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Heritability and Genetic Components Studies of F2 Population of Rice (O. Sativa L.)

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Abstract: Rice is one of the most widely consumed staple crops in Africa and consumption continues to grow at a rapid pace with increasing population is therefore, imperative for production to match the consumption. The objectives of this study were to determine the genetic components for yield improvement and selection of promising genotypes for food security. The research was carried out at the University of Port Harcourt Faculty of Agriculture teaching and research farm. Single cross (FARO 52 x UPN 223) was used to generate population that was advanced to F2 generation and 50 F2 lines were selected for evaluation. FARO 52 is an adapted improved variety while UPN 223 is anther-culture derived from Korea. This was a potted experiment in randomized complete block design in two replications in the screenhouse. All agronomic practices and data collection were carried out at the appropriate stage of the crop phenology. This study showed the existence of a considerable level of diversity among the studied rice genotypes. High heritability plus high genetic advance was observed for plant height, effective tillers, number of seeds per panicle and number of filled seeds per panicle. The lines 11, 17, 19, 46, 49 and 50 had good phenotypic expressions for the desired traits and promising for advancement for to next generations. The grain yield per plant had high and significant correlation with all the yield components in this study. Three lines were observed to be transgressive, line 40, 49 and 43 for grain yield per plant of 5.75g, 5.51g and 5.09g, respectively compared with parental lines FARO 52 (2.51g) and UPN 223 (3.32g) promising for advance in the breeding programme.

Keywords: Oryza Sativa, Phenotypic Coefficient of Variation, Phenotypic Coefficient of Variation, Genetic Advancement, Heritability, Grain Yield

1. Introduction

Rice is one of the most important crops produced worldwide. It provides 21% energy and 15% per capita protein of global human nutrition [20]. It is an important crop which provides nutrition and more than one fifth of calories consumed worldwide. [34]. Rice consumption in world, especially developing countries is growing at such a rapid rate that it has been estimated that about 30 million tons of rice will be required to feed the population [4]. In the developing countries, urban migration, and the increasing influx of women into active work force has also had a notable impact on the increased rate of rice consumption because rice is easy to prepare quick and relatively cheap option for feeding families. [6]. With the growing size of population, increasing the productivity of rice has become an

international urgency to meet up with the national livelihood and food security system. Therefore, developing high yielding genotypes with the desired agronomic traits adapted to various environments is therefore, seen as a requisite, also noted that to attain rice self-sufficiency and meet the future demands, development of high yielding varieties with other desirable agronomic traits is very crucial [21].

The genetic analysis of quantitative traits is extremely important for plant breeding programs, which helps breeders in experimental designs and developing appropriate mating strategies in plant breeding [33]. Therefore, the study of heritability of traits is relevant in determining its responses to selection as genetic improvement for qualitative and quantitative characters requires a reliable estimation of heritability for efficient breeding programs [1]. Heritability is described as a

measure of the phenotypic expression of traits (phenotypic variance) attributed to genetic variances and it has a predictive function in crop breeding [29]. The rice grain yield depends on the various growths and yields component traits like; the filled grain number per panicle, the panicle number per plant and, weight per plant [31]. Panicle affects yielding capacity as yields capacity is determine by number of grains per unit's area and the potential grain size [11]. Tillering ability plays a prominent role in determining grain yield because it is closely associated with panicle number. [7]. Leaf area (LA) and leaf area index (LAI) also plays an important role because it is directly involved in the photosynthetic process and chlorophyll conversion of the rice plant. Reports showed that the difference between effect of environment on traits is indicative of the differences between GCV and PCV [24]. Large differences mean high environmental effect whereas a small difference equals low genetic difference, reports noted that selection for yield improvement based on traits which showed small differences between PCV and GCV would be effective for future breeding programs [33]. Correlation coefficient analysis helps to determine the nature and degree of relationship between plant character variables. As grain yield is a complex character and dependent on several component characters, the knowledge of character association would be useful to plant breeder in the selection of suitable plant type. Therefore, the objectives of this study were to determine heritability and genetic components of yield related traits in early generation of rice for rapid yield improvement.

2. Methodology

The research was carried out at the University of Port Harcourt Faculty of Agriculture teaching and research farm, Choba, Rivers State, located in the southern part of the country along the Niger-Delta coast. The state has an estimated annual rainfall of 2000 – 2680 mm and an average temperature of 28 – 30°C. The experiment was established at the University of Port Harcourt, Faculty of Agriculture teaching and research farm. Single cross (FARO 52 x UPN 223) was used to generate population that was advanced to F2 generation and 50 F2 lines were selected for evaluation. FARO 52 is an adapted improved variety while UPN 223 is anther-culture derived from Korea. This was a potted experiment in randomized complete block design in two replications in the screenhouse. Pots were filled with sterilized top-soil loamy properties. The 50 F2 lines and the parental lines were pre-germinated and the healthy seedlings were transplanted after two weeks at the rate of two seedlings per pot. Normal agronomic practices were carried out as required. Weeding was carried out manually. Irrigation was applied regularly (weekly) to maintain the soil requirement and prevent scorching. Chemical fertilizer NPK (15:15:15) was applied as a basal application of 200 kg/ ha (N_2, P_2O_5 and K_2O). Urea fertilizer was applied in two splits at the rate of 65 kg/ha at tillering stage and the second application at the rate of 35 kg/ha at the beginning of panicle initiative stage. All agronomic practices and data collection were carried out at the appropriate stage of the crop phenology.

2.1. Data Collection

Agronomic data collection was done at appropriate phenological stages of the plant following the standard evaluation system (SES) for Rice [13]. Data was collected from five plants in each line per replication and their means was taken as a representative sample of the line. Parameters were measured every two weeks at the appropriate stage such as plant height (cm) was measured from the base of the plant (top of the soil) to the tip of the longest leaf, leaf area (LA) was determined using a leaf area meter (li-3100, Lincoln, NE USA), leaf area index (LAI) was calculated as was calculated as described [32] as follows. LAI = (sum of the Leaf Area of all leaves per unit area where the leaves have been collected). Number of effective tillers,% full seed per panicle was noted, number of seeds per panicle and number of filled seeds per panicle were counted and recorded. Panicle length was measured in centimeters. Panicle weight, 1000 seed weight and yield per plant were all weighed using a sensitive weighing balance in grams.

2.2. Data Analysis

Heritability estimates as described [10] was carried out on the F2 population. The following equation was used to calculate the broad sense Heritability (H^2);

$$H^2 = (\sigma^2 g / \sigma^2 p) \times 100$$

Where, $\sigma^2 g$ = additive variance, $\sigma^2 p$ = dominance variance, Genetic variances were calculated as describes [14],

$$\sigma_g^2 = (MSG-MSE)/r$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where MSG is the mean square of genotypes, MSE is mean square of error, and r is number of replications, σ_g^2 is the genotypic variance and σ_e^2 is the error variance.

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variance (PCV) were computed as follows:

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$$

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

Where $\sigma^2 g$ = Genotypic variance $\sigma^2 p$ = Phenotypic variance and $\bar{x}$ is the mean of the genotype.

Genetic advance (GA) was computed according to [27] and Genetic advance as percentage of the mean (GAM) also known as expected genetic gain (EGG) was computed according to [25]. GAM was categorized as high, medium and low based on the classification [10]. High = >20%; Moderate = 11-20%; Low = 0-10%

3. Results

3.1. Evaluation of Agronomic Traits of the F2 Progenies

The results obtained from this study (Table 1) showed that for Plant height, about 26 lines performed better than the mean (89.22 cm) and the tallest was lines 11 (106.5cm) and line 50 (104.21cm). The shortest was line 7 (52.3cm) and line 13 (68.15cm) and the tallest parent FARO 52 had (99.00cm) t. For Leaf area index, 25 lines had higher value than the mean (1.86). Highest value was line 11 (2.22) and line 50 (2.17), while FARO 52 recorded (2.13) as compared to UPN 223 (0.75) Table 1.

The effective tillers number, which is the harvestable tiller, about 23 lines had high numbers of effective tiller per plant than the mean (2.5). The line 50 had the highest number of effective tillers per plant (5) and line 17 (4) while the parents UPN 223 FARO 52 had 5 and 3, respectively. While for the panicle length 26 lines had longer panicles than the mean (23.15 cm). The line 6 had panicle length of 32.34 cm the longest and followed by line 26 (28.44cm), while FARO 52 and UPN 223 had (25.11cm) and (22.35cm), respectively. Panicle weight per plant showed that 22 lines had higher panicle weight than the mean (1.38g) and the highest were lines 40 (2.59g) and 6 (2.53g), while UPN 223 (1.75g) as compared to FARO 52 (1.42g) Table 1.

The Number of seeds per panicle recorded in this study showed that 24 crosses performed better than the mean (85.28) and significant variation (P≤ 0.05) was observed among the lines. The lines with higher number of seeds per panicle were lines 6 (191) and 46 (138), while the parents FARO 52 and UPN 223 had 121 and 92, respectively, the number of seeds per panicle.

While in 1000 grain weight, 33 lines performed better than the mean (18.44). Highest was line 46 with 23.64g while the lowest was line 12 with 3.01g. The higher parent was UPN 223 with 24.1g while and FARO 52 had 20.62g. Yield per plant showed that 18 lines performed better than the mean (2.36g). Highest was line 40 (5.75g) and followed by line 49 (5.51g). The higher parent was UPN 223 (3.32g) and FARO 52 (2.51g) (Table 1). Line 40 and line 49 performed better than the parents in all traits. 21 lines performed better than the mean of both parents (Table 1). The genotypes showed high significant differences (0.05) across all traits observed.

Table 1. *Evaluation of agronomic traits of the F2 progenies.*

INES (FARO 52 X UPN223)	PHT (cm)	LAI	ET	LP (cm)	WP (g)	NOSPP	NOFSPP	%FS	1000SW	YPP (g)
FARO 52	99	2.13	3	25.25	1.42	121	59	48.76	20.62	2.51
UPN 223	67.4	0.75	5	22.35	1.75	92	67	72.83	24.1	3.32
1	88.1	1.83	2	23.52	1.05	82	40	49	23.4	1.89
2	87.12	1.81	3	25.51	1.71	105	91	87	17.81	1.42
3	77.51	1.61	2	23.24	1.23	75	69	92	18.62	1.36
4	98.53	2.05	2	21.33	1.25	86	40	47	22.00	1.86
5	93.12	1.94	3	21.72	1.51	103	90	87	19.61	1.42
6	103.01	2.15	2	32.34	2.53	191	92	48	21.21	1.9
7	52.3	1.09	2	20.91	0.67	53	20	38	19.12	1.39
8	81.53	1.7	2	25.13	1.36	81	67	83	16.2	0.97
9	88.21	1.83	3	22.64	1.42	89	73	82	17.41	1.11
10	96.53	2.01	3	25.12	1.86	87	79	91	19.13	2.63
11	106.5	2.22	2	22.64	1.37	90	78	87	20.61	2.17
12	87.12	1.81	1	15.11	0.33	33	13	39	3.01	0.15
13	68.15	1.41	1	20.53	1.08	63	49	78	18.40	0.92
14	87.04	1.81	2	21.21	1.21	81	58	72	15.41	2.21
15	89.42	1.85	3	26.52	1.68	97	75	77	18.60	1.71
16	76.12	1.59	3	23.14	0.54	77	22	29	6.40	0.32
17	86.13	1.79	4	21.14	1.65	79	71	90	20.21	2.17
18	73.51	1.53	2	20.00	0.71	82	40	49	8.04	0.44
19	90.52	1.88	4	27.51	2.16	105	100	95	17.41	1.95
20	79.02	1.64	3	23.22	1.01	59	28	47	12.42	0.69
21	84.1	1.75	2	22.11	1.53	72	58	81	23.63	1.7
22	87.32	1.81	3	20.13	1.41	71	63	89	19.44	2.31
23	70.31	1.46	2	18.34	0.98	56	47	84	18.61	1.57
24	70.5	1.47	1	16.11	0.86	54	39	72	15.01	0.75
25	92.12	1.92	2	23.72	1.72	86	76	88	19.6	2.9
26	103.01	2.15	1	28.44	1.89	110	65	59	20.32	1.23
27	81.31	1.69	2	23.41	1.14	92	47	51	17.23	1.65
28	89.21	1.85	2	24.53	1.75	95	74	78	22.31	2.93
29	76.13	1.59	3	18.24	1.24	60	56	93	19.41	2.65
30	88.12	1.84	3	16.62	0.72	79	51	65	13.8.3	2.66
31	95.11	1.98	3	22.31	1.54	79	73	92	19.22	3.1
32	103.21	2.15	3	28.34	0.67	71	26	37	20.43	1.82
33	86.93	1.81	2	24.23	0.91	56	29	52	19.42	1.1
34	87.14	1.81	2	25.54	1.13	107	43	40	18.41	1.12
35	91.41	1.89	2	23.62	0.79	71	27	38	20.02	1.45
36	90.24	1.87	2	20.31	1.07	70	40	57	21.13	2.19
37	94.34	1.96	2	23.44	1.86	103	86	83	19.41	2.79

INES (FARO 52 X UPN223)	PHT (cm)	LAI	ET	LP (cm)	WP (g)	NOSPP	NOFSPP	%FS	1000SW	YPP (g)
38	100.21	2.08	2	23.22	1.89	105	94	90	17.62	1.72
39	90.53	1.88	3	21.53	1.43	88	70	80	18.41	3.17
40	98.14	2.04	4	26.54	2.59	114	96	84	21.32	5.75
41	94.12	1.96	3	23.42	1.25	15	54	47	19.12	2.16
42	86.22	1.79	1	23.34	1.1	70	35	50	20.31	1.28
43	103.31	2.14	4	24.61	2.32	99	85	86	20.21	5.09
44	103.21	2.14	2	23.93	1.69	128	83	65	20.26	3.04
45	96.33	2	3	23.52	1.33	77	44	57	22.63	2.53
46	100.24	2.08	3	27.93	2.52	138	93	67	23.64	5.14
47	94.33	1.95	2	23.42	1.21	98	41	42	20.21	2.52
48	93.31	1.94	3	25.14	1.66	101	48	48	20.82	4.25
49	103.24	2.15	4	26.22	1.85	97	70	72	22.41	5.51
50	104.21	2.17	5	24.44	1.32	84	63	75	15.23	2.78
Mean	89.22	1.86	2.5	23.15	1.38	85.28	59.42	34	18.44	2.36
S.E	63.127	0.865	1.873	16.528	1.041	63.173	44.985	61.28	13.34	1.758
LSD	0.52*	0.35*	0.5*	0.65*	7.55*	7.50*	6.50*	6.53*	1.50*	0.75*

*, significant at 0.01. PHT: Plant height, LAI: Leaf area index, ET: Effective tiller, LP: Length of panicle, WP: Weight of panicle, NOSPP: Number of seeds per panicle, NOFSPP: number of feed grain seed per panicle, %FS full seeds, 1000 SW: 1000 Seed weight, YPP: Yield per plant.

3.2. Genetic Variances and Heritability

NOSPP, PHT and NOFSPP showed the highest genotypic variance (σ^2g). NOSPP, PHT and NOFSPP also showed the highest phenotypic variance (σ^2p). The σ^2p observed for all traits were all higher in value than the σ^2g (Table 2). Similarly, the phenotypic coefficient of variation (PCV) had higher percentages than the genotypic coefficient of variation (GCV) for all the traits measured except plant height (PHT). All traits showed a high heritability (above 70%) except for 1000 SW and YPP with heritability of 13.10 and 22.21 respectively. Genetic advance (GA) was significant at (P$\leq$ 0.01) for all the traits measured but higher in number of seeds per plant (NOSPP) at 89.98% (Table 2).

Table 2. *Genotypic and phenotypic coefficient of variability (GCV and PVC), heritability (h^2), genetic advance and components of variance for different characters in F2 progenies and parental lines of the FARO 52 x UPN 223 Cross.*

	PHT (cm)	LAI (cm^2)	ET	PL (cm)	PW (g)	NOSPP	NOFSPP	1000 SW (g)	YPP (g)
GCV%	22.25	46.65	27.27	15.32	20.67	35.39	25.82	2.43	10.42
PCV%	22.25	47.95	29.46	15.90	23.73	36.74	27.08	3.45	22.12
Heritability% (Broad base) h^2	99.99	94.65	85.71	902.87	75.85	92.77	90.91	13.10	22.21
Genetic advance as% of mean (GAM)	58.74**	1.8**	66.66**	10.1**	0.8**	89.98**	48.1**	0.3**	0.4**
Genotypic variance (σ^2g)	404.43	0.47	1.00	15.83	0.14	1006.83	365.00	8.33	0.09
Phenotypic variance (σ^2p)	404.46	0.49	1.17	17.05	0.18	1085.33	401.50	8.63	0.39
Environmental variance	0.003	0.03	0.17	1.22	0.04	78.50	36.50	0.30	0.30

** significant at 0.01 PHT: Plant height, LAI: Leaf area index, ET: Effective tiller, PL: Panicle length, PW: Panicle weight, NOSPP: Number of seeds per panicle, 1000 SW: 1000 Seed weight, YPP: Yield per plant.

Table 3. *Correlation coefficient between yield and yield related traits in F2 progenies.*

	PHT (cm)	LAI (cm^2)	ET	PL (cm)	PW (g)	NOSPP	NOFSPP	%FS	1000 SW (g)	YPP (g)
PHT										
LAI	0.974**									
ET	0.896**	0.855**								
PL	0.972**	0.945**	0.902**							
PW	0.907**	0.863**	0.870**	0.929**						
NOSPP	0.925**	0..851**	0.845**	0.950**	0.949**					
NOFSPP	0.894**	0.914**	0.869**	0.903**	0.973**	0.930**				
%FS	0.748**	0.724**	0.740**	0.742**	0.728ns	0.612ns	0.757**			
1000 SW	0..948**	0.870**	0.870**	0.963**	0.922**	0.914**	0.894**	0.748**		
YPP	0.807**	0.751**	0.847**	0.873**	0.873**	0.805**	0.832**	0.639**	0.835**	

**= significant at 0.01 and ns = not significant. PHT: Plant height, LAI: Leaf area index, ET: Effective tiller, PL: Length of panicle, WP: Weight of panicle, NOSPP: Number of seeds per panicle%FS:% Filled Seeds, 1000 SW: 1000 Seed weight, YPP: Yield per plant.

3.3. Correlation Coefficient Between Yield and Yield Related Traits in F2 Progenies of (FARO 25 x UPN 223)

There was significant correlation (P$\leq$ 0.01) among all traits with yield, as well as 1000SW. The Pearson's correlation coefficient (r) values were all above 0.6. Yield per plant (YPP) had higher correlation value for PL and PW (0.873). The highest correlation value was observed between PHT and LAI (0.974). Thus, the results from this study showed that there was a highly significant correlation amongst all traits and yield in the F2 generations (Table 3).

4. Discussion

4.1. Evaluation of Agronomic Traits

Plant height and leaf area are very important traits in rice which have been reported to affect panicle traits, and consequently yield. This was attributed to increase in panicle traits in some rice varieties and partly due to increase in plant height and large leaf area of such rice varieties [15]. They also stated that varieties with good leaf area and increased plant height utilizes more efficiently the energy from the sun for photosynthesis, this is a good attribute for the tallest line 11 (106.5cm) and the highest LAI value line 11 (2.22). A report noted that nitrogen response and plant lodging behaviour of rice is partly determined by the height of the plant [10]. Hence, such rice varieties with increased height and large leaf area have the potential for high yield due to effective utilization of nitrogen and sunlight which would increase the rate of photosynthesis. Leaf area index is leaf area per unit ground area and is an important crop biophysical parameter. High leaf index was reported to be a good selection index for increasing grain yield of rice [8].

The effective tillers number, which is the harvestable tiller. The higher in the number of harvestable tillers the higher the yield output. One of the parental lines UPN 223 had 5 effective harvestable tillers with yield output of 3.32g/plant. Grain weight is a veritable parameter in rice, in comparison with other cereals [32] and 1000 grain- weight is significantly associated with yield components that could be exploited for higher yield. This study showed significant variations among the lines for 1000 grain- weight, which is an indication for higher grain yield. Panicle traits, which include panicle number, panicle weight, panicle length, spikelet fertility, and number of grains per panicle, are important yield components for rice and they are traits to be considered when evaluating individual varietal performance. Some of the panicle traits evaluated (Table 1) showed significant variations among the lines. Reports noted that grain yield in rice is a function of many panicle traits also, panicle traits affect the total grain yield of rice and are often used as an index to assess the performance of any particular rice varieties [9, 22]. It was reported that an increase in grain yield could be effectively achieved through yield component improvement since yield components have higher heritability than grain yield (Xiong 1992). Three lines were observed to be transgressive line 40, 49 and 43 with grain yield per plant of 5.75g, 5.51g and 5.09g, respectively compared with parental lines FARO 52 (2.51g) and UPN 223 (3.32g), which can advance to the next generation of the breeding cycle.

4.2. Genetic Variances

The presence of high genetic variability in the breeding materials is believed to give better chances for developing desirable plant variety [12]. This study showed that considerable genetic variation exists among the lines, which might be because of the differences in the genetic composition of the parental lines. Such variations are beneficial to breeders for selecting better parental materials in a breeding programme. Similar results have been reported in some rice genotypes and in 17 recombinant rice inbred lines and in some Korea rice germplasm [26, 16, 17]. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values are very useful in crop improvement through selection [32, 28]. These parameters are used for comparing the relative amount of phenotypic and genotypic variation observed in different characters. The study showed reasonable level of high PCV and GCV for all the traits measured, similar results were also reported in rice [33, 16]. However, the small differences between the GCV and PCV observed in this study indicates that there is little environmental influence in the expression of these traits. Therefore, selection based on the phenotypic expression of the traits could be effective.

The concept of heritability estimates in genetic study of quantitative characters is its predictive role to indicate the dependability of the phenotypic value as a guide to breeding value [10, 2] In this study, high heritability estimates were observed in most of the traits, which indicates additive gene action. Similar results were observed and noted high heritability (above 60%) for number of productive tillers per plant, panicle weight, number of grains per plant and 1000 grain weight [19]. However, traits like 1000 seed weight and grain yield per plant showed low heritability estimates, which is likely to be affected by environment hence, lower the effectiveness for their selection, similar reports [4].

High heritability estimates coupled with high genetic advancement for traits provide confidence for selection of desirable genotypes [3], The traits observed in this study showed higher heritability estimates and genetic advancement, which could give confidence for effective selection of genotypes. In related development, high values of genetic advance as percentage of mean (GAM) are indicative of additive gene effect whereas low values are indicative of non-additive gene effect [23], therefore, most of the traits observed in this study showed additive gen effects.

4.3. Correlation Coefficient Between Yield and Yield Related Traits

Selection based on the detailed understanding of magnitude and direction of association between yield and its related traits is very important in identifying the major traits, which can be exploited for crop improvement through suitable breeding programme. In this study, data analysis between yield and yield related traits showed high significant association (P≤ 0.01) among all measured traits with grain yield per plant. Similar reports stated that highly heritable characters showing high correlations with single plant yield might be used as an indirect selection for yield in early generations as observed in this study for plant height, effective tiller and panicle length [18]. Tillering ability plays an important role in determining rice grain yield as it is closely correlated with the yield components measured in this study. Corroborative reports showed that that 1000-grain weight were highly associated with rice grain yield and grain

yield significantly correlated with component traits like the number of productive tillers and the number of filled grains per panicle [6, 5, 30].

5. Conclusion

The results from this study revealed that a highly significant association amongst all traits measured with grain yield per plant in this early generation, which could be used as an indirect selection for grain yield. Among the progenies, line 11 had the highest value for plant height and leave area index 106.5cm and 2.22, respectively. This study showed that considerable genetic variation exists among the lines. The study showed reasonable high PCV and GCV for all the traits measured. High heritability estimates observed in most of the traits observed in this study indicates additive gene action. The traits observed in this study showed higher heritability and genetic advancement. In this study, data analysis between yield and yield related traits showed high significant association (P≤ 0.01) among all measured traits with grain yield per plant.

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