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GENETIC ANALYSIS OF YIELD AND YIELD COMPONENTS IN *Oryza sativa* x *Oryza sativa* CROSS

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ABSTRACT

The number one goal of most rice improvement programmes around the world is breeding for high potential to take care of the increasing consumption of rice. The objective of this experiment was to study the inheritance of yield and yield components and to estimate the heritabilities of important quantitative traits in rice (*Oryza sativa* L.). Six generations *viz*., P_1, P_2, F_1, F_2, BCP_1 and BCP_2 of a cross between IET6279 and IR70445-146-3-3 were used for the study. Generation mean analysis suggested that additive effects had a major role for the expression of plant height, number of panicles, number of spikelets per panicle, percentage spikelets fertility per plant and grain yield per plant, which further suggested that phenotypic selection was possible at an early stage. Both additive and non-additive gene actions were important for the expression of number of fertile spikelets per panicle and 100-grain weight. Therefore, selection for these characters would be fruitful, if delayed till epistasis effects are reduced to a minimum. High broad sense heritability estimates were observed for characters viz. plant height and 100-grain weight, suggesting that the characters under study are less influenced by environment in their expression. Thus, selection based on phenotypic value of these characters would be reliable and effective. Low estimates of broad sense heritability were observed for number of panicles per plant, number of spikelets per panicle, number of fertile spikelets per panicle, percentage spikelets fertility per plant and grain yield per plant, indicating that influence of the environment was high for these characters. Therefore, superior genotypes selection based on phenotypic performance for these characters may not effective.

Key Words: Additive, gene action, heritability, inheritance, non- additive, rice

RÉSUMÉ

La majorité des objectifs des programmes d'amélioration du riz dans le monde est relative à la sélection pour le désire croissant de la consommation du riz. L'objectif de cette expérimentation était d'étudier l'héritage du rendement et des composantes du rendement et d'estimer les héritabilités des traits importants sur le riz (*Oryza sativa* L.). Six générations *viz*, P_1, P_2, F_1, F_2, BCP_1 et BCP_2 du croisement entre IET6279 et IR70445-146-3-3 étaient utilisés pour cette étude. L'analyse de la moyenne des générations a suggéré que les effets additifs ont un rôle majeur pour l'expression de la taille de la plante, le nombre de panicules, le nombre d'épillets par panicule, le pourcentage de fertilité d'épillets par plant et le rendement en grain par plant qui davantage ont suggéré que la sélection phénotypique était possible à une étape précoce. Les actions de gènes de type additifs et non-additifs étaient importantes pour l'expression du nombre d'épillets fertiles par panicule et le poids de 100-grains. Toutefois, la sélection pour ces caractères serait utile ; si elle est retardée jusqu'à ce que les effets d'épistasis soit réduits au minimum. La valeur élevée de la grande héritabilité était observée pour les caractères *viz*. La taille de la plante et le poids de 100 grains, suggéraient que les caractères sous investigation sont moins influencés par l'environnement dans leur expression. Donc, la sélection basée sur les valeurs phénotypiques de ces caractères serait plus efficace. De faibles valeurs estimées de la grande héritabilité étaient observées pour le nombre panicules par plant, nombre d'épillets par panicule, nombre d'épillets fertiles par panicule, le pourcentage d'épillets fertiles par plant et le rendement en grain par plant, indiquant que l'influence de l'environnement était élevée pour ces caractères. Toutefois, la sélection supérieure des génotypes basée sur la performance phénotypique pour ces caractères pourrait être non efficiente.

Mots Clés: Action de gène, additif, héritabilité, héritage, non- additif, riz

INTRODUCTION

Rice (*Oryza sativa* L.) belongs to the family Poaceae. It is a staple food for more than half of the world's population. The world population is expected to reach 8 billion by 2030 and therefore, rice production must be increased by 50% in order to meet the growing demand (Miah *et al*., 2013). However, with an increasing world population and gradually deteriorating environment, food security has become a major challenge, especially in Asia and Africa (Sasson, 2012). In sub-Saharan Africa (SSA), rice consumption is increasing at a rate of 6% per *annum*, the highest in the world. The rate of increase in the consumption of rice in Africa has not been matched by corresponding increases in production, and the demand-supply gap is widening. To attain rice self- sufficiency and meet the future demand's, development of high yielding with other desirable agronomic traits is crucial (Mulugeta *et al*., 2012).

Many studies show that rice yield related characters (tiller number, grain number and grain weight) and agronomic character (plant height) are inherited quantitatively, related genetically to one another and influenced by changing environments (Kobayashi *et al*., 2003). Hence, rice breeders are interested in developing cultivars with improved yield and other desirable agronomic characters. Genetic variability for agronomic traits is the key component of breeding programmes, for broadening the gene pool of rice. Plant breeders commonly select for yield components, which indirectly increase yield. Heritability (h^2) of a trait is important in determining its response to selection.

Genetic improvement of plants for quantitative traits requires reliable estimates of heritability and gene action in order to plan an efficient breeding programme. Anyanwu and Obi (2014) and Tuhina *et al.* (2015) recorded high broad sense heritability for plant height and 100 grain weight per plant, respectively. On the other hand, Anyanwu and Obi (2014) recorded low broad sense heritability for 1000 seed weight (13%) and percentage fertile spikelet (29.7%), possibly because the author used different genotypes and the environmental conditions under which their study was conducted was different. Kato (1997) estimated low broad sense heritability of 16% for the number of panicles per plant and 20 to 33% for number of spikelets per panicle. Perera *et al.* (1986) suggested that genes with additive, dominant, and epistatic effects controlled both the number of tillers at maturity and the number of panicles per plant. According to Padmaja *et al.* (2008) and Liu *et al.* (2010), there is a predominance of additive gene action for number spikelet per panicle. However, Panwar and Paroda (1983) showed that grain yield is controlled by both additive and dominant gene effects.

The objectives of this study was to elucidate the gene action associated with yield and yield component attributes and estimate of heritability of quantitative traits.

MATERIALS AND METHODS

Site of experiment. The study was conducted at the CSIR- Crops Research Institute (CRI) Fumesua- Kumasi, Ghana. Two rice genotypes, namely, IET6279 and IR70445-146-3-3, were used for the study. IET6279 is high yielding, high tillering, has heavy panicles and short grains. IR70445-146-3-3 has long slender grains, low tillering ability and low yield potential (personal communication, Dr. Maxwell Asante, Crops Research Institute, Kumasi, Ghana).

A cross, IET6279 x IR70445-146-3-3 was made and the F_1 was selfed to obtain an F_2 populations. The F_1 was also backcrossed to either parent, to obtain two backcross populations (BC) —BCP_1 (backcross to IET 6279) and BCP_2 (backcross to IR70445-146-3-3). During the generation of the BC populations, new crosses between the parents were also made to generate fresh F_1 seeds. All six populations, P_1, P_2, F_1, F_2, BCP_1 and BCP_2, were planted in a rainfed lowland field (with supplementary irrigation) at CSIR-CRI, Fumesua, during the minor season (September-December) of 2014. The field layout was randomised complete block design with three replications. Each replicate had 60 plants of parents, 25 F_1s, 300 F_2, 60 BCP_1 and BCP_2 plants. Spacing was 40 cm and 20 cm between-row and within-row, respectively; at a density of a single plant per hill.

The recommended fertiliser rate of 90-60-60-kg ha^{-1}- $N-P_2O_5-K_2O$ was applied; 60-60-60 kg ha^{-1} applied two weeks after transplanting top-dressed with 30 kg ha^{-1} N at panicle initiation. Weeds were controlled by spraying with a post-emergence selective weedicide, Pronil-plus and Propanil. This was followed by hand picking. The plots were irrigated uniformly whenever necessary using rain water from a fabricated lake through canals with flood method.

Data collection. Data for all the measured traits were taken on all plants within each population. Plant height was measured from individual plants at maturity, from the base of the plant to the top of the latest spikelet on the tallest panicle, excluding the awn. Number of panicles per plant was counted from individual plants at maturity, before harvesting. Number of spikelets per panicle was counted from individual plants, after harvesting. Number of fertile spikelets per panicle was also determined by pressing the spikelets with fingers and noting those that do not have grains after harvesting. Percentage spikelets fertility was calculated from the total number of spikelets per plant divided by total number of fertile spikelet per plant multiplied by 100%.

One hundred grain weight was measured from individual plant dried to 14% moisture content, using an electronic balance. Grain yield per plant was obtained weighing grains from individual plants and finding the mean.

Data analysis. Generation mean analysis (Equation 1) was used to estimates genetic control of the seven quantitative traits according to the methodology proposed by Mather and Jinks (1971):

$$Y = m + \alpha a + \beta d + \alpha 2aa + 2\alpha\beta ad + \beta 2dd \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{Equation 1}$$

Where:

α and β are the coefficients for a and d, respectively;

Y = the observed mean;
m = mean = mean of the F_2;
a = pooled additive effects;
d = pooled dominance effects;
aa = additive x additive gene interaction effects;
ad = additive x dominance gene interaction effects; and
dd = dominance x dominance gene interaction effects;

The mode of inheritance of the seven quantitative traits was estimated by generation mean analysis, with six generations (P_1, P_2,

F_1, F_2, BCP_1 and BCP_2) of IET6279 and IR70445-146-3-3. Generation mean analysis was performed using Statistical Analysis System (Version 9.2).

Broad sense heritability (H^2_b), of seven quantitative traits of rice was estimated by the formula of Allard (1960). $H^2_b = (VF_2 - VE) / VF_2$ .... Equation 2

Where:

H^2_b = Broad sense heritability;

V E = Error variance = $(VP_1 + VP_2 + VF_1) / 3$;

VF_2 = Variance of F_2 family;

VP_1 = Variance of parent 1;

VP_2 = Variance of parent 2; and

VF_1 = Variance of F_1 family

Narrow sense heritability (h^2_n) was calculated according to the method of Halloran *et al.* (1979)

h^2n = [2VF2 -VBCP1 - VBCP2] / VF2 .... Equation 3

Where:

VF_2, $VBCP_1$, and $VBCP_2$ are the variances of the F_2, IET6279 x F_1 and IR70445-146-3-3 x F_1 respectively.

RESULTS

The means, standard deviation, range and coefficient of variation of the six populations of the cross between IET 6279 and IR70445-146-3-3 are presented in Tables 1 and 2. Heritability was estimated for all the traits studied (Table 3).

Plant height. The maximum and minimum plant height was 134.27 and 113.15cm for IET 6279 and IR70445-146-3-3 respectively. The mean plant height of F_1, F_2, BCP_1 and BCP_2 were all within the parental limits (Table 1). The range of variation in F_2 was higher than F_1, BCP_1, BCP_2 and parents, The CV in F_2 was highest (12.73%) followed by BCP1 (10.06%) and IET6279 (Table 1). Heritability estimate was high for plant height. It recorded the highest broad sense (71%) and narrow sense (48%) heritabilities compared to the other traits studied (Table 3). Results obtained from regression analysis revealed that additive gene effect (a) alone was significant for plant height. Dominance gene effect (d) and epistasis (aa), (ad) as well (dd) were not significant for plant height (Table 4).

Number of panicles per plant. Number of panicles per plant varied between 4 and 43 (Table 1). IET6279 recorded the highest mean for number of panicles per plant (22.17), followed by IR70445-146-3-3 (19.70); while F_2 had the lowest mean (17.12). The mean for both parents were slightly greater than F_1, F_2, BCP_1 and BCP_2. The CV in F_2 was the highest (36.46%) followed by BCP_2 (34.34%) and IET6279 recorded the lowest (18.22%) (Table 1). Broad sense heritability estimates were low for number of Number of panicles per plant (Table 3). The analysis of gene effects in six-parameter model revealed that additive effects only was involved in the inheritance of number of panicle per plant, while dominance and gene interaction were non-significant for this character.

Number of spikelets per panicle. There was a high variation in number of spikelets per panicle, within and between the populations (Table 1). The maximum and minimum number of spikelets per panicle was recorded for IET6279 (191.40) and IR70445-146-3-3 (150.30) respectively. The number of spikelets per panicle for F_1, F_2 and BCP_1 was all within parental limits. The F_2 recorded the highest CV (28.28%) and IET6279 (12.80 %) recorded the lowest (Table 1). Low broad sense heritability was observed for number of spikelets per panicle.

TABLE 1. Mean, standard deviation, ranges and coefficient of variation (c v) of plant height, number of panicles per plant, number of spikelets per plant and number of fertile spikelets per plant of six generations in IET6279 X IR70445-146-3-3 cross

Traits	Generation	Mean	Standard deviation	Range	C.V
Plant height (cm)	P_1	134.27	6.40	122-150	4.77
	P_2	113.15	9.42	108-137	8.32
	F_1	123.66	9.13	116-147	7.38
	F_2	123.70	15.74	77-187	12.73
	BCP_1	123.61	12.44	96-162	10.06
	BCP_2	119.88	11.01	90-139	9.19
	Grand mean	128.18			
	L S D (0.05)	3.80			
Number of panicles / plant	P_1	22.17	4.04	20-30	18.22
	P_2	19.70	5.25	11-23	21.09
	F_1	18.36	5.99	18-28	22.63
	F_2	17.12	6.33	5-43	24.46
	BCP_1	18.19	5.23	4-39	23.19
	BCP_2	17.36	5.13	5-38	24.34
	Grand mean	17.69			
	L S D (0.05)	1.63			
Number of spikelets / panicle	P_1	191.40	24.50	188.60-245.40	12.80
	P_2	150.30	34.96	118.20-153.60	13.26
	F_1	161.80	43.55	148.65-208.20	18.91
	F_2	150.50	42.58	61.31-298.20	22.28
	BCP_1	156.20	40.50	72.55-295.20	21.95
	BCP_2	148.60	33.70	69.57-223.10	20.67
	Grand mean	153.30			
	L S D (0.05)	10.93			
Number of fertile spikelets / panicle	P_1	165.30	21.77	162.80-203.40	13.17
	P_2	107.90	28.54	103.65-150.50	16.45
	F_1	145.00	39.17	130.65-174.00	17.02
	F_2	125.40	38.35	54.38-273.40	20.58
	BCP_1	134.60	36.96	53.68-262.00	21.46
	BCP_2	124.80	30.48	49.70-207.90	14.43
	Grand mean	128.30			
	L S D (0.05)	9.83			

The results obtained from regression analysis revealed that additive gene effect only was significant for number of spikelet per panicle; while as dominance gene effect and epistasis were not significant for number of spikelet per panicle (Table 4).

Number of fertile spikelets per panicle. The maximum and minimum number of fertile spikelets per panicle were recorded in IET6279 (165.30) and IR70445-146-3-3 (107.90) respectively (Table 1). The number of spikelets per panicle for F_1, $F_{2,}$ BCP_1 and BCP_2

TABLE 2. Mean, standard deviation, ranges and coefficient of variation (c v) of the percentage spikelets fertility /plant, 100-grain weight per plant and Grain yield per plant (g) of six generations in IET6279 X IR70445-146-3-3 cross

Traits	Generation	Mean	Standard deviation	Range	C.V
Percentage spikelets fertility / plant	P_1	86.39	3.28	83.26-94.89	3.80
	P_2	72.39	7.25	52.36.88.99	8.78
	F_1	89.76	5.61	67.76-98.15	6.25
	F_2	83.16	7.86	57.31-98.33	9.45
	BCP_1	85.95	6.82	53.79-95.29	7.74
	BCP_2	83.85	6.80	62.20-95.59	8.11
	Grand mean	82.25			
	L S D (0.05)	2.02			
100-grain weight / plant (g)	P_1	2.69	0.10	2.46-2.92	3.71
	P_2	3.04	0.13	2.77-3.33	4.43
	F_1	2.76	0.14	2.49-3.12	5.03
	F_2	2.77	0.23	2.27-3.91	8.12
	BCP_1	2.74	0.19	2.24-3.21	7.06
	BCP_2	2.80	0.22	2.28-3.57	7.72
	Grand mean	2.78			
	L S D (0.05)	0.06			
Grain yield / plant (g)	P_1	97.78	21.02	95.75-130.60	11.49
	P_2	65.64	27.69	60.67-111.10	22.18
	F_1	74.05	33.11	72.98-100.70	24.71
	F_2	59.13	28.95	10.79-188.90	25.95
	BCP_1	66.41	28.95	11.90-193.50	21.60
	BCP_2	59.74	26.09	15.48-156.50	23.67
	Grand mean	62.82			
	L S D (0.05)	7.71			

were all within parental limits. BCP1 recorded the highest CV (37.46%); followed by F_2 (30.58%) and IET6279 recorded the lowest (13.17%). Low heritability estimate was observed for number of fertile spikelets per panicle (Table 3). Both additive gene effect (a) and additive x dominance gene effect (ad) were significant for number of fertile spikelets per panicle; while dominance gene effect (d), (aa) as well as (dd) were not significant for these character. The magnitude of non-fixable gene effect (additive x dominance gene effect) was greater than the corresponding fixable gene effect (additive gene effects) (Table 4).

Percentage spikelets fertility per plant. Percentage spikelets fertility per plant ranged from 52.36 to 98.33%. Surprisingly, the percentage spikelets fertility per plant means was highest for the F_1 (89.76%) followed by IET6279 (86.39) while the lowest was recorded for IR70445-146-3-3 (72.39 %). Means for F_2, BCP_1 and BCP_2 were all within parental limits. The range of variation in F_2 was higher than IR70445-146-3-3 and BCP_1. F_2 recorded the highest CV (9.45%); followed by IR70445-146-3-3 (8.78%) and IET6279 recorded the lowest (3.80%). Low heritability estimate was observed for percentage spikelets

TABLE 3. Heritability estimates for yield and yield component characters calculated from estimated variance component in IET 6279 X IR70445-146-3-3 cross

Characters	Heritability	
	Broad sense (%)	Narrow sense (%)
Plant height (cm)	71	48
Number of panicles / plant	30	14
Number of spikelets / panicle	32	29
Number of fertile spikelets / panicle	36	27
Percentage spikelets fertility / plant	49	47
100 grain weight / plant (g)	67	50
Grain yield / plant (g)	32	19

TABLE 4. Analysis of variance and parameter estimates for genetic control of yield and yield component characters obtained through generation mean analysis of IET6279 X IR70445-146-3-3 cross

Variables	Characters						
	Plant height (cm)	Number of panicles / plant	Number of spikelets / panicle	Number of fertile spikelets / panicle	Percentage spikelets fertility / plant	100 grain weight / plant (g)	Grain yield / plant (g)
Intercept	131.83**	15.71*	157.89**	112.25**	72.02**	2.84**	46.62
Rep	0.20	1.03	3.33	3.62	0.54	0.00	6.20
a	-9.97**	-1.30*	-20.61**	-28.89**	-6.63**	0.17*	-17.32*
d	-26.83	-3.99	-55.85	-4.26	22.72	-0.20	-22.57
aa	-7.25	2.72	5.70	16.26	6.59	0.01	17.48
ad	12.19	0.56	26.25	38.46*	10.12	-0.24*	21.63
dd	18.35	5.02	55.99	32.38	-4.79	0.10	41.20

*, ** significant at 5 and 1% levels respectively. (a) additive; (d) dominance; (aa) additive x additive; (ad) additive x dominance; (dd) dominance x dominance gene effects

fertility per plant and this indicate high influence of the environment on this trait. (Table 3). The results obtained from regression analysis revealed that additive gene effect only was significant for percentage spikelets fertility per plant, while as dominance gene effect and epistasis were not significant for percentage spikelets fertility per plant (Table 4).

100-grain weight. The maximum mean performance of 100-grain weight was recorded for IR70445-146-3-3 (3.04 g) and the minimum was recorded for IET6279 (2.69 g). Means for F_1, F_2, BCP_1 and BCP_2 were all within parental limits. The range of variation in F_2 was higher than the corresponding parents, F_1, BCP_1 and BCP_2 populations. F_2 recorded the highest CV (8.12%); followed by BCP_2 (7.72%) and IET6279 recorded the lowest (3.71%). High broad sense heritability estimates was observed for 100 grain-weight, (Table 3). Both additive gene effect (a) and additive x dominance gene effect (ad) were significant; while dominance gene effect (d), (aa) as well as (dd) were not significant. However, the magnitude of non-fixable gene effect (additive x dominance gene effect) was greater than the corresponding fixable gene effects (additive gene effects) for 100-grain weight (Table 4).

Grain yield per plant. Grain yield per plant varied between 10.79 g and 193.50 g. IET6279 registered the maximum grain yield per plant (97.78 g); followed by F_1 (74.05 g) and F_2 recorded the minimum (59.13 g) per plant. The range of variation in F_1 and BCP_1 was higher than their corresponding F_2. This deviates from how the various generations normally behave. However, F_2 recorded the highest CV (48.95%) and IET6279 recorded the lowest (21.49%). Low broad sense heritability estimate was observed for grain yield per plant (Table 3). Additive gene effect (a) alone was significant for grain yield per plant, while dominance gene effect (d) and epistasis (aa), (ad) as well (dd) were not significant (Table 4**).**

DISCUSSION

Plant height. High broad sense heritability was recorded for plant height (Table 3) indicating that the phenotype is highly correlated with the genotype. Hence, selection based on phonotypic performance of this character will be reliable and effective. Other authors (Lingaiah *et al.*, 2014; Ketan and Sarkar, 2014 and Tuhina *et al.*, 2015) also reported high broad sense heritability for plant height in rice. High heritability in broad sense values indicate that the characters under study are less influenced by environment in their expression. Therefore, the rice breeders may make superior genotypes selection based on phenotypic performance for these trait. The analysis of gene effects in six-parameter model revealed that additive effects only was involved in the inheritance of plant height. Dominance gene effect and epistasis were not significant for plant height, suggesting the predominance of additive gene action controlling this character. Additive effects are exactly what an individual contributes to its progeny, unaltered by segregation and recombination. Consequently, there is a high probability of success in selecting for plant height in early generations. The significant and negative additive gene action (a) for plant height indicates that gene action was in the direction of the reducer parent. Upadhyay and Jaiswal, (2015), reported the predominance of additive gene effects in rice for plant height.

Number of panicles per plant. Broad sense heritability estimates was low for number of panicle per plant (Table 3), which indicates greater role of environment on the expression of the traits. Thus, direct selection for these traits will be ineffective. Therefore, methods of selection based on families and progeny testing are more effective and efficient. Other investigators Rafii *et al.* (2014) also reported similar results for number panicle per plant in rice.

Results from the regression analysis revealed that additive gene effect (a) alone was significant for number of panicles per plant; while dominance gene effect (d) and epistasis (aa), (ad) as well (dd) were not significant for these trait, suggesting the predominance of additive gene action controlling these character. The non-significance of non-additive gene effects and their interactions suggest that improvement of this character can be done through mass selection in early generations. The significant and negative additive gene action (a) for number of panicle per plant shows that gene action was in the direction of the reducer parent. Jarwar *et al.* (2014), reported similar results in rice.

Number of spikelets per panicle. Low broad sense heritability estimate was observed for number of spikelets per panicle (Table 3). This indicates that this trait was highly influenced by environment. Low heritability in broad sense value indicate that the characters under study are highly influenced by environment in their expression. Therefore, superior genotypes selection based on phenotypic performance for this trait may not effective. Other researchers also obtained low broad sense heritability estimates for this trait (Anyanwu and Obi, 2014; Osekita *et al.*, 2014) in rice.

For number of spikelets per panicle in the six parameter model revealed that additive gene effect (a) only was significant for number of spikelets per panicle, while as dominance gene effect (d) and epistasis (aa), (ad) as well (dd) were not significant for number of spikelet per panicle, suggesting the importance of additive gene action controlling these character. Hence, the non-significance of non-additive gene effects and their interactions for number of spikelet per panicle could be explained by additive gene action. The significant and negative additive gene action (a) for number of spikelets per panicle shows that gene action was in the direction of the reducer parent. Similar results were earlier reported by Mulugeta *et al.* (2012) for number of spikelets per panicle in rice. Hence, improvement of this character can be done through mass selection in early generations of F_2 population.

Number of fertile spikelets per panicle. In contrast to other characters, number of fertile spikelets per panicle had low heritability (Table 3), which indicates greater role of environment on the expression of the trait. Thus, direct selection for these traits will be ineffective. Therefore, methods of selection based on families and progeny testing are more effective and efficient. Similar results were reported by Osekita *et al.* (2014) for number of fertile spikelets per panicle. Both additive gene effect (a) and additive x dominance gene effect (ad) were significant for number of fertile spikelet per panicle; while dominance gene effect (d), (aa) as well as (dd) were not significant for these character, suggesting the importance of both additive and non-additive gene actions in control of this character. The magnitude of non-fixable gene effect (additive x dominance gene effect) was greater than the corresponding fixable gene effects (additive gene effects). Consequently, the postponement of selection to later generations in pedigree breeding is advised. One or two cycles of recurrent selection, followed by pedigree breeding, will be effective and useful to utilise both the additive and non-additive gene effects. Similar results were reported by Bagheri *et al.* (2008), Kundu *et al.* (2008) and Venkata *et al.* (2011) for predominance of additive gene effects in controlling the inheritance of number of fertile spikelets per panicle in rice. Li *et al.* (1997) who found that epistasis has important effect on complex traits such as number fertile spikelets per panicle

Percentage spikelets fertility per plant. Low heritability estimate was observed for percentage spikelets fertility per plant (Table 3), low heritability in broad sense value indicate that the character under study was highly influenced by environment in it expression. Therefore, superior genotypes selection based on phenotypic performance for this trait may not effective. This possibly occurred because of the genotypes used and the environmental conditions under which the study was conducted. Other authors reported low heritability for Percentage spikelets fertility per plant in rice (Vanisree *et al.*, 2013 and Anyanwu and Obi, 2014). The results obtained from regression analysis revealed that additive gene effect (a) only was significant for percentage spikelets fertility per plant; while dominance gene effect (d) and epistasis (aa), (ad) as well (dd) were not significant. This suggested the predominance of additive gene action controlling these characters. This is an indication that additive gene effect determined to some extent by the genotypes used for the study. However, the non-significance of non-additive gene effects and their interactions for percentage spikelets fertility per plant could be explained by additive gene action and, hence, improvement of this character can be done through mass selection in early generations of F_2 population. The significant and negative additive gene action (a) for percentage spikelets fertility per plant shows that gene action was in the direction of the reducer parent. Saleem *et al.* (2005) reported similar results for percent spikelets fertility per plant in rice.

100 - grain weight. High broad sense heritability estimates was observed for 100 grain-weight (Table 3). High heritability value indicate that the characters less influenced by environment in their expression, which suggested that these traits would respond to selection owing to their high genetic variability and transmissibility. Thus, selection based on phenotypic value of this character would be reliable and effective. Other authors (Rita *et al.*, 2009 and Tuhina *et al.*, 2015) reported similar results for 100-grain weight in rice.

Both additive gene effect (a) and additive x dominance gene effect (ad) were significant for 100-grain weight, while dominance gene effect (d), (aa) as well as (dd) were not significant for this character. However, the magnitude of non-fixable (additive x dominance gene effect) was greater than the corresponding fixable gene effects (additive gene effects) for 100-grain weight, suggesting the predominance of both additive and non-additive gene actions in control of this character. Consequently, selection for 100-grain weight will be effective during later generations. One or two cycles of recurrent selection, followed by pedigree breeding, will be effective and useful to utilise both the additive and non-additive gene effects. However, the magnitude of non-fixable gene effects (additive x dominance gene effect) was greater than the corresponding fixable gene effects (additive gene effects) for 100-grain weight. Both additive effects (Praveen *et al.*, 2009; Pallabi *et al.*, 2013) and epistasis (Bagheri *et al.*, 2008) have been reported to play major roles in controlling the inheritance of seed weight in rice.

Grain yield per plant. Low broad sense heritability estimates were observed for grain yield per plant (Table 3), indicating that the phenotype is not correlated with the genotype and that contribution of environmental was relatively high for this trait. Therefore, superior genotypes selection based on phenotypic performance for this trait may not effective. Mulugeta *et al.* (2012) and Rafii *et al.* (2014), reported similar results for grain yield per plant in rice. Additive gene effect (a) alone was significant for grain yield per plant; while dominance gene effect (d) and epistasis (aa), (ad) as well (dd) were not significant for these characters. This suggested the predominance of additive gene action controlling these characters. However, the non-significance of non-additive gene effects and their interactions for grain yield per plant could be explained by additive gene action and, hence, improvement of this character can be done through mass selection in early generations of F_2 population. Similar results were reported by Singh *et al.* (2014) for grain yield per plant in rice.

CONCLUSION

Broad sense heritability estimates were high for plant height and100 grain weight per plant in IET6279/ IR70445-146-3-3 rice population in Ghana. Low broad sense heritability estimate is evident for number of panicle per plant, number of spikelets per panicle, number of fertile spikelets per panicle, percentage spikelets fertility per plant and grain yield per plant. Additive effects played a major role in the expression of plant height, number of panicles, number of spikelets per panicle, percentage spikelets fertility per plant and grain yield per plant. The performance of some of the characters studied manifesting non-allelic interactions for number of fertile spikelets per panicle and 100-grain weight per plant is an indication that epistasis is determined to some extent by the genotypes used for the study.

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