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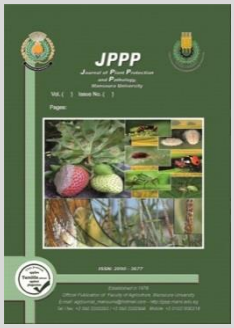
Determination of Resistant on New Highly Productivity Lines for Major Rice Diseases

Selim, M. E.[1*]; A. A. Hassan[2*]; M. A. A. El Sayed[1] and E. A. Z. El Shamey[1]

[1]Rice Research and Training Center, Field Crops Research Institute, Agricultural Research Center, Egypt.
[2]Rice Pathology Department, Plant Pathology Research Institute, Agricultural Research Center, Egypt.



ABSTRACT

This study focused to produce new resistant rice genotypes to major rice diseases and its highly productivity. Rice accessions Giza 177, Sakha 105, Sakha 106 and Gz.7768 were used as male parents and TG-60-6 lines were used as female parent in addition to F_n lines obtained from four crosses. The best genotype has highly productivity and resistance to blast; TG-60-6/Sk.105-2, TG-60-6/Sk.106-3, TG-60-6/GZ.7768-2, TG-60-6/GZ.7768-5, TG-60-6/GZ.7768-6 and TG-60-6/GZ.7768-8. The results of yield and its compounds characters were influenced by environmental effect and the selection should be practiced successfully in late generation. Twenty four *Pyricularia grisea* isolates were identified as five main groups. Under artificial inoculation eleven genotypes were resistant to all rice blast races, but at field condition, eighteen genotypes were resistant at Sakha location and twenty two genotypes resistant at Gemmiza location. The biochemical changes of antioxidant enzymes and total protein were estimated after 24, 96 and 120 h of inoculation with blast race p23 (ID-15) at seedling stage. The maximum activity of perioxidase (POX), polyphenol oxidase enzyme (PPO) and total protein was recorded at 96 h after inoculation and then decreased. Under artificial inoculation with *Bipolaris oryzae* the causal fungus of brown spot disease, TG-60-6/G. 177-1 and TG-60-6/GZ.7768-2 rice genotypes were the lowest for disease severity. For artificial inoculation with *Fusarium fujikuroi* the casual fungus of bakanae, TG-60-6/GZ.7768-1and TG-60-6/G. 177-8 rice genotypes were the lowest seedling death percentages. TG-60-6/G. 177-8 rice genotype was proved the lowest disease incidence. While, the rice genotype TG-60-6/Sk.106-1 showed the lowest disease severity index.

Keywords: Rice, Genotypes, Resistance, Blast disease, Biochemical, *Bipolaris oryzae*

INTRODUCTION

Rice (*Oryza sativa* L.) is considering one of the most cereal crops not only in Egypt but also all over the world. The green revolution technology in China was the reason to increase rice production during last four decades, however, the rate of growth of rice production has slowed down. Whereas, rice production in Egypt increased at the annual growth rate of 2.85% during 1970–1990, the annual growth rate was 1.94% during 1990-2000 and only 1.68% during 2000–2012 (RRTC, 2013). The population of rice consumers is continuing to increase and demand for rice is also going up due to improved living standards particularly in Africa. According to various estimates have to produce 30% more rice in 2030. To meet this challenge, we need rice varieties with higher yield potential and greater yield stability. Although yield potential of rice is 10 tons per hectare, farmers on the average harvest about 5 tons per hectare from irrigated lands. This yield gap is due to the losses caused by biotic and abiotic stresses (Khush and Jena, 2009). Biotic stresses such as fungal diseases, which cause economic losses (Kumar *et al*., 2009). To control diseases, an approach was used in breeding and selected resistant rice cultivars. This method was highly effective and environmentally friend compared with use fungicides (Dodds and Rathjen, 2010). The causal fungus of rice blast is *Magnaporthe oryzae* as teleomorph stage and [anamorph *P. grisea* (Cooke) Sacc.]. In the worldwide blast disease is considered dangers for rice crop yield (Scheuermann *et al*., 2012). About 60 million of the people each year can feed and covered their needed from rice if they can control the blast disease and keep rice free from blast to reduce the yield losses caused by this disease (Divya *et al.*, 2014).

Blast pathogen produce different physiological races and these races can develop and breakdown the resistant in rice cultivars (Urashima, 2014). Management of rice blast disease depending on identifies the resistant of different sources of rice genotypes. The second disease after blast is brown spot in reducing the yield as foliar diseases. The caused fungus is *B. oryzae* (Breda de Haan) Shoemaker (Ou, 1985). Development of resistant lines can reduce the severity of brown spot disease (Bonman *et al*., 1991). Also, bakanae disease is one of the most serious and affected on rice production in the world. *F. moniliforme* is the casual fungus of bakanae Sheldon, *F. fujikuroi* Niremberg [teleomorph *Gibberella fujikuroi* (Sawada)] (Ghazanfar *et al*., 2013). The yield losses of bakanae disease ranged from 50% to more 70% in different rice growing countries. Bakanae considered as soil and seed-borne disease and the disease infected rice plants from the seedling stage until mature stage, with results to infection rice seeds (Wulff *et al.*, 2010). The present study aimed at evaluate and selection some developed new genotypes has

* **Corresponding author.**
E-mail address: m.selimrrtc@gmail.com - amr_ab_2028@yahoo.com
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resistance to some major rice disease *i.e*. blast, brown spot and bakanae and its highly productivity.

MATERIALS AND METHODS

The experimental investigation was carried out at the Farm of Rice Research Department, Sakha, Kafrelsheikh, Egypt, during two successive summer seasons of 2018 and 2019, in addition to Rice Pathology Laboratory and Greenhouse during three successive seasons 2018, 2019 and 2020.

Plant materials and hybridization

The plant materials were including F_n lines to four crosses. The crosses were produced from hybridization between one thermo sensitive genic male sterile (TGMS) line (TG-60-6) as a female line with three Egyptian cultivars; Giza 177, Sakha105, Sakha106 and one new promising line GZ.7768 as male lines in cross I, cross II, cross III and cross IV, respectively. Rice parental lines, parentage origin and grain type are shown in Table 1. Hybridization was followed by pedigree selection methods in segregation generation from F_2 to F_6 into stability. The used F_n lines were divided into eight F_n lines from cross I, two F_n line from cross II, eight F_n lines from cross III and nine F_n line from cross IV. Thirty day old seedlings of each genotype were transplanted in a single seedling per hill in the experimental plots. Each plot consisted of 7 rows, 5 m length with the spacing of 20 × 20 cm. The studied characters were; days to heading (day), flag leaf area (cm^2), flag leaf angel (Ô), panicle $plant^{-1}$, panicle weight (g), and 1000-grain weight (g) and yield $plant^{-1}$ (g). Cultural practices were applied as recorded by RRTC (2013). The experimental was arranged in Randomized Complete Block Design (RCBD) with five replications. Data was subjected to analysis of variance as suggested by Panse and Sukhatme (1954).

Table 1. Rice parental lines, parentage origin and grain type.

No.	Genotypes	Parentage	Origin	Grain type
1	TG-60-6	MJ 5460s / Sakha106	Egypt	Short
2	Giza 177	[Giza 171] Ymji No.1 // PiNo.4	Egypt	Short
3	Sakha105	GZ 5581 / GZ 4316	Egypt	Short
4	Sakha106	Giza 177 / Hexi 30	Egypt	Short
5	GZ.7768	GZ.5320 / Taninung 70	Egypt	Short

Diseases evaluation

Blast disease

Rice blast samples were collected during 2018 growing season from Kafrelsheikh (9 samples), Gharbia (7 samples), Dakahlia (5 samples) and Beheira (3 samples) rice governorates. Typical blast lesion from infected rice samples was isolated according to Shabana *et al*. (2013).

For spore production, isolates were individually grown on banana dextrose agar medium (200, 15 and 15g /1000 ml distilled water) under florescent light for 8 days at 28ºC. The spores were harvested at a density of at least 25 spores/microscopic field, examined by 10x objective Shabana *et al*. (2013).

Pathogenicity test and identification of physiological races

Twenty four blast isolates were isolated and identify as physiological blast races by used eight international differential varieties (I.D.V.) according to Atkins *et al*. (1967). All tested genotypes (32) were planted in plastic trays (30 x 20 x15cm). Each tray comprised 20 rows representing twenty genotypes. The trays were kept in the greenhouse at 28±2 ºC, and fertilized with Urea 46.5%N (5 g/tray). Seedlings were ready for inoculation at 3-4 leaf stage, (about 3-4 weeks after sowing), were inoculated by spraying with spore suspension (100 ml) adjusted to (5×10^4 spores/ml). Each isolate was sprayed using electrical spray gun. The inoculated seedlings were held in a moist chamber with more than 90% R.H. and 25 ± 2^0C for 24 h and moved to the greenhouse conditions.

Biochemical studies

The activities of certain oxidative enzymes, *e.g*. peroxidase (POX), polyphenol oxidase (PPO) and total protein were estimated in eight rice genotypes (TG-60-6, Sakha 106, GZ. 7768, TG-60-6/Sk.105-2, TG-60-6/Sk.106-3, TG-60-6/GZ.7768-2, TG-60-6/G.177-3 and TG-60-6/Sk.106-7) healthy and 24, 96 and 120 h after inoculation with blast race p23 (ID-15) at seedling stage. Enzymes extract were prepared according to the methods recommended by Maxwell and Betman (1967). 500 mg fresh weight of rice leaf samples were ground in a mortar and pestle containing liquid nitrogen. The resulting powder was homogenized with 3 ml of sodium phosphate buffer pH 6.8 (0.1 M) in China mortar. The homogenized samples were centrifuged for 15 min at 10,000 rpm in a refrigerated centrifuge. The clear supernatant was taken as the enzymes source. The absorbance was measured at 425, 495 and 595 nm for POX, PPO and total protein, respectively and recorded at 0, 1, 2, 3, 4 and 5 min. intervals for POX and PPO and only one for total protein using spectrophotometer (Milton Roy, Spectronic, 1201 Digital).

Peroxidase assay

Peroxidase enzyme activity was estimated according to the methods described by Srivastava (1987) The sample cuvette contained 0.5 ml of 0.1 M sodium phosphate buffer at (pH 7.0), 0.3 ml enzyme extract, 0.3 ml of 0.05 pyrogallol, 0.1 ml of 10% H_2O_2 and distilled water to bring cuvette contents to 3.0 ml. Peroxidase activity was expressed as changes in absorbance (mg^{-1} min^{-1}).

Polyphenoloxidase assay

The enzyme was determined according to the method adopted by Matta and dimond (1963). The reaction mixture contained 1.0 ml of 0.2 M sodium phosphate buffer at (pH 7.0), 10.0 ml of 0.001 M catechol, 1.0 ml enzyme extract and 3.0 ml distilled water to bring cuvette contents to 3.0 ml the mixture. Polyphenoloxidase activity was expressed as changes in absorbance (Unit / mg/ min).

Total protein assay

The total protein was determined according to the method adopted by Bradford (1976).The reaction mixture contained 0.1 ml of protein extract, 0.4 ml distilled water and 0.5 ml coomassie brilliant blue G. 250 to bring cuvette contents to 1.0 ml of the mixture. Protein content was expressed as absorbance (mg/ min) and recorded at once time.

Field evaluation at blast nursery test

The tested genotypes (32) were evaluated at two locations Sakha (Kafrelsheikh) and Gemmiza (Gharbia) in 2018 growing season for blast at seedling stage under natural infection (blast nursery). Seedbeds were prepared,

manure fertilizer (5m^3/fad.) and nitrogen as urea 46.5%N (60 Kg/feddan) was added during land preparation. Each genotype was planted in 5 rows with three replicate. Sakha 101 was used as a susceptible check and spreader (source of blast inoculum) while, Giza 178 was used as resistant check. The resistant and susceptible checks were cultivated as alternatively with five rows of each tested genotype. All genotypes were planted with late sown (first week of July) to enhance blast infection that increases temperature and relative humidity with three replications. After sowing by 40-50 days, the typical blast lesions were scored, according to the standard evaluation system using 0-9 scale (IRRI, 2002).

Blast disease assessment

Seven days after inoculation under greenhouse condition, blast reaction, as the typical blast lesions was scored, according to the standard evaluation system using 0-9 scale as follows: 1 – 2, resistant "R"; 3, moderately resistant "MR"; 4 – 6, susceptible "S"; 7 – 9, highly susceptible "HS" IRRI (2002).

Brown spot disease

Rice brown spot fungus was isolated from rice leaves showing typical symptoms of brown spot Giza 177 rice cultivar during 2018 season from Kafrelsheikh according to Kalboush (2007) and identified by the morphological characteristics as *B. oryzae* according to Barnett and Hunter (1972).

Under greenhouse thirty two rice genotypes were planted and fertilized as method of blast with three replications. The isolate was grown on PDA medium under florescent light for 7 days at 28±2^{0}C for spore production. Inoculum of spore suspension was prepared by adding 10 ml sterilized water in each dish. Mycelia mats were gently scraped by spatula and filtered through cheese cloth. Spore suspension was adjusted to (2X10^5 spores/ml). The seedlings were inoculated at 3-4 leaf stage by using electrical spray gun as spray. The inoculated seedlings were held in a moist chamber with at least 90% R.H. and 25±2 ^{0}C for 24 h. and then moved to the greenhouse.

Brown spot assessment

Brown spot disease incidence was assessed as a percentage by counting the number of infected leaves per 25 randomly selected leaves per pot 5 days after infection. Disease severity was calculated as a total number of brown lesions/25 leaves according to Kalboush (2007).

$$\text{Disease incidence \%} = \frac{\text{number of infected leaves}}{\text{total number of leaves}} \text{ X 100}$$

Bakanae disease

Bakanae disease symptoms which collected from infected rice plants of Sakha 105 rice cultivar during 2018 season from Kafrelsheikh (Sakha farm) governorate. The part of steam which has disease was cut into 0.3 to 0.5 cm pieces, sterilized with immersing in 2% sodium hypochlorite solution (NaOH) for two minutes, rinsed twice with sterilized distilled water and then placed onto PDA medium. Plates were incubated at 28±2 °C for 2 to 5 days and the developed fungus was purified using hyphae tip techniques according to Hansen (1926). The morphological characteristics and microscopic examination using the key of imperfect fungi Summerell *et al*. (2003) were used to identify the fungus isolates of *F. fujikuroi*.

Thirty two genotypes inoculated with *F. fujikuroi* isolate were planted in 15x15 cm pots. Seeds of each genotype were sterilized by sodium hypochlorite solution 2% and washed by sterile water several times after that soaked in the pathogen spore suspension (4 x 10^5 spores/ml) for 48 h while check seeds (control) were soaked in sterilized water. Healthy and inoculated seeds were sown on sterilized soils (autoclaved 2 times for 24 h. intermittently at 121^{o}C, 15 psi,). One hundred seeds with triplicate were planted in each tray and arranged with randomized complete design (RCD) in the greenhouse. The fertilization with urea 46.5% N (3 g/pot) was applied one time. The germination percent was recorded after 7 days of sowing and the death seedling %, disease incidence % and disease severity index (DSI) of rice seedling was calculated after inoculation with 45 days for each genotype according to Ooi (2002).

Bakanae disease assessment

The disease scale of bakanae was observed and scoring according to Zainudin *et al*. (2008) the standard evaluation system using 0 to 4 as disease symptoms 0; healthy and uninfected plants (no external symptoms), 1: normal growth but leaves beginning to show yellowish–green, 2: abnormal growth- elongated- thin and yellowish-green leaves; seedlings also shorter or taller than normal, 3: abnormal growth elongated; chlorotic, thin and brownish leaves; seedlings also shorter or taller than normal and 4: seedlings with fungal mass on the surface of infected plants or died. Disease incidence was assessed according to Teng and James (2001) with slight modifications:

$$\text{Disease incidence \%} = \frac{\text{total number of infected plants}}{\text{total number of plant}} \text{ X 100}$$

Disease severity index (DSI) :was calculated for each genotype according to Ooi (2002). DSI was calculated using on the following formula:

$$\text{DSI} = \frac{\sum (\text{number of plants in the specific scale} \times \text{disease scale})}{\text{Total of plants}}$$

Data Analysis: Data were statistically analyzed using standard statistical analysis with MSTATC. in the table of main treatments, Duncan′s (1955) was used to compare the significantly different averages.

RESULTS AND DISCUSSION

The genetic improvement in rice is an inevitable and continuous process to meet the projected future challenges. The available germplasm has to be evaluated to identify potential genotypes which can be exploited for evolving desirable variation to meet future demands which ultimately leads to food and nutritional security of the country.

Mean performance of yield and its components with some vegetative characters

A wide range for yield and its components characters of the genotypes was recorded, the data are summarized in Table 2 showed that, the general mean values of the genotypes were (96.63; 22.40; 46.62; 20.03; 6.14; 29.82; and 74.25) for days of heading, flag leaf area,

flag leaf angle, panicle plant^{-1}, panicle weight, 1000-grain weight, and yield plant^{-1}, respectively. There were, the increase of general mean value for grain yield per plant referring to the increase of seed set %. Generally, for days of heading, the lowest value recorded of TG-60-6/G.177-3 genotype and the highest value recorded of TG-60-6/Sk.106-6 genotype, but the desirable value were (90.53 and 94.37) TG-60-6/G.177-1 and TG-60-6/GZ.7768-2, respectively. As well as, the TG-60-6/GZ.7768-2 genotypes has resistance to blast diseases (Table 6), also, the TG-60-6/G.177-1 genotypes has lowest disease severity to brown spot disease, this could be due to the early maturity. So, should be using these two genotypes to get highly productivity and resistance to blast diseases. As shown in Table 2, the vegetative characters flag leaf area gave desirable values, the data ranged between (29.80 cm^2 and 15.10 cm^2) were recorded with the genotypes TG-60-6/Sk.106-5 and TG-60-6/G. 177-8, respectively.

For flag leaf angle, the desirable value (28.87) was recorded with TG-60-6/GZ.7768-2, and the data ranged between (63.30 ô and 28.87 ô) were recorded with TG-60-6/Sk.106-7 and TG-60-6/GZ.7768-2 genotypes, respectively. The genotypes TG-60-6/GZ.7768-2 has wide area in addition to good adsorb for day light and this might be good to photosynthesis process, also present resistance to blast disease. For panicle plant^{-1}, the data ranged between (13.40 and 26.19) were recorded with TG-60-6/G. 177-4 and TG-60-6/Sk.106-7, respectively, but the desirable value were (21.78, 21.17, 24.95 and 22.63) and recorded with the genotypes; TG-60-6/SK.106-3, TG-60-6/SK.106-4, TG-60-6/SK.106-5 and TG-60-6/GZ.7768-2. As well as, the TG-60-6/GZ.7768-2 genotypes have resistance to blast disease.

For panicle weight, the highest value with TG-60-6/G.177-6 as 8.16 g, but the lowest value 3.26 g and recorded with Sakha 105. While, genotypes TG-60-6/SK.106-6 and TG-60-6/GZ.7768-9 were observed 7.64 and 7.50, respectively.

The highest value was 33.97 g for 1000-grain weight characters and recorded with TG-60-6/G. 177-3, but the lowest value recorded with TG-60-6/GZ.7768-6. For yield plant^{-1}, TG-60-6/Sk.106-7 gave the highest value as (97.80 g) and the rest genotypes ranged between (95.03 g and 41.29 g) with TG-60-6/Sk.106-5 and G. 177, respectively.

Table 2. Means of yield and its components with some vegetative characters

Genotypes	Days to heading (day)	Flag leaf area (cm^2)	Flag leaf angel (Ô)	Panicle plant^{-1}	Panicle weight (g)	1000-grain weight (g)	Yield plant^{-1}
TG-60-6	89.47	18.73	46.65	16.47	7.40	31.53	83.03
TG-60-6/G. 177-1	90.53	17.20	45.03	15.13	6.93	33.87	76.97
TG-60-6/G. 177-2	90.80	19.30	48.58	17.68	7.10	30.53	85.07
TG-60-6/G. 177-3	90.20	19.80	56.20	14.67	7.07	33.97	80.67
TG-60-6/G. 177-4	90.33	27.60	48.44	13.40	6.44	30.07	49.80
TG-60-6/G. 177-5	90.33	24.60	42.18	13.87	6.67	32.53	72.07
TG-60-6/G. 177-6	98.40	22.23	42.69	13.93	8.16	33.03	69.73
TG-60-6/G. 177-7	96.43	24.77	49.22	20.67	6.06	29.20	74.73
TG-60-6/G. 177-8	98.53	15.10	49.71	22.47	5.07	26.20	79.67
TG-60-6/Sk.105-1	100.47	25.07	45.79	18.88	6.18	27.47	67.08
TG-60-6/ Sk.105-2	94.47	24.27	49.43	17.76	5.77	31.47	64.82
TG-60-6/Sk.106-1	102.33	20.07	65.43	21.31	6.83	28.27	69.68
TG-60-6/Sk.106-2	95.73	23.33	52.62	20.00	5.72	30.40	79.70
TG-60-6/Sk.106-3	98.40	18.73	45.52	21.78	5.05	30.73	65.57
TG-60-6/Sk.106-4	98.27	24.00	58.00	21.17	6.68	29.73	89.99
TG-60-6/Sk.106-5	96.73	29.80	42.34	24.95	6.53	29.93	95.03
TG-60-6/Sk.106-6	108.13	20.20	49.03	21.21	7.64	32.13	85.67
TG-60-6/Sk.106-7	98.47	19.80	63.30	26.19	6.00	32.73	97.80
TG-60-6/Sk.106-8	104.33	19.93	54.31	16.85	7.18	28.87	81.80
TG-60-6/GZ.7768-1	94.53	21.00	34.70	22.38	5.52	30.00	74.97
TG-60-6/GZ.7768-2	94.37	22.10	28.87	22.63	5.65	31.97	79.67
TG-60-6/GZ.7768-3	98.40	18.13	49.60	19.97	7.01	29.90	81.83
TG-60-6/GZ.7768-4	94.67	21.40	47.80	22.21	7.03	26.60	75.70
TG-60-6/GZ.7768-5	96.30	23.40	32.78	22.27	6.37	27.33	84.55
TG-60-6/GZ.7768-6	100.33	26.10	38.48	21.97	6.53	25.07	86.03
TG-60-6/GZ.7768-7	98.60	20.07	47.72	23.19	6.02	28.41	79.47
TG-60-6/GZ.7768-8	99.80	20.90	39.82	22.23	6.52	30.00	74.95
TG-60-6/GZ.7768-9	100.80	18.13	49.92	23.19	7.50	31.33	92.17
Giza 177	92.83	27.82	38.80	20.61	3.46	27.99	41.29
Sakha 105	96.27	27.81	42.28	19.85	3.26	28.70	45.48
Sakha 106	98.23	28.22	42.76	21.30	3.55	27.02	46.70
GZ. 7768	94.67	27.04	43.77	20.63	3.66	27.38	44.34
Mean	96.63	22.40	46.62	20.03	6.14	29.82	74.25

Analysis of variance for yield and its components and some vegetative characters

The analysis of variance Table 3 exhibited highly significant differences among the 32 genotypes tested for all studied characters. The mean square values of the studied characters were highly significant for genotypes, but were insignificant for replications, demonstrating that the pedigree method can be utilized to enhance these

characters and develop new hybrid rice varieties. The gauge of the broad sense heritability for the studied characters were sensibly high (Jensen *et al.,* 2008). From the above results it could be led that the pedigree method can be utilized to enhance all characters under investigation and develop new hybrid rice varieties, while, the mean square values of all characters were highly significant.

Table 3. Analysis of variance for yield and its components and some vegetative characters

S.O.V	d.f	Days to heading	Flag leaf area	Flag leaf angel	Panicle plant^{-1}	Panicle weight	1000 grain weight	Yield plant^{-1}
Reps.	2	0.677 n.s	0.835 n.s	0.301 n.s	0.264 n.s	0.111 n.s	0.746 n.s	11.513 n.s
Genotypes	31	56.722**	41.503**	186.757**	32.236**	4.657**	15.621**	661.390**
Error	33	0.148	0.051	0.018	1.854	0.007	0.045	0.698

Estimating of heritability for the studied yield and its components and some vegetable characters

Data shown in Table 4 the heritability was estimates in broad sense. Regarding to heritability estimates, table 4 illustrate that high values were determined in broad sense for all yield and its component and vegetative characters. The heritability ranged between 82.705 % and 99.49 % and was recorded with panicle weight and flag leaf angel, respectively.

Table 4. Estimates of heritability for the studied yield and its components and some vegetable characters

	Days to heading	Flag leaf area	Flag leaf angel	Panicle plant^{-1}	Panicle weight	1000 grain weight	Yield plant^{-1}
Heritability	95.806	93.980	99.490	82.705	92.931	86.778	94.747
CV	0.1536	0.2258	0.0391	9.2570	0.1097	0.1516	0.9397

For panicle weight for instance, the data in Table 4 demonstrated that the dominance genetic variance as a part of the total genetic variance was bigger than additive genetic variance. These results demonstrated that the two genetic variance components may be critical in the inheritance of panicle weight, whereas the dominance genetic variance played an important role in this case. Regarding heritability estimates, Table 4 illustrates the high value (99.49%) was determined in broad sense. These findings agree with those obtained earlier from the partitioning of genetic variance in this study. These results indicated that this character was influenced by environmental effect. This means that selection for panicle weight might be practiced successfully in late generations.

These results were in agreement with those obtained by Elshamey (2016) who found that the influence of non-additive was more than the additive genetic variance for panicle weight. These results suggested that all the materials under this study are very useful for explaining the heterotic effect through the hybrid rice program. These results were also agreed with those of Bansal *et al.* (2000) who they found predominance of non-additive gene effects for number of fertile tillers/plant, grain yield/plant and 1000-grain weight. The genetic variance components *i.e.* additive genetic variance and dominance genetic variance and heritability in broad and narrow senses were useful to determine the inheritance for characters, when additive genetic variance was larger than dominance, this lead to inheritance by the selection in early generations. Similar results were also found by Kumar and Nautiyal (2016) Selim *et al.,* (2018).

Disease evaluation

Pathogenicity test and race identification to blast disease

Rice infected samples with blast collected from different rice cultivars and locations during 2018 growing season in Table 5. Twenty four *P. grisea* isolates were successfully isolated and purification as single spore technique. The data in Table 5 indicated that twenty four isolates were identified as five main groups *i.e.,* IC, ID, IF, IG and IH using the I.D.V., these race groups included eight physiological races (two from each of IC-27, ID-15; one from ID-11, IF-4, IG-1; three from IF-1; six from IF-3 and eight from IH-1). These results are agreement with the findings of Shabana *et al.* (2013) they showed that the distribution of races with different rice entries and location.

Thirty two genotypes were tested under greenhouse and field conditions. The results in Table 6 indicated that, eleven genotypes *i.e.* TG-60-6/Sk.105-2 from cross II; TG-60-6/Sk.106-3 and TG-60-6/Sk.106-8 from cross III; TG-60-6/GZ.7768-2, TG-60-6/GZ.7768-5, TG-60-6/GZ.7768-6 and TG-60-6/GZ.7768-8 from cross IV; in addition, the parental were resistant to all tested blast races under this study. On the other hand, the parent of female TG-60-6 infected with eight races out of the tested races.

Concerning the natural infection under the field conditions data in Table 7 indicated that, at Sakha location, eighteen genotypes were resistant and fourteen genotypes were susceptible. On the other hand, at Gemmiza location, twenty two genotypes were resistant and ten genotypes were susceptible. The susceptible check (Sakha 101) was highly susceptible at both locations. These results will be considered in developing resistant genotypes which is the most important method for control rice blast disease. This approach is friendly for environment and disease management (Bonman *et al,* 1991). Sedeek and Elwhash (2015) evaluated 10 genotypes and their parents for rice blast disease. The breeding lines were resistant to rice blast under artificial inoculation in greenhouse and field condition, but Sakha 101 rice cultivar was susceptible. Fang *et al* (2017) reported that rice varieties were resistant to different races of *M. oryzae* in Australia. The variety SHZ-2 exhibited a resistant reaction to all five races, while, BR-IRGA-409, Ceysvoni, Rikuto Norin 20, NTR587 and Kyeema, were resistant to *M. oryza* at least three races.

Table 5. Source and physiological races of *Pyricularia grisea* isolates collected in 2018 growing seasons

Isolate number	Governorate	District	Rice cultivar	Race
P1	Kafrelsheikh	Kafrelsheikh	Sakha 101	IH-1
P2	Kafrelsheikh	Kafrelsheikh	Sakha l01	IF-3
P3	Kafrelsheikh	Desouq	Sakha 101	ID-15
P4	Kafrelsheikh	Kallien	Sakha 104	IH-1
P5	Kafrelsheikh	Kallien	Sakha 101	IC-27
P6	Kafrelsheikh	Sakha	Giza171	IF-1
P7	Kafrelsheikh	Sakha	Sakha 104	IF-3
P8	Kafrelsheikh	Sakha	Sakha 101	IC-27
P9	Kafrelsheikh	Sakha	Reiho	IG-1
P10	Gharbia	EL-Mahala	Sakha 101	IH-1
P11	Gharbia	Qotour	Sakha 101	IF-3
P12	Gharbia	Qotour	Sakha 101	IH-1
P13	Gharbia	Samanoud	Sakha 104	IF-3
P14	Gharbia	Gemmiza	Sakha 104	IH-1
P15	Gharbia	Gemmiza	Giza171	IF-3
P16	Gharbia	Gemmiza	Sakha 104	IH-1
P17	Dakahlia	Mansoura	Sakha 101	IH-1
P18	Dakahlia	Talkha	Sakha 101	IF-1
P19	Dakahlia	Dekerns	Sakha 101	IF-3
P20	Dakahlia	Dekerns	Sakha 101	IH-1
P21	Dakahlia	Met sweed	Sakha 101	IF-4
P22	Beheira	Itai-El-Barood	Sakha 104	ID-11
P23	Beheira	Itai-El-Barood	Sakha 101	ID-15
P24	Beheira	Kafr El-Dawar	Sakha 101	IF-1

Table 6. Blast reactions for 32 rice genotypes inoculated with 24 *Pyricularia grisea* isolates under greenhouse conditions.

No.	Genotypes	Isolate number / Reaction																						
		P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13	P14	P15	P16	P17	P18	P19	P20	P21	P22	P23	P24
1	TG-60-6	S	S	MR	MR	MR	S	S	R	MR	MR	MR	MR	MR	R	R	R	R	R	R	R	S	S	S	S
2	TG-60-6/G. 177-1	S	S	MR	MR	MR	S	MR	R	MR	MR	MR	S	R	R	R	R	R	R	R	R	S	S	S	R
3	TG-60-6/G. 177-2	S	S	MR	R	MR	S	MR	R	MR	MR	MR	S	MR	R	R	R	R	R	R	R	S	S	S	S
4	TG-60-6/G. 177-3	S	S	MR	R	MR	S	MR	MR	MR	S	MR	MR	R	R	R	R	R	R	R	R	S	S	S	S
5	TG-60-6/G. 177-4	S	MR	S	R	MR	S	R	MR	MR	S	MR	S	R	R	R	R	R	R	R	R	S	S	S	S
6	TG-60-6/G. 177-5	S	S	S	MR	MR	S	MR	S	MR	MR	MR	S	R	R	R	R	R	R	R	R	S	S	S	S
7	TG-60-6/G. 177-6	S	S	S	MR	MR	S	MR	S	MR	S	MR	S	R	R	R	R	R	R	R	R	S	S	S	S
8	TG-60-6/G. 177-7	S	R	R	S	R	R	R	R	S	S	R	R	R	S	MR	R	S	S	S	R	MR	MR	S	MR
9	TG-60-6/G. 177-8	S	S	S	S	MR	S	S	S	S	R	S	S	MR	S	S	R	S	S	S	S	R	R	R	R
10	TG-60-6/Sk.105-1	S	MR	S	MR	R	S	MR	MR	MR	S	MR	MR	R	R	R	R	R	R	R	R	S	S	S	MR
11	TG-60-6/Sk.105-2	MR	R	MR	MR	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
12	TG-60-6/Sk.106-1	S	S	S	S	R	S	MR	S	MR	S	S	R	MR	R	R	R	S	MR	MR	R	R	R	R	MR
13	TG-60-6 /Sk.106-2	MR	R	MR	R	R	S	R	R	R	MR	R	R	R	R	R	R	R	R	R	R	R	R	R	R
14	TG-60-6 /Sk.106-3	R	R	MR	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	MR	R	R
15	TG-60-6/Sk.106-4	S	R	S	S	R	R	R	R	S	S	R	R	R	S	R	R	S	S	MR	R	R	R	R	R
16	TG-60-6/Sk.106-5	S	S	S	S	R	MR	S	S	S	S	S	S	MR	S	MR	R	MR	S	S	MR	R	R	R	R
17	TG-60-6/Sk.106-6	S	R	S	S	R	R	R	R	R	S	R	R	R	R	R	R	R	MR	R	R	S	S	S	S
18	TG-60-6/Sk.106-7	MR	S	S	S	R	MR	MR	S	S	S	S	MR	R	S	MR	S	S	S	R	S	R	S	S	S
19	TG-60-6/Sk.106-8	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
20	TG-60-6/GZ.7768-1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S	S	MR
21	TG-60-6/GZ.7768-2	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
22	TG-60-6/GZ.7768-3	S	MR	MR	MR	MR	MR	MR	R	MR	R	R	MR	R	R	R	R	R	R	R	R	R	R	R	R
23	TG-60-6/GZ.7768-4	S	S	MR	R	R	S	MR	S	MR	R	R	S	R	R	R	R	R	R	R	R	R	R	R	R
24	TG-60-6/GZ.7768-5	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
25	TG-60-6/GZ.7768-6	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
26	TG-60-6/GZ.7768-7	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S	S	S
27	TG-60-6/GZ.7768-8	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
28	TG-60-6/GZ.7768-9	S	MR	MR	R	R	MR	MR	R	MR	R	S	MR	R	R	R	R	R	R	R	R	S	S	MR	MR
29	Giza 177	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
30	Sakha 105	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
31	Sakha 106	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
32	GZ. 7768	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R

Table 7. Reaction of 32 rice genotypes to blast disease under field conditions

No.	Genotypes	Field Reaction	
		Sakha	Gemmiza
1	TG-60-6	S*	S
2	TG-60-6 / G. 177-1	R	S
3	TG-60-6 / G. 177-2	R	R
4	TG-60-6 / G. 177-3	R	R
5	TG-60-6 / G. 177-4	R	S
6	TG-60-6 / G. 177-5	S	R
7	TG-60-6 / G. 177-6	S	R
8	TG-60-6 / G. 177-7	S	R
9	TG-60-6 / G. 177-8	S	S
10	TG-60-6 /Sk.105-1	S	R
11	TG-60-6 /Sk.105-2	R	R
12	TG-60-6 / Sk.106-1	S	S
13	TG-60-6 / Sk.106-2	S	S
14	TG-60-6 / Sk.106-3	R	R
15	TG-60-6 / Sk.106-4	S	S
16	TG-60-6 / Sk.106-5	S	S
17	TG-60-6 / Sk.106-6	S	R
18	TG-60-6 / Sk.106-7	S	R
19	TG-60-6 / Sk.106-8	R	R
20	TG-60-6 / GZ.7768-1	S	R
21	TG-60-6 / GZ.7768-2	R	R
22	TG-60-6 / GZ.7768-3	R	S
23	TG-60-6 / GZ.7768-4	S	S
24	TG-60-6 / GZ.7768-5	R	R
25	TG-60-6 / GZ.7768-6	R	R
26	TG-60-6 / GZ.7768-7	R	R
27	TG-60-6 / GZ.7768-8	R	R
28	TG-60-6 / GZ.7768-9	R	R
29	Giza 177	R	R
30	Sakha 105	R	R
31	Sakha 106	R	R
32	GZ. 7768	R	R
Susceptible check (SK.101)		HS	HS

*** Reactions: R = resistant (1-2), MR = moderately resistant (3), S = susceptible (4-6), HS = highly susceptible (7-9).**

Activity of antioxidative enzymes:

The changes in level of enzymatic defense during host–pathogen interactions were investigated to evaluate level of peroxidase and polyphenol oxidase activity on *P. grisea* through pathogenicity test. POX activity ranged from (0.44 to 3.0 mg^{-1} min^{-1}) in the inoculated seedling (Fig. 1). While, in un-inoculated leaf samples, the POX activity ranged from (0.27 to 0.85 mg^{-1} min^{-1}). The maximum increase in POX activity was recorded at (96 h) after inoculation and then decreased. The highest activity for POX significantly induced in TG-60-6/GZ.7768-2 and TG-60-6/Sk.106-3 as the blast resistant genotype. The least level of induction was recorded in TG-60-6/G. 177-3 and TG-60-6/Sk.106-7 as susceptible rice genotype. POX enzyme in healthy seedling may be due to their presence in healthy seedling tissues as constitutive enzymes.

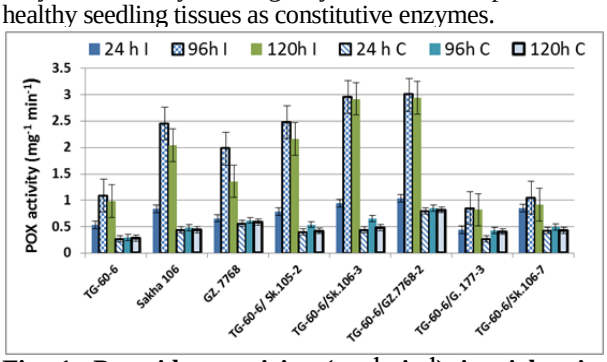

Fig. 1. Peroxidase activity ($mg^{-1}min^{-1}$) in eight rice genotypes either healthy or inoculated 24, 96 and 120 h after artificial inoculation with *P. grisea*. The bar represents standard error (SE ±) of each treatment (n = 3) at Duncan test P≤0.05 probability.

PPO activity profile ranged from 0.25 to 1.95 U/mg in un-inoculated seedling of eight rice genotypes, while, in the inoculated seedling was ranged from 0.25 to 2.24 U/mg. Significantly of PPO activity was increased in both resistant and susceptible as showed in (Fig 2). PPO enzyme showed maximum activity at 96 h in susceptible and resistant seedling and then decreased. The obtained data present high level of PPO activity in TG-60-6/GZ.7768-2 followed by TG-60-6/Sk.106-3 as accession resistant were higher compared with TG-60-6/Sk.106-7 as highly susceptible to blast.

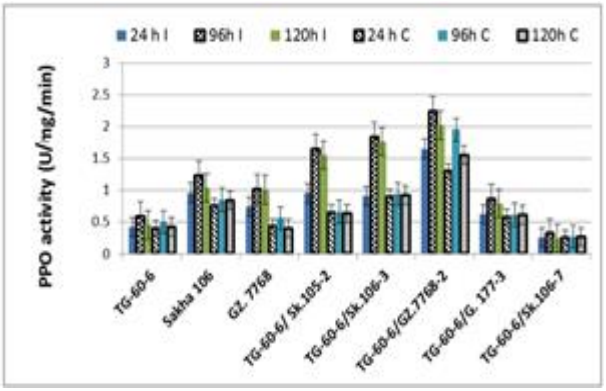

Fig. 2. Polyphenol oxidase activities (U/mg/min) in eight rice genotypes either healthy or inoculated 24, 96 and 120 h after artificial inoculation with *P. grisea*. The bar represents standard error (SE ±) of each treatment (n = 3) at Duncan test P≤0.05 probability.

Total protein content:

Total protein content was measured on the chosen genotypes (Fig. 3). All inoculated seedling showed higher content of total protein than the un-inoculated seedling. There is no significant difference between Sakha 106 rice cultivar and TG-60-6/Sk.106-3 genotypes in protein content and proved the maximum protein content decreased gradually after also 96 h. Total protein content profile ranged from 0.11 to 0.85 mg/g fresh weight in un-inoculated seedling of eight rice genotypes, while, in inoculated seedling was ranged from 0.25 to 1.28 mg/g fresh weight. TG-60-6 rice genotype was less in total protein as susceptible one to blast.

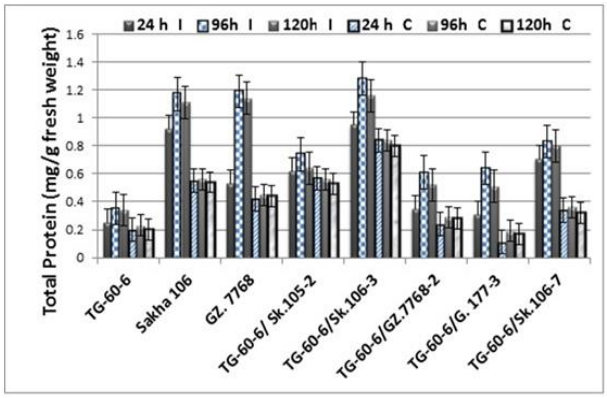

Fig. 3. Total protein content (mg/g) in eight rice genotypes either healthy or inoculated 24, 96 and 120 h after artificial inoculation with *P. grisea*. The bar represents standard error (SE ±) of each treatment (n = 3) at Duncan test P≤0.05 probability.

The results are agreement with Chandrakanth, *et al*. (2018) they reported that the peroxidase and polyphenol oxidase activity as well as total protein was increased after 96h of inoculation with *M. oryzae* and then decreased after 120h. Also, Kalbouh (2019) studied the biochemical change in some Egyptian rice genotypes after inoculation with *P. grisea* and showed the semi results which proved POX activity was increase after 96h of inoculation and then decreased.

The pathogenicity test for brown spot disease under greenhouse

Thirty two rice genotypes were inoculated with *B. oryzae* under greenhouse. Data in Table 8 indicated that all the tested rice genotypes differed in their susceptibility to infection with isolate of *B. oryzae*. However, TG-60-6/GZ.7768-3, TG-60-6/Sk.105-2 and TG-60-6/GZ.7768-5 (825.0, 753.3 and 750.0, respectively) were proved the highest disease severity. While, TG-60-6 / Sk.106-7 and Sakha 106 were gave the highest disease incidence % (99.0). On the contrary, TG-60-6/G. 177-1 and TG-60-6/GZ.7768-2 were the lowest for brown spot disease severity (180) and disease incidence (37.7%). The same results were obtained from Aryal *et al.* (2016) they evaluated rice genotypes against brown spot disease at field condition. The variation in disease increment might be due to variation in susceptibility of cultivar to the pathogen.

The pathogenicity test for bakanae disease under greenhouse

Thirty two rice genotypes were evaluated under artificial inoculation with *F. fujikuroi*. Data in Table 9 indicated that susceptibility to all the tested rice genotypes different in toward infection with the bakanae pathogen. However, TG-60-6/Sk.106-5, and TG-60-6/Sk.106-6 were the highest seedling death (28.67 and 27.00%, respectively). Whereas, TG-60-6/GZ.7768-1, TG-60-6/G. 177-8 and TG-60-6/G. 177-3 rice genotypes were the lowest seedling deaths (2.00, 2.67 and 2.67%, respectively). On the other hand, TG-60-6/G. 177-8 rice genotype was proved the lowest disease incidence (7.33 %), Followed by TG-60-6 / Sk.106-1 (9.0%). While, the rice genotype TG-60-6 / Sk.106-1 showed the lowest disease severity index (1.03) followed by TG-60-6/G. 177-8 (1.04%). The germination % decreased in inoculated genotypes compared with un-inoculated (healthy) genotypes. Thirteen rice cultivars and seven lines were screened by inoculated with ten isolates of *F. moniliforme* under greenhouse in Egypt. Sakha 101 and Giza 177 were the most susceptible cvs followed by Hybrid 1 and Hybrid 2. On the other hand; Sakha 104, GZ 9461-4-2-3-1 and GZ 9626- 2-1-3-2-3 were the least susceptible ones (Abeer and Gabr, 2015).

Table 8. Evaluation of rice genotypes toward infection with *Bipolaris oryzae* the casual fungal of brown spot disease under greenhouse conditions.

No.	Genotypes	Disease Severity (spots/25 leaves)	Disease incidence %
1	TG-60-6	435.0^{ij}	75.0e
2	TG-60-6 / G. 177-1	180.0^{p}	37.7^{k}
3	TG-60-6 / G. 177-2	394.7^{jk}	57.7^{g}
4	TG-60-6 / G. 177-3	394.7^{jk}	57.0^{gh}
5	TG-60-6 / G. 177-4	280.0^{mn}	37.7^{k}
6	TG-60-6 / G. 177-5	500.0^{gh}	98.3^{a}
7	TG-60-6 / G. 177-6	230.0^{nop}	57.0^{gh}
8	TG-60-6 / G. 177-7	500.0^{gh}	87.7^{b}
9	TG-60-6 / G. 177-8	212.7^{op}	60.7^{g}
10	TG-60-6 / Sk.105-1	460.0^{hi}	80.3^{cd}
11	TG-60-6 / Sk.105-2	753.3^{b}	95.0^{a}
12	TG-60-6 / Sk.106-1	530.0^{fg}	83.0^{c}
13	TG-60-6 / Sk.106-2	580.0^{ef}	98.7^{a}
14	TG-60-6 / Sk.106-3	435.0^{ij}	97.7^{a}
15	TG-60-6 / Sk.106-4	230.0^{nop}	37.7^{k}
16	TG-60-6 / Sk.106-5	250.0^{no}	56.7^{gh}
17	TG-60-6 / Sk.106-6	330.0^{im}	76.7^{de}
18	TG-60-6 / Sk.106-7	680.0^{cd}	99.0^{a}
19	TG-60-6 / Sk.106-8	441.7^{hij}	77.3^{de}
20	TG-60-6 / GZ.7768-1	360.0^{kl}	69.0^{f}
21	TG-60-6 / GZ.7768-2	180.0^{p}	37.7^{k}
22	TG-60-6 / GZ.7768-3	825.0^{a}	97.0^{a}
23	TG-60-6 / GZ.7768-4	735.0^{bc}	96.0^{a}
24	TG-60-6 / GZ.7768-5	750.0^{b}	97.0^{a}
25	TG-60-6 / GZ.7768-6	625.0^{de}	96.3^{a}
26	TG-60-6 / GZ.7768-7	225.0^{nop}	47.0^{j}
27	TG-60-6 / GZ.7768-8	625.0^{de}	70.7^{f}
28	TG-60-6 / GZ.7768-9	240.0^{nop}	51.3^{i}
29	Giza 177	275.0^{mno}	53.3^{hi}
30	Sakha 105	624.3^{de}	88.7^{b}
31	Sakha 106	630.0^{de}	99.0a
32	GZ. 7768	499.0^{gh}	95.7a

In a column, means followed by a common letter are not significantly different at the 5% level by DMRT

Table 9. Evaluation of rice genotypes toward infection with *Fusarium fujikuroi* the casual fungal of bakanae disease under greenhouse conditions

No.	Genotypes	Germination %		Seedling death %	Disease incidence %	Disease Severity Index
		Healthy	inoculated			
1	TG-60-6	84.7^{a-f}	78.7^{a-f}	3.30^{hij}	12.67^{g-j}	1.07^{ghi}
2	TG-60-6 / G. 177-1	70.0^{efg}	64.0^{efg}	3.00^{hij}	19.33^{d-j}	1.09^{d-i}
3	TG-60-6 / G. 177-2	71.3^{d-g}	65.3^{d-g}	4.67^{g-j}	10.00^{ij}	1.05^{ghi}
4	TG-60-6 / G. 177-3	84.7^{a-f}	78.7^{a-f}	2.67^{ij}	12.67^{g-j}	1.06^{ghi}
5	TG-60-6 / G. 177-4	80.0^{b-f}	74.0^{b-f}	10.0^{d-j}	13.33^{g-j}	1.08^{e-i}
6	TG-60-6 / G. 177-5	70.7^{efg}	64.7^{efg}	8.00^{e-j}	16.67^{e-j}	1.08^{e-i}
7	TG-60-6 / G. 177-6	79.3^{b-f}	73.3^{b-f}	8.00^{e-j}	18.67^{d-j}	1.18^{a-d}
8	TG-60-6 / G. 177-7	93.3^{ab}	87.3^{ab}	13.34^{c-g}	20.00^{c-j}	1.12^{c-h}
9	TG-60-6 / G. 177-8	78.0^{b-f}	71.0^{b-g}	2.67^{ij}	7.33^{j}	1.04^{hi}
10	TG-60-6 / Sk.105-1	83.3^{a-f}	77.3^{a-f}	5.33^{f-j}	9.33^{ij}	1.07^{ghi}
11	TG-60-6 / Sk.105-2	92.0^{ab}	86.0^{ab}	5.33^{f-j}	31.33^{a-f}	1.21^{abc}
12	TG-60-6 / Sk.106-1	83.3^{abc}	75.3^{a-f}	3.00^{hij}	9.00^{ij}	1.03^{i}
13	TG-60-6 / Sk.106-2	89.3^{abc}	83.3^{abc}	6.00^{f-j}	16.67^{e-j}	1.10^{d-i}
14	TG-60-6 / Sk.106-3	76. 7^{b-f}	62. 7^{fg}	22.0^{abc}	44.67^{a}	1.26^{a}
15	TG-60-6 / Sk.106-4	92.0^{ab}	86.0^{ab}	26.67^{ab}	32.67^{a-e}	1.26^{a}
16	TG-60-6 / Sk.106-5	84.7^{abc}	84.7^{abc}	28.67^{a}	38.00^{ab}	1.23^{ab}
17	TG-60-6 / Sk.106-6	98.7^{a}	92.7^{a}	27.00^{ab}	36.67^{abc}	1.24^{a}
18	TG-60-6 / Sk.106-7	68.7^{fg}	62.7^{fg}	10.00^{d-j}	21.33^{b-j}	1.12^{c-i}
19	TG-60-6 / Sk.106-8	78.0^{b-f}	68.0^{c-g}	14.67^{c-f}	28.67^{a-g}	1.16^{a-f}
20	TG-60-6 / GZ.7768-1	74.0^{b-f}	64.0^{efg}	2.00^{j}	11.33^{hij}	1.06^{ghi}
21	TG-60-6 / GZ.7768-2	84.7^{a-f}	78.7^{a-f}	7.33^{f-j}	27.33^{b-h}	1.20^{abc}
22	TG-60-6 / GZ.7768-3	77.0^{b-g}	71.0^{b-g}	8.00^{e-j}	18.00^{d-j}	1.10^{d-i}
23	TG-60-6 / GZ.7768-4	90.0^{abc}	84.0^{abc}	11.00^{d-j}	31.33^{a-f}	1.17^{a-e}
24	TG-60-6 / GZ.7768-5	69.3^{fg}	63.3^{fg}	10.67^{d-j}	27.33^{b-h}	1.14^{b-g}
25	TG-60-6 / GZ.7768-6	76.0^{b-g}	70.0^{b-g}	12.00^{d-i}	22.67^{b-j}	1.13^{c-h}
26	TG-60-6 / GZ.7768-7	61.3^{g}	55.3^{g}	3.00^{hij}	14.67^{f-j}	1.08^{f-i}
27	TG-60-6 / GZ.7768-8	88.7^{a-d}	82.7^{a-d}	10.67^{d-j}	32.67^{a-e}	1.18^{a-d}
28	TG-60-6 / GZ.7768-9	81.3^{a-f}	75.3^{a-f}	12.67^{d-h}	29.33^{a-g}	1.17^{a-f}
29	Giza 177	91.3^{abc}	85.3^{abc}	17.33^{cde}	34.67^{a-d}	1.20^{abc}
30	Sakha 105	77.3^{b-g}	71.3^{b-g}	12.00^{d-i}	26.00^{b-i}	1.15^{b-g}
31	Sakha 106	89.3^{abc}	83.3^{abc}	14.67^{c-f}	29.33^{a-g}	1.17^{a-e}
32	GZ. 7768	87.3^{a-e}	81.3^{a-e}	18.67^{bcd}	31.33^{a-f}	1.12^{c-i}

In a column, means followed by a common letter are not significantly different at the 5% level by DMRT

CONCLUSION

we can summarize the previous results into two directions; the first one, the best genotypes had resistance to all blast races which used in these study in greenhouse and field conditions as; TG-60-6/ Sk.105-2; TG-60-6/ Sk.106-3; TG-60-6/GZ.7768-2; TG-60-6/GZ.7768-5; TG-60-6/GZ.7768-6 and TG-60-6/GZ.7768-8, the second direction is the yield productivity and earlier maturity. The most important thing is the genotype has resistance to blast disease, earlier maturity and highly yield productivity in addition to have desirable vegetative characters. So we can use above selected genotypes in hybridization program to produce genotypes had highly productivity and resistance to some major diseases. The resistance to some diseases like blast, brown spot and bakanae could be due to the genotypes which used to produce this population (Giza 177, Sakha 105, Sakha 106, and GZ7768) because some of this parent/s may be have the genes which response to the resistance effect and also had maternal effect for these characters.

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تحديد مقاومة سلالات من الارز عالية الانتاج لأمراض الأرز الرئيسية

محمود السيد سليم[1]، عمرو عبد الباري حسن[2]، محمود عبد الله السيد[1] و عصام عادل الشامي[1]

[1]مركز البحوث والتدريب فى الارز، معهد بحوث المحاصيل الحقلية ، مركز البحوث الزراعية ، مصر

[2]قسم بحوث أمراض الأرز ، معهد بحوث أمراض النبات ، مركز البحوث الزراعية ،مصر

تهدف هذه الدراسة الى إنتاج طرز وراثية جديدة من الأرز مقاومة لأمراض الأرز الرئيسية وإنتاجيتها العالية. استخدمت الطرز الوراثية جيزة 177، سخا 105، سخا 106 و السلالة المبشرة 7768 كآباء ذكور وتم استخدام السلالة TG-60-6 كأب مؤنث بالإضافة إلى سلالات F_n التي تم الحصول عليها من أربعة تهجينات. أفضل تراكيب وراثية لديها إنتاجية عالية ومقاومة لمرض اللفحة تحت ظروف الصوبة والحقل ؛ TG-60-6/Sk.105-2، TG-60-6/Sk.106-3، TG-60-6/GZ.7768-2، TG-60-6/GZ.7768-5، TG-60-6/GZ.7768-6 -TG- 60-6/GZ.7768-8 و TG-60-6/GZ.7768-8. وقد تأثر المحصول ومكوناتة بالتأثيرات البيئية ويجب أن يتم الاختيار بنجاح في الجيل النهائي. تم عزل أربعة وعشرين عزلة من فطر *Pyricularia grisea* تشمل خمس مجاميع رئيسية. وجد تحت ظروف العدوي الصناعى احدى عشر طرز وراثى مقاوم لجميع سلالات لفحة الأرز المختبرة، بينما في ظروف الحقل، كان هناك ثمانية عشر طرز وراثى مقاوم في موقع سخا، بينما في موقع الجميزة، اثنان وعشرون تركيب وراثى مقاومً. تم تقدير التغيرات البيوكيميائية للإنزيمات المضادة للأكسدة والبروتين الكلي بعد 24، 96 و 120 ساعة من التلقيح بسلالة فطر اللفحة p23 (ID-15) فى مرحلة البادرة، تم تسجيل أقصى نشاط لأنزيم البيروكسيداز (POX) وإنزيم بوليفينول أوكسيديز (PPO) وكذلك البروتين الكلي عند 96 ساعة بعد التلقيح ثم ينخفض. تحت العدوي الصناعي بالفطر المسبب لمرض التبقع البني *Bipolaris oryzae* ، كانت الطرز الوراثيه TG-60-6/G.177-1 وTG60-6/GZ 7768-2 الاقل فى شدة الاصابة بمرض التبقع البني. اما العدوى الصناعى بفطر *Fusarium fujikuroi* ، كانت طرز الارز الوراثيه TG-60-6/G. 177-8، TG-60-6/ GZ.7768-1, و TG-60-6/G. 177-3 هي أقل النسب المئوية لموت البادرات. وكان الطرز الوراثي للارز TG-60-6/G. 177-8 أقل فى نسبة حدوث للمرض بينما الطرز الوراثى TG-60-6/Sk.106-1 الاقل فلى دليل الشدة المرضيه.