



Variability in Number of Seedling Potentials for Final Yield Evaluation in Rice (*Oryza sativa* L.)

O. S. Osekita^{1,2*}, R. I. Adedoyin¹, B. O. Akinyele³, O. A. Obembe¹, A. C. Odiyi³
and M. G. Akinwale⁴

¹Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba-Akoko, Ondo State, Nigeria.

²Department of Agronomy, Presently in Crop Improvement Unit, Adekunle Ajasin University, Akungba-Akoko, Ondo State, Nigeria.

³Department of Crop, Soil and Pest Management, The Federal University of Technology, Akure, Ondo State, Nigeria.

⁴Reseed Project, International Institute of Tropical Agriculture (IITA), Lilongwe, Malawi.

Authors' contributions

This work was carried out in collaboration between all authors. Author OSO designed the study, wrote the protocol and wrote the first draft of the manuscript. Authors BOA and ACO reviewed the experimental design and all drafts of the manuscript. Author RIA managed the analyses of the study. Author OAO identified the plants. Authors OSO and MGA performed the statistical analysis. All authors read and approved the final manuscript.

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ABSTRACT

Five lowland rice genotypes obtained from International Institute of Tropical Agriculture (IITA) Ibadan were grown during the rainy season of 2013/2014 to study factor analysis for yield and its components in rice (*Oryza sativa* L). The factors are the genotypes and numbers of seedlings planted per hill, the varieties were evaluated in a split plot design replicated three times, and the numbers of seedlings per hill were allotted to the subplot and the rice genotypes in the main plot. The study was conducted on the field of Akungba Akoko Plant Science and Biotechnology

*Corresponding author: Email: oluwatoyin.osekita@aaau.edu.ng, oluwatoyinosekita@gmail.com;

Department, Adekunle Ajasin University, Nigeria. The characters measured include: number of tillers/hill at 30 and 50 days after transplanting, plant height at 30 and 50 days after transplanting, final plant height, flag leaf length, number of effective tillers, number of spikelets per panicle, number of grain per panicle, grain length, grain width, panicle length, panicle weight, 1000 grain weight, and grain yield per hill. The results showed that there were no significant differences between the treatments and the genotypes and that the treatments have no effect on the yield of the genotypes. The PCV was higher than GCV for all characters in most cases.

Keywords: Characters; factor analysis; genotypes; seedlings; yield components.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is the most important cereal crop of the world which is consumed as a staple food and forms the staple diet of over one-half of the world's population with approximately 95% of production in Asia Bhattacharjee et al. [1]. It also provides an excellent entry point for mobilization of national and international resources to achieve the millennium goals and the recommendation of the world food summit. According to FAO [2], the Director General stated that "Rice is a symbol of both cultural identity and global unity". An increase in rice production can be achieved partly through area expansion and increase of yield per unit area by employing high yielding varieties. Rice provides 35-60% of the dietary calories consumed by more than three billion people Fagade [3]. Grain yield is a complex polygenic character controlled by many genes interacting with the environment and is the product of many factors called yield components. The selection of parents based on yield alone is often misleading according to Khan et al. [4]. Population dynamics exerts a strong influence on rice growth and grain yield, because of its competitive effect both on the vegetative and reproductive development, and ultimately quality. Density depended effects on yield are due to the competition between the adjacent plants for the necessary resources Donald [5]; Zia [6]. Grain yield (GY) in cereals is one of the most important and complex traits in plant breeding experiments. Continued improvement of GY remains the top priority in most of the breeding programs Yan et al. [7,8]. In rice, GY depends on various growth and component traits, and is the final outcome of a combination of different yield components, such as the panicle number per plant, the filled grain number per panicle, and the weight per grain. Therefore, it is of significance to reveal the genetic contribution of yield components to GY. Hence Donald [9], opined that many breeders have paid much attention to the concept of plant ideotypes and proposed several models for high-

yielding rice, such as the 'heavy-panicle' and the 'multi-panicle' types. It was suggested that an increase in GY could be effectively achieved through yield component improvement since yield components have higher heritability than GY Xiong [10]. Correlation and path analyses have revealed the relationships between GY and its yield components at both the phenotypic and genetic levels, Xiong [10]. However, the implications of those studies to breeding practice were limited due to complicated correlations between GY and its yield components, which were disturbed to varying degrees by numerous factors such as environmental effects and experimental error etc. Risch [11]; Darvasi and Pisant'e-Shalom [12]. Selection of yield components was not highly effective in increasing GY, because of their negative correlations to each other Li et al. [13]. Different traits may be important to increase the rice grain production. The considered traits may include short plant height, strong culms; moderate tillering, short and erect leaves, large and compact panicles, and early maturation. Tillering in rice is one of the most important agronomic characters for grain production Smith and Dilday [14], because the tiller numbers per plant determines the panicle number, a key component of grain yield [7]. The prime characters among the various grain quality characters in deciding the overall grain quality in rice are grain length, width, shape, and its weight Gravois and Helms [15]; Tan et al. [16]. Rice grain features such as length, width, and shape have a direct effect on the marketability, and therefore on the commercial success of modern rice cultivars Redona and Mackill [17]. Most of the grain quality characters of rice are controlled by QTLs showing continuous phenotypic variation Yano and Sasaki [18]. The objectives of the study, therefore, are; to compare the yield of the genotypes, estimate the significant differences in yield of the various treatments in the sub plot and to recommend appropriate seedlings to be planted per hill.

2. MATERIALS AND METHODS

A field experiment was conducted with five rice genotypes (NL-19, FARO 57, MR 220, FARO 44, WITA 4) during the year 2013/2014 cropping season at the experimental field of the Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba Akoko, Ondo State. The five rice genotypes were obtained from IITA (International Institute of Tropical Agriculture, Africa Rice Centre Ibadan, Oyo State, Nigeria). The rice genotypes were pre-treated to hasten the germination process. The sprouted seeds were sowed in seed trays in the nursery for a period of three weeks before transplanting was done in an open field in a split plot design replicated three times. The seedlings were transplanted (25 x 25) cm row to row and plant to plant spacing. NPK fertilizer (15:15:15) was applied 10-15 days after transplanting. At 30-35 days data was collected on five randomly selected plants on number of tillers/hill and plant height and the values were recorded. At 50 days another set of data was collected on the previously selected plants which include; the number of tillers/hill, plant height, number of effective tillers, final plant height and the flag leaf length. The harvested panicles were sundried to about 14% moisture content, data was collected on the following eight yield components; number of spikelets per panicle, panicle length, number of grains per panicle, panicle weight one thousand grain weight, grain length, grain width and grain yield per hill.

2.1 Statistical Analysis

The data were subjected to statistical analysis using SPSS Version 20 software for the combined analysis of variance and coefficient of variation, the analysis of variance for split plot was done according to the procedure of Gomez and Gomez [19]. The variance component, genotypic and phenotypic coefficient of variation was computed according to the procedure of Miller et al. [20], Osekita and Akinyele [21], heritability, genetic advance and genetic advance as per cent of mean was computed according to Allard [22] and Osekita and Ajayi [23].

3. RESULTS AND DISCUSSION

The mean estimates of the quantitative traits measured across the genotypes were shown in Table 1. NL – 19 and WITA 4 were very tall with final heights of 140.21 cm and 121.53 cm compared to the other three genotypes, the

effect of this on the performance of the genotypes may result to lodging which invariably could bring about yield loss. The panicle length is an important yield component trait of which correlates with the final number of grains set on the panicle, therefore, NL – 19 had the highest mean value of 29.44 cm and the least was observed in MR 220 an Asian genotype with 24.58 cm. The important attribute of the Asian genotypes lies in the fact that it produces good number of effective tillers (14) as shown in the result and the grain yield per hill of 30.32 g and the final yield per hectare of 4.851 tons although, NL – 19 produces higher yield of 6.224 tons per hectare therefore, hybridization programme would be instituted through introgression of tillering tendencies of MR 220 genotypes in order to boost the yield to a higher figure. WITA 4 produces a good number of effective tillers as well but the seed weight had to be improved such that the final yield could be tremendously increased. Table 2 revealed the mean squares and coefficients of variation for the quantitative traits measured similarly; Table 3 indicated the combined analysis of variance and coefficients of variation for the measured traits, therefore, almost all the traits showed significant variations from the results, in Table 2a the number of seedlings planted per hill designated as Factor A did not showed significant variations except in number of tillers at 50 days after transplanting (33.69) that was significant ($P < 0.05$). Factor B the genotypes showed significant variations in almost all the traits except in few cases but the case was different among the interaction effect with significant variation noticed in effective tillers, panicle length and thousand grain weight. The coefficient of variation according to Gomez and Gomez [19] indicates the degree of precision with which the treatments are compared and is a good index of the reliability of the experiment. Hence, only few cases of high CV values were obtained and this goes a long way to show the reliability of the findings. Similar situations were obtained from the combined analysis of variance as shown in Table 3. The above results were in agreement with the findings of Osekita et al. [24,25].

The variance components, genetic advance, heritability and genetic advance as per cent of mean (GAM) among the treatments in the sub-plot and main plot are presented in Tables 4 and 5, respectively. The heritability is used to describe what proportion of total phenotypic variation in a population is due to genetic factor Klug et al. [26].

Table 1. Mean values of fifteen quantitative traits of rice (*Oryza sativa* L.)

Genotypes	PH30DAT	PH50DAT	NT30DAT	NT50DAT	FPH	FLL	EFT	NSP	PL	NGP	TGW	PW	GL	GWDT	GYDH	GY/Ha
NL-19	82.43 ^a	114.96 ^a	8 ^a	12 ^c	140.21 ^a	35.94 ^a	10 ^{ab}	16 ^a	29.44 ^a	218 ^a	28.02 ^a	6.77 ^a	0.90 ^b	1.74 ^{ab}	38.90 ^a	6224
FARO 57	67.16 ^{bc}	95.26 ^{bc}	8 ^a	13 ^{bc}	118.47 ^b	34.23 ^a	8 ^b	15 ^a	26.12 ^b	203 ^{ab}	25.56 ^{ab}	5.23 ^b	0.92 ^{ab}	1.60 ^c	23.42 ^b	3747
MR 220	61.45 ^c	78.41 ^c	7 ^a	17 ^{ab}	84.23 ^c	27.66 ^b	14 ^a	15 ^a	24.58 ^b	139 ^c	24.47 ^b	4.21 ^{bc}	0.95 ^{ab}	1.79 ^a	30.32 ^{ab}	4851
FARO 44	73.70 ^{ab}	101.48 ^{ab}	10 ^a	19 ^a	111.19 ^b	33.15 ^a	12 ^{ab}	14 ^a	26.35 ^b	142 ^c	26.71 ^{ab}	4.24 ^{bc}	0.98 ^a	1.67 ^{bc}	22.36 ^b	3578
WITA 4	74.31 ^a	88.40 ^{bc}	9 ^a	15 ^{abc}	121.53 ^{ab}	37.01 ^a	14 ^a	15 ^a	26.63 ^b	165 ^{bc}	18.09 ^c	3.39 ^c	0.90 ^b	1.63 ^{bc}	17.93 ^b	2869

Note: From the above table mean value with the same alphabet are not significantly different from each other.

PH30DAT and PH50DAT are plant height at 30 and 50 days after transplanting; NT30DAT and NT50DAT are numbers of tillers at 30 and 50 days after transplanting; FPH is final plant height; FLL is flag leaf length; EFT is number of effective tillers; NSP is number of spikelets/panicle; PL is panicle length; NGP is number of grain/panicle; TGW is thousand grain weight; PW is panicle weight; GL is grain length; GWDT is grain width; GYDH is grain yield/hill

Table 2. Mean squares and coefficients of variability for the parameters measured

Source of variation	DF	PH30DAT	PH50DAT	NT30DAT	NT50DAT	FPH	FLL	EFT	NSP	PL	NGP	TGW	PW	GL	GWDT	GYDH
REPLICATION	2	104.37	390.39	56.43	22.42	116.83	20.49	4.865	4.36	1.389	46.38.74	9.825	2.83	0.025	0.000	187.29
FACTOR A	2	1.04ns	35.52ns	0.825ns	33.69*	12.45ns	6.60ns	10.4ns	2.61ns	8.079ns	753.14ns	0.96ns	2.75ns	0.000ns	0.000ns	158.28ns
ERROR (a)	4	12.29	51.84	0.42	3.56	63.51	27.06	8.068	1.37	-1.935	3729.62	7.775	3.18	0.015	0.000	131.13
FACTOR B	4	537.51**	1343.28**	10.145ns	51.42*	3060.24**	165.45**	125.09**	3.78ns	14.76ns	10017.51**	50.79**	13.27**	-0.063ns	0.004ns	643.64**
A*B	8	4.83ns	63.02ns	2.044ns	22.61ns	48.64ns	-20.73ns	22.62**	1.48ns	52.15*	646.16ns	45.31**	0.299ns	0.0013ns	0.000ns	204.86ns
ERROR (b)	24	102.7	256.59	7.145	18.01	332.59	21.69	2.45	4.45	22.13	462.63	5.351	2.409	0.067	0.000	130.37
CV (a)		4.87	7.39	7.33	12.33	6.72	15.39	28.48	7.79	5.22	34.85	11.35	37.31	13.17	0.00	42.41
CV (b)		14.04	16.44	31.89	27.74	15.39	13.78	12.94	14.05	17.67	12.27	9.42	32.47	27.77	0.00	41.81

Note: *, ** significant at 5% & 1% levels respectively, ns is non-significant

PH30DAT and PH50DAT are plant height at 30 and 50 days after transplanting; NT30DAT and NT50DAT are numbers of tillers at 30 and 50 days after transplanting; FPH is final plant height; FLL is flag leaf length; EFT is number of effective tillers; NSP is number of spikelets/panicle; PL is panicle length; NGP is number of grain/panicle; TGW is thousand grain weight; PW is panicle weight; GL is grain length; GWDT is grain width; GYDH is grain yield/hill

Table 3. Combined analysis of variance and coefficients of variation for the quantitative traits measured

Source of var	DF	PH30DAT	PH50DAT	NT30DAT	NT50DAT	FPH	FLL	EFT	NSP	PL	NGP	TGW	PW	GL	GWDT	GYDH
GENOTYPE	4	566.03**	1703.01**	11.05**	76.03**	3715.92**	119.18**	64.30**	3.80**	27.97**	11350.10**	133.85**	15.15**	0.01*	0.06*	604.37**
TREATMENT	2	0.38**	18.52**	0.47**	27.02**	144.50**	9.92**	22.33**	0.70**	1.68**	1175.34**	0.96**	2.03**	0.00*	0.01*	190.59**
GEN*TRT	8	3.59**	113.15**	1.77**	17.38**	178.33**	10.05**	20.80**	0.36**	0.73**	582.87**	3.78**	0.37**	0.00*	0.02*	158.06**
ERROR	30	90.22	323.05	9.69	18.58	436.56	25.43	22.08	4.65	6.24	2696.50	5.97	2.37	0.01	0.01	159.02
CV		13.23	18.78	37.35	28.40	18.15	15.01	39.97	14.31	9.38	29.96	9.95	32.26	8.14	6.93	47.43

*, ** Significant at 5% and 1% probability levels respectively.

Note: From the above table PH30DAT and PH50DAT are plant height at 30 and 50 days after transplanting; NT30DAT and NT50DAT are numbers of tillers at 30 and 50 days after transplanting; FPH is final plant height; FLL is flag leaf length; EFT is number of effective tillers; NSP is number of spikelets/panicle; PL is panicle length; NGP is number of grain/panicle; TGW is thousand grain weight; PW is panicle weight; GL is grain length; GWDT is grain width; GYDH is grain yield/hill

Table 4. Variance components, genetic advance, heritability and genetic advance as per cent of mean (GAM) among the treatments in the sub-plot

Treatments	Vg	Vp	GCV	PCV	H ²	Ga	GAM
PH30DAT	-29.95	60.27	-0.08	0.11	72.73	11.63	16.20
PH50DAT	-101.51	221.54	-0.11	0.16	68.75	21.08	22.03
NT30DAT	-3.07	6.62	-0.21	0.31	67.74	3.59	43.10
NT50DAT	2.81	21.39	0.11	0.31	35.48	3.38	22.27
FPH	-97.35	339.21	-0.09	0.16	56.25	21.34	18.54
FLL	-5.17	20.26	-0.07	0.13	53.85	4.99	14.85
EFT	0.08	22.16	0.02	0.40	5.0	0.49	4.17
NSP	-1.98	2.67	-0.09	0.12	75.0	2.53	16.80
PL	-2.08	4.16	-0.05	0.08	62.50	2.63	9.88
NGP	-507.05	2189.45	-0.13	0.27	48.15	14.69	8.48
TGW	-1.67	4.30	-0.05	0.08	62.50	2.67	10.87
PW	-0.11	2.26	-0.07	0.32	21.88	0.69	14.47
GL	-0.00	0.01	0	0.12	0	0	0
GWDT	0	0.01	0	0.06	0	0	0
GYDH	10.52	169.54	0.12	0.49	24.49	6.57	24.71

Note: From the above table Vp is phenotypic variance; Vg is genotypic variance; GCV is genotypic coefficient of variation; PCV is phenotypic coefficient of variation; h² is heritability; Ga is genetic advance and GAM is genetic advance as percent mean, PH30DAT and PH50DAT are plant height at 30 and 50 days after transplanting; NT30DAT and NT50DAT are numbers of tillers at 30 and 50 days after transplanting; FPH is final plant height; FLL is flag leaf length; EFT is number of effective tillers; NSP is number of spikelets/panicle; PL is panicle length; NGP is number of grain/panicle; TGW is thousand grain weight; PW is panicle weight; GL is grain length; GWDT is grain width; GYDH is grain yield/hill

Table 5. Variance components, genetic advance, heritability and genetic advance as per cent of mean among the genotypes in the main plot

Treatments	Vg	Vp	GCV	PCV	H²	Ga	GAM
PH30DAT	158.60	248.82	0.18	0.21	63.74	20.71	28.84
PH50DAT	459.99	783.04	0.22	0.29	58.74	33.86	35.38
NT30DAT	0.46	10.15	0.08	0.38	4.53	0.30	3.60
NT50DAT	19.15	37.73	0.29	0.41	50.76	6.42	42.29
FPH	1093.12	1529.68	0.29	0.34	71.46	57.58	50.01
FLL	31.25	56.68	0.17	0.22	55.13	8.55	25.45
EFT	14.07	36.15	0.32	0.51	38.92	4.82	40.99
NSP	-0.28	4.37	-0.04	0.14	6.41	0.28	1.86
PL	7.24	13.48	0.10	0.14	53.70	4.06	15.25
NGP	2884.53	5581.03	0.31	0.43	51.69	79.55	45.90
TGW	42.63	48.60	0.27	0.28	87.72	12.60	51.28
PW	4.26	6.63	0.43	0.54	64.25	3.41	71.49
GL	0.002	0.012	0.05	0.12	16.67	0.04	4.30
GWDT	0.02	0.03	0.08	0.10	74.99	0.27	15.98
GYDH	148.45	307.47	0.49	0.66	48.28	17.44	65.59

Note: From the above table Vp is phenotypic variance; Vg is genotypic variance; GCV is genotypic coefficient of variation; PCV is phenotypic coefficient of variation; h² is heritability; Ga is genetic advance and GAM is genetic advance as percent mean, PH30DAT and PH50DAT are plant height at 30 and 50 days after transplanting; NT30DAT and NT50DAT are numbers of tillers at 30 and 50 days after transplanting; FPH is final plant height; FLL is flag leaf length; EFT is number of effective tillers; NSP is number of spikelets/panicle; PL is panicle length; NGP is number of grain/panicle; TGW is thousand grain weight; PW is panicle weight; GL is grain length; GWDT is grain width; GYDH is grain yield/hill

Table 6. Genotypic correlation coefficients on fifteen quantitative traits of rice (*Oryza sativa* L.)

Characters	PH30DAT	PH50DAT	NT30DAT	NT50DAT	FPH	FLL	EFT	NSP	PL	NGP	TGW	PW	GL	GWDT	GYDH
PH30DAT	1.0000	0.7357**	-0.1609	-0.2980**	0.7897**	0.6851**	-0.0097	0.4127	0.7366**	0.4096**	0.2297**	0.3868**	-0.0315	0.1029	0.2317**
PH50DAT		1.0000	-0.1074	-0.1286	0.6597**	0.4043**	-0.2315**	0.4728**	0.6901**	0.5868**	0.5410**	0.6160**	-0.0719	0.1676	0.4397**
NT30DAT			1.0000	0.4697**	-0.0692	-0.1838	0.1686	-0.2106	-0.3033	-0.2301	-0.1478	-0.1991	0.2949**	-0.2121	-0.0726
NT50DAT				1.0000	-0.3375	-0.2724	0.5179**	-0.0897	-0.3443	-0.2515	-0.1271	-0.2067	0.1454	0.1101	0.1206
FPH					1.0000	0.7926**	-0.0298	0.5827**	0.7386**	0.6560**	0.2181**	0.5863**	-0.1652	-0.1056	0.4092**
FLL						1.0000	-0.0225	0.4321**	0.5012**	0.4138**	-0.0286	0.2754**	-0.1453	-0.1482	0.0560
EFT							1.0000	0.1468	-0.0664	-0.1008	-0.3129	-0.1575	-0.0483	0.2267**	0.2882**
NSP								1.0000	0.6453**	0.7929**	0.1701	0.7400**	-0.1531	0.0253	0.6245**
PL									1.0000	0.7216**	0.3421**	0.7438**	-0.0940	0.2367**	0.4908**
NGP										1.0000	0.2943**	0.8697**	-0.3561	-0.0620	0.5733**
TGW											1.0000	0.5830**	0.0827	0.2036**	0.4583**
PW												1.0000	-0.1413	0.1347	0.7482**
GL													1.0000	0.1081	-0.1434
GWDT														1.0000	0.2073**
GYDH															1.0000

*, ** Significant at 5% and 1% probability levels respectively.

Note: From the above table PH30DAT and PH50DAT are plant height at 30 and 50 days after transplanting; NT30DAT and NT50DAT are numbers of tillers at 30 and 50 days after transplanting; FPH is final plant height; FLL is flag leaf length; EFT is number of effective tillers; NSP is number of spikelets/panicle; PL is panicle length; NGP is number of grain/panicle; TGW is thousand grain weight; PW is panicle weight; GL is grain length; GWDT is grain width; GYDH is grain yield/hill

Therefore, for a multifactorial trait in a given population, a high heritability estimate indicates that much of the variation can be attributed to genetic factors, with the environment having less impact on expression of the trait. With a low heritability estimate, environmental factors are likely to have a greater impact on phenotypic variation within the population. Heritability was low in effective tillers, grain length and width as shown in the sub plot and similarly, low heritability was observed in number of tillers at 30 days after transplanting and number of spikelets in the main plot analysis, the above assertion greatly applied to those traits and selection based on those traits for further improvement is advocated. In the same vein, Genetic advance as per cent of mean was also low for the above mentioned traits with emphasizes on the need to further improve the traits in subsequent breeding programme. The genotypic correlation coefficients on fifteen quantitative traits of rice were presented in Table 5: Correlation analysis measures the degree of association between two or more component traits. Hence the association between yield and its components, such as final plant height (0.4092), effective tillers per hill (0.2882), number of spikelets per panicle (0.6245), panicle length (0.4908), number of grains per panicle (0.5733), thousand grain weight (0.4583), panicle weight (0.7482) and grain width (0.2073) are good indicators of the indirect effect of the treatments that eventually results in grain yield due to combinations of the components traits. Similar results were obtained in the works of Akinwale et al. [27] and Osekita et al. [25].

4. CONCLUSION

In conclusion, taking all the yield component traits into account, there is no observable differences in the important factor tested in the sub-plot and as such farmers can make use of one to three seedlings per hill depending on the vigour of the seedlings because this range of number of seedlings does not make significant impact on yield increase. The genotypes show significant differences among themselves in almost all the traits measured. Further breeding work could be centred on varied number of seedlings greater than three to test for significant effect on the final yield.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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