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## GENETIC PARAMETERS AND PRINCIPAL COMPONENT ANALYSIS FOR QUANTITATIVE TRAITS IN RICE (*ORYZA SATIVA* L.)

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### SUMMARY

Conventional breeding is vital in improving yield-related traits and developing high-yielding cultivars. In the presented study, an evaluation of 15  $F_1$  hybrids compared them to their six parental genotypes for genetic variation of various traits. The results showed that the analysis of variance revealed significant ( $P \leq 0.01$ ) differences among the cross combinations and parental cultivars and among the parents and crosses. The mean sum of squares of parents vs. crosses also indicated substantial ( $P \leq 0.01$ ) for all the characteristics. The general (GCA) and specific combining ability (SCA) variances were significant ( $P \leq 0.01$ ) for all traits studied in the  $F_1$  generation. Three varieties, namely, Sakha108, Giza179, and Sakha109, were highly significantly positive for grain yield plant<sup>-1</sup>, which means these varieties can benefit as good combiners to transfer the said trait in the breeding program. In SCA, seven crosses were negative in plant height and a negative value was desirable to avoid lodging and suitable for mechanical harvesting; however, positive significant values are preferable in the rest of the traits. The results indicated that the best crosses for grain yield plant<sup>-1</sup> and plant height were Sakha105 × Sakha102, Sakha105 × Sakha108, and Sakha108 × Sakha109. Conducting cluster analysis also exhibited the genotypes dividing into four groups. The first group included rice genotypes Sakha109 and Sakha108 alone. These cultivars, produced from a common parent Sakha101, could have genetic relations for three quantitative traits (flag leaf area, 1000-grain weight, and panicle weight). The second group, comprising Sakha 102 and Sakha 106, has a very similar genetic background because both cultivars share a common parent, Giza 177. In addition, these two rice cultivars had at par number of tillers plant<sup>-1</sup>, 1000-grain weight, and panicles plant<sup>-1</sup>. The third group included only Giza 179 belonging to Indica-Japonica varieties. A fourth group has Sakha 105 produced by different parents.

**Keywords:** rice (*Oryza sativa* L.), breeding, combining ability, genetic variation, genetic potential, genotypic and phenotypic variances, heritability

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**Key findings:** The half-diallel method was for crossing between six parents of rice to produce 15 crosses. Three parents, namely, Sakha108, Sakha102, and Giza179, were suitable donors for some traits and could serve as better parents for use in breeding programs. Three crosses also gave a good result for grain yield plant<sup>-1</sup> and plant height. PCA and cluster analysis studied the similarity through quantitative traits, providing results that the varieties produced from the same parents cluster in one group.

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## INTRODUCTION

Rice (*Oryza sativa* L.) is a primary staple food grain consumed by most of the world's population, and several countries in Asia and Africa are dependent on rice productivity (Roy and Shi, 2020). Globally, rice demand increases annually with population growth, requiring a rice production upsurge to fill the gap between its demand and population growth (Arbelaez *et al.*, 2015). Researchers must explore the genetic diversity in the germplasm to increase rice production and also investigate the genetic background of parental lines used in various breeding programs (Abebe *et al.*, 2017; Kumar *et al.*, 2021; El-Malky and Al-Daej, 2023).

The success of breeding programs depends on the genetic variability's magnitude and the extent of heritability of the economic traits (Leung *et al.*, 2015; Juliano *et al.*, 2022; Syahril *et al.*, 2022; Chowdhury *et al.*, 2023). The combining ability analysis helps the breeders identify and select the best parental genotypes, aiding the hybridization program to get the desirable new cross combinations with improved genetic potential. General combining ability explores the role of additive gene effects in the inheritance of quantitative traits, and specific combining ability is the relative performance of a particular cross associated with a non-additive gene action, predominantly managed by dominance and epistasis (Gaballah *et al.*, 2022).

In rice, the study of genetic variability is crucial for selecting valuable genotypes and predicting the genetic potential of selected populations, and it also helps the breeders in

simultaneously improving earliness and yield traits through selection (Abdourasmane *et al.*, 2016; Tiwari *et al.*, 2019; Esther *et al.*, 2021). In addition, assessing genetic diversity and variability in agro-morphological features of the existing germplasm is decisive in retrieving information about their genetic makeup.

Principal component analysis (PCA) is an efficient approach to analyzing the genetic diversity in a population (Ganapati *et al.*, 2020) and also scrutinizing the information comprised of numerous correlated and dependent measures of the traits in crop plants (Shoba *et al.*, 2019). The biplot generated through PCA contains essential information, which helps amplify the relationship among the experimental populations and their various groups and associated variables. Therefore, it is an effective tool to generate reliable information during parental selection for a breeding program (Mvuyekure *et al.*, 2018).

With all this information, the study of genetic relationships is very influential in selecting and predicting the progeny, as well as conserving and characterizing the existing germplasm (Shrestha *et al.*, 2021; Zhong *et al.*, 2021; Gaballah *et al.*, 2022). In the presented study, 15 cross combinations, produced from six rice cultivars, underwent evaluation to compare their parental genotypes for various agronomic traits to explore the genetic variability among the populations by determining their mean performance, phenotypic and genotypic coefficients of variability (PCV and GCV), and estimating the GCA, SCA, and heritability in the broad sense ( $H_b$ ).

**Table 1.** Parentage and country of release of the studied six rice cultivars.

No.	Genotypes	Parentage	Origin	Type
1	Sakha105	Gz5581 / Gz4316	Egypt	Japonica
2	Sakha106	Giza177 / Hexi30	Egypt	Japonica
3	Sakha108	Sakha101 / HR5824 // Sakha101	Egypt	Japonica
4	Sakha102	Gz4096-7-1 / Giza177	Egypt	Japonica
5	Giza179	GZ 1368-S-5-4 / GZ 6296-12-1-2	Egypt	Indica/Japonica
6	Sakha109	Sakha101/ Gz6522-15-1-1-3	Egypt	Japonica

## MATERIALS AND METHODS

### Genetic material and study area

Six rice (*Oryza sativa* L.) cultivars, namely, Sakha105, Sakha106, Sakha108, Sakha102, Giza179, and Sakha109, served as study samples (Table 1). Using the half-diallel mating design among six parental genotypes generated 15 cross combinations during the crop season 2020. The seeds of the  $F_1$  hybrids and their parental cultivars, grown and evaluated in the crop season 2021, had a randomized complete block design (RCBD) with three replications at the experimental farm of the Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh. All the grown rice genotypes comprised plots with five rows at a 20 cm  $\times$  20 cm spacing.

### Field data collection

Eight agronomic traits, including plant height (cm), tillers plant<sup>-1</sup>, flag leaf area (cm<sup>2</sup>), panicles plant<sup>-1</sup>, grain yield plant<sup>-1</sup> (g), filled grains panicle<sup>-1</sup>, 1000-grain weight (g), and panicle weight (g) attained collecting and measuring according to the standard evaluation system for rice (IRRI, 2014).

### Statistical analysis

All the recorded data analyses used one-way analysis of variance (ANOVA) for RCBD, as suggested by Panse and Sukhatme (1985), with the further combining ability effects for  $F_1$  analyzed, according to Griffing (1956), using Method Two and Model One. The GCA and SCA mean squares' determination and their outcomes with significance were according to p values ( $P \leq 0.05$  = significant,  $P \leq 0.001$  = highly significant). Correlation coefficients (r) among all the studied traits' computations

followed the method according to Gomez and Gomez (1984). The analyses for GCV and PCV and estimates were according to the formula suggested by Burton (1952). The procedure of calculating genotypic and phenotypic percentages proceeded as proposed by Allard (1961). Finally, the Least Significant Difference (LSD) values' estimation used the formula suggested by Wynne *et al.* (1970). Given that calculating heritability (broad sense) percentage was the ratio of genotypic variance (numerator) to total phenotypic variance (denominator), with the latter reduced by a small component of the  $G \times E$  interaction, it was nonsignificant for most traits (Uguru *et al.*, 2005; Acquaah, 2009). Performing the principal component analysis (PCA) ran the XLSTAT v19.1 software (Addinsoft, Paris, France).

## RESULTS

### Analysis of variance

The analysis of variance (ANOVA) and combining ability ANOVA among the  $F_1$  hybrids and their parental genotypes for all the traits appears in Table 2. Significant ( $P \leq 0.01$ ) mean sum of squares was evident among the parental and cross combinations for all the traits. Both general (GCA) and specific combining ability (SCA) variances resulted in being significant ( $P \leq 0.01$ ) for all the characteristics. However, the GCA/SCA variance was notably greater than unity for flag leaf area, 1000-grain weight, and panicles plant<sup>-1</sup>, indicating that additive and non-additive  $\times$  additive types of gene action were more valuable for inheritance in these traits, and the non-additive type of gene action was weightier for the other features.

**Table 2.** Mean sum of squares estimates of ordinary analysis and combining ability for all studied characters.

S.O.V.	d.f.	Plant height	Tillers plant <sup>-1</sup>	Flag leaf area	Grain yieldplant <sup>-1</sup>
Replications	2	7.62	9.27	0.73	17.43
Genotypes	20	62.30**	19.26**	103.26**	104.26**
G.C.A	5	47.30**	14.52**	116.87**	60.76**
S.C.A	15	67.23**	37.68**	100.40**	118.75**
Error	40	1.173	29.52	0.57	1.60
G.C. A/S.C. A		0.704	0.039	1.114	0.512
S.O.V.	d.f.	1000-grain weight	Panicle weight	Panicles plant <sup>-1</sup>	Filled grains panicle <sup>-1</sup>
Replications	2	0.011	0.023	2.99	7.42
Genotypes	20	8.02**	0.72**	19.13**	607.11**
G.C.A	5	14.68**	0.612**	19.13**	171.38**
S.C.A	15	5.81**	0.757**	2.472**	752.5**
Error	40	0.118	0.017	0.427	8.58
G.C. A/S.C. A		2.527	0.808	7.739	0.228

**Table 3.** Mean performance of parental cultivars and their F<sub>1</sub> crosses for some agronomic traits in rice.

Genotypes	Plant height (cm)	Tillers plant <sup>-1</sup>	Flag leaf area (cm <sup>2</sup> )	Grain yield plant <sup>-1</sup> (g)	1000-grain weight (g)	Panicle weight (g)	Panicles plant <sup>-1</sup>	Filled grains panicle <sup>-1</sup>
Sakha105	104.9	23.04	30.30	42.17	26.60	2.88	22.44	147.33
Sakha106	104.2	21.94	31.43	40.20	26.69	3.08	20.88	131.43
Sakha108	102.3	21.56	30.50	45.33	28.86	3.21	19.79	140.93
Sakha102	108.0	22.54	35.41	50.66	26.83	4.48	21.49	168.53
Giza179	101.6	18.25	48.01	52.42	23.01	2.52	17.37	139.88
Sakha109	110.6	23.30	31.59	54.54	28.92	3.54	23.13	133.00
Sakha105 × Sakha106	112.9	17.33	29.72	41.18	25.43	2.50	16.67	142.48
Sakha105 × Sakha108	107.5	16.93	25.82	49.88	26.67	2.42	16.04	139.07
Sakha105 × Sakha102	103.4	17.88	34.29	52.50	26.04	2.17	18.08	127.52
Sakha105 × Giza179	111.5	23.21	42.51	53.08	27.73	2.51	22.47	150.37
Sakha105 × Sakha109	110.2	18.26	29.04	51.22	30.25	2.64	17.42	127.17
Sakha106 × Sakha108	103.7	22.27	37.36	58.00	25.99	2.79	21.33	152.52
Sakha106 × Sakha102	105.3	16.59	33.43	41.45	24.68	2.37	16.33	118.67
Sakha106 × Giza179	106.9	22.19	25.38	52.86	25.49	2.04	21.57	141.15
Sakha106 × Sakha109	110.3	17.13	25.14	50.34	27.28	2.32	16.16	150.97
Sakha108 × Sakha102	108.7	20.23	30.70	40.13	27.60	3.10	19.50	129.63
Sakha108 × Giza 179	105.4	19.68	35.17	52.44	28.94	2.65	18.72	128.04
Sakha108 × Sakha109	96.4	21.28	43.43	56.90	26.81	3.19	20.01	170.35
Sakha102 × Giza179	99.1	24.43	33.67	44.67	25.77	3.17	24.13	167.77
Sakha102 × Sakha109	102.5	17.56	31.10	45.38	26.62	2.16	16.51	149.58
Giza179 × Sakha109	96.9	20.63	30.27	40.30	28.16	3.76	19.53	139.10
L.S.D 0.05	1.180	0.750	0.580	1.160	0.120	1.21	0.625	3.521
0.01	1.320	0.840	0.650	1.810	0.140	1.359	0.701	3.946

### Mean performance

The mean performance of parental cultivars and their 15 F<sub>1</sub> hybrid populations for all studied traits is available in Table 3. Regarding plant height, a short plant stature is desirable

to avoid lodging, which is also suitable for mechanical harvesting. The results enunciated that the four parental cultivars, namely, Giza179, Sakha106, Sakha108, and Sakha105, provided the lowest mean values (101.6, 102.3, 104.2, and 104.9 cm, respectively), and

the crosses Sakha102 × Giza179, Sakha108 × Sakha109, and Giza179 × Sakha109 also had the lowest average values (96.49, 96.97, and 99.17 cm, respectively). However, the cross Sakha105 × Sakha106 revealed a high rate for plant height (112.94 cm). These results indicated that the most recent F<sub>1</sub> generation dominates this trait.

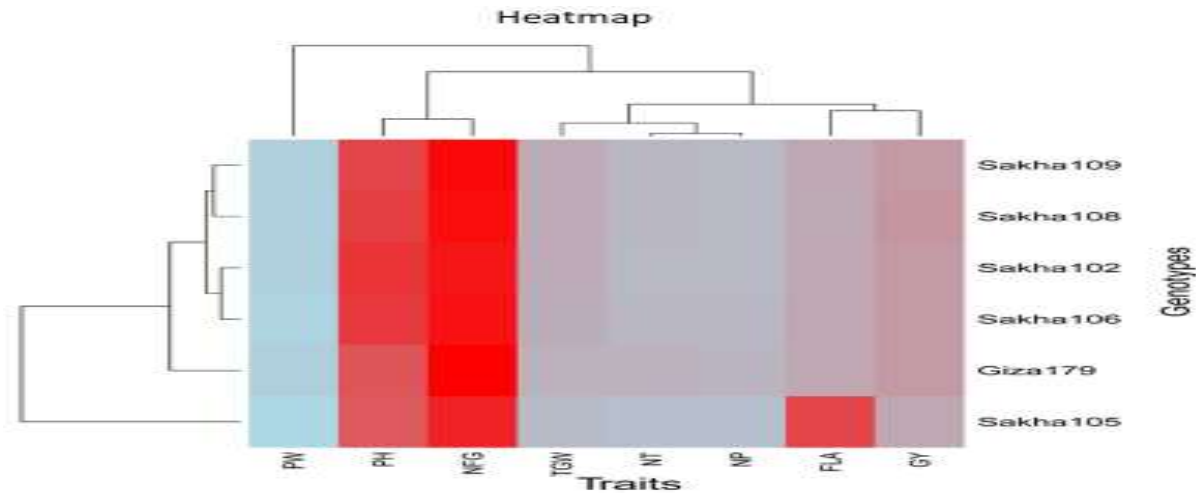
For tillers plant<sup>-1</sup>, the most desirable mean value toward the highest values compared with the mean parental genotypes varied from 16.59 to 24.73. Concerning the flag leaf area, the parent cultivar Giza179 showed the highest value (48.01 cm<sup>2</sup>) compared with the other parents and their F<sub>1</sub> progenies. In data regarding the grain plant<sup>-1</sup>, the F<sub>1</sub> hybrid Sakha105 × Sakha108 gave the highest grain yield plant<sup>-1</sup> (58 g), whereas the cross combination Sakha108 × Sakha102 occurred with the lowest grain yield plant<sup>-1</sup> (Table 3). For 1000-grain weight, the parental genotype Giza179 produced the lowest value (23.01 g), whereas the cross Sakha105 × Sakha109 gave the highest value (30.25 g). Regarding panicle weight, the parent cultivar Sakha102 provided the highest value (4.48 g) compared with the other parental genotypes and their F<sub>1</sub> generations. On the contrary, the cross combination Sakha105 × Sakha108 had the lowest value (16.04), but the cross Sakha102 × Giza179 produced the highest value (24.13) for panicles plant<sup>-1</sup>, indicating an overdominance. For the number of filled grains panicle<sup>-1</sup>, the F<sub>1</sub> hybrid Sakha108 × Sakha109 cross furnished a higher value (170.35 filled grains panicle<sup>-1</sup>), with the cross Sakha106 × Sakha102 presenting the lowest value (118.67 filled grains panicle<sup>-1</sup>).

Heatmap data analysis also observed significant differences among the rice genotypes for the studied traits (Figure 1). The cluster analysis divided all the rice genotypes into four groups, with the first group including the genotypes Sakha109 and Sakha108. These cultivars came from a common parent (Sakha101) and could be genetically close to each other for three quantitative traits (flag leaf area, 1000-grain weight, and panicle weight) (Figure 1). The second group comprised the rice cultivars Sakha 102 and Sakha 106, having a very similar genetic

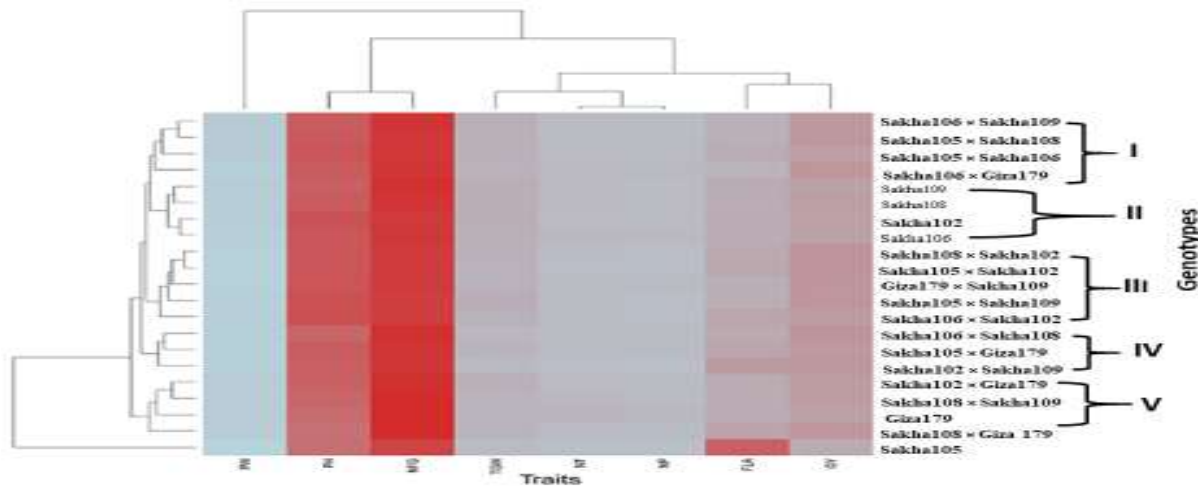
background because these two cultivars also shared a common parent (Giza 177). These two rice cultivars had an equal number of tillers plant<sup>-1</sup>, 1000-grain weight, and panicles plant<sup>-1</sup>. The third group had the genotype Giza 179 alone in branch one, as the said cultivar belonged to an Indica-Japonica type, and their quantitative traits were short stature and increased flag leaf area. The fourth group only has the rice cultivar Sakha 105 because its development resulted from different parents versus other parental genotypes.

The heatmap analysis also authenticated the genetic degree among the rice genotypes under study, which played a vital role in the cluster analysis with quantitative traits (Figure 1). The cluster analysis for the 21 rice genotypes under scrutiny is visible in Figure 2. The heatmap results showed the distribution of the genotypes into five groups, with the first one including four crosses, i.e., Sakha106 × Sakha109, Sakha105 × Sakha108, Sakha105 × Sakha106, and Sakha106 × Giza179, and the first two cross combinations were similar in tillers plant<sup>-1</sup>, flag leaf area, grain yield plant<sup>-1</sup>, 1000-grain weight, panicle weight, and panicles plant<sup>-1</sup>, but latter two hybrids were close to each other for 1000-grain weight and filled grains panicle<sup>-1</sup>.

Moreover, the heatmap analysis further classified the studied traits based on the genetic background of the genotypes (Figure 2). The second group included four parental genotypes (Sakha109, Sakha108, Sakha102, and Sakha106), and all these cultivars belonged to the Japonica type with a short duration and shared parents. The third group comprised five cross combinations, i.e., Sakha108 × Sakha102, Sakha105 × Sakha102, Giza179 × Sakha109, Sakha105 × Sakha109, and Sakha106 × Sakha102. The fourth group contained the three crosses, viz., Sakha106 × Sakha108, Sakha105 × Giza179, and Sakha102 × Sakha109. The fifth group also included three F<sub>1</sub> hybrids, i.e., Sakha102 × Giza179, Sakha108 × Sakha109, and Sakha108 × Giza 179, and a cultivar, Giza179. However, existing alone is the last genotype, Sakha105 (Figure 2).



**Figure 1.** Heatmap analysis of six rice genotypes for eight traits. Heatmap analysis data based on the main values of the traits of each genotype. The abbreviations used were: plant height (PH), tillers plant<sup>-1</sup> (NTP), flag leaf area (FLA), grain yield plant<sup>-1</sup> (GYP), 1000-grain weight (1000-Gw), panicle weight (PW), panicles plant<sup>-1</sup> (NPP), and filled grains panicle<sup>-1</sup> (NFGP).



**Figure 2.** Heatmap analysis of eight traits across 21 rice genotypes. Heatmap analysis data based on the main values of the traits of each genotype. The abbreviations used were: plant height (PH), tillers plant<sup>-1</sup> (NTP), flag leaf area (FLA), grain yield plant<sup>-1</sup> (GYP), 1000-grain weight (1000-Gw), panicle weight (PW), panicles plant<sup>-1</sup> (NPP), and filled grains panicle<sup>-1</sup> (NFGP).

**Combining ability analysis**

**General combining ability effects**

The general combining ability (GCA) effects of the individual parental lines for all the traits are prominent in Table 4. Theoretically, an estimate of the GCA effects of a parental line

depends upon the group of parental genotypes to which its crossing was in the full and half-diallel mating system. When the line is precisely as the average in its GCA effects, an expected result is also zero. Significant deviation from zero, where the direction indicates the line is significantly better or worse than the overall average of the parental

**Table 4.** Estimates of general combining ability effects for all studied characters.

Parents	Plant height	Tillers plant <sup>-1</sup>	Flag leaf area	Grain yield plant <sup>-1</sup>	1000-grain weight	Panicle weight	Panicles plant <sup>-1</sup>	Filled grains panicle <sup>-1</sup>
Sakha105	2.053**	-0.309**	-0.180*	-0.815	0.149**	-0.188**	-0.120*	-2.153**
Sakha106	1.091**	-0.347**	-2.192**	-1.748**	-0.734**	-0.765**	-0.338**	-3.731**
Sakha108	-0.565**	0.166*	0.257**	1.224**	-0.701**	0.133**	-0.168*	0.372
Sakha102	-0.465**	-0.014	0.322**	-1.658**	-0.469**	0.053**	0.126*	3.967**
Giza179	-1.973**	0.593**	3.949**	1.184**	-0.752**	-0.043**	0.579**	0.962**
Sakha109	-0.140	-0.090	-1.158**	1.813**	1.104**	0.206	-0.079	0.384
L.S.D 0.05	0.202	0.160	0.141	0.236	0.064	0.024	0.121	0.545
	0.01	0.313	0.248	0.365	0.099	0.037	0.188	0.845

lines involved. However, the GCA effects computed herein appeared to differ significantly from zero in most cases. The positive GCA effects would be of interest in most traits except plant height, where the negative value would be desirable.

The three rice parental cultivars, Sakha108, Sakha102, and Giza179, showed highly significant negative GCA effects for plant height, revealing that these cultivars could be good general combiners for developing short-stature rice genotypes. For the traits tillers per plant and flag leaf area, the parental cultivars Sakha108, Giza179, and Sakha102 exhibited substantial positive GCA effects (Table 4). The parental genotypes Sakha 108, Sakha 109, and Giza 179 had significant positive GCA effects for grain yield plant<sup>-1</sup>. All the parent cultivars recorded had significantly negative GCA effects for 1000-grain weight, except Sakha 105 and Sakha 109, with these two genotypes recorded with negative GCA effects for panicle weight. The parent cultivars Sakha105 and Sakha106 had significant negative GCA effects for panicles per plant and the filled grains panicle<sup>-1</sup> (Table 4).

#### **Specific combining ability effects**

The estimation of specific combining ability (SCA) effects in the specific F<sub>1</sub> cross combinations for all studied traits occurs in Table 5. Seven out of 15 F<sub>1</sub> hybrid combinations exhibited significantly ( $P \leq 0.01$ ) negative SCA effects for plant height. The results revealed that these crosses can be helpful in future breeding programs to develop short-stature rice genotypes, which will be

more suitable for mechanical harvesting that avoids lodging. However, the four F<sub>1</sub> hybrids, Sakha105 × Giza179, Sakha105 × Sakha108, Sakha106 × Giza179, and Sakha108 × Sakha109, showed significance positive SCA effects for all the traits.

The results concerning GCA and SCA effects indicated that the excellent cross combinations showed desirable SCA effects, resulting also through crossing good × good, good × low, and low × low general combiners. Consequently, a conclusion can be that the GCA effects of the parental cultivars had no overall connections with the SCA effects of their receptive crosses.

#### **Estimates of genetic parameters**

The recorded high estimates of genotypic ( $\sigma^2_g$ ) and phenotypic ( $\sigma^2_{ph}$ ) variances for all characters studied indicated a better scope for the genetic improvement and showed that the environment did not have a critical impact on the variability patterns of these traits (Table 6). Data comparison indicated that the magnitude of genetic variance ( $\sigma^2_G$ ) was better than the environmental variance ( $\sigma^2_E$ ) for all the studied traits.

Results revealed the difficulty of comparing the variances for different attributes because they do not unite freely. Therefore, the estimates of genotypic and phenotypic coefficient of variability (GCV % and PCV %), broad sense heritability (%), and genetic advance as a percentage of the mean for all study traits attained calculation, as presented in Table 5. The phenotypic coefficient of variability (PCA %) was comparatively higher

**Table 5.** Estimates of specific combining ability effects for all studied characters.

Genotypes	Plant height	Tillers plant <sup>-1</sup>	Flag leaf area	Grain yield plant <sup>-1</sup>	1000-grain weight	Panicle weight	Panicles plant <sup>-1</sup>	Filled grains panicle <sup>-1</sup>
Sakha105 × Sakha106	4.211**	-2.306**	0.032	-4.645**	-0.860**	0.067**	-2.375**	5.722**
Sakha105 × Sakha108	0.447	-3.239**	-6.317**	1.082**	-1.055**	-0.312**	-3.175**	-1.791**
Sakha105 × Sakha102	-3.713**	-2.109**	2.087**	6.585**	-0.515**	-0.482**	-1.429**	-16.936**
Sakha105 × Giza179	5.865**	2.613**	6.680**	4.322**	1.457**	-0.047	2.508**	8.919**
Sakha105 × Sakha109	2.772**	-1.652**	-1.682**	1.834**	2.121**	-0.164**	-1.884**	-13.903**
Sakha105 × Sakha108	-2.330**	2.139**	6.234**	10.636**	-0.851**	0.036	2.333**	13.237**
Sakha106 × Sakha102	-0.820**	-3.361**	2.238**	-3.531**	-0.991**	-0.304**	-2.961**	-24.208**
Sakha106 × Giza179	2.267**	1.630**	-9.438**	5.036**	0.101	-0.539**	1.825**	1.277*
Sakha106 × Sakha109	3.805**	-2.745**	-4.571**	1.887**	0.035	-0.507**	-2.926**	11.470**
Sakha108 × Sakha102	4.176**	-0.234	-2.941**	-7.824**	0.494**	0.127*	0.039	-17.351**
Sakha108 × Giza 179	2.344**	-1.392**	-2.097**	1.644**	2.116**	-0.228*	-1.195**	-15.936**
Sakha108 × Sakha109	-8.389**	0.893**	11.270**	5.473**	-1.870**	0.064	0.754**	26.752**
Sakha102 × Giza179	-3.976**	3.838**	-3.663**	-3.243**	0.116	0.372*	3.921**	20.199**
Sakha102 × Sakha109	-2.420**	-2.647**	-1.126**	-3.163**	-0.890**	-0.885**	-3.040**	2.387**
Giza179 × Sakha109	-6.501**	-0.186	-5.582**	-11.085**	0.932**	0.809**	-0.474**	-5.088**
L.S.D 0.05	0.458	0.363	0.319	0.534	0.145	0.055	0.276	1.238
0.01	0.554	0.439	0.336	0.647	0.176	0.055	0.334	1.499

**Table 6.** Estimates of genotypic, phenotypic, heritability, and genetic advance for all studied characters.

Parameters	Plant height	Tillers plant <sup>-1</sup>	Flag leaf area	Grain yield plant <sup>-1</sup>	1000-grain weight	Panicle weight	Panicles plant <sup>-1</sup>	Filled grains panicle <sup>-1</sup>
Mean X	105.59	20.31	33.06	48.39	26.88	2.785	19.50	142.64
Variance	62.29**	19.26**	103.25**	104.26**	8.02**	0.720**	19.135**	607.11**
Ms Error 6 <sup>2</sup> E	1.17	0.74	0.570	1.599	0.118	0.017	0.428	8.579
Phenotypic 6 <sup>2</sup> ph	21.55	6.91	34.41	34.750	2.674	0.240	6.378	202.37
Genotypic 6 <sup>2</sup> G	20.37	6.17	34.22	34.22	2.634	0.234	6.236	199.51
PCV%	4.40	12.95	17.75	12.18	6.083	17.591	12.949	9.97
GCV%	4.28	12.23	17.69	12.09	6.037	17.370	12.804	17.27
Heritability	94.55	89.30	99.45	98.47	98.53	97.62	97.76	98.58
Genetic advance (%)	8.56	24.81	36.35	24.72	12.35	35.37	26.08	20.58

than the corresponding genotypic coefficient of variability (GCV %) for all the studied characteristics. These results suggested that environmental effects constitute a primary portion of the total PCV % in all traits. In any case, in this study, if the PCV was higher than the GCV, then the genetic improvement will be beneficial, and the selection in early generations is better; the effect is also due to additive genes. However, when the differences between the PCV and GCV are high, then the genetic improvement will be slow; the selection is preferable in late generations, and this is due to the dominant genetic action.

### Heritability (broad sense)

Calculating heritability (broad sense) as a ratio of genotypic variance (numerator) to total phenotypic variance (denominator) and components of the genetic-by-environment interaction (GEI) effects were also not significant for all the studied traits. However, heritability in broad sense estimates were high for all the studied features, indicating that the genetic variance (additive and non-additive) played an influential role in the inheritance of all these traits (Table 6).



**Table 7.** Correlation coefficient among the eight traits under study.

Traits	1	2	3	4	5	6	7	8
1	1.00							
2	-0.153	1.00						
3	-0.364	0.195	1.00					
4	0.025	0.132	0.404	1.00				
5	0.272	0.191	-0.334	0.062	1.00			
6	-0.178	0.555**	0.130	-0.115	0.317	1.00		
7	-0.129	0.986**	0.186	0.136	0.142	0.505*	1.00	
8	-0.296	0.462*	0.278	0.271	-0.153	0.369	0.409	1.00

Note: (1) Plant height, (2) Tillers plant<sup>-1</sup>, (3) Flag leaf area, (4) Grain yield plant<sup>-1</sup>, (5) 1000-grain weight, (6) Panicle weight, (7) Panicles plant<sup>-1</sup>, and (8) Filled grains panicle<sup>-1</sup>.

\*\* . Correlation is significant at the 0.01 level (2-tailed), \* . Correlation is significant at the 0.05 level (2-tailed).

### Genetic advance

The possible genetic gain (GA %) from selection is the percent increase in the value of the genetic advance from generation to generation after selecting 5% of the desirable plants in the whole population for each trait (Table 6). Under selection, estimating the genetic advance appeared to be higher for flag leaf area and panicle weight (36.35% and 35.37%, respectively). However, a low value of genetic gain emerged for the plant height. In the presented investigations, the high genetic gain seemed associated with high heritability estimates for flag leaf area and panicle weight. Consequently, selection for these traits should be suitable and satisfactory for successful breeding.

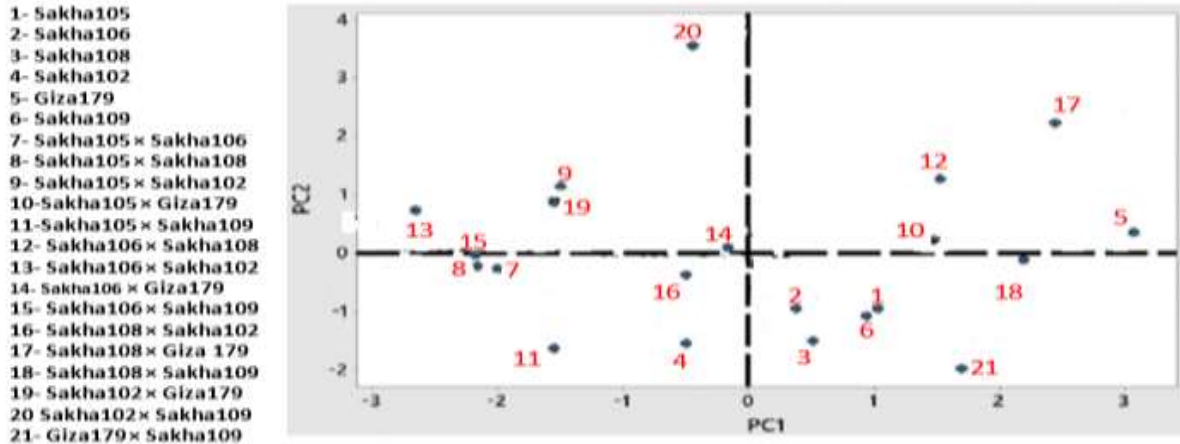
### Correlation coefficients among the traits

Estimates of phenotypic correlation coefficients among all the possible trait combinations are available in Table 7. The trait tillers plant<sup>-1</sup> showed a strong correlation with panicle weight (0.555), panicle plant<sup>-1</sup> (0.986), and the number of filled grains panicle<sup>-1</sup> (0.462). In addition, a significant positive relationship (0.505) was evident between the panicle weight and panicles plant<sup>-1</sup>. Thus, an implication is that these three traits can be

helpful in a breeding program to develop genotypes with the desired panicle traits for yield improvement.

### Principal component analysis (PCA)

The visualization of cluster analysis and the pattern of parental genotypes and their F<sub>1</sub> hybrids ensued by plotting a biplot principal component analysis (Figure 3). In the PCA, the first four components had recordings of the Eigenvalues > 1, which contributed 84.20% of existing variability in the genotypes for yield component traits (Table 8). The remaining components with Eigenvalues < 1 contributed only 15.80% variability. The PC<sub>1</sub> was 36.50% and positively associated with all traits except plant height (-0.213). The PC<sub>2</sub> was 22.60%, also showing positive associations with flag leaf area (0.513), grain yield per plant (0.306), and filled grains panicle<sup>-1</sup> (0.239), and negative with the traits, viz., plant height, tillers plant<sup>-1</sup>, 1000-grain weigh, panicle weight, and panicle plant<sup>-1</sup>. Consequently, the PC<sub>3</sub> contributed negatively for all except panicle weight. Meanwhile, the PC<sub>4</sub> has an associated positive value with flag leaf area (0.307), grain yield plant<sup>-1</sup> (0.281), 1000-grain weight (0.557), and panicle weight (0.363), but negative with plant height, tillers plant<sup>-1</sup>, panicles plant<sup>-1</sup>, and filled grains panicle<sup>-1</sup> (Table 8).



**Figure 3.** Biplot of the principal component analysis (PCA) for six parents and their 15 crosses with eight agronomic traits. PCA was performed using XLSTAT v19.1.

**Table 8.** Eigenvalues, % variance, and cumulative % variance of eight morphological traits for principal components.

Traits	PC1	PC2	PC3	PC4
Eigenvalue	2.92	1.81	1.18	0.81
Variance contribution (%)	36.50	22.60	14.80	10.20
Cumulative variance contribution	36.50	59.20	74.00	84.20
Plant height (PH)	-0.213	-0.363	-0.522	-0.403
Number of tillers /plant (NTP)	0.539	-0.168	-0.064	-0.252
Flag leaf area (FLA)	0.242	0.513	-0.074	0.307
Grain yield /plant (GYP)	0.143	0.306	-0.730	0.281
1000-grain weight (1000-Gw)	0.075	-0.560	-0.273	0.557
Panicle weight (PW)	0.407	-0.293	0.317	0.363
Number of panicles /plant (NPP)	0.520	-0.162	-0.085	-0.300
Number of filled grains/panicle (NFGP)	0.379	0.239	-0.050	-0.261

## DISCUSSION

Developing new rice cultivars through conventional breeding is the best-suited method and continues to be one of the chief objectives in rice breeding programs. Such rice cultivars can adapt well to multiple cropping systems and have a natural advantage of drought avoidance in the later crop cycle. Therefore, the pertinent study transpired to obtain information on the combining ability of parental genotypes and their  $F_1$  cross combinations for economic traits and their correlation with grain yield through a half-diallel mating design involving six parental genotypes. The chosen breeding material and the qualities for evaluation were the most

crucial in breeding for developing new rice cultivars (Kargbo *et al.*, 2019; Behera *et al.*, 2020).

In the relevant study, ANOVA for combining ability revealed significant differences among the genotypes for all the studied traits and the treatments. This finding indicated the presence of notable genotypic variations among the populations for all the studied traits; however, the proportion of genotypic variation to its components varies (Hua *et al.*, 2021; Kumar *et al.*, 2021; Gaballah *et al.*, 2022). The ratio of GCA/SCA variance was more than unity, indicating that additive and non-additive  $\times$  additive types of gene action were more critical for inheritance of these traits (flag leaf area, 1000-grain

weight, and number of panicles plant<sup>-1</sup>), while the non-additive type of gene action was weightier for the other features (El-Malky and Al-Daej 2018; Kargbo *et al.*, 2019; Behera *et al.*, 2020). Therefore, the conclusion of the selection procedure based on the accumulation of additive effects would be more successful in improving the flag leaf area, 1000-grain weight, and number of panicles plant<sup>-1</sup>. However, to maximize the selection advance, procedures effective in shifting gene frequencies when both additive and non-additive genetic variances are participants would be preferable. In combining ability analyses, reports of similar findings for the GCA and SCA variances also emerged in rice populations (El-Malky and Al-Daej, 2018; Fahmi *et al.*, 2018; Gowayed *et al.*, 2020).

The estimates of GCA effects among the genotypes for short-stature traits showed that the three rice parental genotypes, i.e., Sakha 108, Sakha102, and Giza 179, were indicative as the best general combiners for short stature and grain yield plant<sup>-1</sup> except Sakha102, which has the negative GCA effects in grain yield plant<sup>-1</sup> (Srujana *et al.*, 2017; Sandeep *et al.*, 2018; Fahmi *et al.*, 2018; Al-Daej *et al.*, 2022). As for SCA four crosses, namely, Sakha105 × Giza179, Sakha105 × Sakha108, Sakha106 × Giza179, and Sakha108 × Sakha109, these showed significant positive SCA effects for all the traits. It would indicate the importance of both additive and non-additive genetic variances in determining the performance of these eight studied traits. These crosses could be valuable in rice breeding programs to develop new short-stature and high-yielding rice cultivars. The central findings also got support from past studies on the genetic variability in different rice populations (Adjah *et al.*, 2020; Mosleth *et al.*, 2020; Juliano *et al.*, 2022; Syahril *et al.*, 2022; Chowdhury *et al.*, 2023).

Genetic parameters and heritability estimates indicated that a genetic variance (additive and non-additive) played an imperative role in the inheritance of all the traits (Sandeep *et al.*, 2018; Gowayed *et al.*, 2020; Swapnil *et al.*, 2020). Meanwhile, Dixit *et al.* (1970) stated that high heritability is not

always associated with high genetic gain, but to make effective selection, the high heritability should be related to high gain. Complete knowledge of the interrelationship of plant characteristics is supreme to the breeder for improving complex quantitative and economic attributes, as found in the presented study. A correlation coefficient among the traits assessed had the result clarified that tillers per plant were positively associated with panicle weight, panicles per plant, and filled grains per panicle (Okasa *et al.*, 2021). The panicle weight also indicated a positive correlation with panicle per plant, indicating that these traits might have the same genetic makeup controlling the rice genotypes. These results also agree with past findings in different rice populations (Fahmi *et al.*, 2018). Previous studies also revealed that general and specific combining ability and principal component analysis (PCA) were necessary to study the relationship among rice populations' morphological and yield traits (Wei *et al.*, 2018).

## CONCLUSIONS

The analysis of variance revealed that genotypes had highly significant differences for all traits. The variances due to general and specific combining ability were highly significant for all traits, indicating that both additive and non-additive genetic variances were valuable in controlling the inheritance of these traits. For plant height, the rice cultivars Giza179, Sakha106, and Sakha105 and the crosses Sakha102 × Giza179, Sakha108 × Sakha109, and Giza179 × Sakha109 provided the lowest mean values. The cross Sakha106 × Sakha108 was better for grain yield plant<sup>-1</sup> and could benefit selection in the next generation to improve this trait. Heatmap analysis confirmed that quantitative traits played a significant role in measuring distance and dividing clusters. Heritability in the broad sense was high for all studied traits, implying that the genetic variance (additive and non-additive) played an imperative role in inheritance for all traits.

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