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Determining the Gene Action Type for Grain Yield and its Components using Generation Mean Analysis in Rice (*Oryza sativa* L.)

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ABSTRACT

The study was conducted at the Rice Research Department Farm at the Agricultural Research Station in Sakha, Agricultural Research Center - Egypt through the period 2019 - 2022 for two rice hybrids. The study included five populations of each hybrid (P1, P2, F1, F2, and F3), to determine the magnitude of gene action for some using morphological and yield characters using generation mean analysis. Two hybrids GZ9399 × IRRI 148 and Sakha 104 × IM 16 with their parents were used for this study. The results of the scaling tests indicated that the characteristics evaluated in two crosses were not well-suited for the additive-dominance model, indicating the possibility of epistasis in the characters' inheritance. The general mean for each trait was wide significant differences, therefore grain yield/plant of cross 2 (Sakha 104 × IM 16) logged highly significant positive gene action effects. However, 1000 grains weight recorded a highly significant positive gene action effects for cross 1, From phenotypic correlation coefficient, in both crosses, grain yield/plant were positively and highly-significant correlated with branches number/panicle, number of panicles/plant and number of spikelets /panicles. Grain yield/plant of cross 1, it was positively and highly-significant correlated with panicle length, panicle weight. While cross 2, it was positively and significantly correlated with panicle length and positively highly significantly correlated with fertility percentage and 1000 grains weight.

Keywords: rice, scaling test, gene action, generation mean, grain yield and its components
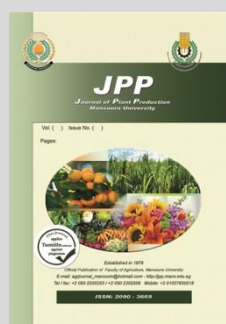
INTRODUCTION

The rice crop (*Oryza sativa L.*) is the foremost nutrition for more half of the worldwide inhabitants and will last to get the essential place in global food and retain food security (Al-Wardi *et al*., 2023). Approximately 23% of energy and 16% of protein are found in rice grains per capita globally (Gramaje *et al*., 2020). Over 160 million hectares of land are used to grow rice worldwide, yielding approximately 740 million tons of rice yearly (Kumar *et al*., 2018). Rice production faces many challenges, causes food shortage which become a real problem. Genetic variability of traits is crucial in breeding programs to broaden the genetic pool. A multitude of factors, the majority of which are controlled by polygenes, combine to control yield, a complicated trait. Therefore, identifying key elements and learning about how they relate to yield and other qualities can help build an effective breeding plan for high producing (Zaazaa and Anis, 2014). Hybridization is a valuable approach for improving yield and its components in rice. Screening of type of gene action in generation offspring is significant to estimate the gene effects with selection of new genes that help to develop yielder rice during plant breeding system. The efficiency of selection between the offsprings with variation genetic values is the main determinant of genetic progress. The knowledge needed to choose the appropriate breeding strategies for genotype development programs is provided by the identification of genetic components and actions (Ammar *et al*., 2014). Additive and dominant influences of types of genetic actions, as well as their interactions are related to the breeding value (Xu, 2022). The generation mean analysis has been reflected to be one of method for determining the various

of genetic variance and epistasis presence or absence. Hence, to frame a breeding program the study of genetics of yield and its components traits is important. Analysis of generation mean measures phenotypic performance of numerous quantitative traits of following generations. This is an extremely easy-to-use method for determining the dominant and additive primary gene effects for quantitative traits as well as the digenic (dominance × dominance and additive × additive) interactions that determine how quantitative characteristics are inherited. It facilitates comprehension of the effectiveness of the parents employed in cross combinations as well as the possibility of using cross combinations for heterosis or other selection processes. Since rice's grain yield and quality features are its most significant complex qualities, improving them is a major goal of rice breeding programs (Kour *et al*., 2019). Other morphological and agronomic variables like plant height, panicle length, number of panicles /plant, grains/panicle, 1000-grain weight, fertility percentage, and grain yield/plant have all been shown to be significantly influenced by additive and dominant genes. The correlation coefficients across different agronomic traits are crucial because, by using linked simple measurable traits, correlation can help researchers anticipate the performance of quantitative and sophisticated qualities that are challenging to measure. Therefore, since the environment will have less of an impact on simple features, selection efficiency will be greatly increased (Zaazaa and Anis, 2014). Nevertheless, this study was aimed to identifying the mode gene action type that control in important agronomic traits in rice populations and determine the correlation coefficient between pairs of studied traits.

MATERIALS AND METHODS

The present investigation was carried out at the Rice Research Department Farm, Sakha Agricultural Research Station, Egypt during four consecutive seasons: 2019, 2020, 2021 and 2022. The genotypes GZ9399 and Sakha 104 were used as female parents (Egyptian genotype ad wide adaptability with high yield potential, while IRRI 148 and IM 16 (introduced genotypes from IRRI, good grain yield and its components with resistance for common diseases and pests and tolerance for abiotic stress) were used as male parents. Two rice populations GZ9399 × IRRI 148 and Sakha 104 × IM 16 were crossed to produce F_1 hybrids in 2019. Consequently in 2020, self the F_1 plants were used to produce F_2 seeds. F_2 plants from each population were grown to obtain F_3 plants in season 2021. Five populations grains including P_1, P_2, F_1, F_2, and F_3 were planted in the nursery at 2022 season. The transplant of seedlings was done after sowing by 30 days. Therefore, the experiment was conducted at RCBD (randomized complete block design) with three replications. The agricultural practices, involving sowing, transplanting where single plant in a hill, and each row consisted of 25 plants with 20 × 20 cm spaces between seedlings). It grew in three rows for each of P_1, P_2 and F_1, 30 rows for F_2 and 15 rows for F_3 generation., Urea-based nitrogen fertilizer containing 46.5% N, at level of 165 N/ha was administered in two splits: two thirds of dose was utilized as basal and blended into dry soil prior to flooding irrigation, and one third of dose was applied at maximum tillering stage), and weed control was conducted according the recommended package at Rice Research Department. The results were reported at the maturity stage; 10 plants for each P_1, P_2 and F_1, along with a total 150 plants from F_2 generation, and 75 plants from the F_3 generation were measured for data analyses. The studied traits measurement included, plant height (cm), panicle length (cm), panicle weight (g), number of branches/panicle, number of panicles/plant, number of spikelets/panicle, fertility percentage (%), 1000-grain weight (g) and grain yield/plant (g) were obtained according to the technique of IRRI (2013).

Determination gene action

To ascertain if the additive-dominance model or non-allelic gene interaction was adequate, the scaling tests (C and D) were computed for each trait. However, these scales were found to be significant in indicating the existence of non-allelic interactions. According to Evans, *et al*. (2002), the variance means for these estimations were shown, and the significance from zero was tested using a t-test. A five parameters model was used to calculate estimates of different gene effects, allelic interactions, and their significance test (Hayman, 1958).

Epistasis type:

When dominance (h) and dominance × dominance (l) gene effects have the same sign, the form of epistasis known as complementary epistasis (C) is identified, while duplicate epistasis (D) is identified when the sign differs.

Statistical analysis

The analysis of variance of three generations with their parents (P_1, P_2, F_1, F_2 and F_3), were statistically analyzed based on individual plant using TNAUSTAT (http://sourceforge.net/projects/dosbox/). Correlation co-efficient was performed by Microsoft Excel Program.

RESULTS AND DISCUSSION

Mean performance

The mean performance of the five populations P_1, P_2, F_1, F_2, and F_3 for characters of two crosses are shown in Table 1. The general mean for each trait was wide significant various among parents and generations were found.

Table 1. Mean performance of five generation materials for vegetative, yield and yield component traits.

Trait	Cross	P1 ± SE	P2 ± SE	F1 ± SE	F2 ± SE	F3 ± SE
Plant height	1	105.6±0.67	138.4±0.67	150.4±0.30	143.5±1.21	119.9±1.07
	2	103.6±1.30	110.0±1.66	130.8±1.74	115.2±2.60	91.06±2.70
Panicle length	1	24.2±0.37	24.0±0.44	25.6±0.40	24.1±1.26	23.4±1.35
	2	23.6±0.60	23.5±0.69	25.8±0.70	21.21±0.84	18.29±0.81
Panicle weight	1	4.0±0.02	3.1±0.04	4.6±0.52	3.9±0.88	4.1± 0.77
	2	2.8±0.12	3.1±0.13	3.9±0.09	3.7±0.19	3.8±0.18
Branches/ panicle	1	9.8±0.13	10.6±0.12	13.2±0.15	9.7±0.99	10.7±1.21
	2	9.6±0.37	10.8±0.37	11.8±0.60	11.58±0.80	11.1±0.84
Number of panicles	1	23.0±0.89	23.0±0.44	24.2±0.84	22.9± 1.54	23.3±1.18
	2	22.2±0.86	16.0±0.70	23.6±0.60	23.4±1.61	23.8±1.05
Spikelets/panicle	1	130.2±7.04	132.8±7.99	146.4±6.63	115.3±9.82	141.2±9.75
	2	121.6±1.50	112.2±2.31	139.0±2.46	135.7±3.27	135.3±4.27
Fertility percentage	1	91.4±1.67	86.1±1.82	88.7±0.63	79.3±2.29	90.3±1.83
	2	95.4±0.73	96.4±0.52	92.9±0.25	70.4±2.13	91.4±1.53
1000 grains weight (g)	1	25.4±0.35	22.0±0.35	28.2±0.32	22.3±0.44	25.1±0.41
	2	25.8±0.24	28.8±0.04	29.3±0.24	28.6±0.40	28.8±0.42
Grain yield /plant (g)	1	45.2±0.87	63.4±0.74	58.0±1.61	54.7±3.53	53.9±2.92
	2	46.4±1.32	45.6±2.48	56.9±1.50	39.3±3.42	55.1±3.20

Cross 1: GZ9399 × IRRI 148, cross 2: Sakha 104 × IM 16

Along with the wide differences in performance between the two crosses populations for all traits existed. Regarding plant height, the shorter mean values were found with cross Sakha 104 × IM 16 however, the plant height for P_1, P_2, F_1, F_2 and F_3 were 103.6, 110.0, 130.8, 115.2 and 91.06 cm, respectively. Concern panicle length, the highest values were 24.2, 24.0, 24.1and 23.4 cm, for P_1, P_2, F_2 and F3, respectively for cross GZ3999 × IRRI 148. While F_1 gave the highest value (25.8 cm) for cross Sakha 104 × IM 16. For

panicle weight, the heaviest panicles were 4.0, 3.1, 4.6, 3.9 and 4.1 g for five populations of cross GZ3999 × IRRI 148. With respect to 1000-grain weight, the highest values were 25.8, 28.8, 29.3, 28.6 and 28.8 g for five populations, respectively, for cross Sakha 104 × IM 16. Regarding branches/ panicle, the superior values were 9.8 and 13.2 for P_1 and F_1 of cross GZ3999 × IRRI 148, and 10.8, 11.58 and 11.1 for P_2, F_2 and F_3 of cross Sakha 104 × IM 16, respectively. Regarding number of panicles plant[-1], the

superior values were 23, 23 and 24.2 panicles plant[-1] for P_1, P_2 and F_1 of cross GZ3999 × IRRI 148, while 23.4 and 23.8 panicles plant[-1] for F_2 and F_3 of cross Sakha 104 × IM 16 for five population, respectively. For spikelets No. /panicle, the highest values were 130.2, 132.8, 146.4 and 141.2 spikelets for P_1, P_2, F_1 and F_3, respectively for cross GZ3999 × IRRI 148 however F_2 recorded highest value 135.7 for cross Sakha 104 × IM 16. Concerning fertility percentage, the highest values of five population were recorded 95.4, 96.4, 92.9 and 90.3 %, respectively, for P_1, P_2, F_1 and F_3 of cross Sakha 104 × IM 16, and 79.3 % for F_2 of cross GZ3999 × IRRI 148. Regarding 1000 grains weight, the superior values were 25.8, 28.8, 29.3, 28.6 and 28.8 g, respectively for five population of cross Sakha 104 × IM 16. For grain yield /plant, the maximum values recorded for P_1 and F_3 of cross Sakha 104 × IM 16 were 46.4 and 55.1 g, respectively. Whereas for P_2, F_1 and F_2 of cross GZ3999 × IRRI 148 were the highest values 63.4, 58 and 54.7 g, respectively. These results are agreement with results were obtained by Solanke *et al.*, (2019). Gaballah *et al.* (2020) and Ganapati *et al.*, (2020) found that the panicle length is significant trait that should be chosen in the early segregating generation.

Scaling test.

Table 2 displayed the estimated scaling test parameters (C and D) for the characteristics under study in the two crosses. Scaling test parameters with significant findings show that the additive-dominance model is not sufficient to describe the gene effects present in the materials. Epistasis plays a significant role in how these traits are inherited. For every attribute under study, the scaling test's calculated parameters were significant except for C scaling test for plant height and thousand grains weight in cross 2 (Sakha 104 × IM 16) and panicle length, branches No. panicle[-1] and grain yield/plant in cross 1 (GZ9399 × IRRI 148). In addition to the D scaling test was insignificant for panicle weight, number of panicles/ plants, spikelets No./panicle and 1000 grains weight in cross 2 (Sakha 104 × IM 16), panicle length for cross 1 (GZ9399 × IRRI 148) and branches/panicle and grain yield/plant for both cross. It was not significant for C and D scaling test for panicle length in cross 1 (GZ9399 × IRRI 148), 1000 grains weight in cross 2 (Sakha 104 × IM 16). These results refer to five parameters model is effective to illustrate the type of gene action for these significant characteristics. The comparable outcomes were found by Hassan (2012) and Hassan *et al.*, (2023) displayed one as a minimum of calculated parameters (C and D) were significant for the traits studied. This finding suggests that allelic interaction is necessary for the genetic regulation of these traits.

Table 2. Scaling test estimate for vegetative, yield and yield component traits

Cross	Plant height (cm)		Panicle length (cm)		Panicle weight (g)	
	C	D	C	D	C	D
1	29.41**	-51.24**	-2.75	-2.52	7.88**	2.94*
2	-14.32	-79.77**	-13.82**	-16.37**	5.13**	0.83
	Number of branches/panicle		Number of panicles/ plant		Spikelets number / panicle	
	C	D	C	D	C	D
1	-0.52	-0.93	-15.72**	-19.43**	-94.25**	71.29**
2	1.19*	0.82	9.03*	6.51	31.38*	35.80
	Fertility percentage		1000 grains weight (g)		Grain yield /plant (g)	
	C	D	C	D	C	D
1	-37.55**	25.16**	-14.68**	8.25**	-5.8	-14.10
2	-95.89**	33.30**	1.41	3.42	-62.57*	21.84

Cross 1: GZ9399 × IRRI 148; cross 2: Sakha 104 × IM 16, *: At 0.05 % level is significant, **: At 0.01% level is significant,

Type of gene actions for studied characters for two rice crosses; mean effect (m), additive effects, dominance effects, and epistasis type were shown Table 3. The mean effect (m) was highly significant for the traits were studied at both crosses. The various genetic effects used means of the different generations (Kumar *et al.*, 2018). A highly significant and significant additive negative gene effects were observed for plant height for two crosses. A highly significant negative additive gene effects were reported for 1000-grain weight for cross Sakha 104 × IM 16 and grain yield/plant for cross GZ9399 × IRRI 148. A highly significant positive gene actions were reported for number of panicles/plant for both crosses, spikelets number /panicle for cross Sakha 104 × IM 16, 1000 grains weight for cross GZ9399 × IRRI 148 and grain yield/plant for cross Sakha 104 × IM 16. Simple pedigree selection can be used to take advantage of the additive component of variation. The quickest and least expensive process would be to adjust the frequencies of desired genes using mass selection for multiple early generations to improve the heterozygous population. Single plant selection would then be conducted on the resulting material. In such a scenario, offspring may be produced and selection is postponed until subsequent generations. These findings concur with those of Vinoth *et al.* (2015) and Kumar *et al.* (2017).

The dominance effects were highly significant with positive for plant height of both crosses, branches/panicle for cross GZ9399 × IRRI 148 and panicle length for cross Sakha 104 × IM 16. It is note that there are no significant dominance gene action effects in some traits of both crosses. Sultana *et al.* (2016) found the same trend for spikelets number /panicle and 100 seeds weight. Concerning the third types of epistasis, the significant positive additive × additive was detected for plant height and panicle length for cross Sakha 104 × IM 16, number of branches/ panicle for cross GZ9399 × IRRI 148.. Indicated to the additive × additive gene action had important role in the inheritance of these traits. However, the presence duplicate type of epistasis for number of spikelets /panicle and 1000 grains weight for cross 1, plant height for cross 2, and fertility percentage for both crosses could impede the improvement of this characteristic caused by early generations' selection. By using a cyclic breeding strategy, which selects and crosses desirable recombinants to combine the advantageous genes for creating an elite population, these crosses could be improved. Chamundeswari *et al.* (2013), Rani *et al.* (2015) and Solanke *et al.* (2019) reported the similar results therefore, Vadivel *et al.*, (2003) confirmed the

existence of non-additive gene action for grain yield/plant the majority of the yield components in the hybrids led to a high level of vigor in the F_1, suggesting the potential for using heterosis to increase yield. Together with Tan *et al*., (2022) also noted a less-than-additive or negative effect on the epistasis of additive by additive interaction between lines.

Dominance × dominance type of epistasis was highly significant and positive for panicle weight, 1000-grain weight and spikelets number /panicle for cross GZ9399 × IRRI 148,

and fertility percentage for both crosses. It was only significant and positive for grain yield/plant for cross Sakha 104 × IM 16.. While, negative with highly significant dominance × dominance found with plant height for both crosses. The gene action of dominance × dominance played vital role in the inheritance of these traits. The dominance × dominance sign component has positive in one or both crosses indicative of improved effect in the character expression.

Table 3. Type of gene actions for studied characters for two rice crosses.

Trait	Cross	m	a	d	aa	dd	Type of epistasis
Plant height (cm)	1	143.55**	-16.40**	67.46**	6.26	-107.54**	D
	2	115.21**	-3.20*	74.79**	44.39**	-87.26**	D
Panicle length (cm)	1	24.16*	0.10	2.72	1.42	0.31	C
	2	21.21**	0.05	10.86**	8.71**	-3.39	D
Panicle weight (g)	1	9.72**	-0.40	-0.27	-4.07**	14.42**	D
	2	11.58**	-0.60	0.50	-0.89	-5.73*	D
Branches number / panicle	1	3.98**	0.48**	1.60**	1.49**	-0.54	D
	2	3.77**	-0.15	0.65	-0.65	-0.48	D
Number of panicles / plant	1	22.91**	6.50**	5.03	23.33**	-4.95	D
	2	23.40**	3.10**	1.26	3.36	-3.35	D
Spikelets number / panicle	1	115.38**	-1.30	-48.33**	-65.83**	220.72**	D
	2	135.79**	4.70**	3.45	-9.24	5.90	C
Fertility percentage (%)	1	79.37**	2.63	-23.03**	-17.75**	83.62**	D
	2	70.42**	-0.50	-41.18**	-39.18**	172.26**	D
1000 grains weight (g)	1	22.35**	1.71**	-3.40**	-4.53**	30.58**	D
	2	28.66**	-1.51**	-0.07	-5.06**	2.68	D
Grain yield /plant (g)	1	54.70**	-9.10**	12.16	-9.77	-11.00	D
	2	39.34**	14.40**	-35.01*	3.80	112.55*	D

Cross 1: GZ9399 × IRRI 148; cross 2: Sakha 104 × IM 16, *: Significant at 0.05 % level, **: Significant at 0.01% level. C and D are complementary and duplicate gene effect, respectively

The expression of these traits in these crosses was significantly influenced by the non-fixable gene effect, which may be taken advantage of through bi-parental mating under recurrent selection or by using the population improvement concept in place of more traditional methods. The dominance × dominance effect sign was negative, suggesting that these characters' expressions were being reduced. On the other hand, the other characters' dominance × dominance component was positive, suggesting that they enhanced the expression of those characters. You *et al*. (2006) observed the interaction of additive × additive had superior effect than dominance × dominance in most crosses. The duplicate epistasis was achieved for studied traits for both crosses excepting panicle length for cross GZ9399 × IRRI 148 and number of spikelets / panicle for cross Sakha 104 × IM 16 were complementary.

In traits under study, both complimentary and duplicate epistasis were found. This makes it challenging to fix genotypes with higher levels of character manifestation in duplication epistasis, as the negative influence of one parameter would cancel out the opposite effect of another. Whereas, epistasis of complementary refers to suggestions for selection in early generation might be effective. Ganapati *et al*., (2020) indicate epistasis effect, epistasis of duplicate was main for entirely the traits excluding panicle length, therefore, the epistasis of duplicates, as demonstrated by Solanke *et al*. (2019), may delay the selection of a single plant. Instead, biparental mating or diallel selective mating, in which a few cycles of crossing of promising segregates in F_2 and subsequent generations are followed, may aid in the integration of desired genes into a single genetic background.

Phenotypic correlation

Determination relationship between characteristics such as grain yield with other characteristics is one of

principal target to the breeding for improving these traits. Although, direct selection for grain yield is not effective. Hereafter, correlation coefficient performed to identify the selection direction and characters to be measured in grain yield improvement. Assessed phenotypic correlations between the studied traits of both crosses are presented in Table 4. For plant height of cross 1, it was positively significant correlated with branches number /panicle. It was highly significant correlated with panicle length. Although, it was negative and highly significant correlated with fertility percentage and 1000 grains weight. While plant height of cross 2, it was highly significant positive correlated with panicle length, panicle weight, branches number /panicle as well as spikelets number /panicle. While it was not correlated with grain yield/plant in both crosses, and this was not in accord with Kumar *et al*. (2017) and Zaazaa and Anis (2014) who showed that grain yield had significantly and positively correlation with plant height. Concerning panicle length of cross 1, had positive and highly significantly correlation with branches number /panicle, spikelets number /panicle and grain yield/plant. Panicle length was only positively significant with 1000 grains weight. Concerning panicle length of cross 2, was positively and highly significantly correlation with branches number /panicle, spikelets number /panicle. As cross 1, was positively significantly with panicle weight and grain yield/plant. Kumar *et al*. (2017) and Al-Wardi *et al*. (2023) showed that grain yield plant[-1] was significantly and positively correlated with panicle length. Therefore, the length of panicle can be measured phenotypic trait for adopt as index of selection for the grain yield for both crosses. For panicle weight, cross 1 was positive and highly significant with grain yield /plant. Number of panicles/plants of cross 1 was positively and highly significant correlated

with grain yield/plant as well in cross 2 which positively and highly significant correlated. Concern spikelets/panicle of cross 1, was positively and highly significant correlated with grain yield /plant. While cross 2 was not. For 1000 grains weight of cross 1 was not associated with grain yield. While, cross 2 was highly positive and significant correlated with grain yield/plant. This disagree with Al-Wardi *et al.* (2023)

for cross 2 and agree in cross 1 who showed that grain yield was non-significantly with weight of 1000-grains. For grain yield/plant of both crosses, it was highly positively and significantly correlated with branches number /panicle, number of panicles/ plant and spikelets number /panicle. For grain yield/plant of cross 1, it was positively and highly significant correlated with panicle length, panicle weight.

Table 4. Phenotypic correlation of studied characters of both crosses

	Cross	Plant height (cm)	Panicle length (cm)	Panicle weight (g)	Branches/ panicle	Number of panicles	Spikelets / panicle	Fertility percentage	1000 grains weight (g)
Panicle length (cm)	1	0.23**							
	2	0.37**							
Panicle weight	1	-0.07	0.03						
	2	0.32**	0.14*						
Branches/ panicle	1	0.17*	0.37**	0.27**					
	2	0.26**	0.29**	0.25**					
Number of panicles	1	-0.04	0.00	0.00	0.05				
	2	-0.01	0.12	0.13*	0.18				
Spikelets / panicle	1	-0.11	0.22**	0.33**	0.30**	0.05			
	2	0.29**	0.22**	0.57**	0.42**	0.19*			
Fertility percentage	1	-0.23**	-0.10	0.24**	0.01	-0.09	0.11		
	2	-0.01	-0.04	-0.09	0.30**	-0.13	-0.07		
1000 grains weight (g)	1	-0.22**	0.14*	0.09	0.20	-0.01	0.32**	0.12	
	2	0.07	0.07	0.10	0.38**	0.05	0.15*	0.37**	
Grain yield /plant (g)	1	0.12	0.20**	0.18**	0.29**	0.47**	0.23**	-0.02	0.11
	2	-0.03	0.14*	0.04	0.44**	0.53**	0.22**	0.35**	0.39**

*: Significant at 0.05 % level, **: Significant at 0.01% level

While cross 2 was positively significant correlated with panicle length and highly positively with correlated significant of fertility percentage and 1000-grains weight. This was in accordance with Zaazaa and Anis (2014), Al-Wardi *et al.* (2023), Heera *et al.* (2023), Streck (2018) and Chhangte *et al.* (2023) for both crosses who showed grain yield has positively significantly correlated with number of panicles. This was in harmony with Chhangte *et al.* (2023), Al-Wardi *et al.* (2023), Heera *et al.* (2023) and Streck (2018) for cross 2 with fertility percentage, who showed that grain yield /plant was highly significant correlated with fertility percentage. Also, this is agreed with Chhangte *et al.* (2023) for cross 1 with panicle weight, who showed that grain yield /plant was highly significant correlated with panicle weight. This was found to be helpful in encouraging rapid improvement of yield.

CONCLUSION

For every character assessed in both crosses, the additive-dominance model was insufficient, indicating that there is epistasis in the characteristics' inheritance. Epistasis plays a significant role in how these features are inherited. Grain yield/plant of cross Sakha 104 × IM 16 logged a highly significant positive gene action effects while cross GZ9399 × IRRI 148 recorded highly significant negative additive gene effects. The observe duplicate of epistasis was in studied characters for both crosses except panicle length for cross 1 and number of spikelets / panicles for cross 2, had complement. The positive with significant or highly significant correlation values among the grain yield with related traits as panicle length, branches number /panicle, number of panicles/plant and spikelets number / panicle for both crosses and panicle weight for cross 1, and fertility percentage and 1000 grains weight for cross 2, could be measured as index for selection to enhance the grain yield and could contributing in rice grain yield.

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تحديد نموذج الفعل الجيني للمحصول ومكوناته باستخدام تحليل متوسط الأجيال في الأرز

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الملخص

أجريت الدراسة بمزرعة قسم بحوث الأرز بمحطة البحوث الزراعية بسخا مركز البحوث الزراعية – مصر خلال الفترة من 2019 إلى 2022 لهجينين من الأرز. شملت الدراسة خمس عشائر لكل هجين (P1، P2، F1، F2، وF3)، والتي تم اختيارها لصفات محصول الحبوب ومكوناته لتقدير الفعل الجيني باستخدام تحليل متوسط الاجيال. تم استخدام هجينين من الأرز جي زد9399 × أري 148 وسخا 104 × أي أم 16 في هذه الدراسة. أظهرت الاختبارات أن فعل السيادة والاضافة للفعل الجيني الوراثي غير كافي لجميع الصفات التي تم تقييمها في كلا الهجينين، مما يشير إلى وجود التفوق للفعل الجيني الوراثي في وراثة هذه الصفات. حيث أظهر المتوسط العام لكل صفة اختلافات عالية المعنوية للهجين والتراكيب الوراثية المستخدمة، لذلك سجل محصول الحبوب / نبات بالهجين 2 (سخا 104 × أي أم 16) تأثيرات جينية إيجابية عالية الأهمية. ومع ذلك، سجل وزن 1000 حبة تأثيراً جينياً موجباً عالي المعنوية للهجين 1. ومن خلال معامل الارتباط المظهري، ارتبط محصول الحبوب/ النبات ارتباطا إيجابي عالي المعنوية مع عدد الفروع/نبلة، وعدد السنابل/نبات وعدد السنيبلات/ سنبلة في كلا الهجينين. بينما ارتبط محصول الحبوب/نبات في الهجين 1 ارتباطا موجباً وعالي المعنوية مع طول السنبلة ووزن السنبلة. بينما اظهر ارتباطا موجبا مع صفة طول السنبلة وعالي المعنوية مع صفة نسبة الخصوبة ووزن 1000 حبة في الهجين 2.