EVALUATION OF SOME DEVELOPED HIGH YIELDING RICE GENOTYPES RESISTANT TO BLAST, BAKANAE AND WHITE TIP NEMATODE

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ABSTRACT

Rice diseases is the most destructive biotic constrains for high yield potential and cause breakdown of resistance. The objective of this investigation is to evaluate and screen some developed elite resistant rice genotypes for blast, bakanae and white tip nematode diseases with high yielding potentiality. Eighteen commercial and promising rice genotypes *i.e.*, six varieties and 12 promising lines were evaluated for their agronomic traits, yield and resistance to various diseases under natural and artificial inoculation at experimental farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt during 2014 and 2015 seasons. Among studied traits, No. of filled grains panicle^{-1} exhibited the highest estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), followed by No. of panicles plant^{-1}. Broad sense heritability values were high for all studied traits and ranged from 91.06 % to 99.05 %. The promising lines SP70-6-4 and SP70-6-1 produced the highest grain yield with 11.73 and 11.72 t ha^{-1} compared with its respective parent Sakha 101 (10.63 t ha^{-1}). The result of principal component analysis (PCA) showed that most important traits in divergence of evaluated genotypes were; filled grains panicle^{-1} and showed the contribution of these parents Giza 178, GZ 6296, super rice varieties IR 66298, IR 65600. IR 66159 as good donors for improving filled grains panicle^{-1}. All the studied genotypes had wide range of genetic variability, therefore they provided broad spectrum of blast resistance levels. The three developed lines; GG-46-2006, GG-42-1 and GG-42-2 were highly resistant to blast. The super rice genotypes; IR 66298, IR 65600, IR 66159 and HR 5824 and the elite developed lines; GZ 5310 and BY 6-20 could be considered as promising donors to bakanae resistance. For white tip nematode, the derived lines from Giza 177 crossed to HR 5824 dropped the No. of nematodes per 10 g rice grains from 153.67 individual larvae to 0 and 1.67. The line BY 6-20 reduced the No. of nematodes to 4.33 comparing with 106 larvae of its parent Sakha 101. The highly resistant genotypes Giza 178, GZ 6296 and their derived lines recorded the lowest no. of nematodes ranged from 0.67 to 12.33. Giza 178, GZ 6296 and their derived line BY 6-20 were considered as good donors for white tip nematode resistance. The breeder successfully improved elite varieties; SP70-6-1, BY 6-20, Giza 178-1 and GG-46-2006, with wide spectrum of resistance level to blast, bakanae and white tip nematode. Giza 178 and GZ 6296 were considered as good donors of all tested diseases in breeding program.

Keywords: *Rice, Oryza sativa L., varietal improvement, disease resistance, blast, bakanae, white tip nematode.*

INTRODUCTION

Rice (*Oryza sativa* L.) is the world's most important food crop and energy source for about half of the world's population and ranks second in production after maize, Manjappa and Shailaja (2014). With the increasing population pressure, the demand of cereal is increased day by day. The world population is expected to reach 8 billion in 2025 and it is estimated that 50 % more food is required to feed the increased population (Khush, 2004). The narrow genetic base of rice breeding programs and the inadequate use of the species genetic variability are some of the main factors limiting increments in grain yield. The need for expansion of rice cultivation depends not only on cultural practices but also on their inbuilt genetic variability. The genetic variability is the basic tool to develop desirable varieties. The studies already conducted have described greater variability in various rice genotypes. Significant variation in various yield components has been noted by many investigators (Zheng-jin *et al.* 2006, Shimono *et al.*, 2009, Huang *et al.*, 2011, Paikhomba *et al.* 2014 and Abacara *et al.* 2016). Genetic diversity triggers the improvement of rice yield and disease resistance with plant breeding.

Rice blast disease, caused by *Magnaporthe grisea*, is one of the most serious constraints minimize rice yield. This fungus has a high level of diversity, mutability and epidemic nature, therefore it can be causing severe yield losses (Khush and Jena, 2009). The unstable nature and rapid changes in virulence characteristics of pathogen populations is a constant threat to the most effective resistant genes in high yielding varieties. In Egypt, race shifting of this fungus resulting in breakdown of some high yielding rice cultivars and promising lines (Marchetti and Bomman 1989, Veillet *et al.* 1996, EL-Shafey 2002, Sehly *et al.* 2008, and El-shafey *et al*. 2015). Therefore, continuous efforts of breeding are considering the only way to overcome the breakdown of effectiveness of existing blast resistance varieties. The most effective strategy to deal with this nature of blast fungus as extreme diversity among the large number of races, or pathotypes, produced by the disease's fungal pathogen (*Pyricularia grisea*) is depend on broaden genetic background and wide genetic diversity of Egyptian rice varieties (El-Refaee *et al*. 2011 and El-shafey *et al*. 2015). The lack of genetic diversity is the main constraint of resistance breeding progress. Therefore, the successful selection for improvement of blast resistance and high yield must depend on wide phenotypic and genotypic variability to extend the genetic diversity. Diversity could perform an essential role in the management and reduce expansion of pathogens (Mundt, 2002).

Rice bakanae, caused by *Fusarium moniliforme* Sheldon, *Fusarium fujikuroi* Niremberg [teleomorph *Gibberella fujikuroi* (Sawada)] is an important rice pathogen. The most characteristic symptoms of this disease are yellowing and abnormal elongation of infected seedlings, as a result of gibberellic acid

production. The pathogen can cause yield loss attribute to seedling infection, weak tillering and poor grain filling capacity. The disease is seed-borne and primarily seed transmitted (Desjardins *et al*. 2000, Nur Ain Izzati and Salleh 2010, Wulff *et al*. 2010 and Wan Nur Ain *et al*. 2015). There are a wide range of variation and varietal resistance to bakanae under Egyptian field conditions. Sakha 101 and Giza 177 cultivars were considered the most abundant susceptible cultivars (El-Refaee *et al*. 2011). The application of fungicides was not effective, therefore, extensive screening for resistant varieties and economic management strategies are required.

White tip disease of rice caused by the plant-parasitic nematode *Aphelenchoides besseyi* Christie 1942, as a foliar nematode, is an important disease caused severe yield losses of rice. In Egypt, white tip nematode causes losses ranged from 18.8 with the most tolerant cultivar Sakha 101 up to 47% of highly susceptible cultivars Giza 171 and Reiho. There are varietal differences in resistance to white tip nematode (El-Shafey 2007, El-Shafey *et al*. 2010 and El-Shafeey *et al*. 2014). The nematicides application to control *A. besseyi* was an expensive and cause serious environmental problems. Thus, the development of resistant rice cultivars has been considered as the most vital and effective strategy for management of white tip disease. There is a wide range of variation for varietal resistance, whereas some varieties are resistant such as Giza 178, Giza 182, Egyptian hybrid 1, others are moderately susceptible like Sakha 101 and Giza 177 while, Giza 171 and Reiho are highly susceptible (El-Shafey 2007 and El-Shafey *et al*. 2010).

The aim of the present investigation was to evaluate some developed new elite rice lines resistant to blast, bakanae and white tip nematode combined with high yield potential. As well as, improve blast resistance of the high yield and most popular cultivar Sakha 101 by hybridization with blast resistant genotypes.

MATERIALS AND METHODS

This experiment was carried out at Sakha Agricultural Research Station Experimental Farm and Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt during the two successive seasons of 2014 and 2015. Eighteen rice genotypes (commercial and promising lines) were used in this study (Table 1). An evaluation experiment was laid out in a randomized complete block design with three replications. Genotypes were transplanted in seven rows with 5m long as individual plants and 20x20 cm distance. All recommended cultural practices for rice cultivation were applied. Nine agronomic characteristics were studied *i.e.*, duration (day), plant height (cm), number of panicles plant^{-1}, panicle length (cm), No. of filled grains panicle^{-1}, 1000-grain weight (g), grain yield (t ha^{-1}), hulling % and milling %. Estimates of genotypic ($\sigma^2 g$) and Phenotypic ($\sigma^2 ph$) variances were obtained from the analysis of variance according to Comstock and Robinson (1952). Heritability in broad sense (h^2_B %) was estimated according to Falconer (1989). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were obtained according to Singh and Chaudhury (1985). Genetic advance (GA) was calculated with the method suggested by Allard (1960) and Singh and Chaudhury (1985). The collected data were analyzed for analysis of variances according to Gomez and Gomez (1984).

Plant materials

Eighteen Egyptian rice genotypes including commercial and newly developed elite lines were used in this study. The pedigree and type of the studied rice genotypes used in the present investigation are shown in Table 1.

Table 1: Pedigree and type of the studied eighteen rice genotypes.

No.	Entry	Pedigree	Type
1	Giza 177	Giza 171/Yomji No.1// PiNo.4	J
2	Giza 177-1	Giza 177 x HR 5824-B-3-2-3	J
3	Giza 177-2	Giza 177 x HR 5824-B-3-2-3	J
4	Giza 178	Giza 175 x Milyang 49	IJ
5	Giza 178-1	Giza 178 x GZ 6296	IJ
6	Giza 178-2	Giza 178 x GZ 6296	IJ
7	GZ 6296	AC 1225 x Hua LienYu 202	IJ
8	Sakha 101	Giza 176 x Milyang 79	J
9	SP 70-6-1	Sakha 101/HR 5824//Sakha 101	J
10	SP 70-6-2	Sakha 101/HR 5824//Sakha 101	J
11	SP 70-6-3	Sakha 101/HR 5824//Sakha 101	J
12	SP 70-6-4	Sakha 101/HR 5824//Sakha 101	J
13	SP 70-6-5	Sakha 101/HR 5824//Sakha 101	J
14	BY-6-20	GZ 5310-20-3-3/Sakha 101//GZ 5310-20-3-3	J
15	HR 5824-B-3-2-3	Akiyudaka x Suweon 310	J
16	GG-46-2006	Sakha 101 x IR 66298-5-3-3-2-1 (super rice)	J
17	GG-42-1	Sakha 101 x IR 65600-38-1-2-1 (super rice)	J
18	GG-42-2	Sakha 101 x IR 66159-189-5-5-3 (super rice)	J

J: Japonica Type, I: Indica Type and I/J: Indica-japonica Type

Principle component analysis (PCA) was performed to evaluate associations among the genotypes and among the variables. The genotypes were classified as loading plot on principal component axis.

Blast evaluation under natural infection at blast nursery

The eighteen Egyptian rice genotypes were sown at two locations *i.e.* Sakha and Gemmiza for blast resistance at seedling stage for major gene resistance with natural infection at blast nursery. Seedbeds were prepared and sowing during end of June. The varieties were naturally infected at seedling stage with mixed races of pathogen populations. About forty-five days from sowing, the typical type-4 blast lesions were scored, according to the standard evaluation system using 0-9 scale (IRRI 2014) as follows: 0, 1 – 2, resistant (R); 3, moderately resistant (MR); 4 – 6, susceptible (S); 7 – 9, highly susceptible (HS).

Blast evaluation under artificial inoculation at greenhouse condition

Eighteen Egyptian varieties were sown in plastic trays (30x20x15 cm). Each tray included 20 rows, each row for each variety in three replications. At 3-4-leaf stage, seedlings were inoculated with ten specific virulent isolate of blast. Spore suspension of each isolate at 5×10^4 spores ml^{-1} was sprayed. The inoculated seedlings were kept in a moist growth chamber with at least 90% R.H. at 25 – 28°C for 24 hrs., then transferred to the greenhouse. After 7 – 9 days after inoculation, blast typical type 4 lesions were appeared on different rice cultivars and scored, according to the Standard Evaluation System of IRRI (2014).

Evaluation of White tip nematode infection

Under field condition: Almost 45 days after transplanting, the typical symptoms of white tip nematode full appeared, so the total infected hills were counted in compared with total hills in 1m^2 and infection % was calculated based on this formula:

$$\text{Infection \%} = \frac{\textbf{No. of infected hills m}^{-2}}{\textbf{Total No. of rice hills m}^{-2}} \times 100$$

At laboratory condition: Ten grams of grains were de-hulled with small equipment. The husk of each genotype was soaked in water for one hour in petri dishes. All rice grains components and husk were sieved through double layers of muslin clothes. The clear extraction was checked under binuclear. The extracted nematodes from 10 g seeds of each variety were counted. The number of extracted nematode reflect and considered as early prediction to the sensitivity and tolerance of each genotype of white tip nematode and the ability of nematode multiplication in rice grains.

Evaluation of bakanae disease infection under artificial inoculation

Pathogenicity test for bakane disease: The eighteen genotypes were artificially inoculated with the most aggressive *Gibberella fujikuroi* isolates 7 and 10. One hundred grains from each rice genotypes was soaked for 24 hrs. in *Fusarium fujikuroi* spore suspension. The concentration of the inoculum suspension was adjusted using a haemocytometer to 1×10^6 spores ml^{-1} with

sterile water. The inoculated seeds were incubated for 48 hrs. at 28°C±2 to enhance both germination and infection. The untreated check of each genotype was sown from healthy seeds. Under greenhouse at 30-35°C, all rice genotypes after incubation were sown in pots as 15x15 cm diameter with three replications. Two weeks after sowing, the infected seedlings with typical bakanae symptoms were counted.

Bakanae disease evaluation under field condition: Genotypes were grown in five-meter-long as individual plants with 20x20 cm. The characteristic symptoms of bakanae disease were scored 45 days after transplanting. The genotypes Sakha 101, Giza 178, Giza 179 (as indica japonica check) and GZ 6296 were evaluated under both greenhouse and field conditions for their behavior to bakanae and transmission capacity after artificial inoculation of grains. The inoculated seeds with sever isolate No.10 were sown in pots and permanent fields for the evaluation of varietal response to artificial inoculation. The infected plants were counted in 2m^2 45-days after sowing in both locations, Sakha and Gemmiza.

RESULTS AND DISCUSSION

Mean performance

According to the results, days to maturity suggested that dominant effect was variable and depends on the cross itself for each line. Days to maturity indicated a wide range of means from 106.0 and 145.0 days among all rice genotypes. HR 5824 showed minimum number of days to maturity while, Sakha 101 recorded maximum days to maturity. The promising lines; Giza 177-2 and Giza 177-1 were early maturing and recorded 120.33 and 121.00 days, respectively. Rice genotypes indicated variable expressions of plant height (cm), selection of rice genotypes with appropriate plant height and non-lodging characteristic is important for high yield potential hybrids (Ikehashi *et al.* 1994). Highest plants were observed for genotypes Giza 178-1 (107.0 cm) and Giza 178-2 (104.0 cm) and the lowest value observed for HR 5824 (73.33 cm). The results obtained are in a close agreement with those reported by Hammoud *et al.* (2013) and Sedeek and El-Wahsh (2015). Concerning No. of panicles plant^{-1} (PnP) data presented in Table 2 indicated significant differences among studied rice genotypes. The promising lines, SP 70-6-5, SP 70-6-2 and Giza 178-1 showed the highest values of PnP, while, HR 5824 exhibited the lowest value (10.0 panicles). Similar trend was found by Hammoud (2005), Hammoud *et al.* (2013) and Sedeek and El-Wahsh (2015). Regarding panicle length (PnL) the mean values of the 18 rice genotypes ranged from 14.43 cm for the early variety HR 5824 to 28.2 cm for GG-42-1 (Table 2). Meanwhile, the promising lines GG-26-2006, GG-42-2 and Giza 178-2 recorded high mean values for this trait with 27.95, 27.52 and 27.33 cm, respectively. Number of filled grains panicle^{-1} (FGP) is the important and relative trait to high yielding. Data in Table 2

revealed that the promising lines, GG-42-2, GG-26-2006 and GG-42-1 recorded the highest values of FGP with values of 264.0, 256.0 and 254.3 grains, HR 5824

recoded the lowest value (87.33 grains).

Table 2: Mean performance of studied rice genotypes for some agronomic studied traits during 2014 and 2015 seasons.

No.	Genotypes	Duration (day)	Ht (cm)	PnP (No.)	PnL (cm)	FGP (No.)	TGW (g)	GYL (t ha⁻¹)	Hulling %	Milling %
1	Giza 177	124.67	98.67	19.67	18.13	118.33	27.73	9.44	80.77	70.96
2	Giza 177-1	121.00	102.00	19.67	19.93	131.00	28.00	10.11	81.03	71.31
3	Giza 177-2	120.33	101.00	21.00	20.76	137.33	28.40	10.85	81.86	72.97
4	Giza 178	135.00	103.33	21.00	25.92	176.00	20.67	11.12	79.32	69.96
5	Giza 178-1	129.33	107.00	23.33	26.90	184.67	25.00	10.83	81.41	71.33
6	Giza 178-2	129.33	104.00	22.00	27.33	192.67	24.32	10.58	80.20	71.93
7	Gz6296	126.00	91.67	23.00	25.71	167.33	27.23	10.73	81.17	69.35
8	Sakha 101	145.00	90.33	23.00	21.95	140.67	28.77	10.63	81.26	70.37
9	SP70-6-1	134.00	93.67	19.33	23.26	153.67	29.97	11.72	82.89	71.33
10	SP70-6-2	136.00	93.33	23.33	22.61	147.33	30.43	10.97	81.80	71.02
11	SP70-6-3	134.33	93.33	22.67	23.72	148.00	29.80	10.91	83.37	73.22
12	SP70-6-4	126.33	95.00	21.00	23.21	149.33	30.53	11.73	80.03	69.93
13	SP70-6-5	131.33	98.33	25.67	24.28	148.00	29.63	10.62	80.58	70.62
14	BY 6-20	130.67	99.00	17.67	20.97	145.00	28.07	10.68	80.11	71.50
15	HR 5824	106.00	73.33	10.00	14.43	87.33	23.00	6.88	77.27	71.07
16	GG-46-2006	128.00	97.00	14.00	27.95	256.00	25.87	8.99	79.64	67.41
17	GG-42-1	128.67	96.00	12.67	28.20	254.33	23.47	10.16	78.70	66.46
18	GG-42-2	127.67	95.33	12.00	27.52	264.00	23.80	10.47	78.59	65.67
	LSD 5 %	0.754	3.16	2.341	1.08	14.81	0.75	0.64	1.07	1.15

Abbreviations: Ht, plant height; PnP, No. of panicles Plant⁻¹; PnL, Panicle length (cm); FGP, Filled grains Panicle⁻¹; TGW, 1000- grain weight (g); GYL, Grain yield (t ha⁻¹).

Regarding 1000-grain weight (TGW) rice genotypes differed significantly for this trait. The rice genotypes, SP 70-6-4 and SP 70-6-2 showed the heaviest weight of grains comparing with the commercial rice variety Sakha 101, while Giza 178 showed the least weight of grains. The promising lines SP 70-6-4 and SP 70-6-1 produced highest grain yield with 11.73 and 11.72 t ha⁻¹ compared with its parent Sakha 101 (10.63 t ha⁻¹). Also, lines Giza 177-1 and Giza 177-2 yielded 10.11 and 10.85 t ha⁻¹, respectively compering with the commercial variety Giza 177 (9.44 t h⁻¹). The superiority of these rice lines in grain yield might be due to their PnP, FGP and TGW. These results are in agreement with those obtained by Sedeek and El-Wahsh (2015). Data in (Table 2) revealed that highly significant differences existed among the tested rice genotypes for hulling %. SP 70-6-3 surpassed significantly the other rice genotypes under study for this trait, While, HR 5824 rice variety showed the lowest value. Concerning milling % trait the rice genotypes, SP 70-6-3 and Giza 177-2 exhibited the highest values of 73.22 and 72.97%, respectively compared with their parents Sakha 101 (70.37%) and Giza 177 (70.96%). On the other hand, the rice genotype GG-42-2 showed the lowest value with 65.67%.

Genetic variability

Analysis of variance (ANOVA) for the nine traits is presented in the Table 3. The results revealed that varietal differences are signified and wide variability present among the genotypes with respect to all studied traits. The estimation of genetic parameters like genotypic coefficient of variation, heritability and genetic advance are presented in Table 3. Phenotypic variance was higher than the genotypic variances for all studied traits thus indicated the influences of environmental factor on these traits. Similar findings were earlier reported by Singh and Chakraborty (1996) and Devi *et al.* (2006). Coefficient of variation studied indicated that estimates of phenotypic coefficient of variation (PCV) were slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the traits. Among the all traits FGP exhibited high estimates of GCV and PCV (28.65% and 29.14%) followed by PnP (22.22% and 23.37%). The high values of GCV and PCV for these traits suggested the possibility of yield improvement through selection of these traits. PnL (15.73% and 15.97%), TGW (10.83% and 10.96%) and GYL (10.18% and 10.84%) showed moderate value of GCV and PCV. The rest of studied traits exhibited low GCV and PCV. Low GCV and PCV values for these traits were reported by Anandrao *et al.* (2011). Heritability is a good index of transmission of traits from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population. Broad sense heritability was higher for all studied traits and ranged from 91.06% to 99.05%, which suggested that these traits would respond to selection owing to their high genetic variability and transmissibility. Similar findings were reported by Verma (2010). Maximum and minimum genetic advance as percentage of mean was recorded for FGP (59.01%) and Hulling % (3.65%), respectively. PnP, PnL, TGW and GYL showed high genetic advance. High genetic advance for number of spikelets per panicle was earlier observed by Ukaoma *et*

al. (2013). High heritability coupled with high genetic advance was recorded for FGP (98.30 % and 59.01 %), PnP (95.09 % and 45.78 %) and PnL (98.49 % and 32.40%). Thus, it is interpreted that these traits were controlled by additive gene action, which could be improved through simple selection methods

Table 3: Phenotypic, genotypic coefficient of variation, and genetic advance of the rice genotypes for some agronomic traits.

	Duration	Ht	PnP	PnL	FGP	Hulling	Milling	TGW	GYL
MS genotypes	194.99	160.07	60.32	41.79	7001.50	6.97	12.40	25.92	3.67
MS error	1.24	3.62	1.99	0.423	79.63	0.42	0.48	0.20	0.15
Mean	128.53	96.24	19.50	23.49	166.72	80.55	70.35	26.92	10.41
σ^2 Ph	65.41	54.56	20.77	14.07	2360.38	2.46	4.29	8.71	1.27
σ^2 G	64.17	50.94	18.78	13.65	2280.74	2.04	3.81	8.50	1.12
PCV%	6.29	7.68	23.37	15.97	29.14	1.95	2.94	10.96	10.84
GCV%	6.23	7.42	22.22	15.73	28.65	1.77	2.78	10.83	10.18
Heritability %	99.05	96.63	95.09	98.49	98.30	91.06	94.25	98.82	93.95
Genetic advance	16.50	14.70	8.93	7.61	98.38	2.94	4.02	6.01	2.18
GA %	12.84	15.28	45.78	32.40	59.01	3.65	5.72	22.32	20.98

Abbreviations: Ht, plant height; PnP, No. of panicles Plant[-1]; PnL, Panicle length (cm); FGP, Filled grains Panicle[-1]; TGW, 1000- grain weight (g); GYL, Grain yield (t ha^{-1}).

Principal components analysis

Principal components analysis (PCA) concurrently inspects difference in agronomic and biotic stress variables and indicates the relative contribution of each trait in genetic divergence. PCA appeared to explain patterns of variation in agronomic attributes.

The first three principal components were significant and accounted for about 81.8% of the total variance of all traits, (Table 4 and Fig. 1). While PC1, PC2 and PC3 explained 32.40, 60.10 and 21.70 %, of the multivariate variation among genotypes showing the highest Eigen values 3.88, 3.32 and 2.60, these values could measure the explained variance associated with variable (Table 4).

PC1 recorded higher loading to PnP (0.458) and GYL (0.408) while, PC2 revealed higher loading to PnL (0.499), FGP (0.484), blast (-0.347), Bakanae (-0.257) and white tip nematode (-0.241). The most important traits in divergence of evaluated genotypes were FGP; GYL, PnL, blast, bakanae and white tip nematode (Table 4 and Fig.1). Thus it is possible to include the corresponding amount of variance in the two dimensional plot of the components. Each genotype is plotted at its principal component score on each axis (Brown 1991).

Table 4. Principal component analysis of rice traits and variation proportions associated with PC1 and PC2 axes and Eigen vectors of each trait.

Eigen value	3.8874	3.3287	2.6017	0.7927
%	32.40	27.70	21.70	6.60
Cumulative Percentage	32.40	60.10	81.80	88.40
	Eigen vector			
	PC1	PC2		
Panicle length (PnL)	0.067	0.499		
Filled grains/ Panicle (FGP)	-0.134	0.484		
Plant height (Ht)	0.260	0.333		
Duration days	0.317	0.147		
No. of panicle plant[-] (PnP)	0.458	-0.043		
Hulling %	0.453	-0.314		
Milling %	0.298	-0.070		
1000- grain weight (TGW)	0.346	-0.220		
Grain yield (GYL)	0.408	0.220		
Blast	-0.096	-0.347		
Bakanae	0.062	-0.257		
White tip nematode	-0.075	-0.241		

The genotypes were scattered into four groups according to their values of PCA that reflect existing of significant diversity among them. PCA is predictable to be more helpful about differentiation among different genotypes and each agronomic trait and clarified the relative contribution of each in divergence.

The scattered diagram for rice genotypes of different types revealed that genotypes, Giza 178, GZ 6296 as well as super rice lines, GG 46, GG 42-1 and GG 42-1 were grouped and clearly allocated to distinctive group in the PCA separated from all genotypes which suggesting more diverged from the other genotypes based on their higher filled grains panicle[-1] (Fig. 1 A and B). Therefore, these genotypes could be used as good sources for improvement of filled grains panicle[-1] trait in breeding program. All

susceptible genotypes for both bakanae and white tip nematode allocated in the same group such as Giza 177 and Sakha 101, while all completely resistant genotypes for all biotic stress, blast, bakanae and white tip nematode combined with high yielding ability genotypes such as, Giza 177-2, Giza 178-2, SP 70-6-1 to SP 70-6-6 and By 6-20.

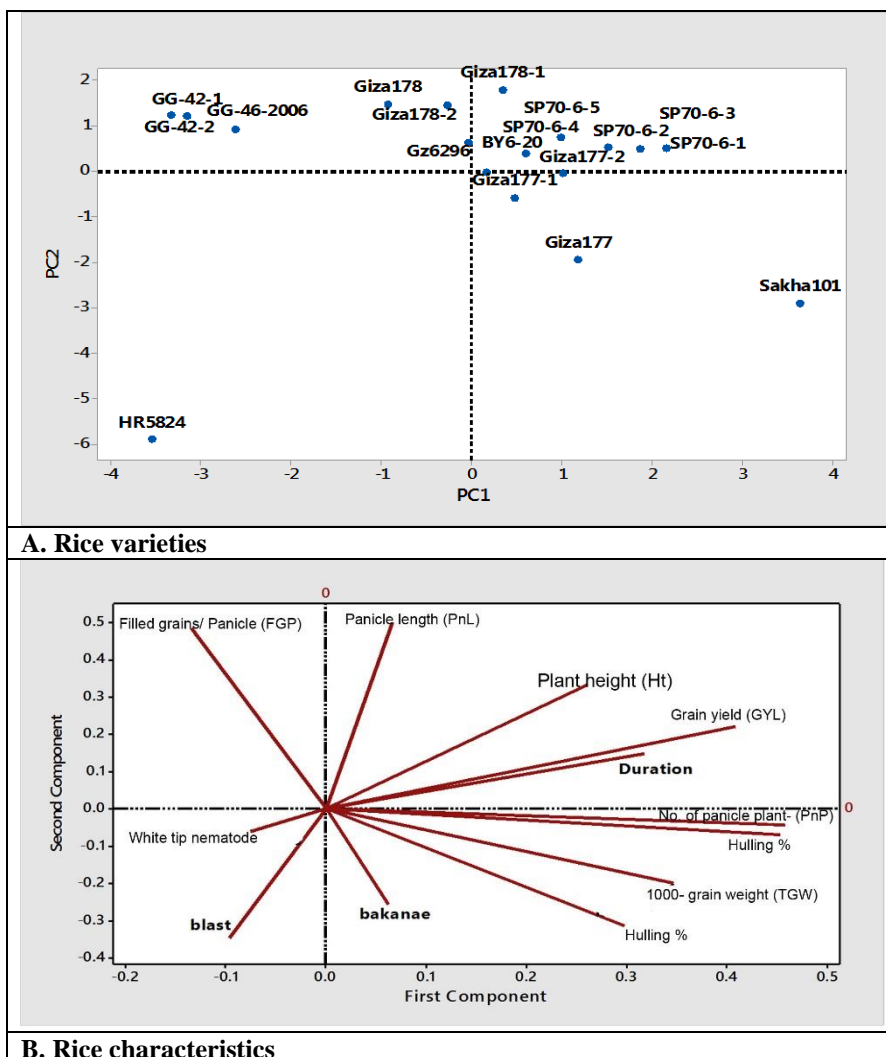**A. Rice varieties**

B. Rice characteristics

Figure 1. Two dimensional plot of PCA for the 18 rice genotypes (A) and their 12 characteristics (B) contributed to genetic diversity based on their PCA scores.

It is well-meaningly to found that, the genotypes Giza 177, Sakha 101 and BY 6-20 were existing in two divergent groups and other lines of Giza 178, GZ 6296 and super rice lines distributed in a unique group with wide distance. Cox *et al.* (1985) suggested crossing distantly related lines in an inbred improvement, thus high heterotic response and good segregates could obtain from crossing among Egyptian and high divergent parents such as GZ 6296, IR 66298, IR 65600, IR 66159 and HR 5824.

Principal component analysis could be used to create genetic variability, also multivariate techniques to determine the relative contribution of traits on variation and grouping the genotypes into varied clusters (El-Mansy, 2009 and Abdel-Salam *et al.*, 2010).

Evaluation of blast disease

All derived lines and their respective parents were evaluated under blast nursery condition with mixed prevalent races and artificially inoculated with 10 aggressive specific races in greenhouse as; IB-45, IC-15, IH-1, IB-63, IC-5, IB-54, ID-13, IB-19, ID-15 and IG-1.

Giza 177 and its derived lines *i.e.* Giza 177-1 and Giza 177-2 were highly resistant to blast under blast nursery test at seedling stage, field condition at adult stage while, HR 5824 was susceptible to blast. Giza 177 and its derived lines exhibited a resistant reaction for all prevalence races at both seedling and adult stages under field condition as well as under artificial inoculation with different races. This proved that selection was go through right direction for resistance through advanced generations and also, good selection for the source of resistance. Although, both Sakha101 and HR 5824 as susceptible parents to blast, but all their derived promising lines with backcross technique were completely resistant under natural and artificial infection. Therefore, it proved that backcross is a successful tool to improve broken-down variety. The resistant lines could be attributed to transgressive segregation that allows the two

favorable parents' alleles derived together and gave resistant lines. The derived lines of Sakha101 showed more genetic variation than their parents. The genetic variation was reflected through highly resistance to blast and other tested diseases. Also, due to recombination of additive alleles, recombination results in new pairs of alleles at two or more loci, which cause extreme phenotypic and genotypic changes in undesirable traits (Arama *et al* 2008 and Schwarzbach *et al* 2001). Giza 178, GZ 6296 and their derived lines Giza 178-1 and Giza 178-2 were highly resistant to prevalent races in blast nursery and ten specific races under artificial inoculation (Table 5). These results exhibited that Giza 178 and GZ 6296 were still as good donors for blast resistance. BY 6-20 was completely resistant under blast nursery test and all tested blast races, that contributed to highly resistant parent GZ 5310 (Hammoud *et al.* 2009 and Hammoud *et al.* 2011). BY 6-20 can be used in advanced breeding program as new promising resistant donor for blast. The three lines; GG-46-

2006, GG-42-1 and GG-42-2 which derived from super rice varieties were highly resistant. All studied parents had wide range of genetic diversity, therefore they provided broad spectrum of blast resistance levels. Consequently, the breeder finally succeeded to improve the broken-down rice cultivar Sakha 101 and produce new resistant promising lines to prevalent aggressive blast races. Frequently, these results are in harmony with those obtained by Sehly *et al.* (2008) and Hammoud *et al.* (2009).

From the reaction of rice genotypes to blast, these varieties exhibited a broad spectrum of resistance, thus, they could be considered as resistant resources for transferring the resistance genes to new promising lines. These results are in agreement with those of El-Refaee *et al* (2011), Hammoud *et al.* (2013) and El-shafey *et al.* (2015).

Table 5: Blast reaction under natural and artificial inoculation of studied rice genotypes during 2014 and 2015 seasons.

No.	variety	Blast nursery at		Blast reaction under artificial inoculation										
		Gemmiza	sakha	IB-45	IC-15	IH-1	IB-63	IC-5	IB-54	ID-13	IB-19	ID-15	IG-1
1	Giza 177	R	R	1	2	1	1	1	1	2	2	1	2
2	Giza 177-1	R	R	2	1	1	1	1	1	1	1	1	1
3	Giza 177-2	R	R	1	1	1	1	1	1	1	1	1	1
4	Giza 178	R	R	1	1	1	1	1	1	1	1	1	1
5	Giza 178-1	R	R	1	1	2	1	1	1	1	1	2	1
6	Giza 178-2	R	R	1	1	1	1	1	1	1	1	1	1
7	Gz6296	R	R	1	1	1	1	1	1	1	1	1	1
8	Sakha 101	S	S	5	4	2	6	4	6	2	5	2	4
9	SP70-6-1	R	R	1	1	1	1	1	1	1	1	1	1
10	SP70-6-2	R	R	1	1	1	1	1	1	1	1	1	1
11	SP70-6-3	R	R	1	1	1	1	1	1	1	1	1	1
12	SP70-6-4	R	R	1	1	1	1	1	1	1	1	1	1
13	SP70-6-5	R	R	1	1	1	1	1	1	1	1	1	1
14	BY 6-20	R	R	1	1	1	1	1	1	1	1	1	1
15	HR 5824	S	S	5	5	3	4	5	5	6	5	3	5
16	GG-46-2006	R	R	1	1	1	1	1	1	1	1	1	1
17	GG-42-1	R	R	3	3	1	1	1	1	3	3	1	1
18	GG-42-2	R	R	1	1	2	1	1	1	1	1	2	1

Evaluation of Bakanae infection

The mean performances of infection by Bakanae disease for the rice genotypes are presented in Table 6 and the symptoms of Bakanae disease as abnormal elongation of Sakha 101 seedlings under artificial inoculation are shown in Figure 2. With artificial infection by two diverse isolates of *Fusarium fujikouri*, the severe isolates were significantly differed in their interaction with various genotypes (Table 6). Some isolates recorded high infection % with some varieties such as on Giza 178. The isolate 7 recorded the highest infection 77.3% compared with 38.66% of isolate 10 for Giza 178. On the other hand, isolate 10 showed the highest infection with line Giza 178-1 as 73.33% and isolate 7 showed 53.33%. The reaction differed from isolate to another and based on different varieties under interaction. These results agreed with Leslie *et al.* (2007), Kvas *et al.*

(2009), Gabr (2010), Nur Ain Izzati and Salleh (2010) and Hsuan *et al.* (2011), they revealed that there were a wide range of virulence and variability among isolates of Fusarium and pathogenicity tests on a susceptible rice seedlings confirmed that only isolates identified as *F. fujikuroi* were pathogenic and able to produce typical bakanae symptoms.

Concerning the reaction of varieties under artificial inoculation, all tested genotypes were significantly differed according to their response to infection with *Fusarium* during seedling stage. Giza 177, Giza 178 and Sakha 101 were highly susceptible and exhibited high level of infection. All lines that derived from Giza 177 and Sakha 101 recorded low levels of infection compared with their parents, so the selection go through resistance direction. The infection of susceptible cultivar Giza 177 reduced from 77.33 to 9.33%

with line Giza 177-2. All derived lines from highly susceptible parent Sakha 101 successfully reduced the higher level of infection from 53.33 to 20%. Depend on super rice such as, IR 66298, IR 65600 and IR 66159 as new parents to improve Sakha 101 create wide range of variation and reduced the infection from 53.33 to 13.33% (Table 6).

Under natural infection at nursery bed and field conditions, all tested varieties exhibited high level of resistance to Bakanae disease except Giza 177 and Sakha 101. All lines significantly surpassed their highly susceptible cultivars Giza 177 and Sakha 101 in

reducing bakanae infection level. Subsequently, the super rice varieties IR 66298, IR 65600, IR 66159, and HR 5824 and the lines GZ 5310 and BY 6-20 could be considered as promising donors to Bakanae resistance. The variation ranged from highly susceptible to resistant genotypes especially under natural infection in field conditions for long period of evaluation. So, this reflected the proper and right behavior of cultivar against this disease. Wan Nur Ain *et al*. (2015) reported that a total of 31 Malaysian rice varieties screened for Bakanae disease had variable susceptibility.

Table 6: Mean performance of the rice genotypes for bakanae infection.

No.	Genotype	No. of healthy plants				No. of bakanae infected plants				Infection %				Bakanae Infection % under field
		control	Isolate 7	Isolate10	Mean	Control	Isolate 7	Isolate10	Mean	Cont.	Isolate 7	Isolate10	Mean	
1	Giza 177	18.3	7.3	5.7	10.4k	6.7	17.6	19.3	14.5a	26.7	70.6	77.3	58.2a	10
2	Giza 177-1	23.7	20.0	22.3	22.0ab	1.3	5.0	2.6	3.0jk	5.3	20.0	10.6	12.0jk	0
3	Giza 177-2	23.7	20.3	22.6	22.2ab	1.3	4.7	2.3	2.8jk	5.3	18.6	9.3	11.1jk	0
4	Giza 178	23.7	5.7	15.3	14.9h	1.4	19.3	9.6	10.1d	5.3	77.3	38.6	40.4d	0
5	Giza 178-1	22.6	11.6	6.7	13.7ij	2.2	13.3	18.3	11.3bc	9.3	53.3	73.3	45.3cb	0
6	Giza 178-2	22.3	9.8	7.6	13.2j	2.6	15.3	17.3	11.8b	10.6	61.3	69.3	47.1b	0
7	Gz6296	23.6	13.3	6.7	14.5hi	15.3	17.3	1.3	10.4cd	5.3	46.6	73.3	41.7cd	0
8	Sakha 101	18.0	11.6	16.3	15.3gh	11.6	18.3	7.0	9.6de	28.0	53.3	34.6	38.6ed	30
9	SP70-6-1	24.6	20.0	21.6	22.1ab	13.3	8.6	0.3	2.9jk	1.3	20.0	13.3	11.6jk	0
10	SP70-6-2	23.7	16.4	20.6	20.2de	1.3	8.6	4.3	4.7gh	5.3	34.6	17.3	19.1gh	0
11	SP70-6-3	24.6	17.3	19.7	20.6cd	0.3	7.6	5.3	4.4hi	1.3	30.6	21.3	17.7hi	0
12	SP70-6-4	23.7	13.0	18.6	18.4f	1.3	12.0	6.3	6.5f	5.3	48.0	25.3	26.2f	0
13	SP70-6-5	23.3	18.6	15.0	19.0f	1.6	6.3	10.0	6.0f	6.6	25.3	40.0	24.0f	0
14	BY 6-20	23.3	19.3	22.3	21.6abc	1.6	5.6	2.6	3.3ijk	6.6	22.6	10.6	13.3ijk	0
15	HR 5824	20.7	15.3	13.3	16.4g	4.3	9.6	11.6	8.5e	17.3	38.6	46.6	34.2e	0
16	GG-462006	23.3	22.5	21.6	22.5a	1.6	2.3	3.3	2.4k	6.6	9.3	13.3	9.7k	0
17	GG-42-1	25.0	17.6	20.7	21.1bcd	0.0	7.3	4.3	3.9ijk	0.0	29.3	17.3	15.5hij	0
18	GG-42-2	22.7	18.0	17.3	19.3ef	2.3	7.0	7.6	5.6fg	9.3	28.0	30.6	22.6fg	0
		22.8a	15.4c	16.3b		2.17c	9.6a	8.6b		8.6c	38.2a	34.9b		
L.S.D 5 %	Variety	1.12				0.40				4.48				
	Isolate	0.46				0.16				1.83				
	V*I	1.94				0.69				7.77				

Figure 2: Symptoms of Bakanae disease as abnormal elongation of Sakha 101 seedlings under artificial inoculation.

The derived lines of Giza 178 and GZ 6296 have the same level of infection as their parents under artificial inoculation. The level of infection ranged from 40.44 to 47.11%. On contrary, under both nursery bed and permanent field the behavior of these varieties were changed totally to resistance side. Therefore, the artificially inoculated plants of different cultivars; Sakha 101, Giza 178, GZ 6296, and Giza 179 were transplanted under field conditions to estimate the reaction against bakanae after inoculation (Table 7). Compared with the behavior of Sakha 101 as japonica highly susceptible cultivar to bakanae, the genotypes; Giza 178, GZ 6296, and Giza 179 as indica-japonica

were considered highly resistant to bakanae disease under field conditions. While, No. of infected plants of Sakha 101 under artificial inoculation was 80.5 plant for each 15 cm^2 pot, it reduced to 25.75 plant for 2 m^2 plot as a mean of both locations. The infection disappeared after transferring the inoculated rice grains to the permanent field for indica-japonica genotypes. The infection of both Giza 178 and Giza 179 under artificial inoculation was 68.3 and 50.0 plant for 15 cm^2 pot, while it was 1.41 and 1.08 plant for 2m^2 at the permanent field, respectively.

Table 7: Infection % of Bakanae disease under greenhouse and field conditions

No.	Variety	Under greenhouse (No. of infected plants /pot)			Under field (no. of infected plants/2 m^2)					
					Sakha		Gemmiza			
		Healthy seed	Inoculated seed	Mean	Health seeds	Inoculated seeds	Health seeds	Inoculated seeds	Mean
1	Sakha 101	11.0	150.0	80.5	12.33	46.67	8.00	36.00	25.75
2	Giza 178	1.3	68.3	34.8	1.00	1.00	1.33	2.3	1.41
3	GZ 6296	3.0	46.3	24.7	1.33	1.6	3.00	4.00	2.50
4	Giza 179	1.0	50.0	26.0	0.00	1.00	1.00	2.33	1.08
	Mean	4.4	78.7	-	3.67	12.58	3.33	11.15	-
	LSD 5 %	Variety	8.48			Variety	1.167		
		Inocul.	6.00			Location	0.825		
		V*I	11.99			Inoculation	0.825		

The cultivation of resistant cultivars potentially represents an economic and effective way to control this disease. However, even though previous studies have conducted extensive screenings for resistant germplasm, only a few varieties have been reported to exhibit resistance to bakanae (Khokhar and Jaffrey 2002, Kim *et al*. 2014). Hammoud and Gabr (2014) revealed that there are variations among some Egyptian rice varieties for Bakanae susceptibility.

The behavior of indica-japonica varieties and their response to bakanae was very clear as the infection in inoculated seeds not developed with time after cultivation in permanent field compared with the highly susceptible japonica cultivar Sakha 101. Therefore, the highly response of Giza 178, GZ 6296, their lines, and Giza 179 to bakanae infection represented in abnormal elongation that more than 100 %. The abnormal elongation of these varieties not reflected their normal growth in the field after transferred artificially inoculated grains to permanent field (Tables 6 and 7). Their abnormal elongation could be attributed to excessive response to gibberellin hormones which responsible for internode elongation. The results in harmony with those of (Zainudin *et al*. 2008) they reported that *F. fujikuroi* regarded as the most virulent species causing bakanae disease, produced an excessive gibberellin hormones which is responsible for internode elongation of bakanae infected plants. The increase in plant height might be due to the ability of the inoculated species to produce gibberellin. Desjardins *et al*. (2000) reported the bakanae disease due to *F. proliferatum* induces elongation and production of gibberellins in infected plants. Genetically, *F. proliferatum* and *F.*

fujikuroi are closely related species.

Evaluation of white tip nematode

The response of different rice genotypes to infection by white tip nematode was evaluated twice; the first was early prediction by infection through the No. of nematodes in 10g seeds, the second, actual infection under field condition. At lab, the highest extracted nematodes were harvested from grains of highly sensitive cultivar Giza 177 with 153.67 nematodes/10g grains followed by moderately susceptible cultivar Sakha 101 with 106.33. The lines derived from super rice and Sakha 101 reproduced high number of nematode as Giza 177 and Sakha 101.

The derived lines of Giza 177 crossed with resistant variety HR 5824 dropped the nematodes number from 153.67 to 0 and 1.67, while lines of Sakha 101 reduced the nematodes number from 106.33 to 10 nematodes. BY 6-20 reduced the number of nematodes comparing with its parent Sakha 101 to 4.33 nematodes.

Concerning the highly resistant cultivars Giza 178, GZ 6296 and their derived lines gave the lowest number of nematodes ranged from 0.67 to 12.3 nematodes.

For reaction at field, the response of tested varieties was significantly differed according to the variety, there are significant difference among varieties in their infection of white tip nematode. The highest infection was exhibited with cultivar Sakha 101 (53.3%) followed by Giza 177 (38.3%). Although, the derived lines of super lines GG-46-2006, GG-42-1, and GG-42-2 recorded highest number of nematode/10g grains but were symptomless and considered as resistant varieties at field conditions with acceptable yield. These varieties

were more tolerant to infection with white tip nematode although the buildup and reproduction of nematode as similar as sensitive varieties Giza 177 and Sakha 101 but their yield considered high. Most of resistant cultivars were lack of the characteristic symptom of white tip nematode. These results in lines with those of El-shafey (2007) who reported that some varieties were nematode symptomless and their grains harvested more buildup of nematodes associated with high yield and their yield not affected with the highest content number of nematode in their grains. Therefore, the early prediction to the infection of white tip nematode with check the nematode content in grains of tested varieties was highly associated with infection % in the field. These results agreed with those of Feng *et al* (2014), whom reported that the final nematode population indicated that the threshold of economic damage had also been exceeded in 10 cultivars and none of them was immune.

Table 8: Mean performance of the rice genotypes for nematode infection.

No.	variety	Plant height (cm)				Elongation %			White tip Infection % under field	No. of nematode /10g seeds
		Control	Isolate 7	Isolate10	Mean	Iso.7	Iso. 10	Mean		
1	Giza 177	10.13	13.26	15.50	12.97 b	30.92	52.96	41.94	38.33	153.67 a
2	Giza 177-1	10.13	12.20	12.53	11.62 ed	20.39	23.68	22.04	10	1.67 d
3	Giza 177-2	13.00	11.66	10.00	11.56 ed	0	0	0	1.33	0.00 d
4	Giza 178	5.66	16.33	11.70	11.23 ef	188.52	106.47	147.50	0	12.33 d
5	Giza 178-1	6.66	13.66	12.00	10.78 fg	105.00	80.00	92.50	0	7.67 d
6	Giza 178-2	8.33	18.00	9.66	12.00 cd	116.00	16.00	66.00	0	2.67 d
7	Gz6296	6.90	11.83	18.46	12.40 bc	71.49	167.63	119.25	0	0.67 d
8	Sakha 101	6.33	15.06	9.43	10.28 gh	137.89	48.95	93.42	53.33	106.33 b
9	SP70-6-1	6.03	11.10	9.66	8.93 J	83.98	60.2	70.09	15	0.33 d
10	SP70-6-2	7.00	10.83	10.16	9.33 ij	54.76	45.24	49.72	1.33	9.00 d
11	SP70-6-3	7.66	12.33	8.33	9.44 ij	60.87	8.70	34.79	5	0.67 d
12	SP70-6-4	7.00	12.50	10.33	9.94 hi	78.57	47.61	63.09	5	6.33 d
13	SP70-6-5	9.83	12.33	13.93	12.03 cd	25.42	41.69	33.56	1.33	10.00 d
14	BY 6-20	8.46	11.16	8.96	9.53 ij	31.89	5.90	18.90	0	4.33 d
15	HR 5824	12.83	15.20	14.50	14.18 a	18.44	12.98	15.71	0	1.33 d
16	GG-46-2006	10.00	10.66	11.16	10.61 fgh	6.66	11.66	9.16	0	143.33 a
17	GG-42-1	8.33	14.36	9.86	10.86 fg	72.4	18.40	45.40	0	91.00 bc
18	GG-42-2	11.10	12.30	11.60	11.67 ed	10.81	4.50	7.66	0	71.00 c
	Mean	8.63 c	13.05 a	11.55 b						
	Variety	0.396							2.179	24.42
	Isolate	0.161								
	V*I	0.686								

Finally, breeders in this investigation succeeded to identify the genetic divergence among derived lines combined with highly resistance to biotic stress and high yielding potential. The new combinations of divergence parents and local varieties could be used in breeding programs as resistant resources for blast, bakanae and white tip nematode. The identification of sources of resistance for developing new varieties with high level of resistance to blast, bakanae and white tip nematode disease represents the most economic effective and eco-friendly approach to manage the diseases.

The breeder successfully improved elite lines; SP70-6-1, BY 6-20, Giza 178-1 and GG-46-2006, with wide spectrum of resistance level to blast, bakanae and white tip nematode. Giza 178, GZ 6296 and GZ 5310 were considered as good donors of all tested diseases in breeding program.

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تقييم بعض التراكيب الوراثية المستنبطة من الأرز عالية المحصول مقاومة لأمراض اللفحة وعفن القدم والقمة البيضاء النيماتودي

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مركز البحوث والتدريب في الأرز بسخا ـ قسم بحوث الأرز ـ معهد بحوث المحاصيل الحقلية ـ مركز البحوث الزراعية

تعتبر أمراض الأرز من العوامل الحيوية المحددة للمحصول العالي وكسر المقاومة. يهدف هذا البحث الى تقييم بعض التراكيب الوراثية المستنبطة والمتفوقة في المحصول ذات المقاومة لأمراض اللفحة وعفن القدم والقمة البيضاء النيماتودي. وتم استنباط ١٢ تركيب وراثي مبشر تم تقييمهم بالإضافة الى أباءهم الثمانية وذلك لبعض الصفات الاقتصادية والمحصولية وكذلك مقاومة الامراض تحت ظروف الحقل والعدوى الصناعية بمركز البحوث والتدريب في الارز ، سخا، كفر الشيخ، مصر خلال موسمي الزراعة ٢٠١٤ و٢٠١٥. ومن بين الصفات المدروسة، صفة عدد الحبوب الممتلئة بالسنبلة والتي أعطت أعلى القيم لمعامل التباين الوراثي والمظهري تلتها صفة عدد السنابل لكل نبات. درجة التوريث بالمعني الواسع كانت عالية لجميع الصفات المدروسة وتراوحت من ٩١.٠٦ الي ٩٩.٠٥ %. وانتجت السلالات SP 70-6-4، SP 70-6-1 أعلي محصول حبوب (١١.٧٣ ، ١١.٧٢ طن / هكتار) مقارنة مع الأب سخا ١٠١ (١٠.٦٣ طن / هكتار). وكانت جميع الاباء المختارة للتهجين عالية التنوع الوراثي ولذلك عملت علي توفير مدي مقاومة واسع لمرض اللفحة. وأظهرت السلالات المستنبطة المبشرة GG-46-2006 ، GG-42-1 وGG-42-2 مقاومة عالية لمرض اللفحة. وتعتبر سلالات الأرز السوبر IR 66298، IR 65600 وIR 66159 وكذلك السلالات المستنبطة BY 20-6 و HR 5824 مصادر مهمة لمقاومة مرض البكانا. وبالنسبة لمرض القمة البيضاء النيماتودي، كانت السلالتين المستنبطتين من جيزة ١٧٧ والأب المقاوم HR 5824 وهي جيزة ١-١٧٧، جيزة ٢-١٧٧ أكثر مقاومة وانخفض فيها عدد افراد النيماتودا في ١٠ جم حبوب من ١٥٣.٦٧ فرد نيماتودا الي صفر. بينما السلالة BY 6-20 انخفض العدد الي ٤.٣٣ فرد بالمقارنة مع ابيها سخا ١٠١. وتعتبر الأصناف جيزة ١٧٨ و GZ 6296، وسلالاتهم وكذلك السلالة BY 6-20 مصادر جيدة لمقاومة نيماتودا القمة البيضاء.

تعتبر السلالات SP70-6-1, BY 6-20, Giza 178-1 and GG-46-2006 ذات مدي واسع من المقاومة لمرض اللفحة والبكانا ونيماتودا القمة البيضاء. ويعد الصنف جيزة ١٧٨ والسلالة GZ 6296 من مصادر المقاومة الجيدة للأمراض المختبرة.