

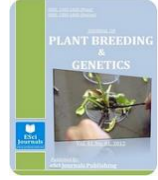


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### ASSESSMENT OF GENETIC PARAMETERS FOR YIELD AND YIELD RELATED-TRAITS IN AN INTRASPECIFIC RICE (*ORYZA SATIVA* L.) POPULATION

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#### ABSTRACT

Rice production in Africa is very far from reaching the required growth rate for various reasons. Breeding and improved yield potential in rice are perceived as an important option to ensure food security in Africa. A rice recombinant inbred line population was evaluated in the field for an estimation of genetic parameters of grain yield and its related-traits. We found that environment had little influence on the expression of days to 50% flowering, plant height, thousand kernel weight and a number of grains per panicle. These traits had high to medium broad sense heritability indicating a good scope of selection. Of all traits, the only number of grains per panicle had the highest genetic advance as percent of the mean, suggesting both additive and non-additive gene action on this trait expression. We also found that grain yield showed significant positive phenotypic and genetic correlation with a date to 50% flowering, plant height and number of panicles, indicating that these traits could be used as target traits for selection to improve grain yield in rice.

**Keywords:** Coefficient, Correlation, Cotonou, Genetic advance, Grain yield, Heritability, Longorola, Yield-related traits.

#### INTRODUCTION

Rice is the second most widely cultivated cereal in the world after wheat but feeds more people than any other crop (Maclean *et al.*, 2002). In Africa, rice is a staple food for millions of people and constitutes a major part of the diet in the region (Atera *et al.*, 2011; Maclean *et al.*, 2013). The overall rice grain yield in the region has increased from 2.3 t ha<sup>-1</sup> in 2004 to 2.7 M t ha<sup>-1</sup> in 2013, which is still very low compared with the average production reported in Asia (4.6 t ha<sup>-1</sup>), South America (5.2 t ha<sup>-1</sup>) and North America (8.5 t ha<sup>-1</sup>) (FAO, 2016). Between 2013 and 2014, the average rice production in Benin and Mali showed an erratic pattern, probably due to unreliability rainfall, limitation on the availability of water for irrigation and/or low fertilizer input. During this period, the average rice yield in Benin and Mali varied from 2.6 to 3.1 and from 1.6 to 3.2 t ha<sup>-1</sup> (FAO, 2016). However, the huge need both for local consumption and export caused a major gap between

demand and supply in these countries. As a result, the countries are currently importing massive quantities of rice to meet the national demand for sustainable food security. Self-sufficiency in the countries may be achieved either by making more agricultural land available for rice cultivation or increasing rice yield per unit area by growing improved varieties that are stable and high yielding with minimal input requirements.

The development of high yielding varieties requires detailed knowledge of the genetic variability presents in the germplasm of the crop, the association among yield components, inputs requirements, cultural practices. (Dutta *et al.*, 2013; Kishor *et al.*, 2008). Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm. Heritability coupled with high genetic advance would be more useful in predicting the resultant effect in the selection of the best genotypes for yield and its attributing traits. It helps in determining the influence of environment on the expression the and reliability of characters (Singh *et al.*, 2011).

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Rice grain yield is a complex trait and is positively correlated with several quantitative traits, including plant height, number of panicles, number of grains per panicle and grain weight (Mohammadi *et al.*, 2009; Sürek, and Beşer, 2005; Xing and Zhang, 2010). The number of panicles is dependent on the ability of the plant to produce tillers, while the number of grains per panicle depends on the number of spikelets and the seed setting rate of the spikelets (Xing and Zhang, 2010). Grain weight is largely determined by grain size (length, width, and thickness), and the degree of filling. Moreover, yield is highly influenced by genotype-by-environment interactions (GEI), showing large variation across years and locations (Karimizadeh *et al.*, 2013; Khush, 2001; Song and Ashikari, 2008) and also often shows low heritability, especially under drought stress (Edmeades *et al.*, 1999; Venuprasad *et al.*, 2007; Ziyomo and Bernardo, 2013). To minimize some of the issues associated with direct selection for grain yield, indirect selection for secondary traits that are easy to measure, highly heritable, and highly correlated with grain yield may be used (Babu *et al.*, 2003).

It is necessary to have a good knowledge of those traits that have a significant association with yield because they can be used either for indirect selection or in developing selection indices to improve the development of high yielding rice varieties. Moreover, knowledge of heritability is essential for selection as it indicates the extent of transmissibility of a character into future generations and the quality of the phenotype data in multilocation trials (Islam *et al.*, 2015; Sabesan *et al.*, 2009). The present study was undertaken to estimate the genetic parameters among 230 rice inbred lines, their 2 parents and 8 checks across four experiments both in Benin and Mali.

#### MATERIALS AND METHODS

**Plant material and phenotyping:** A total of 230 F<sub>5</sub> lines derived from an intraspecific cross between IR64 (a popular Filipino high-yielding *indica* variety) and Kogoni 91-1 (a Malian elite high-yielding *indica* variety) plus the two parents and 8 checks varieties (IRAT104, B6144-MR-6-0-0, BW 348-1, ITA212, Nerica-L-19, Tox 4004-43-1-2-1, WAB 638-1, WITA 4) were used in this study. For each entry, seeds were sown in a seedling bed and seedlings were transplanted to a field 21 days later, with a single plant per hill spaced at 20 x 20 cm. Transplanting was done in an alpha lattice design with two replications for two consecutive growing years

(2013-2014 and 2014-2015) at the Africa Rice research station in Cotonou (CTN2013 and CTN2014), Benin and at the Institute of Rural Economy (IER) station in Longorola (LGL2013 and LGL2014), Mali. The Cotonou field experiments were conducted from February to May 2013 and from June to September 2014. In Longorola, the field experiments were conducted from August 2013 to November 2013 and from July to October 2014. The field experiments in Cotonou were rainfed, with supplementary irrigation whenever needed, while the Longorola experiments were only rainfed. For all experiments, compound fertilizer (NPK 15-15-15) was applied at the rate of 200 kg ha<sup>-1</sup> at the time of transplanting, followed by 100 kg ha<sup>-1</sup> urea (46% N) 15 days and then 30 days after transplanting. The experiments were kept weed clean by regular hand weeding and bird damage was controlled using bird scares.

**Data collection and analyses:** Data collection was done according to Standard Evaluation System for Rice (SES) (IRRI, 2002) and included days to 50% flowering (DTF), plant height (PHT), number of tillers (NT), number of panicles (NP), number of grain per panicle (NGP); thousand kernels weight (TKW), and grain yield (GY). For all traits, except DTF, TKW and GY, data were recorded from 5 randomly chosen plants per plot and their average was used to represent that plot. All panicles from each plot were harvested at physiological maturity, dried to a moisture content of about 14%, shelled and measured. The weighted plot yield was then used to estimate grain yield (GY) per hectare.

**Statistical analysis:** All traits were subjected to analysis of variance (ANOVA) to test the significance of variance sources using XLSTAT2016.05. Maximum, minimum and, Coefficient of variation (CV) were computed using the program Multi-Environment Trial Analysis with R for Windows (METAR) (Alvarado *et al.*, 2015) and the phenotypic and genotypic correlation analysis was conducted to find the relationship of different attributes by using the same program.

**Phenotypic and Genotypic Coefficient of Variation (PCV and GCV):** were calculated according to Burton (1952) as follows:

$$GCV = \frac{\sqrt{\sigma_g^2}}{X} * 100$$

$$PCV = \frac{\sqrt{\sigma_{ph}^2}}{X} * 100$$

Where:

$\sigma_g^2$  = genotypic variance

$\sigma_{ph}^2$  = phenotypic variance

X= General means of the character under study

**Broad sense Heritability:** Heritability in broad sense ( $H^2$ ) was estimated from method given by Falconer et al. (1996).

$$H^2 = \frac{\sigma^2 g}{\sigma^2 ph}$$

**Expected Genetic Advance:** It was obtained by the method given by Johnson et al. (1955).

$$GA = K\sigma H^2$$

K = Selection differential (constant) i.e. 2.06 at 5% selection intensity

**Genetic advance (as percentage of the mean):** Genetic advance was categorized as low (0–10%), moderate (10–20%), and high (>20%) by Johnson et al. 1955).

$$\overline{GA}\% = \frac{GA}{\bar{X}}$$

$\bar{X}$  = General mean of the character under study

## RESULTS

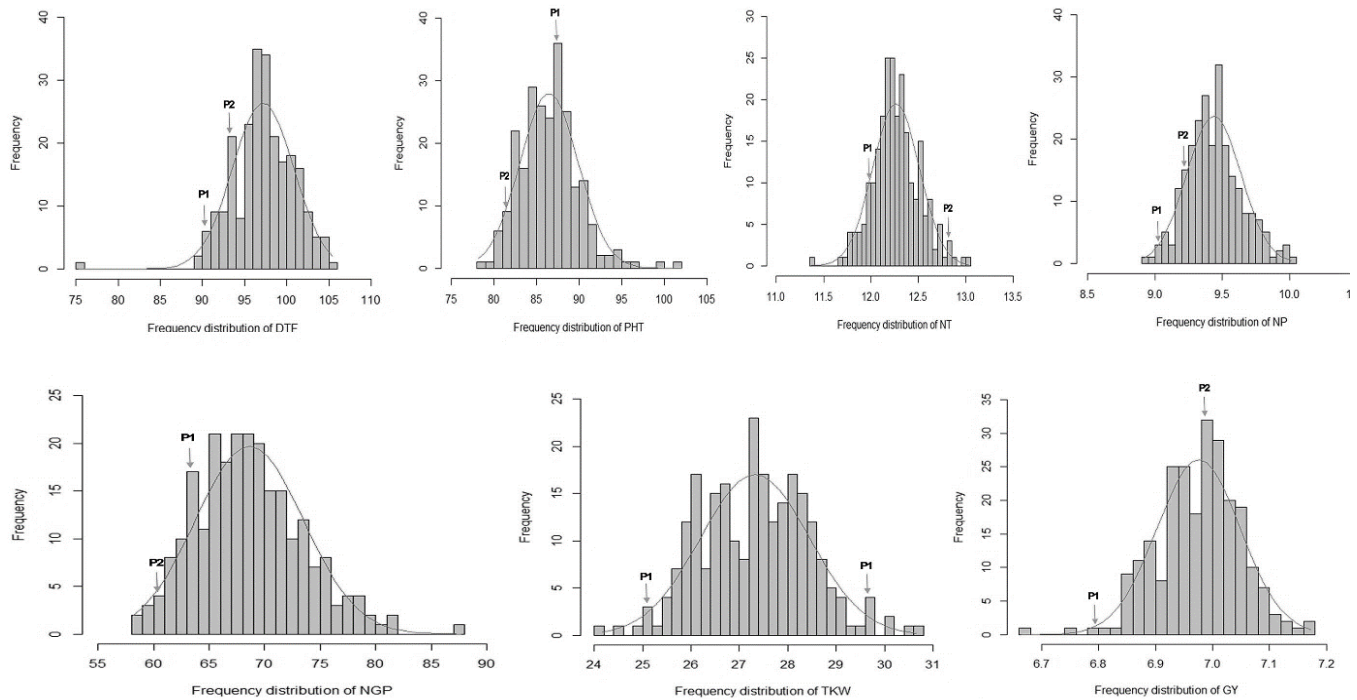
**Phenotypic variation:** The summary statistics for the 7 traits recorded on the 240 genotypes for each experiment and combined across all experiments is showed in Table 1. For all traits except plant height and grain yield, the minimum, maximum and mean values were generally comparable across all four experiments. On average, each genotype was about 86 cm tall, produced about 12 tillers and 10 panicles, and needed 97 days for flowering (Table 1). Mean grain yield across the four experiments varied from 3.3 to 10.6 t ha<sup>-1</sup> and the overall average was about 7 t ha<sup>-1</sup>. The coefficient of variation (CV) is a measure of dispersion of a frequency distribution and it varied from 7.7 to 49.1 (Table 1). Grain yield had the highest coefficient of variation (29.22), followed by number of grains per panicle (22.34), while days to 50% flowering showed the lowest (2.28). The mean phenotype data of all seven traits showed continuous variation and normal or approximately normal distribution (Figure 1).

Table 1. Summary statistics of 7 traits evaluated in 230 rice recombinants inbred lines, their 2 parents and 8 checks varieties across 4 experiments in Cotonou and Longorola locations.

Variable	Location	N	Minimum	Maximum	Mean	StDev	CV
DTF	Cotonou2013	480	74.76	101.87	92.05	3.79	3.93
	Cotonou2014	480	69.7	110.49	98.4	4.44	5.5
	Longorola2013	480	79.37	106.86	92.79	3.64	2.69
	Longorola2014	480	86.54	115.56	105.63	3.31	2.28
	Overall	1920	75.31	105.38	97.18	3.62	3.19
PHT	Cotonou2013	480	77.01	105.75	88.02	4.63	6.61
	Cotonou2014	480	81.75	116.96	94.56	4.69	5.63
	Longorola2013	480	62.27	75.67	67.13	2	6.65
	Longorola2014	480	89.65	107.46	96.13	6.75	5.95
	Overall	1920	78.22	101.96	86.45	3.42	6.02
NT	Cotonou2013	480	9.38	13.16	11.17	0.68	17.03
	Cotonou2014	480	11.18	13.7	12.12	0.43	19.57
	Longorola2013	480	13.58	16.35	15.17	0.32	12.41
	Longorola2014	480	9.41	12.05	10.59	6.75	15.89
	Overall	1920	11.36	13.02	12.26	0.24	16.18
NP	Cotonou2013	480	8.02	11.17	9.11	0.51	19.37
	Cotonou2014	480	8.65	12.47	10.23	0.54	14.38
	Longorola2013	480	11.05	11.13	11.1	0.01	15.52
	Longorola2014	480	7.89	10.29	8.97	0.71	17.36
	Overall	1920	8.91	10.01	9.43	0.2	17.03
NGP	Cotonou2013	480	47.62	69.29	56.06	3.06	18.92
	Cotonou2014	480	34.18	83.2	56.26	9.44	22.34
	Longorola2013	480	50.6	84.45	18.9	4.71	18.9
	Longorola2014	480	70.69	124.5	94.36	12.87	18.87
	Overall	1920	58.10	87.60	68.61	4.86	19.99
TKW	Cotonou2013	480	25.70	33.31	27.92	1.03	7.89
	Cotonou2014	480	27.37	35.09	30.47	1.43	3.95

	Longorola2013	480	24.89	22.39	23.59	2.17	10.01
	Longorola2014	480	23.71	27.71	27.33	2.86	3.91
	Overall	1920	24.16	30.65	27.4	1.1	6.63
GY	Cotonou2013	480	5.76	8.81	7.67	0.38	21.15
	Cotonou2014	480	8.48	12.9	10.82	0.76	14.36
	Longorola2013	480	2.75	4.24	3.38	0.33	29.22
	Longorola2014	480	5.3	7.12	6.05	0.45	25.63
	Overall	1920	6.66	7.17	6.9	0.07	21.00

DTF = days to 50% flowering; PHT = plant height; NT = number of tillers; NP = number of panicles; NGP = number of grains per panicle; TKW = thousand kernels weight; GY = grain yield (t ha-1); Stdev = Standard deviation; CV= coefficient of variation; N = number of plots in both repetitions.



P1 = parent Kogoni91; P2 = Parent IR64; DTF = days to 50% flowering; PHT = plant height; NT = number of tillers; NP = number of panicles; NGP = number of grains per panicle; TKW = thousand kernels weight; GY = grain yield (t ha-1). Figure 1. Phenotypic variation of four 7 traits evaluated in 230 rice recombinant inbred lines their 2 parents and 8 checks varieties across 4 experiments in Cotonou and Longorola Location.

**Analysis of Variance (ANOVA):** Analysis of variance performed on the combined data of the four experiments showed significant ( $P < 0.01$ ) differences among genotypes for all traits studied excepted number of tillers and grain yield. Genotypes  $\times$  locations interactions

were significant for both flowering date and number of grain per panicle, while genotype  $\times$  year interaction was significant only for days to flowering (Table 2), The three ways (genotypes  $\times$  locations  $\times$  years) interactions were significant for all traits except grain yield.

Table 2. Summary of analysis of variance of 230 rice recombinant inbred lines, their 2 parents and 8 checks varieties for 7 traits evaluated in Cotonou and Longorola across 4 experiments.

Trait	Source	DF	SS	MS	F	Pr > F
DTF	Location	1	7253.67	7253.67	488.10	< 0.0001
	Year	1	39761.22	39761.22	2675.55	< 0.0001
	Genotype	239	29706.46	124.29	8.36	< 0.0001
	Location $\times$ Genotype	238	4583.38	19.26	1.30	0.005
	Year $\times$ Genotype	239	5007.99	20.95	1.41	0.000
	Location $\times$ Year $\times$ Genotype	233	7915.85	33.97	2.29	< 0.0001

Continuing table 2

PHT	Location	1	44241.89	44241.89	741.29	< 0.0001
	Year	1	150719.90	150719.90	2525.38	< 0.0001
	Genotype	239	40035.78	167.51	2.81	< 0.0001
	Location × Genotype	239	13118.73	54.89	0.92	0.785
	Year × Genotype	239	13880.09	58.08	0.97	0.597
	Location × Year × Genotype	238	71549.89	300.63	5.04	< 0.0001
NT	Location	1	467.07	467.07	75.09	< 0.0001
	Year	1	1269.80	1269.80	204.15	< 0.0001
	Genotype	239	1870.26	7.83	1.26	0.011
	Location × Genotype	238	1659.31	6.97	1.12	0.128
	Year × Genotype	239	1445.33	6.05	0.97	0.599
	Location × Year × Genotype	233	4564.11	19.59	3.15	< 0.0001
NP	Location	1	24.64	24.64	5.49	0.019
	Year	1	100.58	100.58	22.41	< 0.0001
	Genotype	239	1240.81	5.19	1.16	0.074
	Location × Genotype	238	1252.07	5.26	1.17	0.058
	Year × Genotype	239	973.92	4.07	0.91	0.818
	Location × Year × Genotype	233	2192.73	9.41	2.10	< 0.0001
NGP	Location	1	281267.85	281267.85	1008.1	< 0.0001
	Year	1	69137.42	69137.42	247.80	< 0.0001
	Genotype	239	177173.61	741.31	2.66	< 0.0001
	Location × Genotype	238	82476.24	346.54	1.24	0.015
	Year × Genotype	239	69876.90	292.37	1.05	0.318
	Location × Year × Genotype	233	144040.98	618.20	2.22	< 0.0001
TKW	Location	1	6251.73	6251.73	1752.69	< 0.0001
	Year	1	4272.13	4272.13	1197.70	< 0.0001
	Genotype	239	4059.63	16.99	4.76	< 0.0001
	Location × Genotype	238	968.74	4.07	1.14	0.095
	Year × Genotype	239	983.30	4.11	1.15	0.078
	Location × Year × Genotype	233	1163.39	4.99	1.40	0.000
GY	Location	1	9247.05	9247.05	1805.95	< 0.0001
	Year	1	3661.54	3661.54	715.10	< 0.0001
	Genotype	239	1118.15	4.68	0.91	0.801
	Location × Genotype	238	1122.47	4.72	0.92	0.779
	Year × Genotype	239	1089.31	4.56	0.89	0.863
	Location × Year × Genotype	233	947.69	4.07	0.79	0.984

DTF = days to 50% flowering; PHT = plant height; NT = number of tillers; NP = number of panicles; NGP = number of grains per panicle; TKW = thousand kernels weight; GY = grain yield; DF = degree of freedom; MS = mean of squares; SS = sum of squares; F = Fischer test; Pr = probability.

**Repeatability:** In each experiment, repeatability varied from 0.10 to 0.84 and was highly dependent on the complexity of the trait (Table 3). The flowering date had the highest repeatability, which varied from 0.75 in Cotonou in 2013 to 0.84 in Cotonou in 2014. Thousand kernels weight showed the second highest repeatability followed by plant height and number of grains per panicle which ranged from 0.48 to 0.70 and from 0.34 to 0.64 respectively. Number of tillers and number of panicles showed the lowest repeatability, which varied from 0.10 to 0.33 (Table 3).

**Heritability:** Heritability across the combined data of the four experiments showed a similar pattern to that of

the repeatability and varied from 0.18 for grain yield to 0.91 for flowering. Heritability was highest for days to 50% flowering (0.88), thousand kernels weight (0.77), and plant height (0.76). It was moderate for number of grains per panicle (0.54) and number of tillers (0.31), while it was low for number of panicles (0.22) and grain yield (0.16) (Table 4).

**Genetic variance:** The value of coefficients of phenotypic variation (PCV) were higher than their corresponding coefficient of genotypic variation (GCV) for all trait but the difference between the values were generally low. The number of grain per panicle showed the highest value of the coefficient of variation with

14.37%. Grain yield also showed high phenotypic coefficients of variation with 10.93% followed by number of panicle and number of tiller with 9.26 and 8.17%, respectively. In the same way, the highest value of the genetic coefficient of variation was recorded for number of grains per panicle. In contrast to the phenotypic coefficient of variation, the lowest value for the genetic coefficient of variation was observed for grain yield (Table 4).

**Estimates of Expected Genetic Advance:** Table 4 shows the values of the expected genetic advance for the 7 traits. These values are also expressed as a percentage of the genotypes mean for each character. The highest value 15.38% of genetic advance as per cent of the mean was recorded only for a number of grain per panicle with a value of and was low in all other traits ranging from 2.36% in grain yield to 8.66% in thousand kernels weight.

Table 3. Repeatability per experiment of 7 traits measured in 230 rice recombinant inbred lines, their 2 parents and 8 checks varieties evaluated in Cotonou and Longorola across 4 experiments.

	Location	DTF	PHT	NT	NP	NGP	TKW	GY
Repeatability	Cotonou 2013	0.75	0.66	0.40	0.34	0.34	0.48	0.30
Repeatability	Cotonou 2014	0.80	0.70	0.23	0.41	0.64	0.79	0.50
Repeatability	Longorola 2013	0.84	0.53	0.22	0.1	0.41	0.2	0.32
Repeatability	Longorola 2014	0.82	0.48	0.33	0.32	0.53	0.82	0.30

DTF = days to 50% flowering; PHT = plant height; NT = number of tillers; NP = number of panicles; NGP = number of grains per panicle; TKW = thousand kernels weight; GY = grain yield.

Table 4. Estimates of phenotypic and genotypic coefficients of variability, heritability and expected genetic advance of 7 traits evaluated in 230 rice recombinant inbred lines, their 2 parents and 8 checks varieties across 4 experiments in Cotonou and Longorola.

Traits	$\sigma_g^2$	$\sigma_{ph}^2$	Mean	GCV	PCV	H <sup>2</sup>	GA	GA%
DTF	16.05	18.98	97.19	4.12	4.48	0.88	6.98	7.20
PHT	15.73	22.53	86.45	4.59	5.49	0.76	6.55	7.61
NT	0.23	1	12.26	3.93	8.17	0.27	0.59	5.19
NP	0.18	0.76	9.44	4.53	9.26	0.23	0.4	4.20
NGP	44.85	97.24	68.62	9.76	14.37	0.54	10.52	15.38
TKW	1.66	2.24	27.32	4.72	5.47	0.77	2.37	8.66
GY	0.05	0.58	6.98	3.23	10.93	0.11	0.16	2.36

DTF = days to 50% flowering; PHT = plant height; NT = number of tillers; NP = number of panicles; NGP = number of grains per panicle; TKW = thousand kernels weight; GY = grain yield,  $\sigma_g^2$  = genotypic variance;  $\sigma_{ph}^2$  = phenotypic variance; GA = genetic advance.

**Phenotypic and genetic correlation among traits:** The phenotypic and genetic correlation coefficients among the seven traits are presented in Table 5. The highest significant positive phenotypic correlation was observed between number of tillers and number of panicles (r = 0.81; P<0.01), followed by days to 50% flowering and grain yield (r = 0.34; P<0.01) and plant height and grain yield (r = 0.23; P<0.01). The significant phenotypic correlation was also recorded between number of grain per panicle and plant height (r = 0.23 P< 0.01) and between grain yield and number of panicle and number of grain per panicle. At the genetic level, similar patterns correlation were observed between traits but the genotypic correlation coefficients were higher than their corresponding phenotypic correlation in most of the

cases. The highest genotypic coefficient was observed between grain yield and days to 50% flowering (r = 0.99; P<0.01) and between number of tiller and number of panicle (r = 0.99; P<0.01). Grain yield was significantly correlated with all traits excepted thousand kernels weight. It was correlated positively with number of panicles (r = 0.68; P<0.01), with plant height (r = 0.45; P<0.01), number of tillers (r = 0.50; P<0.01). On the other side, it was negatively correlated with number of grain per panicle (r = -0.13; P<0.05). Negative genetic correlation was also recorded between number of grain per panicle and number of panicle (r = -0.82; P<0.01) and number of tiller (r = -0.64; P<0.01), and between plant height and number of tillers (r=-0.75; P<0.01) and number of panicles (r = -0.61; P<0.01).

Table 5. Genotypic (above diagonal) and phenotypic (below diagonal) correlations testing the relationships among 7 trait evaluated in 230 rice recombinant inbred lines, their 2 parents and 8 checks varieties across 4 experiments in Cotonou and Longorola.

Traits	DTF	PHT	NT	NP	NGP	TKW	GY
DTF	1	0.44**	0.06	0.36**	0.16**	-0.02	0.99**
PHT	0.40**	1	-0.75**	-0.61**	0.26**	0.07	0.45**
NT	0.03	-0.29**	1	0.99**	-0.82**	0.06	0.50**
NP	0.22**	-0.17**	0.81**	1	-0.64**	-0.13*	0.68**
NGP	0.07	0.23**	-0.23**	-0.140*	1	-0.61**	-0.13*
TKW	-0.01	0.11	-0.01	-0.08	-0.37**	1	-0.11
GY	0.34**	0.23**	0.07	0.17**	0.11	0.06	1

DTF = days to 50% flowering; PHT= plant height; NT = number of tillers; NP = number of panicles; NGP = number of grains per panicle; TKW = thousand kernels weight; GY = grain yield; DF = degree of freedom; MS = mean of squares; \*, \*\*level of significance at 5% and 1% probability respectively.

## DISCUSSION

In the combined data of all experiments, grain yield, number of tillers, number of panicles and thousand kernels weight showed the lowest range between the minimum and the maximum values, while it was very large for number of grains per panicles, days to 50% flowering and plant height, indicating the presence of large variability among the genotypes used in the present study for these traits. This variability is useful in selecting the best genotypes for advanced trials in multi-location environments. The experiments at Longorola were conducted under rainfed conditions and there was limited rainfall in 2013, which reduced thousand kernel weight by 14-38%, plant height by 24 -43%, and grain yield by 44-69% as compared with the other three experiments. In contrast, a number of tillers and number of panicles at the Longorola experiment in 2013 were higher by 25-30% and 9-24%, respectively, as compared with the other three experiments. Although none of our experiments was designed for drought evaluation, the data obtained at Longorola in 2013 could be considered as drought for different reasons. First, the tillering ability is an important trait to be considered during drought screening. Upon relief from the drought, some rice genotypes are able to produce more tillers, which are productive if the remaining growing season is long enough to complete grain filling (Lilley and Fukai, 1994), which was the case in our experiment conducted at Longorola in 2013. Second, drought stress experiments showing a yield reduction of 30% or less are considered mild stress, those with a reduction of 31-65% are termed moderate stress, and those with yield reduction above 65% are described to as severe stress experiments (Dixit *et al.*, 2014; Kumar *et al.*, 2008). Based on these criteria, therefore, the extent of drought

stress at Longorola in 2013 could be considered moderate to severe and provides a good indication of genotypic differences under random drought stress. Water deficit during flowering period results in poor assimilation reduced translocation of photosynthesis to the grain and higher respiratory losses (Al-Khatib and Paulsen, 1984; Shpiler and Blum, 1990) which lead to grain abortion and consequently yield reduction. Therefore, in the present study the effect of water deficit at Longorola in 2013 resulted in short plants and low grain yield, which is in agreement with other studies reported for tef (*Eragrostis tef*) (Shiferaw *et al.*, 2012; Teferra *et al.*, 2000), wheat (*Triticum spp.*) (Nouri-Ganbalani *et al.*, 2009) and rice (Ndjiondjop *et al.*, 2010). The coefficients of variation in our data seem dependent on the complexity of the traits, with relatively easy traits, such as days to flowering showing the lowest CV, while complex traits, such as grain yield and number of grains per panicle showed the highest CV. Similar results were reported in other studies which showed the higher coefficient of variation for grain yield (Kole and Hasib, 2008) and higher coefficient of variation for number of tillers (Golam *et al.*, 2011).

There was no significant difference between genotypes for number of panicles and grain yield. The 230 lines used in the present study were derived from an intraspecific cross that involved IR64 and Kogoni 91-1, both of which are popular high-yielding *indica* varieties. For grain yield, number of tillers and number of panicles, the values of the two parents were very similar (Figure 1), showing clearly the lack of genetic difference between the two parents for these traits. This could partly explain why there was no significant difference between genotypes for these traits. Some other studies have also reported a lack of significant genotypic

differences for both grain yield and number of panicles in rice (Atif and Khalid, 2013; Xu *et al.*, 2015).

The phenotypic variance is the sum of environmental variance, genetic variance and their interaction. However, the phenotypic and genotypic variance values cannot be used for comparing degrees of variability since different traits have different means across environments as noticed by Tewodros *et al.* (2013). Thus the genotypic and phenotypic coefficients of variations were used to compare variability in traits. The genotypic coefficient of variation (GCV) measures the extent of genetic variability present in a crop species and also enables quantification of the extent of variability present in different characters. The phenotypic coefficient of variation (PCV) of a character is the manifestation of genotypes, environment and interaction between the genotypes and environment. Therefore, the total variance needs to be partitioned into heritable and non-heritable components to assess the true breeding nature of that particular trait (Chakraborty and Hazarika, 1994). In the present study, it is clear that environment played an important role in the expression of some characters as the PCV was found to be higher than the corresponding GCV for all characters studied. Similar findings were reported by earlier studies (Devi *et al.*, 2006; Islam *et al.*, 2015; Prajapati *et al.*, 2011). The GCV values were close to their corresponding PCV values for all the characters except for number of tillers, number of panicles and grain yield. Indeed the PCV values for these characters were generally 3 times higher than their corresponding GCV. These greater differences between GCV and PCV showed clearly that environment played an important role in the expression of these characters. On the other hand, the narrow differences observed between GCV and PCV in days to flowering, plant height and thousand kernels weight indicates the low sensitivity of these traits to environmental effects. Moderate GCV and PCV were observed for number of grains per panicle. The findings were supported by Senapati and Kumar (2015) who also reported moderate GCV for number of grains per panicle. Days to 50% flowering, plant height, number of panicles, number of tillers, thousand kernels weight and grain yield exhibited low values of genotypic as well as the phenotypic coefficient of variation. This may be attributed to the presence of both positives and negative alleles in the population studied. A similar suggestion was given by Iftekharuddaula *et al.* (2001). Our findings

are supported by those of Akinwale *et al.* (2011) Sabesan *et al.* (2009b) and Sinha *et al.* (2004) for days to flowering and plant height and by those of Islam *et al.* (2015) for thousand kernels weight.

Heritability is a measure of the magnitude of the phenotypic variation caused by the action of genes. High heritability for quantitative traits is useful because it is the basis of selection made on phenotypic performance. Heritability is classified as low when it is <0.30, moderate when it is between 0.30 and 0.60 and high when > 0.60 (Johnson *et al.*, 1955). In the present investigation, high heritability was recorded for days to 50% flowering, plant height, thousand kernels weight, number of grains per panicle, and days to 50% flowering. This indicates that these traits were simply inherited characters controlled by additive gene effects or a few major genes, therefore selection for of these traits would be more effective for improvement. Similar results were previously reported by Karthikeyan *et al.* (2010) for days to 50% flowering and thousand kernels weight and by Sankar *et al.* (2006) and Ukaoma *et al.* (2013) for days to 50% flowering, plant height and number of grains per panicle. The expression of a quantitative trait depends on the cumulative action of many genes and their interaction with the environment, so performance only partially reflects the genetic values of the individuals (Sham *et al.*, 2002). Low heritability indicates the greater role of environment on the expression of the trait, which was the case for grain yield number of tillers and number of panicles.

Although a high heritability value shows the genetic component of phenotypic variation, it gives no indication of the level of genetic progress resulting from the choice of the best individuals. The estimate of heritability is more advantageous when expressed in terms of genetic gain (Paikhomba *et al.*, 2014). According to Johnson *et al.* (1955) calculating heritability and genetic progress together, might be more useful in predicting the effect resulting from the selection made a basic phenotypic expression. Genetic advance under selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Wolie *et al.*, 2013). In this study, high heritability along with low genetic advance as percent of the mean was observed for the days to 50% flowering, plant height, thousand kernels weight suggesting a predominance of non-additive gene action for the expressions of these



three characters. Selection could be postponed for such traits or they could be improved by intermating of superior genotypes of segregation population from recombination breeding as emphasised by Singh *et al.* (2011) and Roychowdhury and Randrianotahina (2011). These results were earlier corroborated by Sabesan *et al.* (2009b) for days to 50% flowering, Konate *et al.* (2016) for plant height and Islam *et al.* (2015) and Akhtar *et al.* (2013) for thousand kernels weights. Moderate heritability in conjunction with moderate genetic advance as percent of the mean was recorded in number of grain per panicle. This indicates the action of both additive and non-additive genes. Low heritability along with low genetic gain was recorded for number of panicles, number of grain and grain yield indicating that the dominance/epistasis effect is very important in the expression of these characters. These results are in agreement with those obtained by Fentie *et al.* (2014) for grain yield but do not agree with those of Oladosu *et al.* (2014) and Ukaoma *et al.* (2013) who reported high heritability along with high genetic advance for number of panicles.

Selection of traits contributing simultaneously to a character will improve it in subsequent segregation population (Nor Aishah *et al.*, 2014). Based on the correlation values obtained in this study, selection of plants with more tillers could indirectly be used for developing plants with a high number of panicles. Plant height showed moderate to high significant positive phenotypic correlation with flowering time, number of grains per panicle and grain yield, which suggests that high yielding and late flowering rice varieties could be developed by indirectly selecting for taller plants. However, selection for taller plants may increase lodging, which would negatively affect grain yield. On the other hand, late flowering and late maturity require availability of sufficient moisture for a long period of time, which may not be possible in areas where there is limited rain within a short period of time. Plant height exhibited a negative correlation with number of tillers and number of panicle in both phenotypic and genetic level suggesting that selection for short genotypes would result in developing varieties with a higher number of tillers and panicles. Our results from correlation analysis are supported by previous findings (Al-Tabbal and Al-Fraihat, 2011; Bai *et al.*, 1992; Fellahi *et al.*, 2013; Girish *et al.*, 2006; Ukaoma *et al.*, 2013). Although the positive and negative correlation coefficients obtained in our

study may be useful for conducting indirect positive or negative selection for developing improved rice germplasm, the outcome may not be desirable if selection would have to be made based on two or few traits. We, therefore, think that indirect selection for developing high yielding rice germplasm requires developing a selection index that combines more traits that showed moderate to high correlation, each given a different weight depending on trait heritability. In developing a selection index, more weight may be given to traits with higher heritability values and lower weight to traits with lower heritability values.

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