

Assessing Phenotypic Diversity, Stem Borer Infestations, and Blast Resistance of Some Hybrid and Inbred Rice Genotypes

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ABSTRACT

Quantitative traits and resistance to diseases and insects are among the most important factors determining the selection of new rice varieties and hybrids. A field experiment was conducted on eight rice genotypes, including three hybrids and five varieties. ANOVA showed significant differences at the 0.01 level among all quantitative traits under study. Agronomic traits, showed that Giza182, Giza177 and Sakha108 varieties gave low value (96.20, 97.40, 97.60 cm), while Hybrid 27P31 and Hybrid 28P67 gave the highest value (137.2 and 133 cm) in plant height, tillers plant⁻¹, panicles plant⁻¹, panicle weight, grain yield plant⁻¹, grain yield day⁻¹, field grains panicle⁻¹. Stem borer infestation revealed that the varieties Giza177, Sakha104, Sakha101, Sakha108, and Giza182 were resistant and moderately resistant compared with Hybrid 27P31, Hybrid 28P67, and Egyptian Hybrid 1, which were susceptible. Leaf blast reaction exposed that the varieties Saka101, Sakha104, and Sakha108 were susceptible, while the rest of the genotypes, namely, Giza177, Giza182, Hybrid 27P31, Hybrid 28P67, and Egyptian Hybrid 1, were resistant to leaf blast reaction. All traits under study exhibited the highest heritability broadly, with the coefficient of variation (PCV) values surpassing the genotypic coefficients of variability (GCV) in all characteristics. Correlation analysis revealed that the plant height trait had a significant positive association with panicle weight, grain yield day⁻¹, grains panicle⁻¹, unfilled grains panicle⁻¹, and infestation of stem borer. Also, grain yield plant⁻¹ was positive with field grain panicle⁻¹, and grain yield acre⁻¹, while grain yield day⁻¹ was positively correlated with field grain panicle⁻¹, grain yield acre⁻¹, and the infestation of stem borer percentage. The principal component analysis (PCA) agreed with cluster analysis and divisions into four groups, with the first one included Sakha101, Sakha104 and Sakha108, while Quitters-II and IV included the genotypes Hybrid 27P31 and Hybrid 28P67.

Keywords: genotypes, heritability, PCA, genetic diversity, cluster analysis, quantitative traits.

INTRODUCTION

Rice (*Oryza Sativa* L.) is a staple food for most of the world's population (Bin Rahman and Zhang, 2023), especially in developing and poor countries (Arouna et al., 2017), this is because it is rich in important nutrients for all human ages (Naomi and Ziska, 2019; El-Beltagi et al., 2022), and also its cheaper food compared to other crops (GRiSP, 2013). Therefore, rice-producing countries it working to increase production by developing new high-yielding inbred varieties or hybrids genotypes to decrease the gap between the annual population increase and the demand for rice. Genetic improvement in the conventional breeding system depends

on to making several crosses between parents that provide some of the desired traits with the commercially grown varieties in order to obtain new combinations that are high-yielding and resistant or tolerant to different conditions (Villegas et al., 2018; Bairagi et al., 2021; El-Malky, 2024; Rezk et al., 2024). Studying the behavior of desired traits in different generations and selecting until obtaining genetic homogeneity of new lines is considered very important (Rezk et al., 2022; Al-Khayri and EL-Malky, 2023). Also, the heritability, genetic advance and genetic relationship between them are important to know the degrees of dominance, genetic stability and segregation in different generations (Roy and Shi, 2020). While, hybrid rice

production technology depends on using the phenomenon of hybrid vigor present in the F1 generation, which helps increase production by from 25 to 30% in yield (Abo-Yousef et al., 2023). However, increased grain yield trait is a multifaceted trait that is affected by the arrangement of genes, the environment in which they develop, and the degree and types of variation in genotypes (Faysal et al., 2022).

In Egypt during the last thirty years, rice varieties have been improved significantly in the yield average per unite area, grain quality, and other desirable traits such as plant height, short growth duration and disease resistance. During this period, many varieties were developed, such as Giza177, Japonica type and short-duration variety (125 days), Giza178 an (Indica-Japonica type variety), Sakha101, Sakha102, Sakha103, Sakha104, Sakha105, Sakha106, Sakha107, Sakha108, Sakha109 (Japonica type), Giza179 (Indica-Japonica type), Giza182 (Indica type) and Giza183 Indica-Japonica type (Hammoud et al., 2020; Abdallah, et al., 2022; Sedeek et al., 2023). However, improving and developing new genotypes is the best way to increase production per unit area (Esther et al., 2021; El-Malky and Al-Daej, 2023). This will need to study the genetic diversity and genetic background for each variety, which will be useful to improve the agronomic traits (Sabri et al., 2020; Zhong et al., 2021; Rezk et al., 2025). In any case, breeding programs that are designed using conventional breeding methodologies, which are based on observed variations in traditional varieties or on controlled crosses, primarily depend on the differences and

similarities among genotypes. Nevertheless, the length of time needed to achieve the desired gain may make these methods less practical. In addition, hybrid rice is used, through the three lines system (A, B, R lines) or the two lines. through this method, the hybrid vigor phenomenon increased the yield by about 25% compared with the inbred varieties, such as Egyptian hybrid 1.

In this research, genetic diversity, heritability, genetic advance, and correlation were studied in some traditional and hybrid varieties to determine the contribution of quantitative traits to increasing the grain yield, also, PCA were analyzed to provide selection criteria for high-yielding rice varieties.

MATERIAL AND METHODS

Rice genotypes

This study included eight rice genotypes, three hybrids (Hybrid 27P31, Hybrid 28P67, and Egyptian Hybrid 1), and five inbred varieties (Giza177, Giza182, Sakha101, Sakha104, and Sakha108) (Table 1). The current research was conducted at the experimental farm of Rice Research and Training Center (RRTC). Seeding at 30 days was transferred to the permanent field after and transplanted spacing of 20 × 20, with 7 rows wide and 5 m long, using a randomized complete block design (RCBD) with three replications. All agronomic practices, such as fertilization, irrigation, and weed and pest control, were done as recommended with the rice crop during both seasons of the study.

Table 1. Eight rice genotypes, parentage, type, origin and grain type

No.	Genotypes	Parentage	Type	Origin	Grain type
1	Giza177	Giza171 / Yamji No.1 / /PiNo.4	Japonica	Egypt	Short
2	Giza182	Giza181 / IR39422-163-247-2-2-3	Indica	Egypt	Long
3	Hybrid 27P31	Exotic	Indica	India	Long
4	Hybrid 28P67	Exotic	Indica	India	Long
5	Egyptian Hybrid 1	Gz69M/Giza178	Indica Japonica	Egypt	Short
6	Sakha101	Giza 176/Milyang 79	Japonica	Egypt	Short
7	Sakha104	GZ 4096/GZ 4100	Japonica	Egypt	Short
8	Sakha108	Sakha101/HR5824/Sakha101	Japonica	Egypt	Short

Agronomic traits

Twelve agronomic traits included plant height (cm), tillers plant⁻¹, duration (days), panicles plant⁻¹, 1000-grain weight (g), panicle weight (g), grain yield plant⁻¹, grain yield day⁻¹ (g), panicle length (cm), field grains panicle⁻¹, unfilled grains panicle⁻¹ and grain yield acre⁻¹ (ton) all these traits were recorded according to IRRI (2014).

Stem borer (Chilo agamemnon Bles.) infestation

Collecting 100 plants at the maturity stage to calculate the damage of white head percentage and the standard evaluation system of Rice Research and Training Center (RRTC), Sakha, Egypt (Sherif, 2002). Resistance (R)=0-3%, moderately resistant (MR) = 3-6%, moderately susceptible (MS) = 6-9%, Susceptible (S) = 9-12%, and highly susceptible (HS) = 12%. While the percentage of white heads was calculated by using the following formula according to Islam et al., (2013). The percentage of white heads was determined after the milking stage:

$$WH\% = \frac{\text{Number of the white heads (WH)\%}}{\text{Total number of tillers with panicles}} \times 100$$

Blast scoring under field conditions

The eight genotypes under study were evaluated under the natural infestation of blast races under the optimum conditions for blast infection, like delaying of sowing dates, increasing the amount of nitrogen fertilization, growing a susceptible check (blast spreader), and applying in different locations. The plant materials were evaluated for their reaction against *M. grisea* at the Sakha location for blast resistance at the seedling stage. About forty-days from the sowing date, the typical blast lesions were scored according to the Standard Evaluation System using a 0-9 scale (IRRI 2014) as follows: 1-2 = resistant (R), 3 = moderately resistant (MR), 4-6 =

susceptible (S), and 7-9 = highly susceptible (HS).

Statistical analysis

Analysis of variance was conducted for each season separately. Two experiments were statistically combined over two seasons because the error variances of the experiments were statistically homogeneous, as reported by Le Clergue et al. (1962). Experiments were then subjected to analysis using analysis of variance, which was utilized to separate gross phenotypic variability into components attributed to genetic (hereditary) and non-genetic (environmental) factors and estimate their relative magnitudes. Comparably, the overall diversity among phenotypes when produced in a variety of relevant conditions is known as phenotypic variance (Dudley and Moll, 1969). Thus, the formula of Wricke and Weber (1986); Prasad et al. (1981) was used to estimate variance components, genotypic (Vg), phenotypic (Vp), or error (Ve) variances. According to Allard (1999), broad-sense heritability (h²b) was calculated on a genotypic mean basis. To assess the genetic relationships among genotypes, dissimilarity coefficients were calculated according to Sneath and Sokal (1973). Similarity matrices were generated using NTSYS-PC version 2.1 (Rohlf, 2000).

RESULTS AND DISCUSSION**ANOVA**

The analysis of variance (ANOVA) for all studied quantitative and grain traits revealed the presence of highly significant differences (P < 0.001) among eight rice genotypes (Table 2), which shows the existence of high and inherent variation among genotypes. Therefore, there is a high possibility for improvement of agronomic and grain quality traits through the selection and hybridization of better parental genotypes.

Table 2. ANOVA of 18 grain quality and 12 quantitative traits of eight rice genotypes under study

Source of variance	Df	Plant height (cm)	Tillers plant ⁻¹	Duration (days)	Panicles plant ⁻¹	1000-grain weight (g)	Panicle weight (g)
Replication	2	0.878	0.230	0.586	0.190	0.142	0.023
Genotypes	7	859.02**	5.528**	169.28**	3.54**	3.92**	4.01**
Error	14	0.737	0.036	1.037	0.037	0.127	0.043
Source of variance	Df	Grain yield plant ⁻¹ (g)	Grain yield day ⁻¹ (g)	Panicle length (cm)	Field grains panicle ⁻¹	Unfiled grains panicle ⁻¹	Grain yield acre ⁻¹ (ton)
Replication	2	0.195	0.980	0.101	0.86	1.07	1.12
Genotypes	7	134.07**	27.99**	12.05**	3613.50**	1064.27**	32.88**
Error	14	0.090	0.078	0.037	0.39	0.07	0.65

*, ** Significant at 5% and 1% probability levels, respectively.

Mean performance of field quantitative traits

The inbred varieties Giza182, Giza177 and Sakha108 were short stature by 96.20, 97.40 97.60 cm, respectively, while the genotypes Hybrid 27P31 and Hybrid 28P67 have highest value (137.2 and 133 cm), also the rest genotypes Egyptian hybrid 1 and Sakha104 gave 109.0 and 107.3 cm (Table 3). This trait is critical and must be bred to produce short-stature varieties, because short varieties are resistant to lodging and suitable for mechanical harvesting. According to Tillers plant⁻¹, four genotypes, Sakha101 (27.03), Sakha108 (26.30), Giza182 (25.43), and Egyptian Hybrid 1 (25.20) gave high value in Tillers plant⁻¹. As for the duration trait, Giza177 (125.0 days) and Giza182 (128.7 days) were early genotypes (Table 3). For panicles plant⁻¹, Sakha101, Hybrid 27P31, and Sakha108 gave the highest value (25.73,

24.17, and 24.07), while in 1000-grain weight, Sakha108, Giza182, and Sakha104 were the heaviest genotypes (28.53, 28.27, and 28.20 g), respectively. The results in Table 3 also showed that the Indian hybrids (Hybrid 27P31 and Hybrid 28P67) had the highest values in panicle weight, grain yield/plant, grain yield/day, field grains panicle⁻¹, and grain yield acre⁻¹ (ton). These hybrids belonged to the Indica type and had high hybrid vigor compared to the inbred genotypes. Giza182 was highly productive and belongs to the inbred Indica type, which was the second highly productive following the Indian hybrids. In conclusion, Indica types are distinguished by their tolerance to different weather conditions and their high yield. This is because they were native to hot and semi-hot regions. However, the expansion of its cultivation depends on the extent of personal preferences.

Table 3. Mean performance for agronomic traits of eight rice genotypes

Traits Genotypes	Plant height (cm)	Tillers plant ⁻¹	Duration (days)	Panicles plant ⁻¹	1000-grain weight (g)	Panicle weight (g)
Giza177	97.4	23.10	125.0	22.40	27.23	2.99
Giza182	96.2	25.43	128.7	23.77	28.27	3.64
Hybrid 27P31	137.3	24.73	147.3	24.17	27.70	6.03
Hybrid 28P67	133.0	23.37	138.5	22.77	27.10	6.36
Egyptian Hybrid 1	109.0	25.20	136.0	23.10	24.90	4.55
Sakha101	95.0	27.03	145.2	25.73	27.33	3.90
Sakha104	107.5	24.27	137.3	22.73	28.20	4.13
Sakha108	97.60	26.30	136.5	24.07	28.53	4.36
LSD at 0.01	0.44	2.08	0.46	2.47	0.47	0.87
0.05	0.32	1.50	0.33	1.78	0.34	0.62
Traits Genotypes	Grain yield plant ⁻¹ (g)	Grain yield day ⁻¹ (g)	Panicle length (cm)	Field grains panicle ⁻¹	Unfiled grains panicle ⁻¹	Grain yield acre ⁻¹ (ton)
Giza177	41.13	29.50	26.63	136.6	4.73	3.76
Giza182	42.37	35.03	28.23	176.6	11.60	4.74
Hybrid 27P31	55.00	37.67	27.23	198.5	44.43	5.40
Hybrid 28P67	43.20	37.58	26.63	211.6	54.50	4.82
Egyptian Hybrid 1	35.67	33.13	24.87	163.7	5.67	4.42
Sakha101	35.21	30.80	24.37	125.8	23.50	4.45
Sakha104	34.60	31.17	25.23	120.5	26.67	4.23
Sakha108	37.67	33.89	21.83	132.5	6.93	4.59
LSD at 0.01	0.51	0.73	0.68	0.47	1.51	0.92
0.05	0.36	0.53	0.49	0.34	1.09	0.87

Rice stem borer estimation (*Chilo agamemnon* Bles.)

Eight rice genotypes were evaluated for stem borer infestation (Figure 1), showing that the variety Giza177 was resistant (R) and gave 2.25%, while the varieties Sakha104, Sakha101, Sakha108, and Giza182 were

moderately resistant (MR) and gave the percentages 3.53, 4.11, 4.94% and respectively. On the other hand, the three hybrid genotypes, Hybrid 27P31, Hybrid 28P67, and Egyptian Hybrid 1, were susceptible, and the infestation percentages were 10.25, 11.7, and 9.72, respectively (Figure 1).

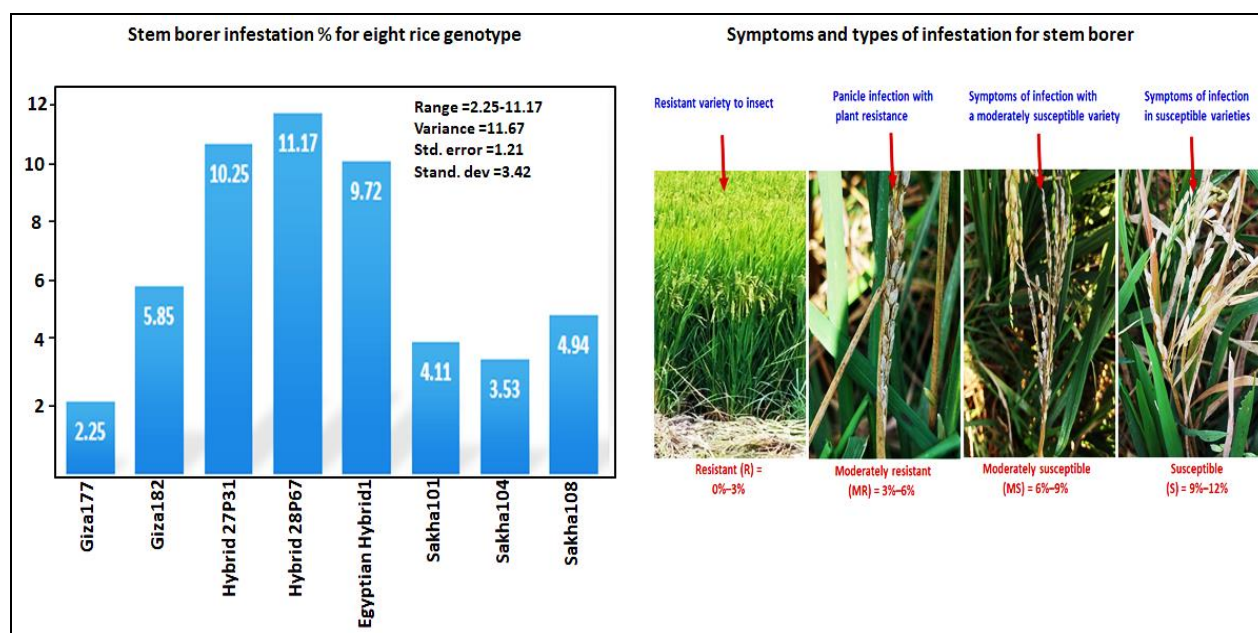


Figure 1. Infestation of eight rice genotypes against rice stem borer attack under study

Evaluation for blast reaction under field conditions

Leaf blast reactions were recorded for the eight rice genotypes under Egyptian conditions in the field conditions in the summer season. The results indicated that three rice varieties,

Sakha101, Sakha104, and Sakha108, were susceptible to leaf blast reaction, while the rest of the genotypes, namely Giza177, Giza182, Hybrid 27P31, Hybrid 28P67, and Egyptian Hybrid 1, were resistant to leaf blast reaction (Figure 2).

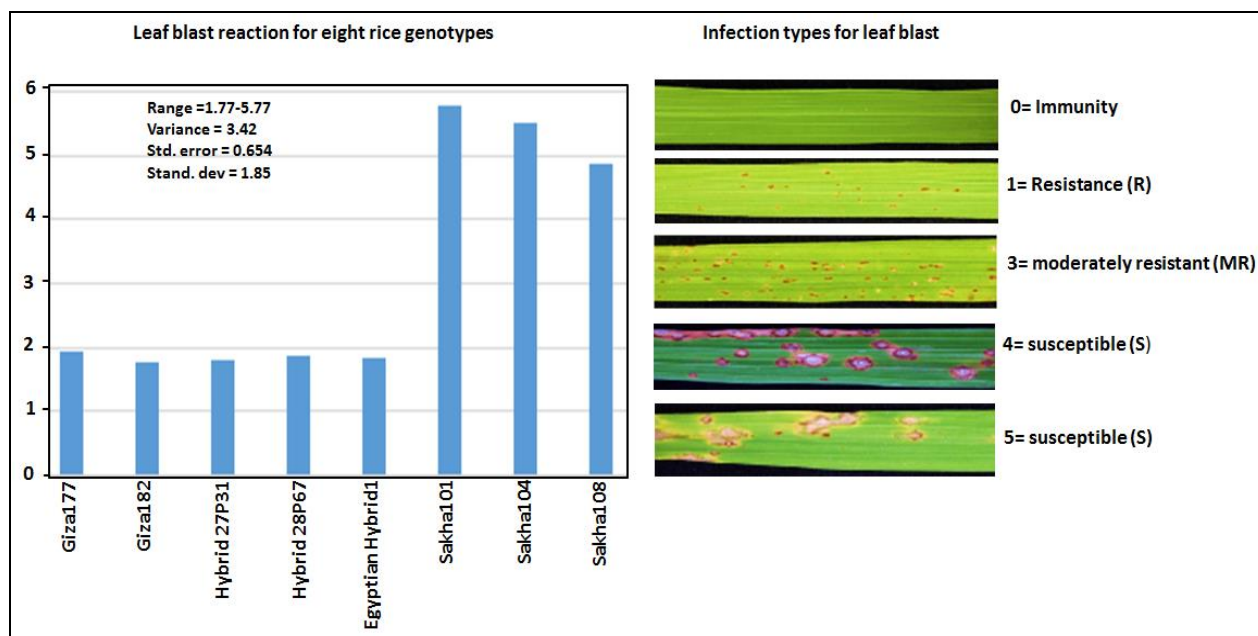


Figure 2. Rice plants showed resistance against leaf blast reaction for eight rice genotypes under study

Phenotypic and Genotypic Variability

The results in Table 4 showed that high estimates of genotypic (σ^2_g) and phenotypic (σ^2_{ph}) variances for all characters studied indicated an improved scope for the genetic improvement and showed that the environment did not have a critical impact on the variability patterns of these traits (Table 4). The data indicated that the magnitude of genetic variance (σ^2_g) was higher than the environmental variance (σ^2_e) for all studied traits. 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 were calculated, as presented in Table 4. For genotypic coefficient (GCV%),

the results ranged between 4.10% and 25.60% for 1000-grain weight and panicle weight. Heritability (h^2_b) for the traits ranged from 69.98 to 95.74 with unfilled grains panicle⁻¹ and plant height (Table 4). The phenotypic coefficient of variability (PCV%) was higher than the corresponding genotypic coefficient of variability (GCV%) for all studied characteristics, indicating that a significant portion of PCV% was primarily influenced by environmental effects. In contrast, the genetic coefficient of variability was higher for all studied characteristics, suggesting that these characteristics may be more predominately determined by genotypic factors, making further improvements feasible.

Table 4. Genetic parameters for agronomics traits of eight rice genotypes under study

Genetic parameters	Mean	Rang	$\sigma^2 g$	$\sigma^2 e$	$\sigma^2 Ph$	PCV	GCV	h^2b
Traits								
Plant height	109.1	95.0-137.3	86.1	0.74	86.8	15.52	15.50	95.74
Tillers plant ⁻¹	24.92	23.1-27.0	1.83	0.04	1.87	5.48	5.43	92.07
Duration	136.9	125.0-127.3	56.08	1.04	57.12	5.52	5.47	94.18
Panicles plant ⁻¹	23.6	22.4-25.7	1.16	0.04	1.20	4.65	4.58	96.93
1000-grain weight	27.4	24.9-28.5	1.26	0.13	1.39	4.30	4.10	90.86
Panicle weight	4.49	2.99-6.36	1.32	0.04	1.36	26.02	25.60	86.85
Grain yield plant ⁻¹	40.23	36.6-55.0	44.66	0.09	44.75	16.63	16.61	94.80
Grain yield day ⁻¹	33.59	29.5-37.6	9.30	0.08	9.38	9.12	9.08	95.17
Panicle length	25.62	21.8-28.2	4.00	0.04	4.04	7.85	7.81	92.08
Grains panicle ⁻¹	158.3	120.5-211.6	1204	0.39	1204.8	21.93	21.92	93.97
Unfiled grains panicle ⁻¹	22.25	4.7-54.5	54.7	0.07	54.8	14.68	14.65	69.98
Grain acre ⁻¹ (ton)	4.55	3.7-5.4	4.56	0.98	2.21	24.45	23.13	93.77

The genetic coefficient of variability refers to both additive and non-additive genetic variance, which played a significant role in the inheritance of these characteristics. Heritability and genetic advance are presented in Table 4. However, heritability estimates in a broad sense were high for all the studied features, indicating that genetic variance (both additive and non-additive) had a substantial impact on the inheritance of all these traits.

Correlation among the traits under study

Pearson's correlation analysis for the 14 quantitative traits across eight rice genotypes revealed varying degrees of correlation (Figure 3). The plant height trait exhibited a significant positive association with panicle weight, grain yield per day, grains per panicle, unfilled grains per panicle, and the percentage of stem borer

infestation. Additionally, panicle weight showed a significant positive correlation with grain yield per plant, grains per panicle, unfilled grains per panicle, grain yield per acre, and stem borer percentage. Grain yield per plant had a significant positive correlation with field grains per panicle and grain yield per acre, while grain yield per day was positively correlated with field grains per panicle, grain yield per acre, and the percentage of stem borer infestation. Conversely, field grains per panicle demonstrated a significant positive correlation with grain yield per acre and stem borer percentage, but a significant negative correlation with leaf blast reaction. Finally, grain yield per acre was positively correlated with the percentage of stem borer infestation (Figure 3).

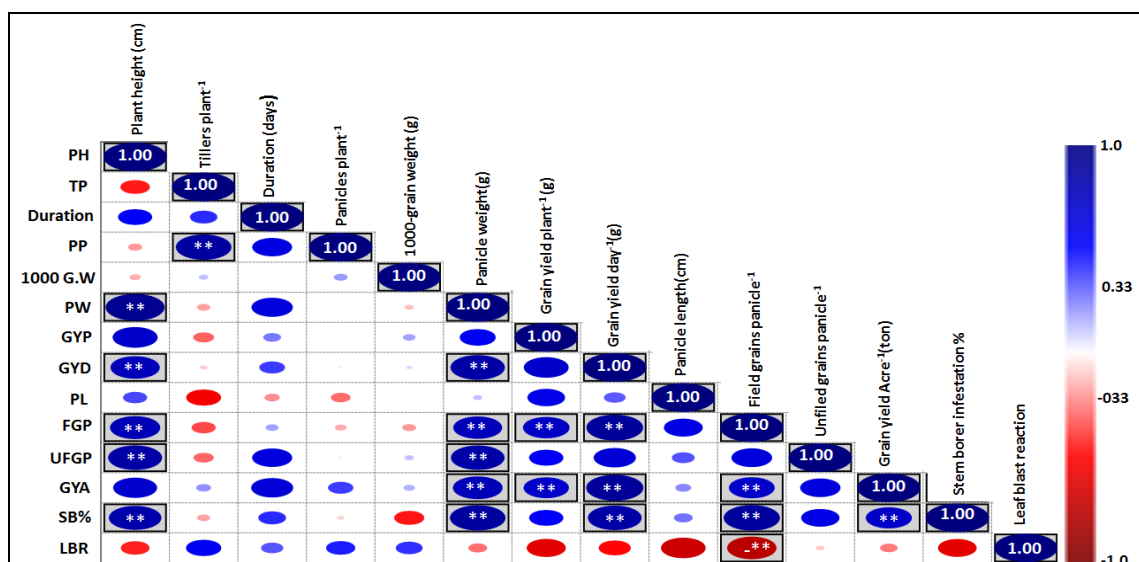


Figure 3. Pearson correlation analysis between 14 quantitative traits for the eight rice genotypes under study

Principal component analysis

The principal component analysis (PCA) helped explain the genetic diversity among the eight rice genotypes through 14 quantitative traits. The cumulative variance of 98.90% for the first five axes with an Eigenvalue of >1.0 indicates that the identified traits within the axes exhibited better influence on the phenotype of the eight rice genotypes (Table 5). The results showed that the control on PC1 and PC2 was for the distribution of the genotypes, with all the genotypes widely scattered across different

quarters (Figure 4). These rice genotypes incurred divisions into four groups, with the first one including Sakha101, Sakha104, and Sakha108 being similar in tiller plant⁻¹, panicle plant⁻¹, 1000-grain weight, and leaf blast reaction. Quitters-II and IV included the genotypes Hybrid 27P31 and Hybrid 28P67, which, characterized by the highest values for days to heading, grain yield acre⁻¹, unfilled grain panicle⁻¹, panicle weight, grain yield per plant, high infestation by stem borer, plant height, grain per plant, filled grain panicle and panicle length.

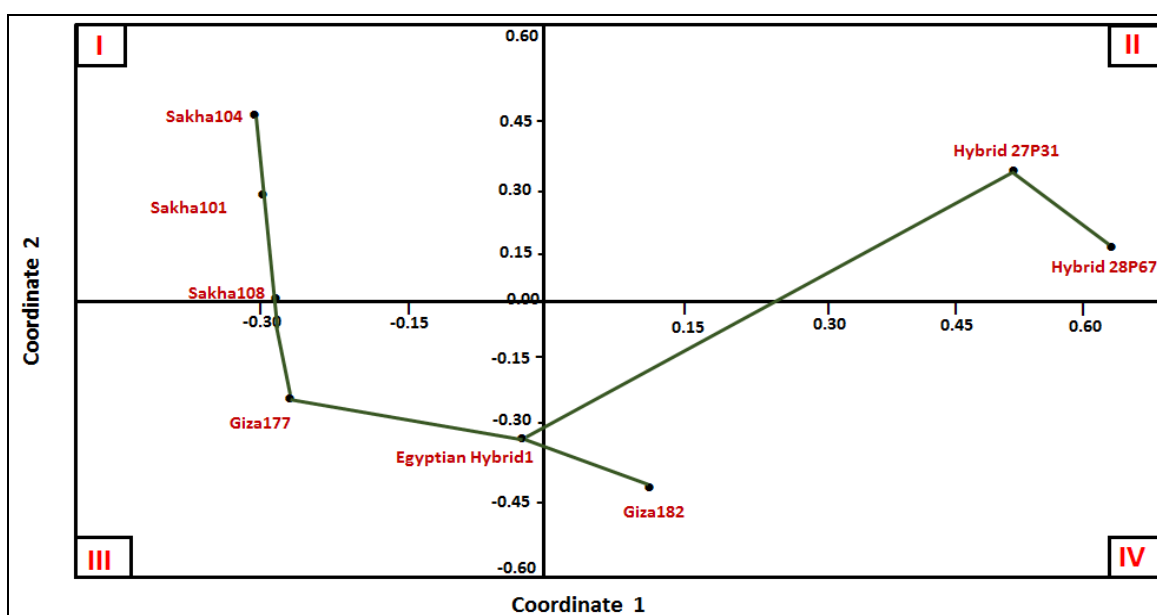


Figure 4. Distribution of eight rice genotypes across two components

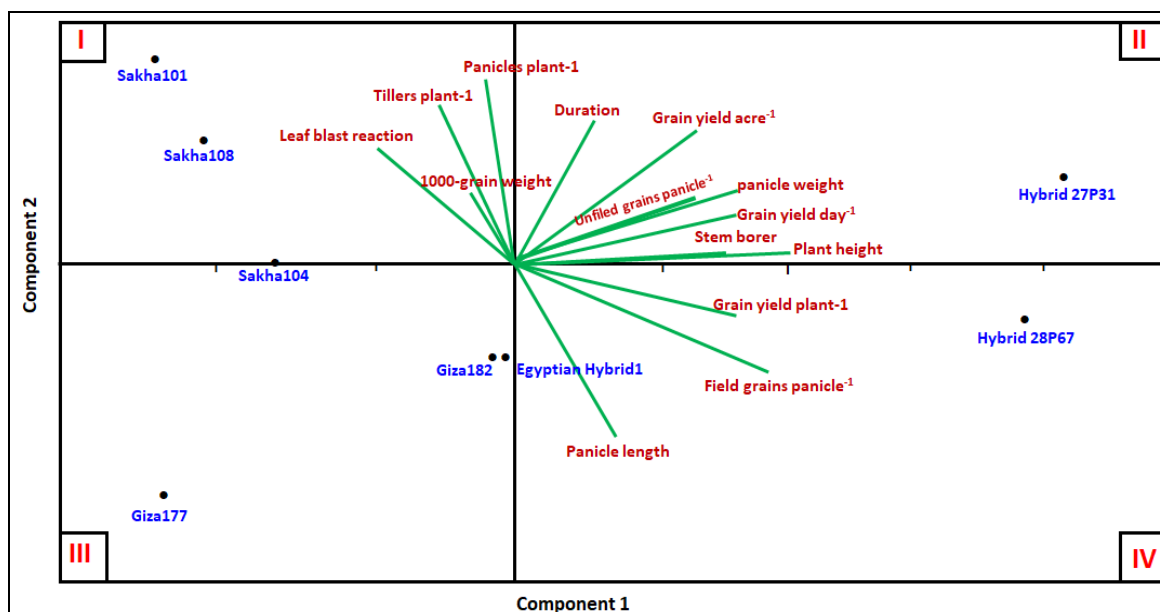


Figure 5. Biplot of the principal component analysis (PCA) for eight rice genotypes with 14 agronomic traits. PCA was performed using XLSTAT v19.1.

Table 5. Eigenvalues, % variance, and cumulative % variance of eight morphological traits for principal components

Traits	PC1	PC2	PC3	PC4	PC5
Eigen value	7.071	3.259	1.423	1.201	0.610
Variance contribution (%)	50.508	23.281	10.165	8.576	4.359
Cumulative variance contribution	67.77	91.74	95.80	98.27	99.32
Plant height	0.373	0.361	0.714	-0.331	-0.252
Tillers plant ⁻¹	-0.013	0.003	-0.013	0.228	0.034
Duration	0.062	0.333	0.226	0.832	0.063
Panicles plant ⁻¹	-0.004	0.016	-0.026	0.176	0.093
1000-grain weight	-0.004	0.019	-0.058	-0.030	0.163
Panicle weight	0.025	0.026	0.028	0.034	-0.051
Grain yield plant ⁻¹	0.125	-0.015	0.285	-0.092	0.896
Grain yield day ⁻¹	0.068	-0.011	0.015	0.123	0.031
Panicle length	0.028	-0.034	-0.074	-0.135	0.151
Grains panicle ⁻¹	0.835	-0.489	-0.149	0.147	-0.047
Unfiled grains panicle ⁻¹	0.362	0.715	-0.557	-0.137	0.084
Grain acre ⁻¹ (ton)	0.009	0.004	0.009	0.043	0.027
Stem borer (%)	0.073	-0.016	0.112	0.147	-0.237
Leaf blast reaction	-0.030	0.075	-0.047	0.085	-0.018

Cluster analysis based on quantitative characteristics

The mean performance and normality for all traits were checked, which indicated that all traits had good approximations of normal distributions. The results indicated the presence of two groups (Figure 6). The first group included the two hybrids (Hybrid 27P31 and Hybrid 28P67), which are imported from the same origin, long grains, Indica type, similar characteristics in plant height, duration, and most other characteristics. The second group included the remaining of genotypes but was further divided into two sub-groups. The first sub-group included the two genotypes Giza182,

which belongs to the Indian type, and the Egyptian hybrid 1, which belongs to the Indica-Japonica type and were similar in tillers plant⁻¹, panicles plant⁻¹ and field grains panicle⁻¹ (Figure 6). The last sub-group included Sakha101, Sakha108 Sakha104 and Giza177, these genotypes from Japonica type. Otherwise, Sakha101 variety was used as a parent to produce Sakha108, so closely together. There is also a similarity in characteristics in plant height (cm), tiller plant⁻¹, and field grain panicle⁻¹. On the other hand, Giza177 variety was in a branch alone because it is characterized by the shortest duration, compared with all the genotypes under study.

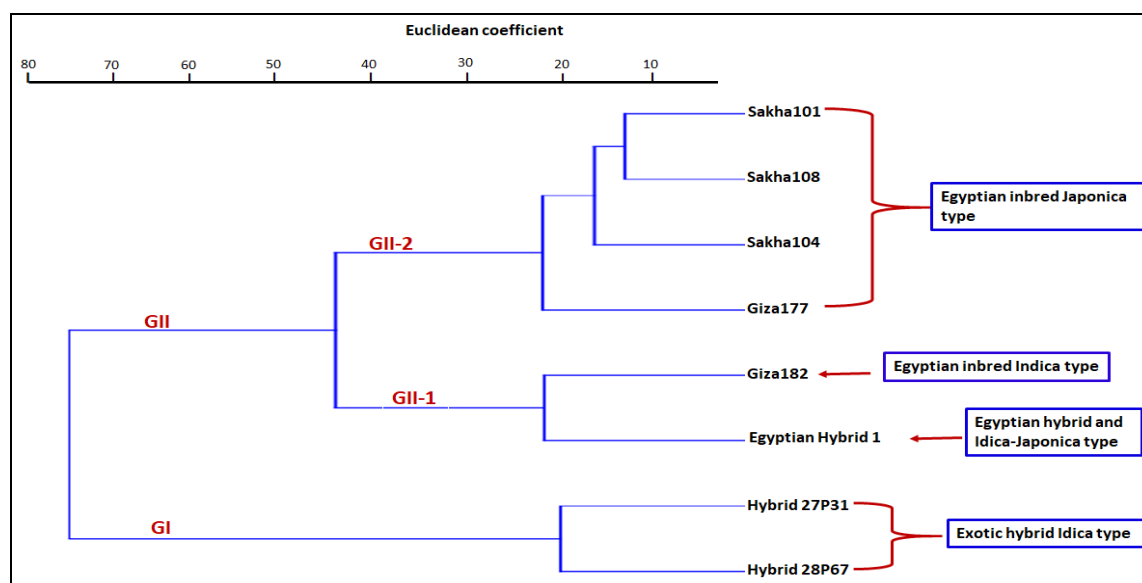


Figure 6. Morphology-based phylogenetic tree based on 30 characters of eight rice varieties

Producing new varieties with high-quality characteristics is one of the main challenges due to global climate change (Li et al., 2014; Bassuony et al., 2022; Nofal et al., 2024). The current study was conducted to obtain genetic information for these traits and their correlations in addition to determining the similarity between the varieties. In the present study, ANOVA for all traits revealed significant differences among all genotypes for all traits. These results indicated a considerable amount of variability among genotypes for various traits and a substantial amount of heterosis among hybrids. These results were in agreement with previous reports on similar traits (Adhikari et al., 2018; Brar et al., 2018; Tewachewu et al., 2018; Demeke et al., 2023). In the previously mentioned studies, the authors highlighted the significant differences between these traits, which are attributed to the difference in the genetic makeup of the varieties. However, the mean performance of agronomic traits showed different genetic systems involved in controlling yield traits, which emphasized the importance of the study of these traits. The results also showed the superiority of Indian hybrids (Hybrid 27P31 and Hybrid 28P67) in crop characteristics, grain yield per plant⁻¹, field grain panicle⁻¹, panicle weight, and grain yield acre⁻¹ (Bian et al., 2021). These are desirable characteristics for increasing the yield trait, plant height, and long duration (Tao et al., 2023; He et al., 2024). In addition, the results showed that Japonica-type varieties were low in the percentage of amylose content, which is a desirable characteristic in the cooking processes compared to Indian varieties and hybrid genotypes. Similar results were previously reported (Bian et al., 2021). Estimates of components of variance genotypic (GCV) and phenotypic (PCV) coefficients of variability, broad sense heritability (h^2B) and genetic advance for all studied traits: The estimates of components of variance, phenotypic (σ^2Ph), genotypic (σ^2g) and environmental (σ^2e) variance; phenotypic (PCV) and genotypic (GCV) coefficients of variability and broad-sense heritability (h^2B) for different traits are presented. The

magnitude of genotypic variance was greater than that of environmental variance for all the studied traits (Aly et al., 2013; Mohamed et al., 2018; Birtucan et al., 2023; Demeke et al., 2023). However, high estimates of phenotypic (σ^2ph) and genotypic (σ^2g) variances were observed for all traits, indicating a better scope for the genetic improvement in these traits. These findings indicate that these specified traits are highly variable, whereas the environment had a moderate influence, revealing moderate estimates of broad-sense heritability. Results of the current study are in confirmation of the findings of (Faysal et al., 2022; Gaballah et al., 2022; Rezk et al., 2024). All characters studied in various years showed high estimates of heritability, indicating the presence of both additive and non-additive genetic variance in the inheritance of most traits, except for breakage in white rice percentage, which varied between 69.98 to 96.93 for unfilled grains panicle⁻¹ and panicles plant⁻¹. These characteristics, however, are more resilient to shifting environments and cultural norms. Thus, it is possible to draw the conclusion that the selection processes it uses are effective in enhancing most of the attributes being evaluated. Some results were previously obtained by Esther et al. (2021), Faysal et al. (2022), Rezk et al. (2024). The correlation among different traits helps to choose components with prior importance to proceed with the selection for improved genetic gain in a population (Brar et al., 2018). It also determines the strength of relationships among different traits to execute a reliable selection of rice genotypes (Al-Daej et al., 2022). Plant height trait showed a significant positive association with panicle weight, grain yield day⁻¹, grains panicle⁻¹, unfilled grains panicle⁻¹, and infestation of stem borer. Also, panicle weight had a significant positive correlation with grain yield plant⁻¹, grains panicle⁻¹, and unfilled grains per panicle⁻¹, grain yield per acre, and stem borer%. Grain yield plant⁻¹ had a significant positive correlation with field grain panicle⁻¹, and grain yield acre⁻¹, while grain yield day⁻¹ had a positive correlation with field grain panicle⁻¹, grain yield acre⁻¹,

and infestation of stem borer percentage. On the other hand, field grain panicle⁻¹ had a positive significant correlation with grain yield acre⁻¹ and stem borer percentage, while a negative significant correlation with leaf blast reaction. Finally, grain yield acre⁻¹ was positively correlated with infestation of stem borer percentage. This positive and significant correlation between these traits is due to their inheritance as one linkage group or were located in chromosome one (Okasa et al., 2021; Shi et al., 2021; Al-Daej et al., 2022). The biplot PCA found remarkable findings regarding the relationship between rice grain quality and agronomic traits (Figure 3). Quadrant-I grouped Japonica type (Giza177, Sakha108, Sakha104 and Sakha101), short grains, Japonica types, and originated from the same origin and common parents, are contribute to the production of some of these varieties (Table 1). Quadrant II included only Egyptian hybrid 1, which belonged to the Indica-Japonica type and had less than 1000-grain weight characteristics compared to the other types. The genotypes in quadrants III and IV included all the Indica types, and most of them were high value in infestation by stem borer, plant height, panicle weight, grain yield plant⁻¹, grain yield day⁻¹, field grain panicle⁻¹, unfilled grain panicle⁻¹, and grain yield acre⁻¹. Similar results appeared with the principal component analysis in rice germplasm for grain quality traits (Mvuyekure et al., 2018; El-Malky and Al-Daej, 2023; El-Malky, 2024). Finally, the cluster analysis was consistent with PCA analysis and was divided into two groups. However, parent, pedigree, grain dimensions, and agronomic traits played a major role in the dendrogram partitioning.

CONCLUSIONS

This study concluded that hybrid rice genotypes (Hybrid 27P31 and Hybrid 28P67) were superior to traditional varieties for yield characteristics and also resistant to leaf blast disease, but were more sensitive to stem borer infestation. Cluster analysis of the eight

rice genotypes was divided based on the genetic background, the types, and the origin. So the Japonica types Giza177, Sakha104, Sakha108, and Sakha101 were together in one group, while the Indica and Indica-Japonica types were in another group.

FUNDING

This research work was supported and funded by the Deanship of Scientific Research, Vice Presidency for Graduate Studies and Scientific Research, King Faisal University, Saudi Arabia, grant number (KFU251748).

ACKNOWLEDGEMENTS

Authors extend their appreciation to the Deanship of Scientific Research, Vice Presidency for Graduate Studies and Scientific Research, King Faisal University, Saudi Arabia for funding this research work (KFU251748).

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