



Research Article

Developing Some Promising Lines Resistant to *Pyricularia grisea* Derived from Egyptian and American Rice Varieties (*Oryza sativa* L.)

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Abstract

Background and Objective: The main disease constraint for rice production in the world is blast, caused by *Pyricularia grisea*. Traditional breeding is one of most economic methods to produce durable resistance. The aim of the study was to develop some promising resistant lines between American and Egyptian in order to study their genetic parameters and investigate correlation co-efficient of agronomic traits. **Materials and Methods:** In this study, the crossing was carried out between blast resistant parents (Egyptian) used as a donors and susceptible parents (Americans). Twenty four promising lines were selected in the late generations and evaluated at three locations; i.e., Sakha, Gemmiza and Zarzora during 2015 up to 2017. **Results:** The results indicated that the Egyptian varieties carry different resistance genes and these genes are dominant under Egyptian condition but the American varieties carry recessive genes for resistance. On the other hand, the genes Pii, Piz, Piz^t, Pit, Pi5^(t), Pi9, Pita, Pita⁽²⁾ and piz⁽⁵⁾ were effective and dominant under Egyptian condition. Concerning agronomic traits, the results showed that the earliest plants were observed in line 18 followed by line 19 and Giza 177, while the latest ones were Giza 178, line 12 and line 13. In addition, line 9 and line 19 had the longest panicles. Lines 14, 20, 21 and 28 produced the highest number of tillers and panicles/plant. Phenotypic (δ^2 ph) and genotypic (δ^2 g) variances were observed for number of filled grains/panicle followed by grain yield/plant, sterility percentage, 1000 grain weight and plant height, indicating a better scope for the genetic improvement in these traits. On the other hand, convenient estimates of Genotypic Coefficients of Variability (GCV) coupled with high broad-sense heritability and high genetic advance were found for duration, plant height, number of tillers/plant, number of filled grains/panicle, 1000 grain weight, sterility percentage and grain yield/plant. The phenotypic correlation coefficients among all possible pairs of grain yield components and grain yield were positive and strongly correlated with each of number of tillers/plant (0.354), number of panicles/plant (0.533), number of filled grains/panicle (0.558) and 1000 grain weight (0.470). **Conclusion:** Egyptian varieties (Giza 177 and Giza 178) carry different dominant resistant and effective genes while the American varieties carry recessive genes for resistance.

Key words: Rice (*Oryza sativa* L.), *Pyricularia grisea*, resistant genes, genetic analysis, genotypic (GCV) and phenotypic (PCV) coefficients, correlation coefficients

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Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Rice (*Oryza sativa* L.) is a principal food crop for more half of the global population¹ and has become in Egypt, the first summer cash crop². This crop is attacked by different diseases, the major one is blast disease caused by *Pyricularia grisea* (Cooke) Sacc. teleomorph, *Magnaporthe grisea* (Hebert) Barr. The resistance genes are used for controlling this disease and are considered cost-effective and environmentally beneficial means for minimizing crop losses caused by the blast³. However, more than 70 genes and 300 Quantitative Trait Loci (QTL) were identified and have been reported^{4,5}. Genetic resistance is a strategy that has long been the mainstay of successful rice production in Egypt. Many rice cultivars contain genes that confer resistance to one or more of the individual races of the fungus found regionally and many contain a high level of resistance to the fungus that is conferred by many other genes. For example, in Egypt, after 1984 breakdown by blast infection, scientists of Rice Research and Training Center (RRTC) started to produce resistant varieties (Giza 177, Giza 178, Sakha 101, Sakha 104, Giza 181, Giza 182, Sakha 102, Sakha 103, Sakha 105, Sakha 106 and Giza 179)⁶. These varieties were produced through classical breeding which is considered an economic way to develop blast resistance rice varieties. All these varieties were resistant but after few years, two cultivars (Saka 101 and Sakha 104) turned to be susceptible^{7,8}. In this way, the new race of the fungus has eluded resistance, which means that the cultivars containing this important resistance gene are very susceptible to the new race, even though they remain resistant to the other races of the fungus. The sources of resistance are very important like durable resistance varieties and monogenic resistant lines can be utilized as donor varieties for blast resistance with different resistance genes^{9,10} which were used in this investigation. The current investigation aimed to: (1) Study the resistance stability of the promising lines, derived from current hybridization between American and Egyptian rice varieties, (2) Estimate the resistance of the varieties to blast under greenhouse condition and (3) Study the genetic parameters and correlation coefficients for agronomic traits for promising lines.

MATERIALS AND METHODS

Three crosses were achieved between American and Egyptian rice varieties, the American varieties (M204 and M202) were used as highly susceptible, while the two Egyptians (Giza177 and Giza178) were used as resistant ones. The crosses and F₁ were sown in the experimental farm of Dr. David J. Mackill, Department of Agronomy and Range

Science, University of California, Davis CA95616-8515, USA. The F₂, F₃ and selected lines were evaluated at the experimental farm of Rice Research and Training Center (RRTC), Sakha, Kafer El-Sheikh, Egypt, during 2015, 2016 and 2017 rice growing seasons. The F₂ and F₃ populations (200 plants each) were planted surrounded by Giza159 cultivar as a spreader to blast. High doses of nitrogen fertilizer were applied to enhance blast infection. From 2012-2017, homogenous lines were selected and evaluated in preliminary yield trials, while the stability of resistance to blast were assessed in 2015-2017. Twenty four promising lines were classified and divided into three categories; SKC23808 (four lines), as produced from the hybridization between M202×Giza 177, SKC2319 (19 lines) as the cross between Giza177×M204 and SKC23824 (one line) as produced from M202×Giza 178 cross.

Blast test

Field evaluation at blast nursery: Twenty eight genotypes were tested at Sakha, Gemmiza and Zarzora fields starting from 2015-2017 for blast resistance at seedling stage for major genes resistance under natural infection at blast nursery. In addition, 32 monogenic lines were identified for possession of resistance genes under Egyptian condition. All genotypes were late sown (1st week of July) to enhance blast infection that increases with high temperature and high relative humidity. Giza181 variety was used as a resistant check. Forty days after sowing, the typical blast lesions were scored, according to the Standard Evaluation System¹¹ using 0-9 scale.

Greenhouse test and race identification: Seeds of each genotypes were seeded in plastic trays (30×20×15 cm) and the seedlings were ready for inoculation at 3-4 leaf stage (about 3-4 weeks after sowing). Seven days after inoculation, blast reaction was recorded according to the standard evaluation system using 0-9 scale¹¹. Also, monogenic lines were cultivated and inoculated with the same races for identification of effective resistance genes. Twenty four isolates collected from three rice-growing governorates; Kafr EL-Sheikh (12 isolates), Gharbia (8 isolates) and Beheira (4 isolates) during 2015 growing season. These isolates were identified as *P. grisea* races according to disease reaction pattern on the international differential varieties and were used in the present study. They were individually grown on banana dextrose agar medium (200 g banana, 15 g glucose, 15 g agar/1000 mL water) under florescent light for 10 days at 28°C for sporulation. The spores were harvested at a density of at least 25 spores/microscopic field, examined by 10x objective. Rice seedlings of about 20 day old, in the trays were inoculated by the spore suspension (100 mL) adjusted to

5×10^4 spores mL^{-1} . Gelatin was added to the spore suspension at a concentration¹² of 2.5 g L^{-1} to enhance the adhesion of spores on leaf surfaces. Each isolate was sprayed using electrical spray gun. The inoculated seedlings were held in a moist chamber with 98-100% relative humidity and $25\text{-}28^\circ\text{C}$ for 24 h and then moved to the greenhouse conditions.

Agronomic traits: Twenty eight lines were evaluated at the Experimental Farm of Rice Research and Training Center, Sakha, Kafr El-Sheikh Governorate, Egypt, during the rice growing seasons from 2015-2017. All these lines were grown in a RCBD in the three replications. Each plot contained three rows and each row contained 25 plants, with growing spacing's of 20×20 cm. Seedlings of 30 day old were transplants in the permanent field. These agronomic traits included duration (day), plant height, no. of tillers per plant, no. of panicles/plant, panicle weight, no. of filled grains per panicle, 1000 grain weight, sterility % and grain yield per plant.

Statistical analysis: Obtained data were statistically combined over the two seasons according to Le Clerg *et al.*¹³ and subjected to analysis of variance (ANOVA). Significant difference means were separated at $p < 0.05$ by the Least Significant Difference (LSD) test. Statistical analyses were made with commercial software which was used to partition the gross phenotypic variability into the components due to genetic (hereditary) and non-genetic (environmental) factors and to estimate their magnitude. Genotypic variance is the part of the phenotypic variance that can be attributed to genotypic differences among the phenotypes. Similarly, phenotypic variance is the total variance among phenotypes when grown over the range of environments of interest¹⁴. Hence, variance components, genotypic (V_g), phenotypic (V_p) and error (V_e) variances were estimated using the formula of Wricke and Weber¹⁵ and Prasad *et al.*¹⁶ as follows:

$$V_g = \frac{MSG - MSE}{r}$$

$$V_{ph} = \frac{MSG}{r}$$

$$V_e = \frac{MSE}{r}$$

where, MSG, MSE and r are the mean squares of genotypes, mean squares of error and number of replications,

respectively. Phenotypic (PCV) and genotypic (GCV) coefficient of variation were evaluated according to the methods of Burton¹⁷, Johnson *et al.*¹⁸ and Kumar *et al.*¹⁹ as:

$$PCV = \sqrt{\frac{V_p}{X}} \times 100$$

$$GCV = \sqrt{\frac{V_g}{X}} \times 100$$

where, V_p , V_g and X are the phenotypic variances, genotypic variances and grand mean per season, respectively for the traits under consideration. Broad sense heritability (h^2_B) expressed as the percentage of the ratio of the genotypic variance (V_g) to the phenotypic variance (V_{ph}) was estimated on genotypic mean basis as described by Allard²⁰. Genetic Advance (GA) expected and GA as percentage of the mean assuming selection of the superior 5% of the genotypes were estimated in accordance with the methods of illustrated by Fehr²¹ as:

$$GA = K (S_{ph}) h^2_B$$

$$GA \text{ (mean \%)} = \frac{GA}{x} \times 100$$

where, k is a constant (which varies depending upon the selection intensity and if the latter is 5%, it stands at 2.06). S_{ph} is the phenotypic standard deviation ($\sqrt{V_{ph}}$), h^2_B is the heritability ratio and x refers to the season mean of the trait.

RESULTS AND DISCUSSION

Field evaluation: Data in Table 1 indicated that the American varieties (M204 and M202) were blast susceptible under the three locations, while the Egyptian varieties (Giza177 and Giza178) were resistant under all locations. These results indicated that the Egyptian varieties carry different blast resistance genes and these genes are dominant under Egyptian condition but the American varieties carry recessive resistance genes. On the other hand, the promising lines derived from crossing between Egyptian and American entries were blast resistant, except the lines number 6, 7, 9, 16, 19 and 24 that were susceptible under Sakha location in 2015 season only (Table 1). These resistant lines could be used as new varieties and to be utilized as donors to blast resistance in the breeding program.

Table 1: Estimates of blast reaction at rice fields of Sakha, Gemmiza and Zarzoura locations during 2015, 2016 and 2017 seasons

Genotype	Location/season/reaction								
	Sakha			Gemmiza			Zarzoura		
	2015	2016	2017	2015	2016	2017	2015	2016	2017
Giza 177	R	R	R	R	R	R	R	R	R
Giza 178	R	R	R	R	R	R	R	R	R
Sakha 102	R	R	R	R	R	R	R	R	R
M202	S	S	S	S	S	S	S	S	S
M204	S	S	S	S	S	S	S	S	S
SKC-23819-189-1-1-1-1-3-1-3-1	S	R	R	R	R	R	R	R	R
SKC-23819-189-1-1-1-3-1-2-4-2	S	R	R	R	R	R	R	R	R
SKC-23808-125-2-3-5-2-2-2-1-1	R	R	R	R	R	R	R	R	R
SKC-23808-125-2-3-5-2-4-1-4-1	S	R	R	R	R	R	R	R	R
SKC-23819-192-2-1-2-1-8-1-1-1	R	R	R	R	R	R	R	R	R
SKC-23819-192-2-1-2-1-8-1-1-2	R	R	R	R	R	R	R	R	R
SKC-23819-192-2-1-2-1-10-2-2-1	R	R	R	R	R	R	R	R	R
SKC-23819-192-2-1-2-2-4-2-1-1	R	R	R	R	R	R	R	R	R
SKC-23819-192-2-1-2-2-4-2-1-2	R	R	R	R	R	R	R	R	R
SKC-23819-192-2-1-2-3-1-1-1-2	R	R	R	R	R	R	R	R	R
SKC-23819-192-2-1-2-4-5-3-1-1	S	R	R	R	R	R	R	R	R
SKC-23819-192-2-1-2-4-5-3-2-1	R	R	R	R	R	R	R	R	R
SKC23808-125-2-1-4-2-1-1-2-1	MR	R	R	R	R	R	R	R	R
SKC23808-125-2-3-1-1-3-1-1-2	S	R	R	R	R	R	R	R	R
SKC23819-189-1-1-2-2-1-1-2-1	R	R	R	R	R	R	R	R	R
SKC23819-189-1-1-2-2-1-1-2-2	MR	R	R	R	R	R	R	R	R
SKC23819-192-2-2-1-1-2-1-2-1	R	R	R	R	R	R	R	R	R
SKC23819-192-2-2-1-1-2-1-2-2	R	R	R	R	R	R	R	R	R
SKC23819-192-2-2-1-1-2-2-1-1	S	R	R	R	R	R	R	R	R
SKC23819-192-2-2-1-1-2-2-1-2	R	R	R	R	R	R	R	R	R
SKC23819-192-3-1-1-1-25-1-1	R	R	R	R	R	R	R	R	R
SKC23819-194-1-2-1-2-5-2-2-1	R	R	R	R	R	R	R	R	R
SKC23824-422-3-3-3-2-1-5-1-1	R	R	R	R	R	R	R	R	R

R: resistant (1-2), MR: moderately resistant (3), S: Susceptible (4-6), HS: Highly susceptible (7-9)

As for resistance dominant genes, under natural infection during 2015 and 2016 seasons. Data presented in Table 2 indicated that the genes; *pii*, *Piz⁻⁵* present in IRBLi-F5, IRBLz5-CA and IRBLz5-CA(R) lines, *Pit*, *Pish* present in IRBLsh-B lines, *Pita⁻²* present in IRBLt-K59 and IRBLta2-Pi were completely resistant in 2015 and 2016 seasons. It could be concluded that the evaluated genotypes are a good source for breeding program for improving resistance against blast. While, *Pi5(t)*, *Pi9* genes were resistant only in 2015 season, as will as *Pik-s* present in IRBLks-S and *Pita-2* present in IRBLta2-Re line in 2016 season. On the other hand, *Pik-s* present in IRBLks-F5 line was Moderately Resistant (MR). The results indicated that these genes are dominant in 2015 and 2016 seasons under Egyptian condition.

Greenhouse test and race identification: Twenty four isolates indicated that 6 race groups were identified i.e., IC, ID, IE, IF, IG and IH, these race groups included 10 races (one from each of IC-17, IC-31, three from IC-19; one from ID-1, two from

ID-15; one from IE-3; two from each of IF-1, IF-3; three from IG-1; and eight from IH-1) were used to evaluate the rice monogenic lines. Data presented in Table 3 summarize that Nine genes namely; *Pii*, *Piz*, *Piz^t*, *Pit*, *Pi5^(t)*, *Pi9*, *Pita*, *Pita⁽²⁾* and *piz⁽⁵⁾* were resistant against twenty four *P. grisea* isolates under greenhouse test. The resistance percentage ranged from 75-100%. This indicated that several effective genes could be used in gene pyramiding for producing new durable resistant genotypes. On the other hand, 14 *P. grisea* isolates selected namely; 2p, 3p, 4p, 5p, 7p, 8p, 9p, 10p, 11p, 15p, 16p, 18p, 19p and 21p were used against the genotypes under study and the results (Table 4) showed that the lines 4 (M202) and 5 (M204) were susceptible and the resistance percentage were 47.2 and 35.7%, respectively, while the other selected lines had complete resistance except the line 18 (SKC23808-125-2-1-4-2-1-1-2-1) that was susceptible and recorded resistance percentage of 14.3% only. The lines 12 (SKC-23819-192-2-1-2-1-10-2-2-1), 14 (SKC-23819-192-2-1-2-2-4-2-1-2), 17 (SKC-23819-192-2-1-2-4-5-3-2-1) and 25

Table 2: Blast reaction of rice monogenic lines during 2016 and 2017 seasons under natural infections

Line	Type of genes	Blast reaction	
		2015	2016
IRBLa-A	Pia	HS	S
IRBLa-C	Pia	S	S
IRBLi-F5	Pii	R	R
IRBLks-F5	Pik-s	MR	MR
IRBLks-S	Pik-s	S	R
IRBLk-ka	Pik	S	S
IRBLkp-K60	Pik-p	S	S
IRBLkh-K3	Pik-h (Pi54)	S	S
IRBLz-Fu	Piz	MR	S
IRBLz5-CA	Piz-5 = pi2	R	R
IRBLzt-T	Piz-t	S	S
IRBLta-K1	Pita = Pi4 (t)	S	S
IRBLta-CT2	Pita = Pi4 (t)	S	S
IRBLb-B	Pib	HS	S
IRBLt-K59	Pit	R	R
IRBLsh-S	Pish	MR	S
IRBLsh-B	Pish	R	R
IRBL1-CL	Pi1	S	S
IRBL3-CP4	Pi3	MR	S
IRBL5-M	Pi5 (t)	R	MR
IRBL7-M	Pi7 (t)	S	S
IRBL9-W	Pi9	R	S
IRBL12-M	Pi12 (t)	S	S
IRBL19-A	Pi19	S	S
IRBLkm-Ts	Pik-m	S	S
IRBL20-IR24	Pi20	S	S
IRBLta2-Pi	Pita-2	R	R
IRBLta2-Re	Pita-2	MR	R
IRBLta-CP1	Pita = Pi4 (t)	S	HS
IRBL11-Zh	Pi11 (t)	S	S
IRBLz5-CA(R)	Piz-5	R	R
Lijiangxintuanheigu	Susceptible	S	S

R: resistant (1-2), MR: moderately resistant (3), S: Susceptible (4-6), HS: Highly susceptible (7-9)

(SKC 23819-192-2-2-1-1-2-2-1-2) were moderately resistant and the resistant percentages were 78.6, 71.4, 64.3 and 64.3, respectively (Table 4).

Analysis of variance: The genotype mean squares (Table 5) exhibited highly significant differences for all the studied traits indicating into wide range of genetic variability among the studied genotypes and this is a primary requirement for further computation.

Mean performance: Data in Table 6 showed that the earliest plants which preferred by rice breeders under water stress conditions were observed in line 18 followed by line 19 and Giza 177, while, the latest ones were belonging to Giza 178, line 12 and line 13 rice genotypes. Line 18 followed by line 22 and line 14, were the shortest genotypes but lines 19, 24 and 28 were the tallest ones. In addition, Giza 178,

M204, line 9 and line 19 had the longest panicles (23.59, 23.42, 22.58 and 22.50 cm, respectively). Highest number of tillers and panicles/plant were detected for Giza 178, line 28 and line 21. Line 14, line 20, line 21 and line 28 had the heaviest of panicles (5.13, 4.63, 5.13 and 5.63 g/panicle, respectively and weight of 1000-grain (38.67, 41.37, 40.47 and 39.67 g/100 grains) and superior grain yield (50.20, 53.40, 48.15 and 57.45 g/plant). The highest number of filled grains/panicle was determined for Giza 178 followed by Giza 177 and line 28 as 191.33, 155.07 and 154.40 grains, respectively. Meanwhile, the lowest values of number of filled grains/panicle were determined for line 15 followed by line 8 and line 7 (91.17, 91.87 and 92.27, respectively). Low sterility (%) was observed for Giza 178, line 10 and line 19 rice genotypes comparing with the other cultivated parents. The parental mean values of grain yield were between 27.15 and 57.45 g/plant for line 15 and line 28, respectively. Similar results were reported by Mohaiuddin *et al.*²², El-Refae *et al.*²³, Munns *et al.*²⁴ and Hassan *et al.*²⁵.

The mean performance of best Egyptian and exotic lines and varieties on different parameters studied can be shown in Fig. 1.

Estimates of components of variance

Genotypic (GCV) and phenotypic (PCV) coefficients of variability, broad sense heritability (h²B) and genetic advance for all studied traits: The estimates of components of variance, phenotypic (σ^2_{ph}), genotypic (σ^2_g) and environmental (σ^2_e) variance; phenotypic (PCV) and genotypic (GCV) coefficients of variability and broad-sense heritability ($h^2 B$) and genetic advance (G.S %) for different traits are presented in Table 7. The magnitude of genotypic variance was greater than that of environmental variance for all the studied traits. However, high estimates of phenotypic (σ^2_{ph}) and genotypic (σ^2_g) variances were observed for number of filled grains/panicle followed by grain yield/plant, sterility (%) 1000 grain weight and plant height indicating into a better scope for the genetic improvement in these traits. Moreover, the extent of variation indicated that high estimates of genotypic (GCV) and phenotypic (PCV) coefficients of variability were found for sterility (%) numbers of filled grains/panicle, numbers of tillers/plant, grain yield/plant and numbers of panicles/plant. These findings indicate that these specified traits are highly variable, whereas the environment had a moderate influence, revealing moderate estimates of broad sense heritability.

Table 3: Blast reaction of rice monogenic lines against 24 *Pyricularia grisea* isolates collected from different rice-growing governorates in 2016 and 2017 seasons, under greenhouse conditions

Monogenic line	Target gene	Race/reaction of isolate											
		1D-15	IH-1	IF-1	IH-1	IH-1	IC-19	ID-1	IG-1	IH-1	IH-1	IF-1	IC-19
IRBLa-A	Pia	S	S	HS	S	S	S	S	S	S	S	S	S
IRBLa-C	Pia	S	S	HS	S	HS	S	S	S	S	S	S	S
IRBLi-F5	Pii	R	R	S	R	R	MR	MR	HS	R	R	S	R
IRBLks-F5	Pik- ^s	S	MR	MR	S	MR	S	S	S	S	S	S	S
IRBLks-S	Pik- ^s	S	MR	S	S	R	S	S	S	S	MR	S	S
IRBLk-ka	Pik	R	S	S	R	R	S	S	S	R	R	HS	S
IRBLkp-K60	Pik- ^p	R	S	S	R	R	MR	S	HS	R	R	S	S
IRBLkh-K3	Pik- ^h	R	S	S	R	R	S	S	S	R	R	S	S
IRBLz-Fu	Piz	R	R	S	MR	R	S	S	S	R	R	MR	MR
IRBLz5-CA	Piz- ^s	R	MR	R	R	R	R	R	R	R	R	R	R
IRBLzt-T	Piz- ^t	S	S	S	S	R	S	S	S	S	S	S	S
IRBLta-K1	Pita	S	R	R	S	R	S	S	S	S	MR	S	R
IRBLta-CT2	Pita	S	S	S	S	R	S	S	S	S	S	MR	S
IRBLb-B	Pib	S	HS	R	S	MR	S	S	S	S	HS	S	R
IRBLt-K59	Pit	MR	R	S	MR	R	S	S	R	S	MR	R	R
IRBLsh-S	Pish	MR	S	S	S	R	S	S	S	S	S	S	R
IRBLsh-B	Pish	MR	R	S	S	R	S	S	S	MR	R	S	R
IRBL1-CL	Pi1	MR	R	S	R	R	S	S	S	R	R	S	S
IRBL3-CP4	Pi3	S	S	S	R	R	R	S	S	R	R	S	S
IRBL5-M	Pi5 (t)	R	R	R	R	R	R	R	S	R	R	MR	R
IRBL7-M	Pi7 (t)	R	R	S	R	R	S	R	S	R	R	S	S
IRBL9-W	Pi9	R	R	R	S	R	S	S	R	R	R	R	R
IRBL12-M	Pi12 (t)	S	S	S	S	R	MR	R	S	S	R	S	S
IRBL19-A	Pi19	S	S	HS	S	R	S	S	S	S	S	S	S
IRBLkm-Ts	Pik- ^m	R	MR	HS	R	R	S	R	S	S	R	S	S
IRBL20-IR24	Pi20	S	S	S	S	R	S	S	S	S	S	S	HS
IRBLta2-Pi	Pita- ²	S	R	MR	R	R	S	MR	MR	R	R	R	R
IRBLta2-Re	Pita- ²	S	R	R	R	R	MR	MR	R	R	MR	R	R
IRBLta-CP1	Pita	S	S	S	S	S	MR	S	HS	S	R	S	S
IRBL11-Zh	Pi11 (t)	S	S	S	S	S	S	S	HS	S	R	R	S
IRBLz5-CA(R)	Piz- ^s	MR	R	R	R	R	R	S	R	R	R	R	R
Ljiangxintuanheigu	-	S	S	S	S	S	S	S	S	S	S	S	S

Monogenic line	Target gene	Race/reaction of isolate												Resistant (%)
		IH-1	IC-31	IH-1	IC-19	IH-1	IF-3	IG-1	IC-17	ID-15	IE-3	IF-3	IG-1	
RBLa-A	Pia	S	S	S	S	S	S	S	S	S	HS	S	S	0.0
IRBLa-C	Pia	S	S	S	S	S	S	S	S	S	HS	S	S	0.0
IRBLi-F5	Pii	R	R	R	R	R	R	R	R	R	R	R	R	87.5
IRBLks-F5	Pik- ^s	R	S	S	S	S	S	S	S	S	S	S	S	12.5
IRBLks-S	Pik- ^s	S	S	S	MR	S	S	S	S	R	S	S	S	20.8
IRBLk-ka	Pik	R	R	R	S	R	R	S	R	R	R	S	R	54.2
IRBLkp-K60	Pik- ^p	R	R	R	S	S	MR	R	S	R	R	S	R	58.3
IRBLkh-K3	Pik- ^h	R	R	R	S	R	R	S	R	R	R	S	R	50.0
IRBLz-Fu	Piz	R	R	R	R	R	R	S	R	R	R	R	R	79.2
IRBLz5-CA	Piz- ^s	R	R	R	R	R	R	R	R	MR	R	R	R	100.0
IRBLzt-T	Piz- ^t	S	S	S	R	S	S	HS	S	S	S	R	S	12.5
IRBLta-K1	Pita	S	S	MR	S	S	S	HS	MR	S	R	MR	MR	41.6
IRBLta-CT2	Pita	S	S	S	S	S	S	HS	S	S	S	S	S	8.3
IRBLb-B	Pib	S	S	S	MR	MR	S	HS	R	HS	S	S	S	25.0
IRBLt-K59	Pit	S	MR	R	R	MR	MR	MR	MR	R	R	R	R	79.2
IRBLsh-S	Pish	S	S	MR	S	MR	S	S	S	S	S	S	S	20.8
IRBLsh-B	Pish	S	R	MR	S	R	MR	S	MR	R	R	MR	MR	63.5
IRBL1-CL	Pi1	MR	R	R	HS	MR	MR	R	S	R	R	S	R	62.5
IRBL3-CP4	Pi3	S	MR	R	MR	S	S	S	R	R	R	MR	R	50.0
IRBL5-M	Pi5 (t)	R	R	R	R	R	R	R	R	R	R	R	R	95.5
IRBL7-M	Pi7 (t)	R	R	MR	S	MR	MR	R	S	R	R	S	R	66.6
IRBL9-W	Pi9	MR	R	S	R	S	S	R	MR	R	R	R	R	75.0
IRBL12-M	Pi12 (t)	S	MR	MR	S	S	S	S	S	R	MR	R	S	37.5
IRBL19-A	Pi19	S	S	S	S	S	S	S	S	S	S	S	S	4.2
IRBLkm-Ts	Pik- ^m	R	R	R	S	R	R	R	S	R	R	S	R	62.5
IRBL20-IR24	Pi20	S	S	S	MR	S	S	HS	S	S	S	S	S	8.3
IRBLta2-Pi	Pita- ²	MR	R	MR	R	MR	S	S	MR	R	R	R	R	83.3
IRBLta2-Re	Pita- ²	MR	R	MR	R	R	MR	S	R	R	R	R	R	91.6
IRBLta-CP1	Pita	S	S	S	HS	S	S	S	S	S	S	S	S	8.3
IRBL11-Zh	Pi11 (t)	S	S	S	S	R	S	S	MR	S	S	S	S	16.6
IRBLz5-CA(R)	Piz- ^s	R	R	R	R	R	R	R	R	R	R	R	R	91.6
Ljiangxintuanheigu	-	S	S	S	S	S	S	S	S	S	HS	S	S	0.0

R: Resistant (1-2), MR: Moderately resistant (3), S: Susceptible (4-6), HS: Highly susceptible (7-9)

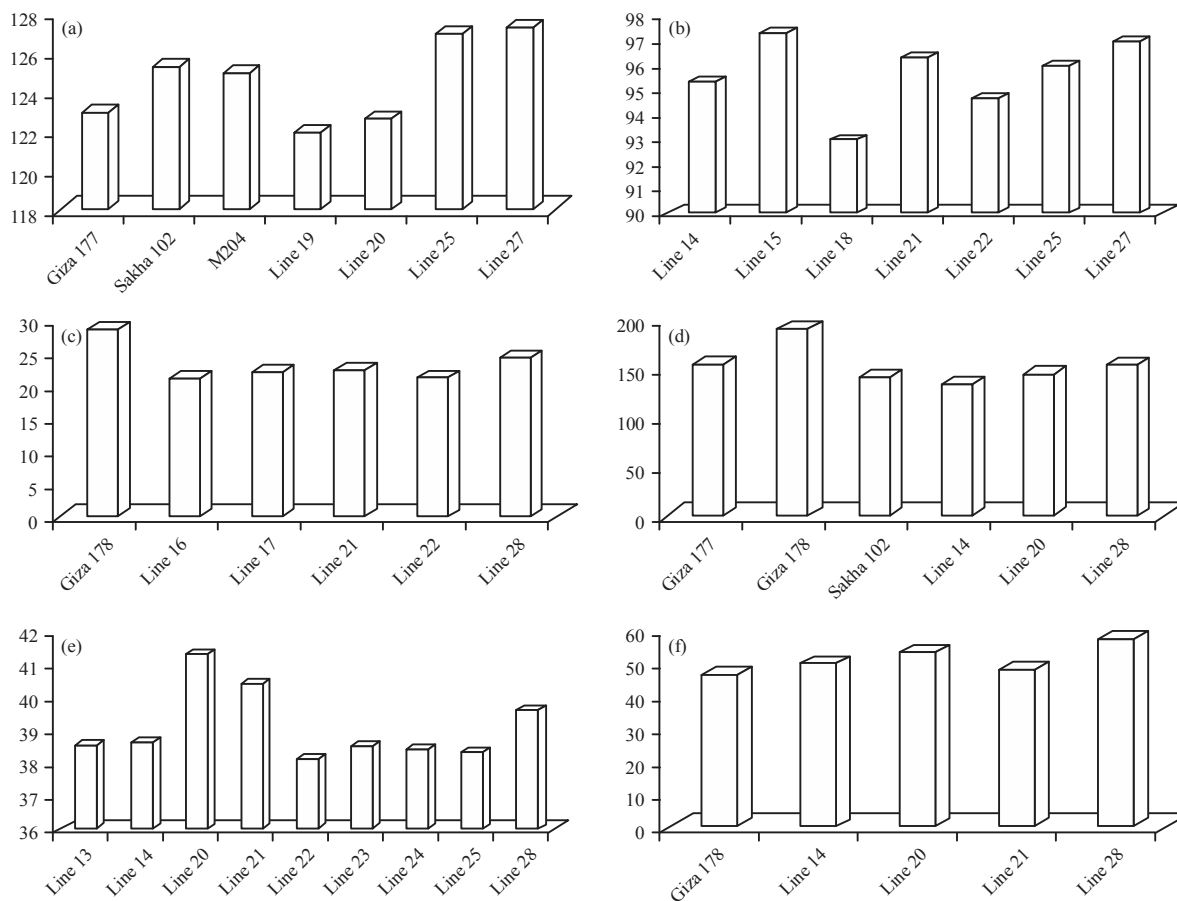


Fig. 1(a-f): Mean performance of the best Egyptian and exotic lines and varieties, (a) Duration, (b) Plant height, (c) Number of Panicles/plant, (d) Number of filled grains/panicle, (e) 1000 Grain weight (g) and (f) Grain Yield/plant (g)

On the other hand, convenient estimates of GCV coupled with high broad-sense heritability and high genetic advance were found for duration, plant height, number of tillers/plant, number of filled grains/panicle, 1000 grain weight, sterility (%) and grain yield/plant, meanwhile, there were not much differences between PCV and GCV, thus, these traits seem to be highly heritable, referring to the predominance of additive gene effect, easily fixable and can be taken as unit traits for effective selection. Sadhukhan and Chattopadhyay²⁶ reported that grain yield/plant had high phenotypic (PCV) and genotypic (GCV) coefficient of variation. However, the highest estimate of GCV was noted in sterility (%). They also added that broad-sense heritability estimates were moderate to high for all studied traits. Results of the current study are in confirmation to the findings of Deosarkar *et al.*²⁷, Soliman *et al.*²⁸, Hassan *et al.*²⁹, Sultan *et al.*³⁰ and Seedek and El-Wahash³¹.

The studies on genotypic coefficient of variation and phenotypic coefficient of variation indicated that the presence of high amount of variance enhances the role of the environment on the expression of these traits. The magnitude

of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters, which may be due to higher degree of interaction of genotypes with the environment²⁹⁻³⁴.

The highest genetic advance was recorded for duration, plant height, number of tillers/plant, number of panicles/plant, number of filled grains/panicle, 1000 grain weight, sterility (%) and grain yield/plant.

A character exhibiting high heritability may not necessarily give high genetic advance; Johnson *et al.*¹⁸ has shown that high heritability should be accompanied by high genetic advance to arrive to a more reliable conclusion. Therefore, it should be combined with information on genetic advance. Thus, a character possessing high heritability along with high genetic advance will be valuable in selection program.

In the current investigation, high heritability coupled with high genetic advance were recorded for duration, plant height, number of tillers/plant, number of filled grains/panicle, 1000 grain weight, sterility (%) and grain yield/plant suggesting preponderance of additive gene action in the

Table 4: Blast reaction of 28 rice genotypes against 14 *Pyricularia grisea* isolates collected from different rice-growing governorates in 2016 and 2017 seasons, under greenhouse conditions

Genotype	Race/reaction of isolates															Resistant (%)
	2p	3p	4p	5p	7p	8p	9p	10p	11p	15p	16p	18p	19p	21p		
Giza 177	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
Giza 178	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
Sakha 102	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
M202	R	R	MR	S	R	HS	S	S	R	S	R	S	R	R	47.2	
M204	R	R	R	S	S	R	S	S	S	S	S	S	S	R	35.7	
SKC-23819-189-1-1-1-1-3-1-3-1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC-23819-189-1-1-1-3-1-2-4-2	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC-23808-125-2-3-5-2-2-2-1-1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC-23808-125-2-3-5-2-4-1-4-1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC-23819-192-2-1-2-1-8-1-1-1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC-23819-192-2-1-2-1-8-1-1-2	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC-23819-192-2-1-2-1-10-2-2-1	R	R	R	S	R	HS	HS	R	R	R	R	R	R	R	78.6	
SKC-23819-192-2-1-2-2-4-2-1-1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC-23819-192-2-1-2-2-4-2-1-2	R	R	R	S	R	HS	HS	R	R	R	R	S	R	R	71.4	
SKC-23819-192-2-1-2-3-1-1-1-2	R	R	R	R	R	R	R	R	R	R	MR	R	R	R	100	
SKC-23819-192-2-1-2-4-5-3-1-1	R	R	R	R	R	R	R	R	R	R	MR	R	R	R	100	
SKC-23819-192-2-1-2-4-5-3-2-1	S	R	R	R	MR	S	MR	MR	S	S	S	MR	R	R	64.3	
SKC23808-125-2-1-4-2-1-1-2-1	HS	R	MR	HS	S	S	S	S	S	S	S	HS	S	S	14.3	
SKC23808-125-2-3-1-1-3-1-1-2	R	R	R	R	R	R	R	R	R	R	MR	R	R	R	100	
SKC23819-189-1-1-2-2-1-1-2-1	MR	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC23819-189-1-1-2-2-1-1-2-2	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC23819-192-2-2-1-1-2-1-2-1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC23819-192-2-2-1-1-2-1-2-2	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC23819-192-2-2-1-1-2-2-1-1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC23819-192-2-2-1-1-2-2-1-2	R	R	R	R	S	S	R	S	R	MR	S	S	MR	R	64.3	
SKC23819-192-3-1-1-1-25-1-1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC23819-194-1-2-1-2-5-2-2-1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	
SKC23824-422-3-3-3-2-1-5-1-1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100	

R: Resistant (1-2), MR: Moderately resistant (3), S: Susceptible (4-6), HS: Highly susceptible (7-9)

Table 5: Mean squares of rice genotypes of studied traits

S.O.V	d.f	Duration (day)	Plant height (cm)	Panicle length (cm)	No. of tillers/plant	No. of panicles/plant
Replication	2	2.51	1.86	1.35	7.20	2.59
Treatment	27	39.09 **	77.77**	4.49**	34.00**	29.32**
Error	54	1.56	4.03	0.92	1.84	6.99
S.O.V	d.f	Panicle weight (g)	No. of filled grains/panicle	1000 grain weight (g)	Sterility (%)	Grain yield/plant (g)
Replication	2	0.12	29.19	0.28	4.85	0.15
Treatment	27	1.41**	1609.83**	81.95**	95.36**	126.01**
Error	54	0.18	48.55	3.40	4.45	1.21

***Significant at 0.05 and 0.01 probability levels, respectively

expression of these characters. Therefore, selection may be effective for these characters in segregating generations^{25,29-31,35}.

The characters like panicle length and panicle weight exhibited high heritability coupled with low genetic advance suggesting preponderance on non-additive gene action in the inheritance of these traits; hence in this case selection may not be effective. Most of the above results in respect to heritability and genetic advance are in agreement with reports of Sawant and Patil³⁶ and Sarawgi *et al.*³⁷ for their potential to selection.

Estimates of phenotypic correlation coefficients: The phenotypic correlation coefficients among all possible pairs

of grain yield components traits were presented in Table 8. Grain yield was positively and strongly correlated with each of number of tillers/plant (0.354), number of panicles/plant (0.533), number of filled grains/panicle (0.558) and 1000 grain weight (0.470). These results indicated that these traits are principle yield components. Therefore, any selection based on these traits will bring the desired improvement in grain yield. Sterility (%) showed significant negative correlations with number of filled grains/panicle (-0.658) and grain yield/plant (-0.350). Among yield related traits, duration was significantly and positively associated with number of tillers/plant (0.373) and number of panicles/plant (0.403). However, a highly significant and positive estimate of phenotypic correlation

Table 6: Mean performance of studied traits of 28 Egyptian and exotic lines and varieties

Genotypes	Duration (day)	Plant height (cm)	Panicle length (cm)	No. of tillers/plant	No. of panicles/plant
Giza 177	123.00	107.00	19.70	19.37	17.53
Giza 178	139.00	98.00	23.59	33.85	28.78
Sakha 102	125.33	105.00	21.17	22.22	13.60
M202	128.33	99.00	21.40	19.07	16.58
M204	125.00	102.00	23.42	20.38	17.29
SKC-23819-189-1-1-1-1-3-1-3-1	131.33	99.00	19.53	21.40	20.20
SKC-23819-189-1-1-1-3-1-2-4-2	131.33	104.33	19.85	19.37	17.60
SKC-23808-125-2-3-5-2-2-2-1-1	131.00	99.67	20.35	17.52	15.80
SKC-23808-125-2-3-5-2-4-1-4-1	132.00	103.00	22.58	17.73	16.47
SKC-23819-192-2-1-2-1-8-1-1-1	132.00	100.67	20.58	17.70	17.00
SKC-23819-192-2-1-2-1-8-1-1-2	132.00	103.67	21.17	19.20	17.57
SKC-23819-192-2-1-2-1-10-2-2-1	133.60	105.00	21.37	19.23	17.47
SKC-23819-192-2-1-2-2-4-2-1-1	133.00	99.67	21.35	16.53	15.33
SKC-23819-192-2-1-2-2-4-2-1-2	131.00	95.33	19.18	20.27	18.27
SKC-23819-192-2-1-2-3-1-1-1-2	131.00	97.33	19.68	22.03	20.47
SKC-23819-192-2-1-2-4-5-3-1-1	131.00	101.67	19.45	23.13	21.30
SKC-23819-192-2-1-2-4-5-3-2-1	131.00	98.00	21.47	23.10	22.27
SKC23808-125-2-1-4-2-1-1-2-1	122.00	93.00	19.59	18.70	17.70
SKC23808-125-2-3-1-1-3-1-1-2	122.67	114.67	22.5	20.17	18.80
SKC23819-189-1-1-2-2-1-1-2-1	129.67	98.00	19.68	19.63	18.27
SKC23819-189-1-1-2-2-1-1-2-2	130.00	96.33	21.57	23.43	22.47
SKC23819-192-2-2-1-1-2-1-2-1	130.00	94.67	20.03	22.77	21.53
SKC23819-192-2-2-1-1-2-1-2-2	129.67	104.00	19.99	21.70	20.57
SKC23819-192-2-2-1-1-2-2-1-1	130.00	109.67	19.53	19.50	18.67
SKC23819-192-2-2-1-1-2-2-1-2	127.00	96.00	19.70	16.77	15.53
SKC23819-192-3-1-1-1-25-1-1	128.00	104.67	20.50	18.33	17.17
SKC23819-194-1-2-1-2-5-2-2-1	127.33	97.00	19.77	20.53	19.53
SKC23824-422-3-3-3-2-1-5-1-1	128.00	109.33	20.22	25.17	24.40
L.S.D 0.05	1.70	2.740	1.31	1.85	3.61
L.S.D 0.01	2.10	3.38	2.04	2.28	4.45

Genotypes	Panicle weight (g)	No. of filled grains/panicle	1000 grain weight (g)	Sterility (%)	Grain yield/plant (g)
Giza 177	4.23	155.07	28.57	6.80	43.25
Giza 178	4.57	191.33	21.21	5.48	46.15
Sakha 102	3.85	141.67	25.15	6.21	42.50
M202	3.23	120.67	25.55	10.83	41.38
M204	3.36	128.00	26.68	9.10	44.65
SKC-23819-189-1-1-1-1-3-1-3-1	4.33	112.27	32.17	8.54	35.30
SKC-23819-189-1-1-1-3-1-2-4-2	4.43	92.27	34.27	16.44	31.50
SKC-23808-125-2-3-5-2-2-2-1-1	3.23	91.87	31.17	23.94	30.33
SKC-23808-125-2-3-5-2-4-1-4-1	3.93	127.20	30.07	16.00	40.70
SKC-23819-192-2-1-2-1-8-1-1-1	5.13	126.10	37.57	5.18	31.95
SKC-23819-192-2-1-2-1-8-1-1-2	5.73	123.60	33.27	8.87	34.05
SKC-23819-192-2-1-2-1-10-2-2-1	4.63	109.60	37.17	14.22	37.48
SKC-23819-192-2-1-2-2-4-2-1-1	5.03	111.77	38.57	11.17	39.50
SKC-23819-192-2-1-2-2-4-2-1-2	5.13	134.87	38.67	11.87	50.20
SKC-23819-192-2-1-2-3-1-1-1-2	3.93	91.17	33.17	15.31	27.15
SKC-23819-192-2-1-2-4-5-3-1-1	4.23	116.07	36.47	12.01	32.00
SKC-23819-192-2-1-2-4-5-3-2-1	5.53	126.30	38.27	7.82	42.80
SKC23808-125-2-1-4-2-1-1-2-1	4.03	124.80	30.57	12.78	39.88
SKC23808-125-2-3-1-1-3-1-1-2	4.63	103.20	30.27	5.17	41.50
SKC23819-189-1-1-2-2-1-1-2-1	4.63	145.50	41.37	9.94	53.40
SKC23819-189-1-1-2-2-1-1-2-2	5.13	128.67	40.47	26.29	48.15
SKC23819-192-2-2-1-1-2-1-2-1	4.53	95.27	38.17	11.47	42.85
SKC23819-192-2-2-1-1-2-1-2-2	4.93	100.07	38.57	13.73	36.05
SKC23819-192-2-2-1-1-2-2-1-1	5.03	104.17	38.47	10.16	44.35
SKC23819-192-2-2-1-1-2-2-1-2	3.83	95.35	38.37	12.07	38.10
SKC23819-192-3-1-1-1-25-1-1	4.43	102.60	35.27	20.59	42.70
SKC23819-194-1-2-1-2-5-2-2-1	5.13	95.40	36.47	23.34	41.98
SKC23824-422-3-3-3-2-1-5-1-1	5.63	154.40	39.67	10.17	57.45
L.S.D 0.05	0.58	9.50	2.51	2.88	1.50
L.S.D 0.01	0.71	11.72	3.10	3.55	1.85

Table 7: Estimates of components of variance; genotypic (GCV) and phenotypic (PCV) coefficients of variability, broad sense heritability (h^2B) and genetic advance (G.S %) for all studied traits

Character	Grand mean	Component of variance		Genetic variability		h^2B		Genetic advance	
		σ^2g	σ^2e	σ^2ph	PCV	GCV		G.S	G.S %
Duration (day)	129.45	12.51	0.52	13.03	2.79	2.73	96.01	24.74	19.11
Plant height (cm)	101.29	24.58	1.34	25.92	5.03	4.89	94.82	48.01	47.40
Panicle length (cm)	20.68	1.19	0.31	1.50	5.92	5.28	79.51	1.95	9.43
No. of tillers/plant	20.67	10.72	0.61	11.33	16.29	15.84	94.59	20.89	101.05
No. of panicles/plant	18.86	7.44	2.33	9.77	16.57	14.46	76.16	11.68	61.91
Panicle weight (g)	4.41	0.41	0.06	0.47	15.55	14.53	87.23	0.74	16.71
No. of filled grains/panicle	117.81	520.43	16.18	536.61	19.66	19.36	96.98	1039.75	882.57
1000 grain weight (g)	33.92	26.18	1.13	27.32	15.41	15.09	95.85	51.70	152.42
Sterility (%)	12.34	30.30	1.48	31.79	45.69	44.61	95.33	59.51	482.30
Grain yield/plant	41.33	41.60	3.57	45.17	16.26	15.60	92.09	78.92	190.93

Table 8: Estimates of phenotypic correlation coefficients among studied traits

Characters	Duration (day)	Plant height (cm)	Panicle length (cm)	No. of tillers/plant	No. of panicles/plant	Panicle weight (g)	No. of filled grains/panicle	1000 grain weight (g)	Sterility (%)
Duration (day)	-								
Plant height (cm)	-0.231	-							
Panicle length (cm)	0.177	0.196	-						
No. of tillers/plant	0.373**	-0.060	0.309	-					
No. of panicles/plant	0.403**	-0.099	0.150	0.882**	-				
Panicle weight (g)	0.233	0.231	-0.059	0.153	0.322*	-			
No. of filled grains/panicle	0.055	0.270	0.577**	0.486**	0.277	0.140	-		
1000-grain weight (g)	0.114	-0.073	-0.518**	-0.259	0.056	0.482**	-0.670**	-	
Sterility (%)	0.056	-0.280	-0.194	-0.210	-0.067	-0.146	-0.658**	0.272	-
Grain yield/plant	-0.136	0.074	0.125	0.354*	0.533**	0.120	0.558**	0.470**	-0.350*

***Correlation is significant at the 0.05 and 0.01 levels, respectively

coefficient (0.577) was recorded between panicle length and number of filled grains/panicle, while highly significant and negative estimate of phenotypic correlation coefficient (-0.518) was recorded between panicle length and 1000 grain weight. In addition, significant positive estimates of phenotypic correlation coefficients were recorded between number of tillers/plant and each of number of panicles/plant (0.882) and number of filled grains/panicle (0.486), between number of panicles/plant and panicle weight (0.322) and between panicle weight and 1000 grain weight (0.482). On the other hand, significant negative estimates of phenotypic correlation coefficients were recorded between number of filled grains/panicle and each of 1000-grain weight (-0.670) and sterility (-0.658)^{25,29,30,38-41}. However, the current results do not coincide with the findings of Aslam *et al.*⁴² who reported that grain yield per plant was positively correlated with plant height. The difference in results may be attributed to the difference in genetic material and environmental condition of the experiments.

Blast disease is the main constraint of rice production in the world. In Egypt, the disease infected area, in 1984, was mainly cultivated with Reihō variety, introduced from Japan in 1978 and adapted and grown in 40% from the total rice area. This cultivar has been quickly susceptible to blast because of new races that broke its resistance^{43,44}. Since that time, the plant breeders at Rice Research and Training Center (RRTC)

started to produce new varieties of short duration and resistant to blast. Plant pathologists isolated and identified different races from different locations, that help the breeders in selection and production of new varieties⁴⁵⁻⁴⁸. Identification of blast resistant genes are very important to produce durable resistant and gene pyramiding, gene accumulation and gene rotation. Monogenic lines, produced by Fukuta *et al.*⁹ are used as differential varieties and a good source for resistance in rice breeding programs. In this study, the American varieties proved to carry the recessive genes, while the Egyptian varieties carry the dominant ones and inherited as a dominant under Egyptian condition. However, the resistant lines appeared as controlled by many different genes (Pii, Piz-5 = Pi2, Pit, Pish, Pita-2 and Piz-5) that could be confirmed through molecular markers⁴⁹. Earliness, preferred by rice breeders to saving water and time was observed in line 18 followed by line 19 and Giza 177 and these entries could be used as donors for short duration program. For short stature, the lines 18, 22 and 14, were the shortest rice genotypes, which are suitable for mechanical harvesting as tolerant for logging. Genotypic (GCV) was greater than phenotypic (PCV) coefficients of variability in number of filled grains/panicle grain yield/plant, sterility (%) 1000 grain weight and plant height indicating better scope for the genetic improvement in these traits.

CONCLUSION

Egyptian varieties (Giza177 and Giza178), are carrying dominant resistant genes. Different genes were found to be effective (Pii, Piz, Pizt, Pit, Pi5⁽¹⁾, Pi9, Pitat, Pita⁽²⁾ and piz⁽⁵⁾). These genes could be used for gene pyramiding and gene accumulation to produce durable resistance to blast. On the other hand, the best genotypes for earliest were SKC23808-125-2-1-4-2-1-1-2-1, SKC23808-125-2-3-1-1-3-1-1-2 and Giza177. While, lines 14, 20, 21 and 28 produced the highest number of tillers and panicles/plant and would be valuable materials for in breeding programs.

SIGNIFICANCE STATEMENT

This study produced new promising lines resistant to blast in addition to the good agronomic characters. It may help the researchers to cover the critical area of the complex qualitative characters such as blast resistant that many researchers were not able to explore. On the other hand, it may help the plant breeders to build the gene pyramiding or gene accumulation for blast resistant in the breeding program.

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