

Stability analysis of yield and yield related traits of rainfed rice (*Oryza sativa* L.) in an upland ultisol in Owerri

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Abstract

An experiment was conducted during the early seasons of 2004 and 2005 in Owerri to assess the stability of yield and yield components in fourteen genotypes of rice (*Oryza sativa* L.) collected from four states of Eastern Nigeria. Ten randomly selected plants were sampled in the middle row of each plot and were used for the analysis. Genotypic stability analysis was performed on yield and the most related traits to yield using mean yield coefficient of variation (C.V.). All the yield components were significant ($P = 0.05$) and positively correlated with yield in both years with the exception of number of tillers/plant in 2004 and 1000-seed weights in 2005. The genotype Fadama significantly ($P = 0.05$) produced highest grain yield as well as number of tillers/plant. Genotype NERICA 1 statistically ($P = 0.05$) produced the same grain yield with Fadama but had the highest % fertile spikelets. Genotypes independently expressed their traits in different stability groups formed. Four groups of yield estimates established were high yield and low variation, high yield and high variation, low yield and low variation and low yield and high variation. This study has shown that yield traits are complementary in action therefore selection for high and stable yield in an upland condition should include such traits as high percentage fertile spikelets, number of tillers/plant and 1000-seed weights. [Life Science Journal. 2009; 6(1): 90 – 93] (ISSN: 1097 – 8135).

Keywords: rainfed rice; *Oryza sativa* L.; stability analysis; yield parameters

1 Introduction

Rice (*Oryza sativa* L.) is speedily overtaking the regular staple crops in its consumption in Nigeria. So there is an increasing demand for rice in Nigerian markets. The performance of wetland rice is constrained by limitation in nutrient availability. Plant development and yields are severely affected by soil conditions such as moisture and soil reaction. Water requirement is larger in rice than any other annual crops. El-Hissewy *et al* (1997) reported that rice water requirement vary with variety, soil, climate and cultivation practices. Rice production under irrigation is expensive and many farmers in Nigeria cannot afford it. The most possible option would be reduction of water requirements through breeding. To achieve this, it is imperative to identify stable yield contributing characters prior to commencing

the breeding programme. Rice production in Nigeria had previously been concentrated in lowland rainfed conditions. In spite of an increased production of upland rice in Nigeria which has improved rice production. It is yet to attain self-sufficiency (Courtois, 1988). Therefore this study was undertaken to assess the stability parameters of some rainfed rice genotypes in South Eastern Nigeria in an upland condition.

2 Materials and Methods

The experiments were conducted at the Teaching and Research Farm of the Federal University of Technology, Owerri, Nigeria (5° 27' N and 7° 02' E) on an elevation of 55.10 m above sea level. The meteorological data collected from Owerri meteorological center showed that the experimental field had mean annual rainfall of 2334.40 mm and 2397.01 mm in 2004 and 2005 cropping seasons respectively. The experimental site had a mean

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annual temperature of 31 °C and relative humidity of 89%. The particle size analysis showed that the soil had a sand value of 84.1%, silt 9.6% and clay fraction of 6.3% while the chemical soil analysis revealed a pH of 4.86, organic matter was 1.78%, total nitrogen 0.103%, 9.62 ppm Bray 2-P and exchangeable cations magnesium, potassium and calcium of 0.88, 0.52 and 0.48 cmol/ kg.

Table 1 describes the rice genotypes used in the study. The lines included five lines collected from the National Cereal Research Institute (NCRI), Baddegi, the other nine lines were collected from farmers fields in Abia, Ebonyi, Enugu and Imo States all in South Eastern Nigeria. The planting materials for the 2005 cropping season were seeds harvested from 2004 plantings.

Table1. Source, location and habitat of rice lines

S/n	Designation	Source	Habitat
1	IR-8	Abia State	Lowland
2	R Box	Imo State	Lowland
3	Mass	Ebonyi State	Lowland
4	1416	Enugu State	Lowland
5	SML	Ebonyi State	Lowland/Upland
6	Fadama	Enugu State	Lowland
7	IR-5-47	Abia State	Lowland
8	1515	Abia State	Lowland
9	BG90	Imo State	Lowland
10	NERICA2	NCRI, Badeggi	Upland
11	WAB96-1-1	NCRI, Badeggi	Upland
12	WAB450-1-B-P-160-HB	NCRI, Badeggi	Upland
13	NERICA3	NCRI, Badeggi	Upland
14	NERICA1	NCRI, Badeggi	Upland

The field was ploughed, harrowed and laid out in a complete block design with three replications. Each plot measured 1m having 5 rows with spacing of 0.25 m. The rice seeds were sown directly in the field on May 25, 2004 and 5th June, 2005 by seed-drilling four seeds in each planting hole and later maintained at two stands per hole at three weeks after planting (WAP). The soil was fertilized with 100 kg NPK/ha in split-application as boost application after planting and as top dressing at booting stage. The experimental field was weeded at 5 WAP and 10 WAP. The field was secured by fencing with wire mesh to protect the rice from grass-cutter and other rodents and scare-scrows were kept for bird scaring. Post harvest operations of threshing and winnowing were done to obtain the paddy yield.

Data collected included number of days from planting to anthesis (DA), number of productive tillers per

plant (PTP), plant height at flowering (PH), percentage fertile spikelets (PFS), flag leaf area (FLA), spikelets per panicle (SP), spikelets per branch of panicle (SB), a thousand seed weight (TSW) and grain yield (GY). The data were collected according to standard evaluation systems for rice SES, IRRI (1988). Ten randomly selected plants in the middle rows of each plot were used for data collection.

Combined analysis of variance for the two years was carried out for each of the yield and yield components. Genotypic correlation (rg) between yield and yield related traits was obtained from the genotypic covariance between two traits and the geometric of their genotypic variance (Obi, 1990)

$$rg = \sigma^2g(XY) / [\sigma^2g(XX) \sigma^2g(YY)]^{1/2}$$

Where $\sigma^2g(XY)$ is genotypic variance of cross production of the traits X and Y, $\sigma^2g(XX)$ is the genotypic variance traits of X and $\sigma^2g(YY)$ is the genotypic variance of the trait Y.

The genotypic stability of yield and those of the two most related traits to yield were estimated by mean coefficient of variation (C.V.) approach as described by Francis and Kannerberg (1978). Using mean C.V. and grand mean of yields obtained, four groups were obtained as follows:

Group 1 is high yield and low variation, group 2 is high yield and high variation, group 3 is low yield and low variation and group 4 is low yield and high variation.

Stable genotypes for traits are those whose C.V.s are below the mean C.V. and yield higher than the grand mean yield.

3 Results and Discussion

Significant genotypic variation ($P = 0.05$) was observed for all the yield and yield attributes measured (Table 2). Fadama gave the highest mean GY of 2.78 t/ha for both years and performed equally with BG90, WAB96-1-1, WAB450-1-B-P-160-HB, NERICA3, Mass and NERICA1. Genotype Fadama equally produced the highest PTP which was significantly different ($P = 0.05$) from those of IR-5-47, NERICA2, WAB96-1-1, NERICA3, NERICA1 and WAB450-1-B-P-160-HB. NERICA1 had highest PFS and were statistically the same ($P = 0.05$) with genotypes NERICA, WAB450-1-B-P-160-HB, WAB 96-1-1 and NERICA2.

PFS and PTP partitioned the genotypes used for the study into two parallel groups with the upland rice genotypes having significantly higher PFS while the lowland ones had more tiller numbers than the upland genotypes. Genotype IR-8 produced the least GY of

0.91 t/ha and was statistically the same with some of the genotypes.

Table 3 shows the mean square of yield and yield attributes of the genotypes studied for two years. There was significant year effect on three of the yield attributes but not on GY t/ha, PTP and number of spikelets per hectare. Highly significant ($P = 0.01$) year effect was observed for the yield attributes with exception of number SB which varied only at $P = 0.05$, thus indicating genotypic variation for both years. The genotype by year (GxY) interaction was significant for half the number of yield attributes recorded and no effect on others. The variation experienced may be as a result of varietal differences.

The characters that showed non significance for GxY effect indicated stable performance inspite of differing environmental conditions for both years and thus agree with Kang (1998). Table 4 shows multiple genotypic

correlation coefficients (rg) of the rice yield and related yield traits.

All the yield attributes were significantly ($P = 0.05$) and positively correlated with yield in 2004 with exception of PTP which negatively correlated with yield in 2004 but positively correlated with it in 2005 and was highly significant. It is thought that the environmental conditions prevailing in 2004 may have affected this trait. On the other hand, the number of SB was significant and positively correlation with yield in the first year but not in the second year. Most of the traits studied also inter-correlated positively with others. Number of SP and PFS had highest correlation values for both years and thus agrees with Lavanya *et al* (1997) who observed positive contribution of grains to high yield. Agbo and Obi (2005) reported that seed weight correlated negatively with tillers per plant and panicle per plant. In the present study PTP had no effect on TSW for the two years.

Table 2. Entry codes and yield and yield components of the upland rice genotypes used for the study

Designation	DA	PH	NPTP	PFS	FLA	GY (t/ha)	TSW (g)	NSB	NSP
IR-8	132.32	104.30	6.33	60.9	56.8	0.910	22.17	10.00	84.3
R Box	100.50	86.37	6.33	68.9	33.9	1.633	22.07	10.18	92.4
Mass	117.67	113.60	7.01	61.3	54.1	1.472	18.68	9.20	100.1
1416	113.50	92.32	6.14	54.3	50.2	1.252	19.03	9.30	78.2
SML	137.01	112.75	6.83	75.9	50.1	1.935	21.40	10.77	95.1
Fadama	99.83	80.40	7.33	70.6	38.5	2.783	21.62	10.43	102.4
IR-5-47	134.17	67.23	4.83	54.1	49.4	0.988	21.00	9.58	75.9
1515	134.71	88.25	6.02	53.9	52.6	1.507	20.63	13.20	72.5
BG90	101.17	107.43	6.17	58.0	44.8	2.185	20.08	11.67	85.3
NERICA2	74.01	80.20	5.50	79.5	57.9	1.898	22.52	10.43	77.3
WAN96-1-1	71.50	97.83	5.01	80.3	54.2	2.660	23.03	10.05	87.8
WAB450-1-B-P-160-HB	74.33	74.07	5.33	83.9	44.01	2.403	25.01	10.42	84.4
NERICA3	76.01	74.92	5.21	81.1	53.6	2.280	22.10		88.4
NERICA1	66.33	77.23	4.50	90.7	53.4	2.680	23.13		90.4
LSD	6.849	10.025	1.416	11.60	11.13	0.9056	2.303	1.44	15.47
Se	1.817	2.342	0.375	1.96	1.97	0.0598	0.213	0.365	2.29
C.V.	1.8%	2.6%	6.4%	2.8%	4.0%	3.1%	1.0%	3.5%	2.6%

LSD = Least significant difference, Se = Standard error .

Table 3. Mean square for rice grain yield and yield components in 2004 and 2005

Sources of variation	d.f	NPTP	PFS	NSB	TSW (g)	GY (t/ha)	NSP
Year (Y)	1	50.298**	923.4**	6.914*	37.067**	0.0012	5558.3**
Genotypes (G)	13	4.517 ^{ns}	939.4**	5.875 ^{ns}	16.765*	2.349*	472.4 ^{ns}
GxY	13	2.298 ^{ns}	412.2*	9.690**	12.016 ^{ns}	1.0911 ^{ns}	456.7 ^{ns}
Error	52	1.496	100.5	1.539	3.957	0.611	178.6

*: Significant $P = 0.05$, **: Significant $P = 0.01$.

Table 4. Multiple correlation matrix of yield and yield parameters for 2004 and 2005

Year	NPTP	PFS	NSP	NSB	TSW	GY
2004	NPTP	-0.471	-0.631	-0.28	-0.383	-0.261
	PFS		-0.313	0.724**	0.790*	0.661*
	NSP			0.775**	-0.365	0.607*
	NSB				0.038	0.531*
	TSW					0.521*
2005	NPTP	0.529*	0.266	0.069	-0.392	0.719**
	PFS		0.604*	0.391	0.587	0.623*
	NSP			0.519*	-0.189	0.982**
	NSB				0.008	0.376
	TSW					0.785**

*: Significant $P = 0.05$, **: Significant $P = 0.01$.

In Table 5, genotypes independently expressed their traits to yield in the different stability groups 1 – 4. The table shows these genotypes: NERICA1, NERICA3, WAB450-1-B-P-160-HB, and WAB 96-1-1 with 2.68, 2.28, 2.41 and 2.66 t/ha had high yields and were stable for the years under consideration.

They contrasted with genotypes Fadama, SML and BG90 which though had high yields of 2.78, 1.94, and 2.19 t/ha were unstable for the two years. Fadama also produced highest number of productive tillers but was unstable for both years. It is the opinion of this study that this might be as a result of their natural lowland adaptation since they were being tried in an upland environment. Other genotypes performed variably for the traits studied thus indicating their high contribution to yield. This agrees with Mishra and Dash (1997) and Agbo and Obi (2005) who had earlier reported similar results.

This study shows that in selecting for better GYs and adaptation under upland rice conditions, the genotypes to be grown must be stable in expression of PFS, high number of SP, high tillering ability and high number of filled grains.

4 Conclusion

The high PFS, number of PTP and TSW are highly associated with high yield in rice. Genotypes to be selected for higher yields and adaptation to upland environments should show stable PFS, high number of SP, high tillering ability as well as high number of filled grains. NERICA1, WAB450-1-B-P-160-HB and WAB96-1-1 were the genotypes that met the above

Table 5. Grouping of rice genotypes by yield, PFS, and NPT using yield and C.V. percentage

Group	PFS	NPT	GY (t/ha)
1	NERICA1, SML, WAB450-1-B-P-160-HB, WAB96-1-1, NERICA2	BG90, 1515	NERICA1, NERICA3, WAB450-1-B-P-160-HB, WAB96-1-1
2	WAB450-1-B-P-160-HB, Fadama	Fadama, SML, 1416, Mass, R Box	Fadama, SML, BG90
3	1515, R Box, 1416	WAB450-1-B-P-160-HB, NERICA1, IR-5-47, NERICA2	IR-8, Mass, IR-5-47, NERICA2
4	IR-5-47, IR-8, BG90, Mass	NERICA1	1416, 1515, R Box

requirements and are already being cultivated in upland environments. More trials are recommended in upland environments for Fadama, SML and BG90 to explore the possibility of attuning them to such environments. Some breeding works are suggested to capture the genes for high numbers of productive tillers and GY in Fadama when crossed with stable genotypes like NERICA1, WAB96-1-1 and WAB450-1-B-P-160-HB to create new genotypes.

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