



HERITABILITY AND CHARACTER CORRELATION AMONG SOME RICE GENOTYPES FOR YIELD AND YIELD COMPONENTS

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ABSTRACT

Morphological characterization of 15 rice breeding lines using 15 agronomic traits was done in field experiment in a Randomized Complete Block Design in the Research farm of the National Cereals Research Institute Sub – station at Amakama for two years. The aims were to determine the extent of variability existing among rice lines, the relationship existing between yield and other traits so as to identify few traits that could serve as good yield components to improve rice yield and the heritability of the traits for effective utilization of rice lines for breeding purposes. Correlation coefficient and estimates of broadsense heritability of the 15 characters associated with grain yield for the combined data showed wide significant genetic variability ($p < 0.0001$) amongst the genotypes. Of all the characters evaluated, only number of grains per plant had the highest and significant correlation with grain yield ($r = 0.7643$). Days to booting and days to 50% heading had negative but high correlation. All the characters evaluated showed high heritability estimates ranging from 93 – 99.8764. The use of forward selection multiple regression analysis revealed number of grains per plant, weight of roots and days to 50% heading as the most important yield component traits that could be used to improve rice yield. The study showed that number of grains per plant can be used as the most reliable selection index for yield improvement in rice since it is the most contributing attribute to yield.

Keywords: Correlation coefficient, Heritability, Yield – related traits, rice, yield improvement.

INTRODUCTION

Rice (*Oryzasativa* L) constitutes a principal source of calories in Africa. It is a staple food in Nigeria, Coted’Ivoire, Gambia, Guinea-Bissau, Liberia, Madagascar, Mauritania, Senegal, Sierra Leone among others (Maltonet *et al.*, 1998). Its adaptation as a principal staple food is increasingly spreading to other parts of Africa. Rice is no longer a luxury food but has become the cereal that constitutes a major source of calories for the urban and rural poor. However, self-sufficiency in rice production is declining as demand increases. Hence there is an urgent need to increase and improve the production of rice in Nigeria in order to meet up with high demand.

The need for expansion of rice cultivation depends not only on cultural practices but also on their inbuilt genetic variability. Hence, a successful breeding

programme will depend on the genetic diversity of a crop for achieving the goals of improving the crop and producing high yielding varieties (Padulosi, 1993). To do this, the first step is to evaluate and characterise available rice germplasm or genotypes at both morphological and molecular levels as phenotypic and genotypic diversity will reveal important traits of interest to plant breeders (Singh, 1989).

The availability of morpho-genetic variation in agronomic characters of a crop would be of considerable importance in determining the best method to improve the yield of that crop. It is necessary to have a good knowledge of those characters that have significant association with yield because the characters can be used to direct selection criteria or indices to enhance performances of varieties in a new plant population.

Attempts have been made since 1966 to develop varieties with high yield potentials. Yield per hectare is the most important consideration in rice breeding programme (Ashura, 1997), but yield is a complex

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character in inheritance and may involve several related components.

Crop improvement scientists systematically evaluate germplasm to generate breeding materials, select superior lines for upland rice improvement. Kumar *et al.* (1999) observed considerable differences for agromorphological traits studied in both early and medium maturing rice genotypes, indicating a wide variability and room for improvement through selection. Genetic variability studies are important in selection of parents for hybridization (Chaudhary and Singh, 1982) because crop improvement depends upon magnitude of genetic variability in base population (Adebisi *et al.*, 2001). Once genetic variability has been ascertained, crop improvement is possible through the use of appropriate selection method and increasing total yield would be made easier by selecting for yield components because they are more often easily inherited than total yield itself.

The dependence of grain yield on other traits has been reported for many crops (Dashora *et al.*, 1977). Rice yield is a product of number of panicles per unit area, number of spikelets per panicle, percentage of filled grains, and weight of 1000 seeds (De Datta 1981). It is, therefore, important to know the factors or traits that influence grain yield, to determine heritability and genetic advance under selection of those traits so that response to selection can be predicted.

Genetic improvement of a complex character such as yield may be accomplished through components approach of breeding that assumes strong associations of yield with a number of characters that make up the yield, seed weight, number of plots per plant and plant weight are yield-determining traits that are often selected for the improvement of yield in breeding programmes for cereals and legumes (Ojo and Dashiella, 2002). Quite often characters are correlated and knowledge of the relationships among various quantitative and qualitative characters with heritability aid to the choice of appropriate parameters to be used as selection indices.

Knowledge of interrelationship of the phenotypic traits among each other and their influence on yield as well as correlation of various traits will be of importance in selection of desirable lines to be incorporated in a breeding programme and in selecting suitable lines for subsequent release as new varieties.

A number of techniques are available for determining the extent of variability in a plant population or accessions. Genotypic and phenotypic correlation coefficients tell us the association between and among two or more characters. A significant association suggests that such characters could be improved simultaneously. However, such an improvement depends on phenotypic correlation, additive variance and heritability (Hayes *et al.*, 1955).

Correlation coefficient analysis has been used by breeders to reveal a positive relationship between yield and other traits that enhance yield in rice genotypes. Ashura (1997) obtained a positive direct effect of number of filled grains per panicles, number of panicles per plant, number of filled panicles per plant 1000-grain weight on grain yield. Hence number of filled grain per panicles, and 1000 grain weight had high heritability, estimated genetic advance and could be used as selection criteria in early generation of test population. Correlation studies enable the breeder to understand the major component characters on which selection can be based for genetic improvement. Various workers studied the relationships between different traits in different crops such as soybean (Adebisi *et al.*, 2001), cassava (Varma and Rai, 1993) sweet potato (Islam *et al.*, 2002) Stather *et al.*, 2003, Isegaye *et al.*, 2006, Afuape *et al.*, 2011).

Grain yield per plant has been found to correlate positively with the morphological characters in cereals, although days to 50% flowering in maize was found to be non-significant. Simple and multiple regression analysis have been used to study character association in maize (Ajayi, 1991). Single linkage analysis has also been used to produce a more informative display of the relative position of breeding lines in accessions of yam (Ariyo, 1990), Ojo *et al.* (2006) correlated yield character in maize and obtained differences in the correlated coefficient in terms of magnitude and direction. Moncada *et al.* (2001) evaluated yield among other components and observed the strongest correlation between yield and grains of rice per plant, with significant correlation also found between yield and number of panicles per plant, plant height, panicle length and 1000-grain weight.

Heritability is a critical component of the production formula for computing expected response to selection since it is based on the phenotypic variance. The

broadsenceestimate however, has some environmental component.

Many workers; Asante and Dixon, (2002) obtained heritability per replicate in all traits studied in 10 cassava genotypes to be above 50% as well as high genetic advance. Hence the genotype of these traits can be passed on to their progenies.

Ariyo(1995) stated that phenotypic variability and the heritability of character determine to a large extent the rate of genetic advance. The presence of non- additive effects could lower the expected progress from selection among early segregating generations, and this lower the gain anticipated from continued breeding (Gupta *et al*, (1993).

Kumar *et al* (1999) obtained a considerable higher phenotypic coefficient of variation than the genotypic coefficient of variation in both early-and medium duration rice genotypes. Furthermore, heritability estimate as well as high genetic advance was obtained for 50% heading, plant height, 1000 – seeds weight and number of tillers m². Seed yield had high h₂, and high expected genetic advance indicating a predominance of additive gene effect.

Most yield attributes in rice are usually significant and positive when correlated with rice yield. This gives rise to the need to identify few traits that have the highest influence on yield that could be used in rice yield improvement among the cultivars.

Forward selection multiple regression analysis has been used to analyse yield on other traits. This model identifies which trait that came into the model and left the model significant (p<0.05) after regression with the dependent trait (yield), starting from the most important trait, and followed by progressing addition of new trait in an interactive manner as an important yield component. Afuape *et al.*, (2011) also used forward selection multiple regression to select yield attribute that most contributed to yield of potato and weight of marketable roots, unmarketable works, weight and total root number were significant and most contributing trait to yield of cassava.

Therefore, the objective of this work is to evaluate 15 rice genotypes with the view of selecting those that have better yield attributes for incorporation into hybridization programme. Therefore, an understanding of the gene action associated with the expression of yield related traits will facilitate the exploitation of the component approach in the improvement of rice.

MATERIALS AND METHODS

Field experiment was conducted at the National Cereals Research Institute Sub – station, Amakama, Umuahia.

Two experiments were carried out over a period of two years (2007 – 2008).Umuahia is in the tropical rain forest zone with 7 months of rainfall. Rainfall distribution pattern is bimodal with the peaks in July and September. The total annual rainfall is about 2000mm. (Abia State Map Sheet, 1991). It lies within latitude 5.32°N and Longitude 7.30°E. Loam soil predominates in Amakama (Ofomata, 1975).

The experiment was laid out in Randomized Complete Block Design (RCBD) with three replicates. Land preparation for the planting of seeds involved slashing of the bush, ploughing and harrowing. The seeds were planted at the rate of 2 seeds per hole at a depth of 5cm, with an inter and intra – row spacing of 20 X 20cm.The plot size was 3 X 4m².

Application of pre – emergence herbicide was carried out. Weeding was carried out manually at 4 weeks after planting (WAP) and at the booting stage. There was basal application of NPK 15:15:15: fertilizer which was broadcast immediately after planting at the rate of 30:30:30kg/ha. After the first weeding, the balance of it was applied in form of urea fertilizer at the rate of 30kg/ha as top dressing.

Fifteen genotypes from National Cereals Research Institute Badeggi, Niger State were evaluated. These genotypes are FARO 46, WAB 1079-B-87AB.2, FARO 40, FARO 48, WAB 515-151-4-443915-B342-1, WAB 56-57, WAB 450-B-P-135-HB, NERICA16, WAB 706-19-K5-14, FARO 39, FARO 38, WAB 706-59-K2-KB, WAB 788-56-1-2-HB, WAB 78-1-14-7-HB and WAB 570-35-53.

Morphological data were collected for 15 quantitative characters at appropriate growth stage of rice plant following the description for rice (IRRI, 1980). Data were collected on the following attributes - Weight of plant, Total number of Tillers per m², Number of productive tillers, Plant height at maturity, Days to booting, Days to 50% heading, Number of grains per plant, Grain yield (T/ha), Number of panicles per meter square, 1000 –seed weight, Grain yield /per hectare, Weight Of root, Weight Of shoot, Yield index, Yield per plant, number of unproductive tillers per m².

Phenotypic, Genotypic and environmental variances were done using the formula of Uguru, I. M. (2005) from modification of Asante and Dixon (2002). Heritability estimates were done according to Burton and Devane

(1953). Correlation and regression analyses were done using ProcCorr and ProcReg of SAS (1992).

RESULTS

Variance component analyses: In order to compare the performances of the genotypes in different years and determine the effect and interactions of the genotypes and year, analyses of combined data for the years were

carried out. Analysis of variance of combined data showed very high significant differences ($p < 0.001$) between rice genotypes for all the attributes assessed (table 1). Overall differences between years were significant for all the attributes studied ($p < 0.001$). The mean separation for year is shown in Table (2).

Table 1: Analysis of variance for different components of rice yield.

Source of variation	d.f	Bootling stage	Days to 50% heading	Total no. of tillers	productive tillers	unproductive tillers	Plant height	Plant weight	Shoot weight	Rot Weight	Panicle weight	No. of grains	1000 seed weight	Yield per plant	Yield (tha ⁻¹)	Yield index
Residual	58	4.6	3.3	350.0	294.2	483.5	19.1	57.5	55.6	4.98	16.6	962.0	3.23	10.8	0.62	0.008**
Genotype/Year	14	698.1***	562.21	15562.2**	8738.3***	6616.1***	313.4**	1092.6**	830.6**	428.98**	2210.3**	97148.0**	183.987**	1152.6**	0.35**	0.188**
Year	1	45.5**	677.88	1130.7**	12721.1***	21436.9***	1999.4**	4737.9**	6183.5**	96.1**	26763.4**	49749.5**	1832.511**	16537.8**	0.65**	4.10**
Genotype	14	3749.18***	2581.5**	16322.7**	10296.0***	7254.3***	606.2**	25546.6**	12300.5**	2973.98**	6142.0**	169227.4**	300.495**	6197.97	6.41**	0.36**

** , *** significant at 1% and <1% levels of probability.

Table 2: Mean separation of combined data for years 1 and 2.

Attributes	Means		LSD (0.05)
	Year 1	Year 2	
Bootling Stage	77.80	79.22	0.908**
50% heading	84.89	79.40	0.771***
Total No. of Tillers	250.7	251	7.89NS
No. of Prod. Tillers	128.8	105.0	7.24***
No. of Unprod. Tillers	121.9	152.8	9.28***
Height	92.31	101.74	1.845***
Weight of plant	168.49	153.98	3.201***
Weight of shoot	110.49	93.91	3.147***
Weight of roots	58.00	60.07	0.941***
Weight of panicles	51.64	86.13	1.717***
No. of Grains	297.40	344.4	13.09***
Wt. of 1000 seeds	34.89	43.91	0.758***
Yield per plant	37.71	64.82	1.386***
Yield (t/ha)	1.892	2.063	0.1049***
Yield index	0.3250	0.7518	0.03782***

Rice yield per plant and other yield attributes were highly significant in both years, days to booting, 50% heading, number of productive tillers, weight of plants, and weight of shoot were enhanced in 2007 when compared with their performance in 2008, conversely, plant height, weight of panicles, number of grains per plant, 1000 – seed weight, yield per plant, as well as yield per ha were enhanced in 2008. The genotypes performed differently in the two years for all attributes studied giving highly significant interactions $p < 0.0001$ for all attributes except total number of tillers ($p > 0.05$).

Heritability Estimates: Estimates of genotypic, phenotypic and environmental variances for all attributes based on the combined data are shown in Table (3). The genotypic variance was higher than the environmental variance in all the traits studied except total number of tillers, number of productive tillers, and number of unproductive tillers. Estimates of the phenotypic and genotypic coefficient of variability and the difference between them are shown in Table (4). The highest PCV and GCV estimates obtained were for number of rice grains per plants.

Table 3: Estimates of phenotypic, genotypic and environmental variances for different attributes based on the combined data of two years.

Attributes	Phenotypic variance	Genotypic variance	Environmental variance
Booting stage	1249.726	1248.184	1.541667
50% heading	860.5147	859.402	1.112667
Total no. Of tillers	5440.9	5324.233	116.6667
No. Of prod. Tillers	3432	3333.933	98.06667
No. Of unpd. Tillers	2418.1	2256.933	161.1667
Height	202.0733	195.7033	6.37
Weight of plant	8515.537	8496.363	19.17333
Weight of shoot	4100.16	4081.617	18.54333
Weight of root	991.327	989.6687	1.658333
Weight of panicle	2047.347	2041.83	5.516667
No. Of grains	56409.13	56088.47	320.6667
Wt. Of 1000 seeds	100.165	99.08867	1.076333
Yield per plant	2065.99	2062.397	3.593333
YIELD (t/ha)	2.13792	2.11734	0.02058
Yield index	0.120545	0.117867	0.002678

Table 4: Estimates of phenotypic and genotypic coefficients of variability, heritability and expected genetic advance from the means of rice attributes combined over two years.

Attributes	Phenotypic coefficient of variability (PCV)	Genotypic coefficient of variability (GCV)	PCV – GCV	Broadsense heritability (%)	Genetic advance
Booting stage	45.02798	45.00019	0.027782	99.87664	92.58604
50% heading	35.71284	35.68975	0.023096	99.8707	73.42582
Total no. Of tillers	29.00608	28.69341	0.312667	97.85575	57.84099
No. Of prod. Tillers	50.11401	49.39283	0.721173	97.14258	98.84183
No. Of unpd. Tillers	35.78907	34.57583	1.213237	93.33499	66.47898
Height	14.65188	14.41909	0.232786	96.84768	28.76698
Weight of plant	57.2348	57.17033	0.06447	99.77484	117.5057
Weight of shoot	62.6541	62.51226	0.14184	99.54774	128.1929
Weight of root	53.33787	53.29324	0.044632	99.83272	109.6004
Weight of panicle	65.68096	65.59241	0.08855	99.73055	134.7563
No. Of grains	74.01249	73.80182	0.210668	99.43153	151.1675
Wt. Of 1000 seeds	25.40164	25.26479	0.136847	98.92544	51.48622
Yield per plant	88.6545	88.57737	0.077131	99.82607	182.152
YIELD (t/ha)	73.92127	73.56462	0.35665	99.03738	150.0843
Yield index	64.48652	63.76628	0.720244	97.77869	128.4407

Estimates of heritability and expected genetic advances as percentages of the general mean are also shown in Table (4). Heritability was low for total number of tillers, number of productive and unproductive tillers, while heritability estimate was highest for days to booting (99.10%),

followed by 50% heading (99.02%).

Interrelationship between attributes and yield in combined analysis: The simple correlation coefficient between attributes studied for the combined data is shown in table (5). Rice yield per plant was positively associated with weight of

plants (r=0.3552 p<0.001), weight of shoot (r=0.3308 p<0.001), weight of roots (r=0.3368 p<0.001), weight of panicle (r=0.5898 p<0.0001), number of grains per plant (r=0.7643 p<0.0001) yield per plant (r=0.6924 p<0.0001) and 1000seed weight (r=0.2263 p<0.05).

Table 5: Simple Correlation Matrix between rice attributes based on combined data.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1		0.9562 ***	0.0550 NS	-0.283 *	0.3806 **	0.3858 **	-0.224 *	-0.237 *	-0.155 NS	-0.434 ***	-0.689 ***	-0.224 *	-0.551 ***	-0.651 ***	-0.379 **
2			0.1135 NS	-0.175 NS	0.3442 **	0.2953 **	-0.137 NS	-0.136 NS	-0.113 NS	-0.450 ***	-0.619 ***	-0.300 *	-0.558 ***	-0.635 ***	-0.488 **
3				0.689 ***	0.6214 ***	-0.414 ***	0.0841 NS	0.0437 NS	0.1493 NS	0.0234 NS	-0.074 NS	0.4376 ***	0.0730 NS	-0.041 NS	0.0302 NS
4					-0.140 NS	-0.568 ***	0.2347 *	0.2724 **	0.1144 NS	0.2067 *	0.1478 NS	0.275 **	0.2840 *	0.1440 NS	0.0441 NS
5						0.0489 NS	-0.139 NS	-0.235 *	0.0803 NS	-0.191 NS	-0.261 **	0.3002 **	-0.207 *	-0.212 *	-0.006 NS
6							-0.107 NS	-0.197 NS	0.094 NS	-0.231 *	0.4170 ***	-0.102 NS	-0.304 **	-0.323 **	-0.123 NS
7								0.9610 ***	0.8711 ***	0.5079 ***	0.0670 NS	0.2668 *	0.4339 ***	0.3552 **	-0.219 *
8									0.7244 ***	0.5222 ***	0.1146 NS	0.1972 NS	0.4570 ***	0.3308 **	-0.211 *
9										-0.383 **	-0.041 NS	0.3558 **	0.3050 *	0.3368 **	-0.176 NS
10											0.5365 ***	0.3601 **	0.8431 ***	0.5898 ***	0.5401 ***
11												0.0434 NS	0.6198 ***	0.7643 ***	0.5405 ***
12													0.3642 **	0.2263 *	0.3597 **
13														0.6924 ***	0.6946 ***
14															0.4676 ***
15															

1= Booting Stage, 2= Days to 50% Heading, 3= Total Number of Tillers, 4= Number of Productive Tillers, 5= Number of Unproductive Tillers, 6= Height, 7= Weight Of Plant, 8= Weight of Shoot, 9= Weight of Root, 10 = Weight of Panicle, 11= Number of Grains, 12 = 1000 – seeds weight, 13= Yield per plant, 14= Yield in t/ha, 15= Yield Index.

There was also significant relationship between the attributes contributing to yield; weight of plant was positively correlated with number of productive tillers ($r=0.2347$ $p<0.05$), but negatively correlated to days to booting ($r=-0.2235$ $p<0.05$), weight of shoot showed a high and significant correlation with the weight of plant ($r=0.9696$ $p<0.0001$) and number of productive tillers ($r=0.2724$ $p<0.001$), but showed negative but significant correlation with days to booting ($r=-0.2366$ $p<0.05$) and number of unproductive tillers ($r=-0.2348$, $p<0.05$). Weight of panicle correlated positively with weight of plant ($r=0.5079$, $p<0.001$), weight of shoot ($r=-0.5222$, $p<0.0001$) and weight of roots ($r=0.3825$, $p<0.001$) but correlated negatively with days to booting ($r=-0.4344$, $p<0.0001$) and days to 50% heading ($r=-0.4498$, $p<0.001$); number of grains showed a high positive significant correlation with weight of panicle ($r=0.5365$ $p<0.0001$) and plant height ($r=-0.4170$ $p<0.0001$), but was negatively correlated with days to booting ($r=-0.6388$ $p<0.0001$), days to 50% heading ($r=-0.6192$ $p<0.0001$) and number of unproductive tillers ($r=-0.2609$ $p<0.001$).

Simple regression coefficient analysis between yield and other attributes are shown in table (6), while the equation for the regression line are shown in table (7).

Table 6: Simple Regression Coefficients between grain yield and other rice attributes based on the combined data across the two years.

Attributes	Simple Regression Coefficients
Booting stage	-0.02591***
50% heading	-0.02982***
Ttl. No. of tillers	-0.0059625*
No. of prod. Tillers	-0.00450*
No. of unprod. Tillers	0.00363NS
Height	0.-02539**
Wt. Of plant	0.00573**
Wt. Of shoot	0.00748**
Wt. Of root	0.01530**
Wt. Of panicle	0.01542**
No. Of grains	0.00470***
Wt. Of 1000 seeds	0.02381*
Yield/plant	0.01989***
Yield index	1.32938***

The regression coefficient of yield on weight of plant, weight of shoot, weight of roots, weight of panicle, number of grains per plant, yield per plant and yield

index were highly significant and positive ($P<0.0001$), however, regression coefficient between yield and days to booting and days to 50% heading were negative but significant while number of unproductive tillers were non-significant ($P>0.05$). Number of grains per plant had high coefficient of determination ($R^2 = 58\%$) and yield per plant ($R^2= 47\%$) indicating the major contribution of these attributes to yield (table 8).

Table 7: Regression line equations, for the regression between yield and other attributes based on combined data from two years.

Attributes	Simple Regression Coefficients
Booting stage	4.01203-0.02591X
50% heading	4.42720-0.02982X
Ttl. No. of tillers	2.12923-0.00059625X
No. of prod. Tillers	1.67015+0.00263X
No. of unprod. Tillers	2.55273-0.00419X
Height	4.44089+-0.02539X
Wt. Of plant	1.05434+0.00573X
Wt. Of shoot	1.21267+0.00748X
Wt. Of root	1.07470+0.01530X
Wt. Of panicle	0.91538+0.01542X
No. Of grains	0.00470+0.46853X
Wt. Of 1000 seeds	0.13948+0.02381X
Yield/plant	0.95786+0.01989X
Yield index	1.26190+1.32938X

Table 8: coefficient of determination (r^2), adjusted r^2 and standard error of the estimate for the regression of yield on other attributes.

Attributes	r^2	Adjusted r^2	S.E
Booting stage	0.4241	0.4175	0.00322
50% heading	0.4029	0.3961	0.0087
Total No. of tillers	0.0017	-0.0096	0.00154
Productive Tillers	0.0207	0.0096	0.001930
Unproductive Tillers	0.0447	0.341	0.00206
Height	0.1040	0.0938	-0.02539
Wt. Of plant	0.1262	0.1163	0.00573
Wt. Of shoot	0.1094	0.993	0.00228
Wt. Of root	0.1134	0.1033	0.00456
Wt. Of panicle	0.3479	0.3404	0.00225
No. Of grains	0.5841	0.5794	0.00042301
Wt. Of 1000 seeds	0.512	0.0404	0.01092
Yield/plant	0.4794	0.4735	0.00221
Yield index	0.2186	0.2098	0.26790

S.E = Standard Error.

Table 9: Forward selection multiple regression analysis between total grain yield and other traits were significant ($p < 0.05$) traits in the multiple regression model.

Variable entered	Number of variable	Partial R ²	Model R ²	F value	Pr>F
No. of grains per plant	1	0.5841	0.5841	123.58	<0.0001
Weight of root	2	0.1359	0.7200	42.23	<0.0001
50% heading	3	0.0203	0.7403	6.74	0.0111

DISCUSSION

The genotypes exhibited significant variability ($p < 0.001$) for most traits assessed in year 1, year 2 and combined data. These traits assessed included days to booting, days to 50% heading, total number of tillers, number of productive tillers, number of unproductive tillers, plant height, weight of plant, weight of shoot, weight of root, weight of panicles/ plant, 1000- seed weight, yield per plant, yield /ha and yield index. Various authors Padulosi(1993); Kumar *et al.*(1999); Da Shora *et al.*,(1977) had previously reported wide variation amongst rice genotypes for different traits.

The dependence of grain yield on other traits have, been reported for many crops (Chandhana - Mutta , 1993). In this study grain yield was also positively correlated with all the characters except days to booting and days to 50% heading and unproductive tiller number. However, the negative association between yield and number of unproductive tillers though non-significant was expected since, number of productive tillers had a high positive significant correlation with grain yield.

This negative correlation corroborates the findings of Moncada *et al.* (2001) who also obtained a negative correlation between yield and percentage sterility of rice genotype.

Also negative correlation between yield and days to 50% heading was obtained. Similar result was obtained by (Moncada *et al.*, 2001). This can be explained by the fact that drought differently affected the late maturing genotypes, depressing yields, while early maturing lines escaped the most serious effect of drought. The breeder must however pay attention to negative correlation that exist between grain yield and those attributes that showed negative correlation. Thus, in order to increase yield, it is important to reduce spikelet sterility or increase spikelet fertility. The highest correlation coefficient with grain yield was recorded for the number of grains per plant ($r = 0.7643$) indicating the importance of this component in rice yield. In addition, significant positive correlation obtained between yield and weight of panicles ($r = 0.5898$) was consistent with the result of

Sarathet *al.* (1969) who obtained a positive and significant correlation between rice yield and number of panicles per plant. The findings indicated that plants with heavy panicles tend to have high number of fertile grains thereby increasing rice yield. The positive correlation that was obtained between number of grains and weight of panicles ($r = 0.5365$) implies that increasing the weight of panicle would also effectively increase the number of grains per plant and thus increase grain yield. A significant correlation of traits showed that these traits could be improved simultaneously. The results obtained also showed that differences in correlation coefficient between grain yield and yield characters existed amongst the rice genotypes studied. This is in agreement with the finding of Ojo *et al.* (2006) in maize grain, while the negative correlation between yield and days to 50% heading as well as booting stage and number of unproductive tillers suggest that the breeder should make selection compromises if simultaneous selection for these traits is performed in order to increase yield.

This study showed a high positive effect of agromorphological characters on rice yield. And this agrees with the findings of Ashura (1997) who obtained a positive effect of agromorphological characters on rice yield, although the negative correlation between grain weight and number of filled grains per plant as obtained by Ashura (1977) was at variance with the findings of this work.

However, in this study plant height correlated negatively ($r = -0.3225$ $p < 0.0001$) with grain yield. This result was at variance with the work of Ojo *et al.* (2006) who obtained a positive correlation coefficient between plant height and gain weight. Significant variability amongst the rice genotypes studied for yield component characters as well as highly significant differences over years for all traits studied were obtained. Varma and Mathura (1993) also obtained highly significant differences over years amongst cassava cultivars for the yield component characters. Significant genotypes and year interaction as obtained in this study showed that there was variations

in environmental conditions such as soil types fertility levels, light, temperature and moisture regime, field management practices which allowed for different results to be obtained using morphological grouping (Morakinjo and Ajibade, 1998; Singh and Racline, 1985). Furthermore, a high and significant coefficient of regression on weight of plant, weight of shoot, weight of roots, weight of panicles, yield per plant, number of grains per plant and yield index ($p < 0.001$) was obtained when these traits were regressed against yield.

Estimates of genetic variability within the germplasm was quantified by the broadsense heritability estimates among other genetic parameters. The study showed that high heritability estimates in all the traits studied and high genetic advance were obtained except for plant height. Estimates of genetic variance and heritability are of great importance in breeding programs. In this study relatively higher phenotypic coefficient of variation than the genotypic coefficient of variation was obtained in all the characters studied. This corroborates with the findings of Kumar *et al.* (1999) in both early and medium duration rice genotypes.

Furthermore, high heritability estimates as well as high genetic advance was obtained for all the traits studied ranging between 93 - 99.8% although low genetic advance was obtained for plant height. Similar result was obtained by Kumar *et al.* (1999), indicating a predominance of additive gene effect. High genetic variation in the germplasm studied is a strong indication of significant genetic variability and low environmental variance showing preponderance of additive gene effect in the inheritance of these characters and these traits can be passed on to the progenies (Asante and Dixon 2002).

High heritability estimates were obtained in all the traits studied as has been previously reported by Kaul and Kumar, 1982. The findings showed that these traits with high heritability is mostly controlled by additive gene effect and response to selection can be predicted, while those traits with low heritability estimate are under the control of environment and not heritable.

Forward Selection Multiple Regression Analysis:

Most yield attributes in rice are usually significant and positive when correlated with rice yield. This gives rise to the need to identify few traits that have highest influence on yield that could be used in rice improvement amongst genotypes. Hence, forward selection multiple regression analyses were used to

identify such traits. The traits contributing most to yield were number of grains/plant ($R^2=58\%$ $p < 0.0001$), weight of roots ($R^2=72\%$) and 50% heading ($R^2=74\%$ $p < 0.05$). Afua *et al.* (2011) also used forward selection multiple regression analysis to identify Weight of marketable roots, root weight, total root number as the most contributing trait to yield of cassava. Hence for every 12m² of rice field using the cultivars at the experimental contribution, yield per plant added $Y = 0.95786 + 0.1989X_1 + X_2$ where X_1 = rice weight, X_2 = total rice yield (t/ha).

CONCLUSION

The study showed that rice yield is a complex character and involved several related components that contributed to yield. A significant correlation of traits as obtained in this work showed that these characters could be improved simultaneously. High heritability of some traits indicated that these characters could be improved and that grain yield could depend on other traits. The phenotypic variability and high heritability of the traits studied is manifested in high genetic advance in the traits exhibited in the germplasm. Therefore, the breeding value is important as high genetic gain is an index of high economic value. High heritability indicated a preponderance of additive gene effect and could be transferred to the progeny in F₁ hybrids.

Both morphological and genetic variation existed between the 15 rice genotypes that were evaluated. Genetic coefficient of variation contributed to a greater proportion of variation that existed amongst the rice genotypes. Yield improvement of these rice genotypes will be accomplished through component approach of breeding that have strong association of yield with a number of characters that make up the yield.

Forward regression analysis however revealed that 50% heading contributed significantly to rice yield. High heritability estimates and high expected genetic advance could be used as selection criteria in early generation of test population. The breeder must however pay attention to the negative correlation that existed amongst the characters.

The study showed genetic variability amongst the genotypes and this is important in selection of parent for hybridization. Since crop improvement depends upon magnitude of genetic variability in base population. Therefore, an understanding of the gene action associated with the expression of yield related traits will facilitate the exploitation of the component approach in

the improvement of rice. Thus, the various analysis carried out had shown wide variability among the 15 genotypes for the 15 traits, the extent of heritability (broad sense) of the traits and the different forms of association existing among different traits. The wide range of variability observed for the characters evaluated may be attributed to diverse genetic background of the line varieties studied and these could be used for selection of the genotypes for crosses.

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