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Genetic Analysis to Improve Rice (*Oryza sativa* L) Grain Yield Attributes and Quality Traits

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ABSTRACT

The investigation was carried out in rice growing seasons of 2020, 2021 and 2022, comprising P₁, P₂, F₁ and F₂ for three crosses Giza 179 × Suweon 361, Giza 177 × Milyang 349, Giza 177 × Sakha super 300 were used to improve grain yield attributes and quality traits. Therefore, the highest grain yield plant⁻¹ resulted with Sakha Super 300 (50.80 g). While F₁ of the crosses Giza 177 × Sakha super 300 and Giza 179 × Suweon 361 provided the highest values 55.80 and 55.14 g, respectively, and F₂ of the cross (Giza 177 × Sakha super 300) give 50.80 g. The parent Sakha super 300 reported highest milling percentage value 73.06%. While, F₁ of Giza 177 × Sakha super 300 displayed the highest value 74.60%. However, F₂ of cross (Giza 177 × Milyang349) was noted maximum value 62.83%. The degree of dominance was greater than unity (± 1.0) for all the studied traits for the three crosses except panicle length, panicle weight, and fertility percentage for cross 1, panicle length, number of tillers, grain length and head rice for cross 2, and 1000-grain weight, grain length and grain width for cross 3, suggesting the important of over dominance in controlling traits. The first PCA (PC1) was 98.45% of the difference and directionally positive associated with Suweon 361, F₁ of cross (Giza 179 × Suweon 361), F₁ of cross (Giza 177 × Milyang 349), P₂ of cross (Sakha super 300) and F₁ of cross (Giza 177 × Sakha super 300).

Keywords: grain yield, quality, PCA analysis, phenotypic correlation, prediction selection, rice

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important cereal crops, which blocks humanity nutritional needs (Krishnan *et al.*, 2011), serves as the main dietary source for half of the world population (Rasheed *et al.*, 2022). It provides all humans with about 50–80% of the daily calorie's consumption (Seck *et al.* 2012 and Futakuchi *et al.* 2013), because of its high carbohydrate content, a low fats content, moreover, its contents proteins, vitamins, and minerals (Khush, 2005). Rice must be increase up to 9.5 billion by 2050 (Leridon, 2020) to face the rapidly increase of human population. Breeding high-yielding rice varieties became a goal which must be attained (Kurniasih *et al.*, 2021). Grains quality traits dictate market value and have a pivotal role in the adoption of new varieties (Han *et al.*, 2004). It is crucial for rice breeding quality to have high-yielding, high-quality rice types (Lang and Buu., 2004). The quality of various rice products, such as physical appearance, eating, cooking, and processing qualities, are determined by starch properties such as gelatinization temperature (GT) and other physicochemical properties (Kottarachchi *et al.*, 2014). Grain size, amylose content and other different grain qualities are essentially determining acceptability to rice variety (Hori & Sun, 2022). Milling quality is the important trait for rice producers (Cheng *et al.*, 2005). The premium product is a whole, unbroken grain of the appropriate length with a uniform white translucent color. Broken grains result in sharp price reductions (Dunn and Stevens 2017). Genetic variability is necessary for successful selection of superior breeds from segregating generations for further selection (Priyanka *et al.* 2019). Any crop improvement program's ability to succeed is contingent upon both the quantity of genetic diversity found in a crop and the degree of variation that can be inherited from its parents (Bello *et al.* 2012). There is a necessity

to beget information on genetic variance, coefficient of genetic variation and heritability to estimate the progress of their breeding program in the future (Savitha and Ushakumara, 2015). For plant breeders, heritability is regarded as a crucial characteristic since it tells them how far a given trait may be passed down from parent to offspring (Syukur and Rosidah, 2014). The degree of genetic variability and heritability of desirable traits are the two main determinants of crop improvement success. A detailed understanding of the genetic variety that already exists for yield, its components, and grain quality attributes is necessary for the development of high-yielding cultivars. Only the genetic component of the observed variability—which is a composite estimate of environmental and genetic factors—is heritable. However, estimations of heritability must be taken consideration in conjunction with estimates of genetic advancement, as they alone cannot provide a sense of the projected gain in the following generation. Rice's grain yield characteristic is a quantitative trait that is influenced by polygenes. Grain yield characteristic alone is typically not a particularly effective or efficient foundation for selection (El-Refae *et al.* 2021). On the other hand, selection according to its constituent characters might be more dependable and effective. The most widely used multivariate technique for classifying genotypes from a variety of biological backgrounds is principal component analysis (Liu *et al.* 2010). Its assistances to classify the genotypes of analogous groups together compared to different genotypes (Kim *et al.* 2013 and Khatun *et al.* 2023). One method for converting high-dimensional vector data to lower-dimensional data is principal component analysis. It makes the genetic differences between the genotypes for every trait clearer. The aims of this study are quantifying the extent of genetic variation available for grain yield and its components then grain quality characteristics in the

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F₂ segregating generation of rice, in addition to select superior segregant that have high grain quality and high yield; and to assess the selection gain that can be made by selected plant.

MATERIALS AND METHODS

The present investigation was carried out at the Experimental Farm of Rice Research Department, Sakha, Kafr El Sheikh, Egypt, in seasons of 2020, 2021, and 2022. The genetic materials used in this investigation involved three crosses genotypes Giza 179 × Suweon 361, Giza 177 × Milyang 349, Giza 177 × Sakha super 300. Therefore, the pedigree, type and origin were illustrated in Table 1.

Table 1. Type, origin and description of genetic material were used

Genotype	Type	origin	Description
Giza 177	Japonica	Egypt	short stature, early duration- medium grain yield and high grain quality
Giza 179	Indica/Japonica	Egypt	short stature, early duration- high grain yield and medium grain quality
Suweon 361	Japonica	Korean	short stature, moderate duration- medium grain yield and high grain quality
Milyang 349	Japonica	Korean	medium stature, medium duration- medium grain yield and high grain quality
Sakha Super 300	Japonica	Egypt	long stature, late duration- high grain yield and high grain quality

In season 2020, the studied parents were sown on four sowing dates in the summer season with 10-day-intervals. Seedlings were transplanted to the field. Plants were grown in three rows, 5 m long and 25 cm between the plants and rows. The hybridization was conducted among the parents in 2020 to produce the seeds of three F₁ crosses, using Jordon's method (1938). The hybrid seeds of the three crosses were grown in 2021 season to obtain seeds of F₂ generation. In 2022, all the genetic materials of P₁, P₂, F₁ and F₂ were grown in three rows of each P₁ and P₂, one row of F₁, twenty rows of F₂. Randomized complete block design (RCBD) with three replications were used. Twenty-five plants were planted in each row. From each population of F₂, 200 individual plants were selected randomly and all recorded data of vegetative, yield and its components were taken. The transplant of seedlings was done after sowing by 30 days of. 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). 165 N/ha, urea-based nitrogen fertilizer containing 46.5% N was administered in two splits: two thirds was utilized as basal and blended into dry soil prior to flooding irrigation, and one third was applied at maximum tillering stage), and weed control were conducted according to the recommended package at Rice Research Department. The recorded data of parents, F₁ and F₂ generations for traits, plant height (cm), panicle length (cm), panicle weight (g), number of spikelets panicle⁻¹, fertility %, number of tillers plant⁻¹, 1000-grain weight (g), grain yield plant⁻¹ (g), grain length (mm), grain width (mm), grain shape, hulling percentage, milling percentage, head rice percentage and gelatinization temperature. The data were collected according to standard assessment system for rice (IRRI, 2014).

Biometrical analysis for the estimated traits:

Three parameters consisted of three generations with their parents (P₁, P₂, F₁ and F₂), were statistically analyzed based on individual plant using GENES package software

(<http://www.ufv.br/dbg/biodata.htm>, www.ufv.br/dbg/genes/genes.htm). Heritability, and genetic parameters were calculated according to Mather and Jinks (1982). Genetic advance as percentage of the F₂ mean were estimated as reported by Allard (1960). The t-test was used to determine the significance of these parameters where the standard error (SE) was calculated. On the other hand, the expected and actual genetic advance (Δg) was computed according to Johanson *et al.* (1955). Similarly, the genetic gain percentage of the F₂ mean performance ($\Delta g\%$) was estimated using the method of Miller *et al.* (1958). PCA was performed. And phenotypic correlation was performed for F₂ population.

RESULTS AND DISCUSSION

Variance of F₂ population of three crosses showed significant and highly significant for all traits under study (Table 2).

Mean performance

The mean performance was recorded for the three crosses; cross 1 (Giza 179 × Suweon 361), cross 2 (Giza 177 × Milyang 349) and cross 3 (Giza 177 × Sakha Super 300), as shown in Table 2. The mean performance of plant height for P₁, P₂, F₁ and F₂ showed that P₁ of cross 1 (Giza 179), was the desired and shortest plant height. It recorded 88.00 cm. the parents Milyang349 and Sakha super 300 were the shorter and recorded 97.00 and 105.00 cm, respectively. F₂ of the cross 2 (Giza 177 × Milyang 349) was the shortest F₂ mean and recorded 94.11 cm. While the F₁ of all crosses was the tallest and was not desired. Regards panicle length, the parent Suweon 361 of cross1 (Giza 179 × Suweon 361) which recorded 27.4 cm, was the tallest panicle length. The F₁ of cross1 (Giza 179 × Suweon 361) recorded 25.6 cm and it was the longest panicle length, followed by its F₂ cross 2 which recorded 25.49 cm. Concern panicle weight, the genotype Suweon 361 had recorded 4.98 g, followed by cultivar Sakha super 300 of which recorded 4.7 g, were the heaviest panicle weight between the parents of the three crosses. And between populations, however F₁ of cross3 (Giza 177 × Sakha super 300) recorded 5.34 g followed by its F₂ cross 3 which recorded 3.65 g. The cross 1 (Giza 179 × Suweon 361) for both parents (P₁ and P₂) and populations (F₁ and F₂) had the highest spikelets panicle⁻¹ were values 169.10, 184.12, 214.18 and 162.55, respectively. Consequently, the fertility % was high for all the parents except P₂ of cross 2 was 79.14 %, and its F₁ also was low and recorded 78.00 %. While, in its F₂ generation become more fertile and recorded 92.46%. On the contrary for cross 1 both parents were more fertility and recorded 94.23 and 92.15% and its F₁ which recorded 92.72%, while, F₂ declined in fertility % and recorded 75.05%. Concern number of tillers plant⁻¹, the Sakha super 300 of cross 3 gave the highest value 23.00. while F₁ with Giza 177 got higher tillering number 24.00. Whereas, highest F₂ tillering ability recorded for cross 2 (Giza 177 × Milyang349), which recorded 20.79. With respect to grain yield/plant, the Sakha Super 300 resulted 50.80 g plant⁻¹. While the crosses Giza 177 × Sakha super 300 and Giza 179 × Suweon 361 provided the highest values 55.80 and 55.14 g plant⁻¹, respectively. F₂ of the cross 3 (Giza 177 × Sakha super 300) noted the highest values 50.80 g plant⁻¹. For grain length, the cultivar Giza 177 had reported longest grain (7.80 mm). While, F₁ of cross 2 (Giza 177 × Milyang349) was longest grain and recorded 7.54 mm. F₂ of cross 3 (Giza 177 × Sakha super 300) was the longest grain and recorded 7.39 mm. Regarding grain breadth, the genotype Milyang349 was the widest grain 3.80 mm. While,

cross 2 (Giza 177 × Milyang349) was longest grain 3.82 mm. F₂ of cross Giza 177 × Sakha super 300 was the longest grain 3.57 mm. the genotype Milyang349 was provided the largest shape

value 2.72 mm. While, cross Giza 177 × Milyang349 was obtained largest shape 2.82 mm. F₂ of cross Giza 177 × Sakha super 300 was the largest shape 2.79 mm.

Table 2. F₂ variance and mean performance of vegetative, yield and its yield components, and grain quality characters for three crosses.

Trait	Cross	F2 Variance	Mean performance			
			P1± SE	P2± SE	F1± SE	F2± SE
Plant height (cm)	1	96.06**	89.98±1.41	121.44±0.84	123.84±1.14	108.83±9.77
	2	120.08**	104.80±0.84	97.00±1.58	124.60±1.14	94.11±10.96
	3	129.01**	105.20±0.84	105.00±1.00	122.80±0.84	107.83±11.36
Panicle length (cm)	1	6.90**	23.50±0.55	26.51±0.55	25.76±0.55	25.61±2.61
	2	5.79**	17.60±0.55	23.2±0.84	21.8±0.84	21.03±2.41
	3	5.76**	18.00±0.71	19.4±0.55	20.5±0.50	20.34±2.4
Panicle weight (g)	1	1.38**	4.54±0.35	4.98±0.11	4.69±0.13	3.34±1.17
	2	1.001**	3.50±0.16	3.90±0.16	4.40±0.16	3.21±1.00
	3	1.46**	3.46±0.11	4.70±0.10	5.34±0.15	3.65±1.21
Number of Spikelets panicle ⁻¹	1	1632.16**	169.10±1.58	184.12±1.00	214.18±1.58	162.55±47.72
	2	1987.31**	121.00±1.58	175.00±1.58	190.00±1.58	126.29±44.58
	3	2030.11**	121.6±1.14	170.2±1.48	188.4±2.07	139.26±45.06
Fertility %	1	236.00**	94.23±0.84	92.15±1.30	92.72±0.84	75.05±15.31
	2	54.39**	94.22±2.53	79.14±1.02	78.00±1.58	92.46±7.37
	3	47.26**	95.80±0.83	95.20±0.84	91.80±0.84	91.37±6.87
Number of tillers plant ⁻¹	1	14.8**	20.80±0.84	20.80±0.84	25.26±0.84	15.5±3.85
	2	44.67**	19.20±0.84	22.60±0.55	20.80±0.84	20.79±6.68
	3	59.05**	18.80±0.84	23.00±0.71	24.00±1.00	20.36±7.68
1000-grains weight (g)	1	4.71**	24.30±0.45	25.76±0.96	23.92±0.68	22.07±2.12
	2	5.35**	28.18±0.70	23.48±0.41	29.70±0.71	27.62±4.82
	3	6.98**	27.88±0.37	26.36±0.33	27.16±0.78	26.7±2.64
Grains yield plant ⁻¹ (g)	1	210.74**	49.12±1.00	42.10±1.00	55.14±1.58	44.68±14.42
	2	383.77**	40.20±1.30	44.40±1.67	50.00±2.55	43.36±19.59
	3	548.86*	40.20±1.30	47.00±1.58	55.80±0.84	50.80±23.43
Grain length (mm)	1	0.07**	5.43±0.11	5.01±0.15	5.50±0.22	5.42±0.36
	2	0.062**	7.80±0.13	5.30±0.13	7.54±0.30	5.41±0.35
	3	0.068**	7.80±0.13	6.32±0.08	7.46±0.22	7.39±0.36
Grain width (mm)	1	0.01**	2.62±0.06	2.63±0.08	2.60±0.06	2.59±0.10
	2	0.012**	3.34±0.05	3.8±0.07	3.82±0.08	2.58±0.11
	3	0.012**	3.34±0.05	3.62±0.08	3.60±0.06	3.57±0.1
Grain shape	1	0.02**	2.08±0.06	2.03±0.13	2.13±0.08	2.10±0.23
	2	0.018**	2.3±0.05	2.72±0.06	2.82±0.11	2.11±0.23
	3	0.017**	2.3±0.05	2.06±0.04	2.36±0.06	2.79±0.23
Hulling (%)	1	54.49**	75.92±2.88	87.95±3.05	89.74±3.77	78.79±7.33
	2	53.85**	79.16±1.27	80.2±2.86	81.00±1.58	78.99±7.34
	3	46.87**	79.16±1.27	81.62±1.09	82.40±0.84	78.83±6.85
Milling (%)	1	60.53**	56.66±1.52	63.04±3.03	64.96±1.34	58.65±7.74
	2	48.24**	69.6±0.37	71.2±0.84	74.20±1.92	62.83±6.95
	3	58.01**	69.6±0.37	73.06±1.13	74.60±1.14	58.74±7.62
Head rice (%)	1	64.49**	53.23±2.45	57.03±3.56	59.96±1.52	52.29±7.99
	2	65.15**	60.68±1.25	59.80±1.14	60.40±1.00	52.86±8.07
	3	58.47**	60.68±1.25	66.50±1.3	70.40±4.39	52.78±7.65
Gelatinization temperature (°C)	1	0.75**	2.61±0.55	2.41±0.55	3.22±0.45	2.89±0.87
	2	0.69**	4.60±0.55	5.20±0.5	5.40±0.55	3.03±0.83
	3	0.85**	4.60±0.55	5.12±0.28	4.60±0.18	3.80±0.92

Cross 1: Giza 179 × Suweon 361, Cross 2: Giza 177 × Milyang 349, Cross 3: Giza 177 × Sakha super 300. High significance at 1% ()** and significant at 5% (*) level.

Concern hulling %, genotype Suweon 361 was the superior value 87.95%. While, cross Giza 179 × Suweon 361 was recorded the highest 89.74%. Although, F₂ of cross Giza 177 × Milyang349 recorded the highest value 78.99%. the parent Sakha super 300 reported highest milling percentage value 73.06%. While, F₁ Giza 177 × Sakha super 300 displayed the highest value 74.60%. However, F₂ of cross 2 (Giza 177 × Milyang349) was the noted maximum value 62.83%. For head rice %, P₂ of cross 3 (Sakha super 300) was the highest and recorded 66.50%. While, F₁ of cross 3 (Giza 177 × Sakha super 300) was the highest and recorded 70.40%. However, F₂ of cross 2 (Giza 177 × Milyang349) was the highest and recorded 52.86%. therefore, genotype Milyang349 achieved the highest value of gelatinization temperature were 5.20 °C. While, F₁ of cross 2 (Giza 177 × Sakha super 300) was the highest and recorded 5.40 °C. However, F₂ of cross 3 (Giza 177 × Milyang349) was the highest and recorded 3.80 °C.

As the purpose of this study was to improve yield and yield component and grain quality of parents Giza177 and Giza 179. Although of merit of these smart varieties, but Giza 179 needs to improve hulling %, milling % and head rice % grain quality traits. From range value, maximum value in F₂ showed some improved lines of F₂ values of yield and yield components traits and high grain quality traits; especially for cross 1 (Giza 179 × Suweon 361). Hulling %, milling%, head rice% and gelatinization temperature maximum value in F₂ of cross 1 reached to 93.92, 71.71, 64.49 and 5.05, respectively comparing to the parent Giza 179 which recorded 75.9, 56.66, 53.23 and 2.61, respectively (Table 2). Also, the three crosses improved yield and yield related traits; grain yield plant⁻¹(57.70, 56.40 and 61.00 g plant⁻¹) maximum value F₂ for cross1, cross2 and cross3, respectively, than parents: P₁, P₂ and F₁; 49.12, 40.20 and 40.20), fertility% (98.20, 97.60 and 97.00 %) maximum value F₂ for cross1, cross2 and cross3, respectively, than parents: P₁, P₂ and

F₁; 94.23, 94.22 and 95.80), 1000-grain weight (32.26, 35.70 and 32.30 g), maximum value F₂ for cross1, cross2 and cross3, respectively, than parents: P₁, P₂ and F₁; 24.30, 28.18 and 27.88) and number of tillers plant⁻¹ (31.67, 32.00 and 34.00), maximum value F₂ for cross1, cross2 and cross3, respectively, than parents: P₁, P₂ and F₁; 20.80, 19.20 and 18.80).

Degree of dominance:

As shown in Table 3, the degree of dominance was greater than unity (± 1.0) for all the studied traits for the three crosses except panicle length, panicle weight, and fertility percentage for cross 1, panicle length, number of tillers, grain length and head rice for cross 2, and 1000-grain, grain length weight and grain width for cross 3, suggesting the important of over dominance in controlling traits. On the other side, the degree of dominance was lower than unity for those traits of panicle length, panicle weight, fertility percentage in cross 1, panicle length, number of tillers, grain length and head rice in cross 2, and 1000 grains, grain length weight and grain width for cross 3. This ratio which lies between zero and unity, express partial or incomplete dominance which occupy itself an obvious role in the inheritance of such traits. Similar results were previously reported by Hassan (2012). The estimates of minimum number of effective factors according ($Amp = \text{Max}$

$F_2 - \text{Min } F_2$) were ranged between 2.042 and 10.25 pairs of genes for spikelets panicle⁻¹ and grain shape, respectively in cross 1. While, the estimates of minimum number of effective factors were ranged between 2.06 and 9.44 pairs of genes for spikelets panicle⁻¹ and fertility percentage respectively in the studied cross 2. Also, the estimates of minimum number of effective factors were ranged between 1.82 and 6.61 pairs of genes for milling % and grain length, respectively in cross 3. The results in general, revealed that plant height in cross 1, fertility % and grain shape in cross 2, grain width and milling % cross 3, were controlled by almost one pairs of effective genes suggesting that these traits were inherited as a simple trait. Other remain traits in the three crosses were probably controlled by two to ten pairs of genes, indicating that these traits were inherited as a complicated or quantitative traits. So, selection in late segregating generations plays a basic role in the inheritance traits. The estimates of minimum number of effective factors according ($Amp = \mu P_1 - \mu P_2$) were ranged between zero (for fertility %, number of tillers and grain width) and 1.29 pairs of genes for plant height, in cross 1. While, the estimates of minimum number of effective factors were ranged between 0.002 and 18.45 pairs of genes for head rice and grain length, respectively in the studied cross 2.

Table 3. P₁ mean, F₂ maximum and minimum values, degree of dominance and number of genes

Trait	Cross	P ₁ mean	F ₂		Degree of dominance	Number of genes (Amp = Max F ₂ - Min F ₂)	Number of genes (Amp = $\mu P_1 - \mu P_2$)
			Max.-	Min.			
Plant height (cm)	1	89.98	138.40-	90.00	-1.15	3.062	1.29
	2	104.80	125.00-	65.00	6.08	3.77	0.06
	3	105.20	135.00-	84.00	17.7	2.53	0.00004
Panicle length (cm)	1	23.50	33.33 -	18.12	-0.50	4.47	0.18
	2	17.60	27.00 -	15.00	-0.50	3.27	0.71
	3	18.00	26.00 -	12.00	-2.57	4.65	0.046
Panicle weight (g)	1	4.54	7.16 -	1.31	0.34	3.27	0.02
	2	3.50	5.30 -	0.60	-3.50	2.83	0.02
	3	3.46	7.80-	1.40	-2.03	3.53	0.132
Spikelets panicle-1	1	169.10	216.80-	53.70	-5.00	2.042	0.017
	2	121.00	232.00-	51.00	-1.56	2.06	0.18
	3	121.60	262.00-	58.00	-1.74	2.56	0.145
Fertility %	1	94.23	98.20-	27.27	-0.46	2.83	0.00
	2	94.22	97.60-	54.50	-1.15	9.44	1.06
	3	95.80	97.00-	67.70	-12.33	2.62	0.0009
Number of tillers	1	20.80	31.67-	8.08	88.33	5.32	0.00
	2	19.20	32.00-	7.00	0.06	4.11	0.03
	3	18.80	34.00-	8.00	-1.47	3.77	0.037
1000-grains weight (g)	1	24.30	32.26-	17.14	1.53	6.65	0.06
	2	28.18	35.70-	18.80	1.65	6.84	0.11
	3	27.88	32.30-	20.90	0.052	2.37	0.042
Grains yield plant ⁻¹ (g)	1	49.12	57.70-	15.12	2.71	4.078	0.029
	2	40.20	56.40-	7.40	-3.67	2.65	0.01
	3	40.20	61.00-	14.00	-3.58	2.19	0.010
Grain length (mm)	1	5.43	6.57-	4.89	1.34	6.29	0.38
	2	7.80	6.50-	4.90	0.79	7.56	18.45
	3	7.80	8.50-	6.90	0.540	6.61	5.65
Grain width (mm)	1	2.62	2.82-	2.26	5.11	6.60	0.00
	2	3.34	2.80-	2.30	-1.09	3.32	2.81
	3	3.34	3.80-	3.30	-0.85	3.36	1.05
Grain shape	1	2.08	2.54-	1.79	2.89	10.25	0.05
	2	2.30	2.50-	1.80	-1.48	4.66	1.68
	3	2.30	3.20-	2.50	1.50	4.87	0.57
Hulling (%)	1	75.92	93.92-	61.80	-1.30	2.88	0.40
	2	79.16	93.00-	62.00	-2.538	2.300	0.003
	3	79.16	93.00-	62.00	-1.63	2.65	0.016
Milling (%)	1	56.66	71.71-	41.79	-1.60	2.07	0.09
	2	69.60	78.00-	42.00	-4.75	3.37	0.01
	3	69.60	71.00-	42.00	-1.89	1.82	0.03
Head rice (%)	1	53.23	64.49-	30.99	-2.54	2.58	0.03
	2	60.68	68.00-	31.00	0.364	2.691	0.002
	3	60.68	64.00-	31.00	-2.34	2.39	0.07
Gelatinization temperature (°C)	1	2.61	5.05-	1.99	7.03	2.62	0.01
	2	4.60	5.00-	2.00	-1.667	2.835	0.113
	3	4.60	5.00-	2.00	1.00	2.04	0.06

Cross 1: Giza 179 × Suweon 361, Cross 2: Giza 177 × Milyang 349, Cross 3: Giza 177 × Sakha super 300.

Also, the estimates of minimum number of effective factors were ranged between 0.00004 and 5.65 pairs of genes for plant height and grain length, respectively in cross 3. The results in general, revealed that grain length in cross 2 and 3, grain width in cross 2 were controlled by almost five to eighteen pairs of effective genes suggesting that these traits were inherited as a complicated or quantitative traits. Similar results were previously reported by Hassan (2012). So, selection in late segregating generations was important and play a remarkable role in the inheritance such traits. On the other hand, the other remaining traits were inherited as a simple trait.

Heritability

Heritability ($h^2b\%$) of the characters ranged from 40.20% for grain shape to 99.74% for spikelets panicle⁻¹, in Cross 1. In Cross 2, heritability ranged from 49.54% for fertility % to 99.87 % for spikelets panicle⁻¹. The ranges in Cross 3 were from 64.72% for gelatinization temperature to 99.93% for spikelets panicle⁻¹ (Table 4). It demonstrates that the largest proportion of the phenotypic expression of traits in parents and F₁, F₂ hybrids is genetic variance. High level heritability for grain yield was reported in the three crosses. These data were in accordance with

Gyawali *et al.* (2018) and Talha (2021) may be due to the influence of the environment on the yield as it is polygenic trait. The majority of the studied traits had a high heritability which was in accordance with Jadhav *et al.* (2020), Palaniyappan *et al.* (2020), Gupta *et al.* (2021), and Singh *et al.* (2021),, also reported high heritability for these traits. The moderate heritability was noted for grain length, grain width and grain shape in the three crosses; cross 1 (76.59%, 51.96% and 40.20%), cross 2 (67.92%, 75.81% and 72.45%) and cross 3 (70.75%, 75.60% and 71.52%). Also, moderate heritability was recorded for gelatinization temperature in cross 3 (64.72%). While, moderately heritability was recorded for fertility % in cross 2 (49.54%). The data of spikelet fertility % were in accordance with data of Jaiswal *et al.* (2015). The high heritability indicates greater role of genetic on the expression of the traits, thus, direct selection for these traits will be effective. These genetic and non-genetic components can be explained by using a quantitative genetic model, where the phenotypic variance is a result of possible interactions between environmental and genotypic variance (Demeke *et al.*, 2023). In this study, the genotypic variance values of all traits participates the major partion of phenotype (Table 4).

Table 4. Phenotypic and genotypic variance, heritability, heterosis over mid and better parent for grain yield attributies and quality traits

Trait	Cross	Phenotypic variance	Genotypic variance	Heritability in Broad sense (%)	Heterosis (mid parent) (%)	Heterosis (better parent) (%)
Plant height (cm)	1	96.06	95.61	99.52	17.15*	37.63*
	2	120.09	119.39	99.42	23.49**	28.45**
	3	129.01	128.31	99.45	16.8*	16.7*
Panicle length (cm)	1	6.90	6.46	93.62	3.00	-2.84
	2	5.80	5.50	94.83	6.86	-6.03
	3	5.76	5.26	91.32	9.62	5.67
Panicle weight (g)	1	1.38	1.31	94.94	-0.02	-0.06
	2	1.001	0.976	97.50	18.91*	12.82*
	3	1.46	1.44	99.10	30.88**	13.61*
Spikelets panicle ⁻¹	1	1632.16	1628.04	99.74	21.27**	16.32*
	2	1987.32	1984.82	99.87	28.38**	8.57
	3	2030.11	2028.8	99.93	29.12**	10.69*
Fertility %	1	236.00	234.59	99.40	-0.51	-1.61
	2	54.39	26.94	49.54	-10.01*	-17.22*
	3	47.26	46.56	98.51	-3.8	-4.17
Number of tillers plant ⁻¹	1	14.84	14.1	95.50	21.18**	21.18**
	2	44.67	43.97	98.43	-0.48	-7.96
	3	59.05	58.35	98.81	14.8*	4.34
1000-Grains weight (g)	1	4.71	4.30	91.37	-4.44	-7.14
	2	25.36	24.87	98.08	14.98*	5.39
	3	6.98	6.84	98.03	0.14	-2.58
Grains yield plant ⁻¹ (g)	1	210.74	209.38	99.35	20.8**	12.24*
	2	383.77	382.07	99.56	18.20*	12.61*
	3	548.86	547.16	99.69	27.98**	18.72*
Grain length (mm)	1	0.07	0.06	76.59	5.30	1.29
	2	0.06	0.04	67.92	15.11*	-3.33
	3	0.06	0.048	70.75	5.66	-4.35
Grain width (mm)	1	0.01	0.01	51.96	-1.11	-1.32
	2	0.012	0.009	75.81	7.00	0.53
	3	0.012	0.009	75.60	3.44	-0.55
Grain shape	1	0.02	0.01	40.20	3.66	2.36
	2	0.018	0.013	72.450	12.35*	3.68
	3	0.017	0.012	71.52	8.25	2.60
Hulling (%)	1	54.49	44.76	82.15	9.52	2.03
	2	53.857	52.229	96.977	1.65	0.99
	3	46.87	6.02	96.52	2.50	0.95
Milling (%)	1	60.53	54.09	89.36	8.54	3.04
	2	48.24	48.10	99.70	5.40	4.21
	3	58.01	57.86	99.75	4.58	2.11
Head rice (%)	1	64.49	54.47	84.46	8.77	5.14
	2	65.16	63.60	97.61	0.27	-0.46
	3	58.47	56.92	97.34	10.71*	5.86
Gelatinization temperature (°C)	1	0.75	0.45	59.26	28.18**	23.24**
	2	0.697	0.397	56.95	10.20*	3.846
	3	0.85	0.55	64.72	-5.35	-10.16

Cross 1: Giza 179 × Suweon 361, Cross 2: Giza 177 × Milyang 349, Cross 3: Giza 177 × Sakha super 300. * is significant and ** is high significant

Heterosis and heterobeltiosis

The best desirable significant and high significant heterosis over mid-parents was found with characteristic, panicle weight for crosses 2 and 3, spikelets number panicle⁻¹ for crosses 1, 2 and 3, number of tillers plant⁻¹ for cross 1, 1000-grains weight for cross 2, grain yield plant⁻¹ for crosses 1, 2 and 3, grain length for cross 2, grain shape for cross 2, head rice for cross 3 and gelatinization temperature for cross 1. Therefore, the desirable significant and highly significant heterosis over better parent (heterobeltiosis) were shown with panicle weight for crosses 2 and 3, spikelets number panicle⁻¹ for crosses 1 and 3, number of tillers plant⁻¹ for cross 1, grains yield plant⁻¹ for crosses 1, 2 and 3 and gelatinization temperature for cross 1. Similar results were reported earlier by Shehata *et al.* (2009), El-Rewainy *et al.* (2011) and Hassan (2012).

Selection differential (S):

Refers to the change of mean performance from selected population (X⁻S) to the origin or base population (X⁻0) and consider as an indicator for artificial selection (Acquaah, 2012). In this study the number of selected

individuals was 2 and intensity of selection (i) at 5.8, as shown in Table 5. The cross 1 (Giza 179 × Suweon 361) showed that selection differential (S) ranged from -0.9 to 39.55 for F₂ generation for gelatinization temperature and grain yield plant⁻¹, respectively (Table 4). While, cross 2 (Giza 177 × Milyang 349) ranged from -21.62 to 103.21 for plant height and spikelet panicle⁻¹, respectively. Also, cross 3 (Giza 177 × Sakha super 300) ranged from -23.83 to 119.73 for plant height and spikelet panicle⁻¹, respectively. The selection gain values were recorded the lowest values 12.36 for grain width in cross 1, 18.16 for grain length in cross 2 and 13.59 for grain width in cross 3 of F₂ generation. The highest values 193.45 for panicle weight in cross 1, 260.83 for grain yield plant⁻¹ in cross 2, and 216.25 for number of tillers in cross 3, as shown in Table 4. Our results matched to the findings of Aziz *et al.* (2014) and Kumar and Katageri (2017), who also found positive response to selection for yield and its components. Selecting the characters as fertility % contributing to the yield together will improve the grain yield in the next segregating population (Ibrahim *et al.* 2018).

Table 5. Selection differential, selection gain, selection gain (%) and predicted mean for the first cycle after selection for three crosses of traits studied

Traits	Cross	Selection differential	Selection gain	Selection gain (%)	Predicted mean for the first cycle after selection
Plant height (cm)	1	-18.77	56.57	51.98	52.25
	2	-21.62	63.19	67.14	30.93
	3	-23.83	65.52	60.76	42.31
Panicle length (cm)	1	6.42	14.26	55.69	39.88
	2	5.47	13.24	62.96	34.28
	3	5.65	12.7	62.5	33.06
Panicle weight (g)	1	3.32	6.46	193.45	9.80
	2	2.036	5.66	176.07	8.87
	3	3.80	6.94	190.33	10.59
Spikelets panicle ⁻¹	1	53.74	233.7	143.78	396.28
	2	103.21	258.23	204.48	384.53
	3	119.73	261.16	187.52	400.42
Fertility %	1	24.58	88.57	118.02	163.62
	2	6.85	21.19	22.92	113.64
	3	7.62	39.28	42.99	130.65
Number of tillers plant ⁻¹	1	13.93	21.36	137.7	36.87
	2	19.71	38.16	183.52	58.95
	3	25.63	44.04	216.25	64.41
1000 Grains weight (g)	1	7.69	11.50	52.08	33.57
	2	21.77	28.65	103.69	56.27
	3	5.59	15.02	56.28	41.73
Grains yield plant ⁻¹ (g)	1	39.55	83.65	187.21	128.34
	2	53.48	113.12	260.83	156.49
	3	56.7	135.46	266.65	186.26
Grain length (mm)	1	1.03	1.20	22.08	6.61
	2	0.98	0.98	18.16	6.40
	3	1.005	1.07	14.51	8.46
Grain width (mm)	1	0.23	0.32	12.36	2.91
	2	0.21	0.49	18.91	3.08
	3	0.22	0.48	13.59	4.064
Grain shape	1	0.35	0.30	14.35	2.41
	2	0.38	0.57	26.72	2.68
	3	0.35	0.54	19.64	3.34
Hulling (%)	1	15.13	35.17	44.64	113.96
	2	14.01	41.28	52.26	120.27
	3	14.16	38.33	48.62	117.16
Milling (%)	1	13.03	40.32	68.76	98.97
	2	15.17	40.16	63.92	103.00
	3	12.26	44.06	75.01	102.81
Head rice (%)	1	12.17	39.34	75.23	91.63
	2	14.13	45.70	86.44	98.57
	3	11.22	43.17	81.79	95.95
Gelatinization Temperature (°C)	1	-0.90	2.98	103.33	5.87
	2	1.98	2.76	91.15	5.78
	3	1.20	3.46	91.10	7.26

Cross 1: Giza 179 × Suweon 361, Cross 2: Giza 177 × Milyang 349, Cross 3: Giza 177 × Sakha super 300.

Principle components analysis (PCA):

The first eight principal components with eigenvalues greater than one were found in the principal components of analysis (Table 6). Other principal components showed eigenvalues less than one were deemed non-significant and were therefore overlooked because they were unlikely to have any functional meaning (Altaher & Singh, 2003). Then there were eight main components of which the eigenvalues of PC1-PC8 were 27710.46, 311.13, 60.06, 38.90, 14.41, 6.45,

2.73 and 1.70, respectively. The first and second principal components were responsible for about 98.45 % and 1.11% of the total variation, respectively. Similarly, the overall variation was contributed by the first one major principal component (Subramanian *et al.* 2019, Raiza Christina *et al.* 2021). The percentage proportions of genotypes in the first principal component with higher eigenvectors suggested that these genotypes contributed more to the overall clustering of the populations.

Table 6. Eigen values, variance %, and cumulative variance % of three crosses for principal components.

Component	PC ₁	PC ₂	PC ₃	PC ₄	PC ₅	PC ₆	PC ₇	PC ₈	PC ₉	PC ₁₀	PC ₁₁	PC ₁₂
Eigen-value	27710	311.13	60.06	38.9	14.41	6.45	2.73	1.7	0.36	0.06	0.01	0.01
Variance [%]	98.45	1.11	0.21	0.14	0.05	0.02	0.01	0.01	0	0	0	0
Cumulative Variance [%]	98.45	99.56	99.77	99.91	99.96	99.98	99.99	100	100	100	100	100
Cross 1	P1	0.28	0.32	0.35	0.28	0.24	0.29	0.32	0.24	0.24	0.3	0.32
	P2	-0.11	-0.11	-0.39	-0.13	0.5	-0.2	-0.25	0.35	0.51	0.04	-0.1
	F1	0.69	-0.09	0.1	-0.25	-0.14	0.14	-0.52	0.22	-0.11	0.21	-0.17
	F2	0.09	0.39	0.26	0.27	-0.1	-0.48	-0.16	0.1	-0.07	-0.42	-0.28
Cross 2	P1	-0.15	0.48	-0.1	0.21	0.08	0.41	-0.09	0.12	0.08	-0.02	-0.54
	P2	-0.01	-0.51	-0.13	0.37	-0.13	0.38	0.17	0.41	-0.19	-0.27	-0.2
	F1	-0.19	-0.11	0.05	0.56	0.03	0.13	-0.66	-0.24	0.04	0.06	0.34
	F2	0.54	0.01	-0.54	0.44	-0.02	-0.26	0.22	-0.2	0.1	-0.02	0.03
Cross 3	P1	-0.07	0.31	-0.27	-0.07	-0.14	-0.07	-0.1	0.57	-0.28	-0.2	0.54
	P2	-0.2	0.12	-0.25	0.14	-0.02	-0.19	0.02	0.07	-0.48	0.7	-0.18
	F1	0.08	-0.22	0.3	0.12	0.69	-0.21	0.04	0.1	-0.42	-0.08	-0.04
	F2	-0.14	-0.25	0.32	0.21	-0.37	-0.38	0.07	0.37	0.34	0.28	-0.09

Rice enhancement can be more successful if selection efforts are focused on these genotypes. Generally, data in Table 5 suggest that since the entire variation cannot be explained by a few principal components, the principal component analysis revealed a high degree of variability among the genotypes studied (Tiruneh *et al.* 2019). The first two principal components, which account for 99.56% of the variance, were plotted to see if there were any relationships between the rice characteristics under study. These data were in accordance with Bassuony *et al.* (2022).

The first PCA (PC1) was 98.45% of the difference and directionally positive associated with Suweon 361, F₁ of cross 1 (Giza 179 × Suweon 361), F₁ of cross 2 (Giza 177 × Milyang 349), P₂ of cross 3 (Sakha super 300) and F₁ of cross 3 (Giza 177 × Sakha super 300). It was directionally negative associated with P₁ of cross 1 (Giza 179), F₂ of cross 1 (Giza 179 × Suweon 361) and P₂ of cross 2 (Milyang349). The PC2 represents 1.11% of the total variation and positive associated with P₁ of cross 2 (Giza 177), P₁ of cross 3 (Giza 177) and F₂ of cross 2. It was associated with F₂ cross 3 negative directions. The first component was strongly correlated to F₁

of cross 1 (Giza 179 × Suweon 361) followed by F₂ of cross 2 (Giza 177 × Milyang 349) (Table 5). While, the second component was strongly correlated with P₁ of cross 2 (Giza 177) then, F₂ of cross 1 (Giza 179 × Suweon 361). P₁ of cross 1 (Giza 179) was positively correlated to the third component. Followed by P₂ of cross 2 (Giza 177) was strongly correlated to the fourth component. P₁ of cross 3 (Giza 177) correlated to the fifth component (Figure 1). This explains a wide range of variability between parents and its crosses combination and suggests that these genetic materials vary together.

A two-dimensional diagram (Figure 1) could divide the genotypes into four groups: group1 included the two parents; Suweon 361, Sakha super 300, and all the F₁ of the three crosses; F₁ of Giza 179 × Suweon 361, F₁ of Giza 177 × Milyang 349, and F₁ of Giza 177 × Sakha super 300, which were high yield. Group-2 included genotypes Giza 179 and Milyang 349, and F₂ of Giza 179 × Suweon 3 61 that showed medium performance for grain yield. Group-3 Giza 177 and F₂ of Giza 177 × Milyang 349, included genotypes with lower grain yield. Group-4 includes F₂ of Giza 177 × Sakha super 300, with highest grain yield.

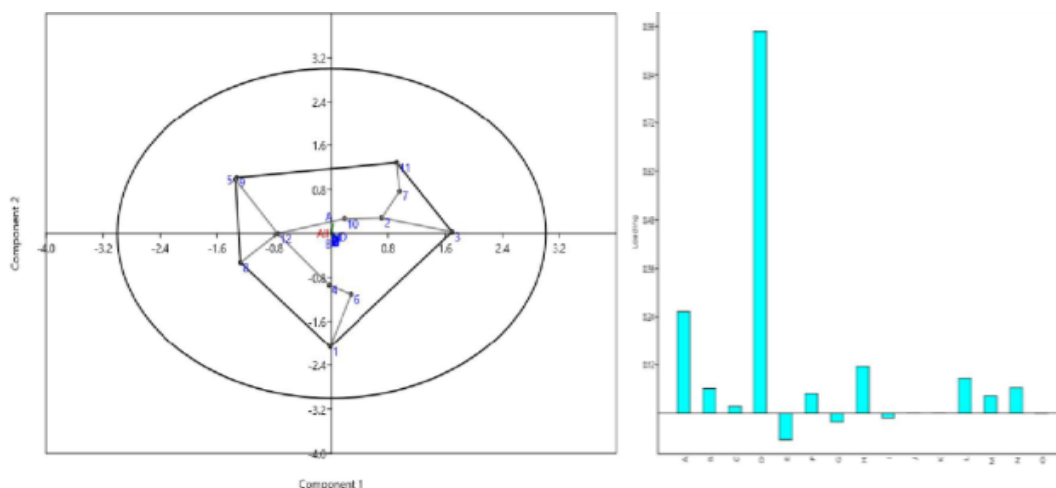


Figure 1. Two-dimensional scheme of PC1 and PC2 for 12 rice genetic components.

Correlation coefficient analysis

Phenotypic correlation measure the relationship between various plant characters and determine the component characters as a basis of selection for yield improvement. Yield is the totality of many component characters which directly or indirectly contribute to it. The estimates of the correlation coefficient among all the studied characters are presented in Table 7. Concerning panicle weight, it was highly significant and positively correlated with panicle length in the three crosses. This result was in accordance with Bassuony *et al.* (2021). Also, panicle weight negatively highly correlated with plant height in cross 3. For spikelets panicle⁻¹, the highly significant and positively correlated with panicle length and panicle weight in crosse 1

and 2. Fertility % was highly significant and positively correlated with panicle weight in the three crosses. Plant height was highly significant and positively correlated with fertility % and grain yield plant⁻¹ in cross 1. Plant height was significant and positively correlated with 1000-grain weight and number of tillers in cross 1. 1000-grain weight was highly significant and positively correlated with panicle weight and fertility %, and significantly and positively correlated with spikelets panicle⁻¹ in cross 3. Grain yield plant⁻¹ was significant or highly significant and positively correlated with panicle weight and spikelets panicle⁻¹ in the three crosses, with panicle length in cross 1 and 3, and with fertility % in cross 2, with plant height and number of tillers in cross 1.

Table 7. Phenotypic correlation of studied characters of three crosses

	Cross	Plant height (cm)	Panicle length (cm)	Panicle weight (g)	Spikelets panicle ⁻¹	Fertility %	Number of tillers plant ⁻¹	1000-grains weight (g)	Grains yield plant ⁻¹ (g)	Grain length (mm)	Grain width (mm)	Grain shape	Hulling (%)	Milling (%)	Head rice (%)
Panicle length (cm)	1	0.06													
	2	0.02													
	3	-0.02													
Panicle weight (g)	1	0.08	0.55**												
	2	0.06	0.46**												
	3	-0.27**	0.31**												
Spikelets panicle ⁻¹	1	0.01	0.52**	0.64**											
	2	0.04	0.43**	0.39**											
	3	-0.18	0.41	0.55											
Fertility %	1	0.30**	0.17	0.51**	0.14										
	2	0.06	0.18	0.38**	0.12										
	3	-0.13	0.14	0.38**	0.16										
Number of tillers plant ⁻¹	1	0.21	0.02	-0.08	0.03	-0.05									
	2	-0.08	0.00	-0.07	-0.02	-0.13									
	3	0.21*	-0.08	-0.11	-0.16	-0.13									
1000-grains weight (g)	1	0.20*	-0.05	0.17	-0.09	0.14	-0.13								
	2	0.11	0.00	-0.02	0.10	0.08	-0.14								
	3	-0.05	0.15	0.44**	0.21*	0.36**	-0.16								
Grains yield plant ⁻¹ (g)	1	0.22*	0.23*	0.25*	0.24*	0.15	0.50**	0.00							
	2	0.03	0.11	0.25*	0.21*	0.26**	-0.11	0.02							
	3	-0.12	0.29**	0.38**	0.29**	0.14	-0.18	0.19							
Grain length (mm)	1	0.03	-0.01	-0.07	-0.06	0.05	-0.14	-0.08	0.04						
	2	0.10	-0.14	-0.10	-0.01	-0.01	0.01	-0.05	0.09						
	3	-0.18	0.12	0.14	0.14	-0.02	0.05	0.11	0.07						
Grain width (mm)	1	0.05	0.06	-0.02	-0.02	0.16	0.05	0.00	0.06	0.08					
	2	-0.15	-0.03	-0.03	-0.03	0.13	0.04	0.21*	0.03	0.12					
	3	-0.11	0.08	0.10	0.09	-0.12	-0.03	0.02	0.16	0.08					
Grain shape	1	-0.01	-0.05	-0.04	-0.03	-0.07	-0.14	-0.06	-0.02	0.74**	-0.61**				
	2	0.07	-0.20**	-0.15	-0.13	-0.04	0.04	-0.08	-0.08	0.50**	-0.32**				
	3	-0.06	0.03	0.04	0.04	0.06	0.06	0.07	-0.05	0.74**	-0.61**				
Hulling (%)	1	-0.11	-0.14	0.02	0.00	0.03	-0.12	-0.06	-0.10	0.01	0.00	0.00			
	2	0.09	0.06	0.02	0.06	-0.18	-0.15	0.10	0.05	-0.02	-0.07	-0.04			
	3	-0.06	-0.03	0.03	-0.02	0.19	0.03	-0.07	0.04	0.03	0.00	0.01			
Milling (%)	1	-0.09	-0.09	0.04	0.02	-0.01	-0.15	0.07	-0.09	-0.02	-0.14	0.08	0.42**		
	2	-0.06	-0.05	0.07	0.00	-0.01	0.01	-0.07	0.09	0.20	0.18	0.17	0.11		
	3	-0.07	-0.09	-0.13	-0.13	0.01	0.11	-0.09	0.00	-0.03	-0.13	0.07	0.37		
Head rice (%)	1	-0.11	-0.06	-0.01	-0.01	-0.04	-0.15	0.05	-0.08	-0.02	-0.11	0.06	0.37**	0.97**	
	2	-0.07	0.00	-0.06	0.04	0.07	-0.07	0.09	-0.03	-0.06	-0.06	0.04	0.34**	0.14	
	3	-0.09	-0.05	-0.11	-0.07	0.02	0.08	-0.11	0.01	0.03	-0.09	0.09	0.26**	0.87**	
Gelatinization Temperature (°C)	1	-0.06	-0.19	0.00	-0.05	0.03	-0.02	0.00	-0.07	0.09	-0.02	0.07	0.39**	0.28**	0.27**
	2	0.03	-0.03	-0.05	0.10	-0.16	-0.12	-0.12	0.06	0.07	-0.11	0.00	0.31**	0.17	0.16
	3	0.10	0.13	0.00	0.05	0.04	-0.03	0.09	-0.02	-0.06	-0.15	0.05	0.09	0.19	0.10

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

Grain shape was significant and positively correlated with grain width and grain length in the three crosses. Milling % was highly significant and positively correlated with hulling % on cross 1. Head rice was highly significant and positively correlated with hulling % and milling % in the three crosses. Gelatinization temperature was highly significant and positively correlated with hulling %, milling % and head rice % in cross 1, and with hulling in cross 2. Panicle weight and

spikelets panicle⁻¹ were positively correlated with grain yield plant⁻¹ for three crosses, therefore, the correlation study revealed that these traits are crucial parameters deserve to take in consideration in selecting. Our data were in accordance with Habib *et al.* (2005), Rahman *et al.* (2020) and Chowdhury *et al.* (2023). The positive and significant association of these traits will provide plant breeders valuable knowledge concerning phenotypic traits and their degree of

association that is beneficial in plant breeding schemes and rice germplasm management. The non-significant relationship of some traits associated with yield may be due to their less contribution to yield improvement or might result from genetic constitution differences in the breeding material evaluated. Therefore, a through selection program needs implementation to synchronize the enhancement of traits having negative and non-significant correlations (Chowdhury *et al.*, 2023).

CONCLUSION

Selection from one generation to the next one in any breeding program will increase homozygosity and additive gene action and reduce variation. Also, the careful selection causes increase genotypic mean performance of the population for certain traits and may get the complete of homozygosity at F₆ generation. So, if there were higher values of additive gene action in early generation, it could be shortening breeding program time or selection cycles and attain homozygosity rapidly. The breeders should choose the most promising families or plants to release as a new variety or to be used as a parent in future hybridization program.

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التحليل الوراثي لتحسين صفات إنتاجية حبوب الأرز وصفات الجودة

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المخلص

أجريت هذه الدراسة في مواسم زراعة الأرز 2020 و2021 و2022، وتضمنت المواد الوراثية الأب الأول والأب الثاني والجيل الأول والجيل الثاني لثلاث هجن جيزة 179 × سويون 361، جيزة 177 × ميلياتج 349، جيزة 177 × سخا سوير 300، لتحسين صفات إنتاجية الحبوب والجودة. ولذلك فإن أعلى إنتاجية للحبوب نباتات كانت سخا سوير 300 × سويون 361، بينما حققت الهجن جيزة 177 × سخا سوير 300 وجيزة 179 × سويون 361 أعلى القيم 55.80 و55.14 جم على التوالي. وسجل الجيل الثاني للهجين (جيزة 177 × سخا سوير 300) أعلى القيم المتوسطة (50.80 جم). بالنسبة لصفة نسبة التبييض %، أظهر الصنف سخا سوير 300 أعلى نسبة تبييض بلغت 73.06%. وبينما حقق الهجين 3 (جيزة 177 × سخا سوير 300) أعلى قيمة بنسبة 74.60%. أما الجيل الثاني للهجين (الجيزة 177 × ميلياتج 349) أعطي أعلى القيم للجيل الثاني 62.83%. وكانت درجة السيادة أكبر من الوحدة (1.0±) لجميع الصفات المدروسة للهجن الثلاثة ماعدا طول السنبل، ووزن السنبل، ونسبة الخصوبة للهجين الأول، وطول السنبل، وعدد الفروع، وطول الحبة، ونسبة الحبوب السليمة للهجين الثاني، ووزن 1000 حبة وطول الحبة وعرض الحبوب للهجين الثالث مما يشير إلى أهمية درجة السيادة لتوريث هذه الصفات. هذا وقد ساهم المكون الأساسي الأول عند تحليل المكونات الأساسية بنسبه 98.45% من التباين وارتبط إيجابيًا بالتراكيب الوراثية بسويون 361، الجيل الأول للهجين (جيزة 179 × سويون 361)، الجيل الأول للهجين (جيزة 177 × ميلياتج 349)، والصنف سخا سوير 300 والهجين (جيزة 177 × سخا سوير 300).