 1000 grain weight ($r = 0.54^*$) and panicle length ($r = 0.86^*$). Thus, these results indicate that these genotypes have possible traits for the improvement to flood tolerance in rice.

Keywords: Traits, Flooding, Genotypes, Yield, Variation.

INTRODUCTION

Rice is ranked 6th in Nigeria based on production in relation to crops like sorghum, millet, cowpea, cassava, and yam (Singh, Mackill and Ismail, 2014). Flooding seriously limits rice production globally and causes enormous financial losses (Dey and Upadhyaya, 2018). About 40 million hectares, or one-fourth of the world's rice harvest, are farmed on lowland rainfed plots that are vulnerable to seasonal flooding. Flooding also is one of the major constraints for rice production particularly in rainfed lowland areas, which threatens global food security (Dar *et al.*, 2017). Flood is one of the biggest challenges to rice production, especially in lowland rainfed areas where most types are severely damaged or destroyed in less than a week due to the tremendous flood effect. They can lower rice yield by up to 22% (Dar, De Janvoy, Emerick, Raitzer and Sadoulet, 2013) and this is becoming a more serious issue with

unpredictable global climate change (Afrin, Nafis, Hossain, Islam and Hossain, 2018). This study aims to close the knowledge gap by presenting data on the variability, heritability, and correlation in some lowland rice (*Oryza sativa* L.) genotypes evaluated for tolerance to flooding in Anwai, Delta State.

MATERIALS AND METHODS

Area of Study

Asaba is located between latitude 6°11'53.66" N and longitude 6°43'54.73"Eat the Equator with a hot humid climate, mixed vegetation of forest interspersed with shrubs and grasses. The rainfall pattern is bi-modal with peaks in July- September, and an annual rainfall amount of 2969mm; a mean temperature of 26.3-33.5°C and relative humidity varies from 61-89% (NIMET, 2021).

Experimental design and layout: The experiment was a 2 x 51 factorial experiment laid out in a Completely Randomized Design and was replicated three times given a total of 306 pots. Screening of germplasm (51 lowland rice varieties) was carried out under a controlled submergence condition using pots and drums. The seeds were sown in seed trays for 21days and afterwards submerged in drums filled with water to the brim for 14 days, and this was done in the two locations. At the end of the 14 days, best varieties that survived in terms of possessing highest survival percentage were identified and taken to the field for planting to assess their variability, correlation and heritability. The experimental design was a split plot laid out in a Randomized Complete Block Design (RCBD) with three replications. The best 21 varieties that had the best survival and growth performance and these genotypes includes: Faro 66 , Faro 15, Faro 16, Faro 17 , Faro 18, Faro 19, Faro 20 , Faro 22 , Faro 24, Faro 26 , Faro 33, Faro 37, Faro 4, Faro 50, Faro 52, Faro 57, Faro 44, Faro 67, Nicro 49,Rasa, and Swana sub 1. They were sown in the field, under 0 –50cm flood water level, at a spacing of 20 cm by 20 cm. Each plot dimension will measure 2m by 2m with 50cm in-between, giving a total of 100 plants per plots.

Data Collection

Data was collected on the following parameters;

- i. Genetic component analysis will be calculated for all the traits. Genotypic and phenotypic coefficient of variability GCV% and PCV% will be estimated according to Singh and Chaudhary (1995) as follows

$$GCV(\%) = \sqrt{\frac{\delta_g^2}{\bar{X}} \times \frac{100}{1}}$$

$$PCV(\%) = \sqrt{\frac{\delta_p^2}{\bar{X}} \times \frac{100}{1}}$$

Where *GCV* = Genotypic coefficient of variability

PCV = Phenotypic coefficient of variability

δ_g^2 = Genotypic variance

δ_p^2 = Phenotypic variance

\bar{X} = Mean

Broad heritability and genetic advance were estimated according to Johnson *et al.* (1955) as follows

$$H^2 = \frac{\delta_g^2}{\delta_p^2} \times \frac{100}{1}$$

$$GA = \frac{k \times \sqrt{\delta_p^2} \times \delta_g^2}{\delta_p^2}$$

$$GAM = \frac{GA}{\bar{X}} \times \frac{100}{1}$$

Where H^2 = Broad-sense heritability

GA = Genetic advance

GAM = Genetic advance as percent of mean

K = 2.06 at 5% selection intensity

Statistical Analysis

As recommended by Panse and Sukhatme (1967), the mean values of all the attributes of each individual genotype per replication were analyzed. Broad sense heritability was done using the Johnson *et al.* (1955) approach. In a similar vein, Genetic Advance was carried out using Lush's recipe (1949).

RESULTS AND DISCUSSION

Table 1: Mean Squares of Analysis of Variance for Phenotypic Performance of Rice Varieties Screened for Flood Tolerance in 4 Environments (2-Locations by 2-Seasons)

Source	Df	Survival (%)	Plant height before submergence (cm)	Plant height after submergence (cm)	Elongation %	Elongation/day (cm)
Rep within loc.	8	317332.00**	1580.90*	1935.73*	6802.79*	485.57**
Varieties	50	424147.30**	1445.64**	2510.16**	824.97**	573.99**
Environment	3	378990.80**	3293.76**	1156.86**	8559.07**	3415.67*
Varieties × Environment	150	1985861.00**	3349.01**	9431.84**	540.01 ^{ns}	59.00*
Year	2	1141025.20**	987.06 ^{ns}	11891.26**	28782.18*	598.55*
Varieties × year	100	1323782.00**	1174.22*	16160.48*	1076.35**	55.59**
Environment × year	7	1876652.00**	2548.14**	9860.65**	1267.41**	56.47**
Error	1165	1411702.00	139.26	11107.35	1895.73	23.14

Where ** = (P<0.01), * = (P<0.05) and ns= Not significant

Table 2: ANOVA Table for 1000 Seed weight(g) of 21 genotypes in Four Environments

Source	Df	Sum of squares	Mean square	F	Value Pr (>F)
Location	3	2118.83	706.2766	56.68	0
Repwithinlocation	8	99.6813	12.4602	0.84	0.5648
Varieties	20	1745.621	87.281	5.92	0
Location x Varieties	63	1220.33	21.0402	1.43	0.0453
PooledError	150	2212.46	14.7497		
Total	239	7396.922			

Table 3: Table for Seed yield/plant (t/ha) in Four Environments

Source	Df	Sum of squares	Mean square	F	Value Pr(>F)
Location	3	39.1819	13.0606	1.32	0.335
Repwithinlocation	8	79.4263	9.9283	1.86	0.0699
Varieties	20	2738.41	136.9205	25.69	0.000
Location x Varieties	63	425.7549	7.3406	1.38	0.0636
PooledError	150	799.4639	5.3298		
Total	245	4082.237			

Table 3: Phenotypic (Vp) and genotypic variance (Vg), phenotypic coefficient (PCV) and genotypic coefficient of variance (GCV), genetic advance (GA) at 5% selection intensity, genetic advance as percent of mean (GAM) and broad sense heritability (H²b) for observed traits in rice genotypes

Traits	Vg	Vp	GA	GAM	H ² b	PCV	GCV (%)
Plant height (cm)	78.54	94.50	14.25	14.68	0.78	12.17	8.91
Panicle length	1.06	3.23	1.88	9.54	0.75	6.86	5.25
No. of tillers/plant	4.23	6.44	2.80	22.29	0.55	23.34	14.67
1000 grain weight (g)	3.56	4.05	3.31	18.29	0.85	7.88	9.02
Grain yield (t/ha)	0.78	0.66	1.61	38.43	0.70	25.64	28.89

Table 4: Phenotypic correlation coefficients of growth and yield characters

	Plant height (cm)	Number of Tiller / Plant (cm)	Panicle length (cm)	Number of Panicle / plant (cm)	1000 grain weight (g)	Grain yield (t/ha)
Plant height(cm)	1					
Number of Tiller/Plant (cm)	0.09	1				
Panicle length (cm)	0.61	0.54	1			
Number of Panicle/plant	0.65	0.37	0.93	1		
1000 grain weight (g)	0.72	0.65*	0.88	0.84*	1	
Grain yield (t/ha)	0.06	0.58*	0.86*	0.60	0.54*	1

Significant at P<0.05

Genetic Variability

It is established that genetic variability is prerequisite for breeding for improvement of any trait and also, efforts made to assess genetic diversity in paddy germplasm for submergence tolerance. Various traits used in screening for submergence tolerance includes germination percentage, seedling vigor, elongation ability, survival percentage, high tillering ability, panicle length, number of grains per panicle and seed yield/plant. As seed yield under submergence is the ultimate criterion traits or indices used for assessing submergence tolerance must be correlated with yield. Tables 1, 2 and 3, presents the mean squares of combined analysis of variance for phenotypic performance of 51 rice varieties screened for flood tolerance in 4 environments (2-Locations by 2-Seasons). Analysis of variance clearly showed that environment x varieties contributed highest (1985861.0) in total mean sum of squares for survival %, followed by environment x year (1876652.0) indicating very greater role played by environments. The analysis of variance also showed that the total mean sum of squares for plant height before and after submergence for varieties x environment was 3349.0 and 9431.8 indicating there were significant difference at P< 0.005 across locations for plant height. The high to moderate difference between the PCV and GCV for all the characters studied indicates a high influence of the environments on the traits and this finding is in line with Gyawali *et al.*, 2018.

Genetic Heritability

The GVC values for 1000 grain yield (g) and grain yield (t/ha) recorded 9.02 % and 28.89 % respectively showing that the environment had no influenced on the genotypes, depicting that these genotypes possibly have flood tolerant trait gene in them. The highest PCV was observed for number of tillers (23.34 %), lowest GCV was observed for panicle length (5.25 %). The Broad-sense heritability ranged from 0.55 for panicle length to 0.74 for the thousand-grain weight (Table 3). The result of the work is in line with Gyawali *et al.*, 2018; Bandhi *et al.*, 2018 and Abebe *et al.*, 2017, who observed high to medium heritability for grain yield. Low heritability estimates could be attributable to differences in the environmental components involved in certain traits. Heritability estimates also showed a high response to selection for flood tolerant traits. As a result, the genetic advance is a valuable indicator for achieving the expected result on a population's trait of interest after selection. Genetic advance as percent mean was categorized as low (0-10%), moderate (10-20 % and high (≥ 20%). In this study, high genetic advance as

percent of mean was observed for grain yield (38.43 %), followed by number of tillers/plant (22.29 %) and 1000 grain weight (18.29 %). This result suggests high component of heritable portion of the variations in these varieties and this is in line with the findings of Bandhi *et al.*, (2018) who reported high heritability for 1000 grain seed weight and the number of panicle per plant in rice.

Correlation

The correlation coefficient is a measure of the degree of association and relationship between two variables. It is important in plant breeding as it can be used for indirect selection. The study of the correlation between different characters may help the plant breeder to know how the improvement of one character will bring simultaneous changes in other characters. Degree of correlation is categorized as weak (0-0.3), moderate (0.3-0.7) and strong (0.7-1.0). The phenotypic correlation between grain yield and yield attributing traits of twelve rice genotypes is presented in Table 4.

Rice grain yield exhibits a positive correlation with thousand grain weight ($r = 0.54^*$) and panicle length ($r = 0.86$) and a positive correlation with no. of tillers/plant ($r = 0.58^*$), and plant height ($r = 0.06$). These findings were similar to those of Lakshmi *et al.*, 2014; Nayak *et al.*, 2001 and Nayak, Reddy, 2005, who found that grain yield was positively correlated with plant height and the number of effective tillers per plant. Ismail and Alvarez, 1986, found a positive correlation between grain yield and panicle length. Grain weight was found to be positively correlated with grain yield in rice by Zhao *et al.*, (2020). The findings of this study is in also in cognizance with Mohammad *et al.*, (2002), who described that differences in plant height depends on genetic makeup of a plant and environmental conditions.

CONCLUSIONS

Twenty one rice genotypes were studied for growth and yield parameters. The result revealed significant variation for grain yield and attributing traits. PCV was greater than GCV in all traits, implying that the environment had an impact. Grain yield, number of tillers/plant, and plant height had the highest GCV, PCV, and GAM values. Individual differences in a population caused by genetic composition and growing environment are referred to as phenotypic variability. Correlation therefore determines the extent of the relationship between yield and its components, as well as the relative importance of their effects, on growth and yield of rice. The information derived from this study could be beneficial for rice research, and for development of flood tolerant rice varieties.

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