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Genetic Variability, Insect and Disease Resistance of some Promising Rice Genotypes

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ABSTRACT



An investigation was carried out during 2019 and 2020 at Farm of Sakha Agricultural Station, Kafrelsheikh, Egypt to study the genetic variation, heritability, genetic advance, correlation coefficient and evaluation the response of fifteen rice genotypes against insects, rice blast, brown spot, and nematodes. The results showed that Sakha108, Giza178, GZ10590-1-3-3-2, GZ10848-1-2-2-1 and Korea 27 yielded more than 10 t/ha compared to GZ10333-9-1-1-3 and GZ10778-17-1-6-1 that yielded 8.89 and 8.74t/ha, respectively. Most of rice genotypes had good desirable values of milling%, except Korea 27 and GZ10686-2-1-3-4 that recorded 69.33 and 69.83%, respectively. The phenotypic variance was higher than genotypic coefficient of variance for all studied traits. The highest phenotypic and genotypic variances were observed in number of filled grains panicle⁻¹. The phenotypic coefficient of variability averaged 0.99 % for hulling % and 19.35% for grain yield. Similarly, the genotypic coefficient of variability averaged 0.44% for hulling % and 19.24% for grain yield. Heritability in broad sense was high for most of studied characters expect hulling percentage. The genotype, Korea 27, GZ10590-1-3-3-2, GZ10778-17-1-6-1 and GZ10848-1-2-2-1 were recorded the highest values of dead hearts and white heads. Eighteen Pyricularia oryzae isolates were identified as four race-groups. Under artificial and natural inoculation with P. oryzae, Giza177, Giza178, Sakha108, GZ10598-9-1-5-5, GZ10101-5-1-1-1 and GZ10848-1-2-2-1 reflected a high level of resistance to rice blast, while for brown spot GZ10333-9-1-1-3, Korea 27, GZ10590-1-1-3-9-1 and GZ10590-1-3-3-2, for white tip nematode resistance were Korea 27, GZ10598-9-1-5-5.GZ10590-1-1-3-9-1 and GZ10590-1-3-3-2. Therefore, they could be utilized as donors for disease resistance in breeding programs.

Keywords: Rice, genetic variation, heritability, insect, diseases.

INDRODUCTION

Planning and execution of breeding program for improvement of quantitative characters depend on the magnitude of genetic variations (Adhikari *et al.*, 2018). Therefore, success of plant breeding activities entirely depends on the existence of genetic variability with respect to desired traits and selection skills of plant breeder. Genetic variation plays a major role in plant breeding, especially for selecting desirable traits and genetic improvement. The maintenance of rice self-sufficiency and meet the future demand due to the increases of population, development of high yielding genotypes with desirable agronomic traits is necessary (Akinwale *et al.* 2011 and Mulugeta *et al.* 2012).

Karthikeyan *et al.* (2010) recorded broad sense heritability estimates of 99.8% for days to heading, 99.2% for days to maturity, 87.3% for plant height, 79.8% for panicle length, 93.4% for number of branches panicle-1, 88.8% for number of filled grains panicle⁻¹, 97.6% for 1000-grain weight and 73.2% for grain yield. Aditya and Bhartiya (2013) reported that heritability estimates along with genetic advance is more precise in predicting the genetic gain under selection than depending on the heritability alone. Also, the relationship between yield and its components is important for direct and indirect selection of traits which contribute to yield. Rashid *et al.* (2017) and Gyawali *et al.* (2018) reported that phenotypic coefficient of variance was higher than genotypic coefficient of variance for all studied traits indicating the environmental influence on the expression of these traits. Also, the estimated high heritability for days to flowering, maturity, 1000-grain weight and plant height suggested that these traits are under high genetic control. High phenotypic variation was observed for grain yield, number of grains/panicle, number panicles m² and straw yield. Also, Adhikari *et al.* (2018) estimated higher phenotypic coefficient of variation as compared to genotypic coefficient of variation, which reveals the influence of environment on the expression of traits.

In Egypt, the key rice insect pest is the rice stem borer (*Chilo agammon* Bles.). The damage of the insect appears as dead hearts in the vegetative stage and as white heads in the reproductive stage (Sherif *et al.* 2005).Insect resistant varieties play an important role in the management of rice pests; particularly they have the unique advantage of not involving extra cash expenditure to the farmer and provide an inherent insect control (Sherif, 2002). In general, rice varieties belonging to Indica or Indica x Japonica sub-species are more susceptible to rice stem borer infestation than those belonging to japonica ones (Bleih *et al.*1991). The resistance of rice varieties to rice stem borer was attributed to non-preference and antibiosis mechanisms of resistance (Sherif, and Bastawisi, 1997).

Biotic stresses are considered as the most destructive constraints for high yield production due to high level of variability. Breeding of blast resistance cultivars are one of the

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most important objectives of rice breeders in Egypt. Utilizing of disease resistance varieties possibly is the maximum costeffective and consistent method of disease management, maintaining clean environment and stable rice production. Blast disease is the most destructive fungal disease caused by Magnaporthe-oryzae-Couch (anamorph: Pyricularia oryzae Cavara) (Couch and Kohn 2002). This fungus caused many high yielding varietal breakdown with the high rate of mutation, race shifting and change of dominant specific races on susceptible cultivars as Sakha101 and Sakha104breakdown (Khush and Jena, 2009, El-Shafey et al. 2015). Broadening the genetic background of new promising lines should utilize a wide range of diversity and new resources of blast resistance (El-Refaee et al. 2011). Brown spot disease caused by Bipolaris oryzae is common in poor soils, bad drainage system, low water quality and saline soil. In addition, white tip nematode disease caused by Aphelenchoides besseyi results in remarkable yield losses of different rice cultivars (El-Shafey 2007 and Selim et al. 2020). There is a wide range of resistance variation in the Egyptian varieties against this nematode (El-Shafey 2007, El-Shafey et al. 2010 and El-Shafey et al. 2015). Therefore, determination of new resistance resources is the most effective and reliable method for disease management.

The objectives of this investigation were to assess the genetic variability, heritability and genetic advance as well as the principal component analysis of some rice genotypes and their agronomic characteristics and their response to biotic stress; stem borer, blast reaction, brown spot, and white tip nematode.

MATERIALS AND METHODS

Plant materials and agriculture practices:

Fifteen rice genotypes were evaluated in 2019 and 2020 rice seasons at the farm of Sakha Agricultural Station,

Kafrelsheikh, Egypt (Table 1). The experiment was laid out in a randomized complete block design (RCBD) with three replications. Seeds of the rice genotypes were sown at the first week of May, and seedlings were transplanted individually 30 days later at a spacing of 20 x 20 cm. Each replication included seven rows of each genotype; the length of the row was 5 m. The rate of NP 60 : 30 Kg/ha was applied as follows; 60 kg N/ha in the form of urea (46.5%N) applied in two splits, the 2/3 of the dose was added as basal application and incorporated into the soil during land preparation, while the 1/3 of the dose was top-dressed 30 days after transplanting. Thirty kg P2O5 ha-1 in the form of single super phosphate (15% P2O5) was applied in the permanent field and incorporated into the soil during land preparation. All agricultural practices, including weed control were applied as recommended. The following traits were recorded i.e., plant height (cm), days to heading (day), number of panicles plant-1, panicle length (cm), number of filled grains panicle-1, grain yield (ton ha-1), hulling (%), milling (%) and head rice (%), measured according to IRRI, (1996).

Evaluation of stem borer, Chilo Agamemnon infestation:

The rice stem borer (*Chilo agammnon* Bles.) damage was recorded as dead heart percentage at vegetative stage and as white head percentage at the maturity stage by counting the number of dead heart or white head per 100 plants according to the standard evaluation system of Rice Research and Training Center (RRTC), Sakha, Egypt. Resistant = 0 - 3%, moderately resistant = 3 - 6%, moderately susceptible = 6 - 9 %, susceptible = 9 - 12 % and highly susceptible ≥ 12 % (RRTC, 2016).

Table 1. Name, parentage and type of the studied rice genotypes

Genotype	Parentage	Туре
Giza 177	Giza 171/Yomji No.1//PiNo.4	japonica
Giza 178	Giza 175/Milyang 49	indica /japonica
Sakha 101	Giza 176/ Milyang 79	japonica
Sakha 108	Sakha 101/HR4856-1-1-1-2//Sakha 101	japonica
GZ 10333-9-1-1-3	SKC23822/Yunlen4	japonica
Korea 27	Introduced	indica
GZ 10101-5-1-1-1	Sakha 103/IRAT 385	japonica
GZ 10598-9-1-5-5	IET16775/ Yunlen 55	japonica
GZ 10590-1-1-3-9-1	GZ 8126-1-3-1-2/ HR17570-21-5-2-5-2	japonica
GZ 10590-1-3-3-2	GZ 8126-1-3-1-2/ HR17570-21-5-2-5-2	japonica
GZ 10631-1-1-2-4	Giza 177/ WAB891S633	japonica
GZ 10686-2-1-3-4	Sakha 104/ WAB450-1-1-P-106	japonica
GZ 10717-3-5-1-1	Sakha 105/ AC 2879	japonica
GZ 10778-17-1-6-1	Giza 178/ IR81326-74-2-2-2	japonica
GZ 10848-1-2-2-1	Sakha 104/ SKC 23819-192-2-2-1-1-1-2-1-2-2	indica/japonica

Rice blast samples collection and identifications of blast physiological races

Eighteen isolates of *Pyricularia oryzea* were collected from infected rice varieties at different locations of rice growing area during 2018 and 2019 seasons. The isolates were grown and multiplied on banana medium (200g Banana, 10g Dextrose, and 20g Agar, 1L water) at 28 °C. The isolates were identified using eight international differential varieties (I.D.V.) according to Atkins *et al.*, 1967. Fifteen rice entries; four commercial rice cultivars and eleven promising lines (Table 1) were used to evaluate its resistance level. Ten Japanese Differential Varieties

(J.D.V.) were used to determine effective blast resistant genes. All tested entries were seeded in plastic trays (30 x 20 x15 cm.). The trays were kept in the greenhouse at 25-30oC, and fertilized with Urea 46.5% N (5 g/tray). Rice seedlings at 3-4-leaf stage (Twenty one-days old) were ready for inoculation by spraying with spore suspension (100 ml) adjusted to 5 x 10^4 spores /ml. The inoculated seedlings were kept in a moist chamber with at least 90% R.H. and 25-28 °C for 24 hr, and then moved to the greenhouse. Seven days after inoculation, blast reaction was recorded according to the standard evaluation system using 0-9 scale (IRRI 2013).

Evaluation of blast under natural field condition:

Fifteen rice varieties were naturally exposed to blast infection through the maximum tillering stage at three locations; Sakha, Gemmeza and Zarzora. Forty-five days from sowing, typical lesions of blast were scored, according to standard evaluation system using 0-9 scale (IRRI 2013) as follows:1-2 = resistant (R), 3 = moderately resistant (MR), 4-6 = susceptible (S), 7-9 = highly susceptible (HS),

Evaluation of brown spot infection:

Severity of brown spot was evaluated as follow: leaf area diseased after Forty-five days of transplanting (IRRI 2013)

Evaluation of White tip nematode infection under field condition:

White tip nematode was evaluated after sixty days from transplanting with full appearance of symptoms. Severity of white tip infection was estimated as the number of infected leaves/m2 according to El-Shafey and Elamawi (2010).

Statistical analysis

Analysis of variance was conducted for each season according to Snedecor and Cochran (1967). Error variances from separate analysis of the data were tested for homogeneity using Bartlett test (1937). Phenotypic (PCV) and genotypic (GCV) coefficient of variability were estimated according to the method of Borton (1952). The expected genetic advance from selection (GA) for the studied plant characteristics as well as the phenotypic correlation between any pairs of traits was calculated according to Johnson *et al.* (1955).

Combined analysis of variance was used (after performing homogeneity test) to estimate the genotypic variance (σ^2 g), environmental variance (σ^2 e), genotypic x environmental variance (σ^2 gy), phenotypic variance (σ^2 ph), genotypic (GCV), phenotypic (PCV) coefficient of variation components and data were statistically analyzed according to Gomez and Gomez (1984).

RESULTS AND DISCUSSION

Mean performance:

Data in Table (2) indicated that all the rice genotypes had desirable values of plant height according to

breeding objectives of Rice Research Department. GZ10848-1-2-2-1 and Sakha 101 exhibited the shortest plants; 91.0 and 92.5cm, respectively. On the other hand, GZ10686-2-1-3-4 and GZ10778-17-1-6-1 recorded the highest values of plant height (100.17cm). Most of rice genotypes matured earlier than the commercial rice cultivars; Sakha 101 and Giza 178 (Table 2). For number of panicles plant⁻¹, Sakha 108, Korea 27 and Sakha 101 showed the highest values of 24.17, 23.5 and 23.00, respectively, while Giza 177 and GZ10778-17-1-6-1 gave the lowest values of 19.33 and 19.50, respectively.

GZ10590-1-1-3-9-1, GZ10590-1-3-3-2 and Korea 27 gave the longest panicle 24.42 and 24.38cm, respectively. On the other hand, Giza 177, GZ10717-3-5-1-1- and GZ10631-1-1-2-4 recorded the shortest panicles 20.60, 20.70 and 20.97 cm, respectively. Data in Table (3) revealed that GZ10590-1-3-3-2, Sakha 108 and Korea 27 gave the highest number of filled grains panicle⁻¹(166.2, 155.5 and 155.3, respectively, while GZ10778-17-1-6-1 recorded the lowest value (109.3) without a significant differences with GZ10598-9-1-5-5 (119.20).

For grain yield, Korea 27, Sakha 108, Giza 178, GZ10590-1-3-3-2 and GZ10848-1-2-2-1 exhibited the highest values (more than 10 t/ha) compared to GZ10333-9-1-1-3 and GZ10778-17-1-6-1 which gave 8.89 and 8.74 ton ha⁻¹, respectively.

As for grain quality characters; hulling %, milling % and head rice % are presented in Table (4). Concerning hulling %, the rice varieties Korea 27 and Sakha 108 gave the highest values; 83.33 and 83.00 % respectively, while Giza 178, GZ10333-9-1-1-3, GZ10598-9-1-5-5-, GZ10590-1-3-3-2, GZ10717-3-5-1-1- and GZ10778-17-1-6-1 recorded the lowest values.

Most of rice genotypes gave good desirable values of milling except Korea 27 and GZ10686-2-1-3-4 which recorded 69.33 and 69.83%, respectively.

The rice genotypes i.e., GZ10848-1-2-2-1, Giza 178 and Giza 177 recorded the highest values of head rice; 63.67, 63.50 and 63.33%, respectively. On the other hand, GZ10598-9-1-5-5 showed the lowest value of head rice (54.33%).

Table2. Means of	plant height, da	ys to heading an	d number of panicles	plant ⁻¹	of the studied rice	genotypes.
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Constrans	Pla	nt height (cm)	Days	Days to heading(day)			No. of panicles plant ⁻¹		
Genotype	2019	2020	Comb.	2019	2020	Comb.	2019	2020	Comb.	
Giza 177	99.00	98.33	98.67	96.00	85.67	90.83	19.00	19.67	19.33	
Giza 178	100.33	97.00	98.67	104.00	98.33	101.17	23.67	21.67	22.67	
Sakha 101	95.33	89.67	92.50	108.33	103.33	105.83	24.33	21.67	23.00	
Sakha 108	97.00	98.67	97.83	100.33	100.00	100.17	24.67	23.67	24.17	
GZ 10333-9-1-1-3	100.00	91.00	95.50	94.67	87.67	91.07	22.00	18.00	20.00	
Korea 27	101.00	97.33	99.17	98.33	101.33	99.83	24.00	23.00	23.50	
GZ 10101-5-1-1-1	95.00	99.33	97.17	97.33	91.33	94.33	24.00	20.67	22.33	
GZ 10598-9-1-5-5	99.00	100.00	99.50	94.67	89.00	91.83	25.00	22.67	23.83	
GZ 10590-1-1-3-9-1	94.00	96.00	95.00	96.33	91.00	93.67	24.00	22.67	23.33	
GZ 10590-1-3-3-2	97.00	97.67	97.33	97.67	90.33	94.00	21.00	23.67	22.33	
GZ 10631-1-1-2-4	98.00	98.67	98.33	92.67	91.00	91.83	21.00	21.67	21.33	
GZ 10686-2-1-3-4	100.00	100.33	100.17	94.67	90.00	92.33	21.00	23.67	22.33	
GZ 10717-3-5-1-1	98.00	99.67	98.83	93.00	90.33	91.67	22.00	19.67	20.83	
GZ 10778-17-1-6-1	105.00	95.33	100.17	95.00	89.00	92.00	21.00	18.00	19.50	
GZ 10848-1-2-2-1	93.00	91.00	92.00	92.67	90.67	91.67	21.00	20.00	20.50	
LSD at 0.05	1.60	5.25	2.68	1.44	2.71	1.51	1.57	4.14	2.16	

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Table3. Means of yield components of the studied rice genotypes.

Construct	Pan	icle lengt	h (cm)	No. of f	filled grains p	anicle ⁻¹	Grai	Grain yield (ton ha ⁻¹)		
Genotype	2019	2020	Comb.	2019	2020	Comb.	2019	2020	Comb.	
Giza 177	21.23	19.97	20.60	142.70	111.00	126.80	9.18	9.49	9.34	
Giza 178	22.53	24.53	23.53	153.70	134.70	144.20	10.70	10.54	10.62	
Sakha 101	22.27	22.80	22.53	151.70	126.00	138.80	10.03	10.41	10.22	
Sakha 108	23.43	24.53	23.98	161.00	150.00	155.50	11.03	10.83	10.93	
GZ 10333-9-1-1-3	21.70	22.53	22.12	124.00	132.70	128.30	8.66	9.13	8.89	
Korea 27	24.93	23.83	24.38	168.30	142.30	155.30	11.51	10.63	11.07	
GZ 10101-5-1-1-1	22.87	22.83	22.85	130.00	119.30	124.70	9.38	9.50	9.44	
GZ 10598-9-1-5-5	22.77	24.70	23.73	113.70	124.70	119.20	9.28	9.36	9.32	
GZ 10590-1-1-3-9-1	24.10	24.73	24.42	136.70	147.70	142.20	9.33	9.59	9.46	
GZ 10590-1-3-3-2	23.83	25.00	24.42	180.00	152.30	166.20	10.68	10.43	10.56	
GZ 10631-1-1-2-4	21.10	20.83	20.97	118.30	136.30	127.30	8.73	10.24	9.49	
GZ 10686-2-1-3-4	20.13	23.23	21.68	136.00	143.30	139.70	8.56	9.18	8.87	
GZ 10717-3-5-1-1	20.00	21.40	20.70	126.00	114.30	120.20	8.70	9.41	9.05	
GZ 10778-17-1-6-1	19.33	21.23	20.28	123.00	95.70	109.30	8.63	8.86	8.74	
GZ 10848-1-2-2-1	20.93	23.50	22.22	124.00	157.30	140.70	9.98	10.47	10.22	
LSD at 0.05	1.55	1.72	1.13	17.76	14.92	11.34	0.284	0.65	0.351	

Table4.	Means	of grain	quality	characters	of the studied	rice genotypes.
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Construis]	Hulling (%)]	Milling (%)	Head rice (%)		
Genotype	2019	2020	Cob.	2019	2020	Cob.	2019	2020	Cob.
Giza 177	82.33	82.67	82.50	73.00	71.33	72.16	65.67	61.00	63.33
Giza 178	81.00	82.67	81.30	71.33	70.33	70.83	67.00	60.00	63.50
Sakha 101	82.67	83.00	82.83	72.33	72.33	72.33	68.00	53.00	60.50
Sakha 108	83.33	82.67	83.00	72.66	72.33	72.50	67.33	61.00	64.17
GZ 10333-9-1-1-3	82.67	81.00	81.83	73.66	70.33	72.00	66.67	51.00	58.83
Korea 27	83.33	83.33	83.33	71.33	67.33	69.33	63.33	57.00	60.17
GZ 10101-5-1-1-1	83.67	80.33	82.00	73.66	70.33	72.00	67.00	51.00	59.00
GZ 10598-9-1-5-5	83.67	80.00	81.83	72.66	68.00	70.33	61.67	47.00	54.33
GZ 10590-1-1-3-9-1	82.67	79.67	81.16	72.66	67.33	70.00	67.00	51.00	59.00
GZ 10590-1-3-3-2	82.67	80.00	81.33	72.66	70.00	71.33	62.67	58.33	60.50
GZ 10631-1-1-2-4	83.67	80.33	82.00	73.33	67.33	70.33	67.00	64.00	58.50
GZ 10686-2-1-3-4	83.69	81.00	82.33	72.66	67.33	69.83	63.33	57.00	60.17
GZ 10717-3-5-1-1	82.67	80.67	81.66	71.66	71.00	71.83	67.00	63.00	62.00
GZ 10778-17-1-6-1	80.67	83.00	81.83	71.66	72.67	72.16	67.00	60.33	63.67
GZ 10848-1-2-2-1	81.33	82.67	82.00	71.50	72.33	72.00	61.00	53.00	57.00
LSD at 0.05	1.08	1.02	0.804	0.983	1.21	0.762	1.47	1.78	0.56

Estimates of genetic parameters:

Parent's means, estimates of genotypic and phenotypic variance, phenotypic coefficient of variance (PCV%), genotypic coefficient of variability (GCV%), heritability in broad sense and genetic advance % are presented in Table 5. The rice genotypes exhibited a wide range of variability for all studied characters over the two seasons, where mean squares were highly significant. Therefore, the selection could be effective among the rice genotypes for these characters. Similar results were obtained by Sedeek et al. (2009). Data indicated that the phenotypic coefficient of variance was generally higher than genotypic coefficient of variance for all studied traits indicating the environmental influence on the expression of these traits, but the biggest portion of P.C.V was contributed by the genotypic component while the leastby environmental component. The highest phenotypic and genotypic variances were observed in number of filled grains panicle-¹. The phenotypic coefficient of variability averaged 0.99 % for hulling % and 19.35% for grain yield. Similarly, the genotypic coefficient of variability averaged 0.44% for hulling % and 19.24% for grain yield.

Heritability percentage is estimated as the ratio between the genotypic variance and the total of phenotypic variance. Heritability in broad sense was high for most of studied characters expect for hulling percentage that was low (Table, 5). High heritability estimates are useful while, making selection as based on phenotype. High heritability coupled with high genetic advance (Table, 5) was observed for number of filled grains panicle⁻¹ and days to heading. This indicates that selection process for these traits would certainly leads to improvement in the genotypes. Burton (1952),Pratap *et al.* (2018) and Dhakal *et al.* (2020) concluded that genotypic coefficient of variance, together with heritability estimates would give a clear image about the value of advance to be expected from the selection. Thus, the expected gain from selection would be a better indication for selection response. All the traits showed relatively high GCV% with high heritability estimates in broad sense. Accordingly, the genetic advance (GA %) from selection appeared to be effective for these characters. **Insect reaction:**

Results in Table (6) show the reaction of the tested 15 rice genotypes to the rice stem borer, *Chilo agamemnon*. The genotypes differed significantly in their level of resistance to rice stem borer as dead hearts and white heads. The indica rice genotype Korea 27 and indica/japonica rice genotypes i.e., GZ10590-1-3-3-2, GZ10778-17-1-6-1 and GZ10848-1-2-2-1 exhibited the highest values of dead hearts and white heads in both seasons of investigation. By contrast, the japonica rice genotypes showed the lowest values of infestation. The obtained results are in accordance with those found by Bleih *et al.*,(1991), who reported that rice varieties belonging to indica or indica/japonica sub-

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species are more susceptible to rice stem borer infestation than those belonging to japonica one. Resistance of japonica rice varieties to the stem borer could be attributed to its higher silica content than indica types. The high level of silica seemed to interfere with feeding and boring of the rice stem borer larvae and could cause defacing of their mandibles (Djamin and Pathak, 1967).

Table 5. Estimates of phenotypic and genotypic coefficients of variability, heritability and genetic advance for studie
traits in the tested 15 rice genotypes (combined data over 2019 and 2020).

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Trait	Gran mean	MS.G	Ms G Y	MS Error	GV	PV	GCV	PCV	h2	GA	GA (%)
Plant height	97.39	39.32	25.13	5.39	5.11	7.64	2.32	2.83	66.88	3.81	3.91
Days to heading	94.82	127.98	15.82	1.69	20.65	22.10	4.79	4.95	93.43	9.04	9.53
Number of panicles plant ¹	21.93	15.09	6.21	3.52	1.85	2.65	6.20	7.42	69.81	2.34	10.67
Panicle length	22.56	13.18	2.39	0.96	1.99	2.27	6.25	6.67	87.66	2.72	12.05
Number of filled grains panicle ⁻¹	135.90	1458.0	611.08	6.16	225.17	276.60	11.04	12.23	81.40	27.88	20.52
Grain yield	9.75	3.67	0.43	0.09	3.52	3.56	19.24	19.35	99.71	3.87	39.69
Hulling %	82.10	2.16	6.11	0.48	0.13	0.67	0.44	0.99	19.40	0.32	0.38
Milling %	71.26	6.66	7.68	0.43	0.83	1.51	1.27	1.72	54.96	1.39	1.95
Head rice %	59.78	54.73	55.52	0.95	7.44	12.14	4.56	5.82	61.28	4.39	7.34

MS. G= maen square genotype, MS GY= mean square genotype x years, GV= genotypic variance, PV= phenotypic variance, GCV= genotypic coefficient of variability, h2= heritability in broad sense, GA= genetic advance and GA%= genetic advance %.

\mathbf{T}	Table 6.	Susceptibilit	v of rice	genotypes to	the rice stem	borer.	. Chilo agammnoi	n Ble
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Constrans	Dead he	earts (%)		White h	eads (%)	
Genotype	2019	2020	2019	2020	Average	category
Giza 177	3.27	2.69	3.58	2.93	3.26	MR
Giza 178	7.18	7.00	7.39	8.38	7.29	MS
Sakha 101	2.77	2.42	3.24	3.09	3.17	MR
Sakha 108	3.57	4.23	3.96	4.54	4.25	MR
GZ10333-9-1-1-3	2.95	3.45	3.31	3.86	3.59	MR
Korea 27	8.73	10.10	8.50	10.43	9.47	S
GZ10101-5-1-1-1	2.92	2.85	3.39	4.27	3.83	MR
GZ10598-9-1-5-5	7.27	6.85	6.93	8.27	7.60	MS
GZ10590-1-1-3-9-1	5.07	4.35	4.98	5.00	4.99	MR
GZ10590-1-3-3-2	8.58	5.57	8.14	8.27	8.21	MS
GZ10631-1-1-2-4	3.43	2.72	3.63	3.27	3.45	MR
GZ10686-2-1-3-4	3.82	3.49	3.15	3.21	3.18	MR
GZ10717-3-5-1-1	3.03	3.52	3.63	2.59	3.11	MR
GZ10778-17-1-6-1	7.75	8.39	8.87	8.01	8.44	MS
GZ10848-1-2-2-1	7.55	9.10	9.29	9.08	8.65	MS
LSD at 0.05%	1.11	1.31	1.58	1.42		

R :Resistant = 0 - 3%, MR: Moderately Resistant = 3 - 6%, MS: Moderately Susceptible = 6 - 9%,

S: Susceptible = 9 - 12 % and HS: highly susceptible ≥ 12 %.

Race identification of rice blast populations:

Eighteen blast isolates were collected from susceptible cultivars Sakha 101, Sakha 104 and Kanto 51 from six rice growing governorate during 2018 and 2019 seasons. The isolates were identified according to their reaction on international differential varieties to race level. The 18isolates were categorized in four race-groups; one race belonging to group IA, there races to group IC, 11 races as most common to ID group from the total isolates, three races II, as a virulent group, Table (7). Race identification and monitoring play an important role to determine race shifting, whereas, current data indicated that race group ID represent the most common races. In addition, absence of group IB, IF, IG and IH. Race identification and shifting are in agreement with (Sehly *et al.* 2008, EL-Shafey *et al.* 2015 and Kalboush, 2019).

Table 7. Rice blast isolates form different governorates, Egyptian rice cultivars and their race identification	Fable 7.	. Rice blast isolates form differe	ent governorates,	Egyptian rice cultivars a	nd their race identification.
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Governorate	District	Rice cultivar	Year	Race identification
Kafrelsheikh	Fowa	SK 101	2018	IC-3
Gharbia	Qutor	SK 101	2018	IA-3
Beheira	Shobrakhit	SK 101	2018	ID-15
Gharbia	Tanta	SK101	2018	ID-15
Dakahlia	Meet al-korashi	SK 101	2018	II-1
Dakahlia	Meet ghamr	SK 104	2018	IC-11
Gharbia	Tanta	SK 101	2018	ID-15
Kafrelsheikh	Sakha	SK 108	2018	ID-11
Dakahlia	Belkas	SK 101	2018	ID-15
Kafrelsheikh	Sakha	Kanto 51	2018	ID-11
Damietta	KafrSaad	SK 101	2018	II-1
Sharqia	Zagazig	SK 101	2018	II-1
Sharqia	AltalElkabeer	SK 104	2019	IC-9
Kafrelsheikh	Qallin	SK 101	2019	ID-15
Kafrelsheikh	Sakha	SK 101	2019	ID-13
Kafrelsheikh	Alhamra	SK 101	2019	ID-11
Kafrelsheikh	Sakha	SK 104	2019	ID-15
Kafrelsheikh	Sakha	SK 101	2019	ID-16

Resistance level of rice promising lines and virulence divergence of blast populations, brown spot and nematode:

Under natural infection in open field, the results showed highly resistance levels through reactions among tested varieties. All tested promising lines reflected highly resistant reactions (1-2) compared with susceptible check Sakha101 at all locations during 2019 and 2020 seasons, while for brown spot GZ10333-9-1-1-3, Korea 27, GZ10590-1-1-3-9-1 and GZ10590-1-3-3-2, for white tip nematode resistance were Korea 27, GZ10598-9-1-5-5.GZ10590-1-1-3-9-1 and GZ10590-1-3-3-2 (Table 8). Whereas, under artificial inoculation with different races of blast fungus, the resistance levels of promising lines were wide-ranging from 72.22 to 100%, Table (9). Promising lines GZ10101-5-1-1-1, GZ10598-9-1-5-5 and GZ10848-1-2-2-1 performed as completely resistant to all tested isolates (18race), which indicates that these three lines may have new resistance genes. The current data show that these promising lines could be employed as distinctive donors for new blast resistant genes in breeding programs. These results are in agreement with those of EL-Shafey et al. (2015) who identified some completely resistant promising lines with high levels of resistance that could be utilized as R-donors in breeding programs. Comparing resistance pattern of promising lines with reaction of Japanese differential varieties that have identified monogenes under artificial inoculation with same isolates, highly significant difference in resistance reactions among Japanese varieties were recorded. The resistance reaction percentage of Japanese varieties to the 18 race ranged from 22.2 to 100%. Therefore, promising lines that reflected high resistance levels compared to some Japanese varieties may be contributed to carry some of highly effective R-genes such as Pi-i-iks, Pi-km, Pi-b, Pi-z (Table 10). In contrast, Pi-ksas ineffective gene in the last years showed complete resistance reaction with100 % against tested races. Out of these results, changes of Pi-ks reaction from highly susceptible as in Sakha 101 to complete resistant reflected high level of race shifting. The current results are in agreement with those of Sehly et al. (2008), found that the resistant genes (Pi-a and Pi-ks) exhibited low levels with 20 and 31 %, respectively, while higher levels of Pi-b, Pi-k and Pi-m genes with 90, 85 and 80 %, respectively. In addition, EL-Shafey et al., (2015) they found that cultivars, Giza 177, Giza 178, still record complete resistance and some promising lines as full matching with current results. So, these varieties could be used as resistant resources to broaden the genetic background (El-Refaee, 2011).

For Virulence variation of blast populations: Each individual isolate was inoculated on fifteen of rice varieties to determine virulence level. The virulence level of tested isolates on promising lines ranged from 6.7 to 33.3 % as a common virulence reaction. So, changes of virulence levels could explain the breakdown of some rice cultivars due to pathogenic variability and wide range of blast fungus mutation. So, understanding changes in the pathogen population and pathogenic variation of *M. oryzae* is critical in overcoming the constraints that many rice breeding techniques face, (Shahriar et al., 2020).

Table 8. promising lines reaction under field conditions against rice diseases

Conotuno	*Blast	score	*Brown s	pot Severity	White tip Nematode Severity (Number infected leaves/m ²						
Genotype	2019	2020	2019	2020	2019	2020					
Giza 177	1	1	10.67	8.00	3.00	6.00					
Giza 178	1	1	1.33	1.00	1.00	1.00					
Sakha 101	5	5	1.00	1.00	1.00	1.00					
Sakha 108	1	1	1.33	1.00	30.00	31.67					
GZ10333-9-1-1-3	2	2	1.33	1.00	26.00	27.00					
Korea 27	3	3	1.33	1.00	1.00	1.00					
GZ10101-5-1-1-1	2	1	11.00	6.67	60.00	72.33					
GZ10598-9-1-5-5	2	1	1.67	1.00	1.00	1.00					
GZ10590-1-1-3-9-1	2	1	1.33	1.00	1.00	1.00					
GZ10590-1-3-3-2	2	1	1.33	1.00	1.00	1.00					
GZ10631-1-1-2-4	1	1	2.67	2.00	32.33	37.33					
GZ10686-2-1-3-4	1	1	20.67	15.67	1.00	1.00					
GZ10717-3-5-1-1	2	1	10.67	8.00	3.67	5.00					
GZ10778-17-1-6-1	2	1	5.33	4.00	2.00	2.00					
GZ10848-1-2-2-1	2	1	1.33	1.00	1.00	1.00					
LSD at 0.05%			1.449	2.060	4.233	2.397					

* = test at 3 locations as mean (Sakha, Gemmiza-Zarzoura) 1-2 = resistant (R), 3 = moderately resistant (MR), 4-6 = susceptible (S), 7-9 = highly susceptible (HS)

Table 9. Promising lines reaction under artificial inoculation against18rice blast race

Isolate no./race identification/ reaction																			
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	Resistance
Variety	IC-3	IA-11	ID-15	1D-15	П-1	IC-11	ID-15	D-11	ID-15	ID-11	II-1	II-1	IC-9	ID-15	ID-13	D-11	ID-15	D-1 6	%
Giza 177	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	100
Giza 178	1	1	1	1	1	1	1	1	1	1	1	2	1	1	2	1	1	1	100
Sakha 101	4	5	6	5	4	4	7	4	6	4	6	7	1	4	4	5	5	6	5.56
Sakha 108	1	1	1	1	1	1	1	4	1	1	1	1	4	1	1	1	1	1	88.89
GZ10333-9-1-1-3	1	1	1	1	1	1	1	1	1	4	1	2	1	1	1	1	1	1	94.44
Korea 27	1	5	1	1	1	2	6	4	1	1	1	1	5	1	1	1	4	1	72.22
GZ10101-5-1-1-1	1	1	1	1	1	1	3	1	1	1	1	2	1	1	1	1	1	1	100
GZ10598-9-1-5-5	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	100
GZ10590-1-1-3-9-1	1	4	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	94.44
GZ10590-1-3-3-2	1	1	1	1	1	1	1	4	4	1	1	3	1	1	4	1	4	4	72.22
GZ10631-1-1-2-4	7	4	1	1	1	1	1	4	1	1	1	4	4	1	1	1	1	1	72.22
GZ10686-2-1-3-4	1	1	1	1	1	4	1	4	1	1	1	4	1	1	4	1	1	1	77.78
GZ10717-3-5-1-1	1	4	1	1	1	1	1	4	1	1	1	4	4	1	1	1	1	1	77.78
GZ10778-17-1-6-1	1	1	1	1	1	1	1	4	1	1	1	4	1	1	4	1	1	1	83.33
GZ10848-1-2-2-1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	3	2	100
Virulence %	13.3	33.3	6.7	6.7	6.7	13.3	13.3	44.4	13.3	13.3	6.7	33.3	16.7	6.7	26.7	6.7	20.0	13.3	

IDV/8	Target	Isolate no./ reaction														Resistance				
JD V.	gene	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	%
Shin2	Pi-ks	1	1	1	1	1	2	1	1	1	1	1	2	1	1	2	1	4	1	94.4
Toride1	Pi-zt	6	1	6	1	1	1	4	6	4	1	1	4	4	5	4	1	4	1	44.4
Tusyake	Pi-km	1	1	1	1	1	6	1	9	1	4	1	1	1	1	4	1	1	1	77.7
Kanto51	Pi-k	6	1	1	1	1	6	1	9	1	4	1	1	1	1	1	4	4	1	66.6
Fukunishiki	Pi-z	1	1	1	1	1	1	1	2	1	1	1	2	1	2	3	1	1	1	100
Ishikari Shiroke	Pi-I &ks	1	2	1	1	1	2	2	2	1	1	1	1	1	1	2	1	2	1	100
BL-1	Pi-b	3	2	4	1	1	2	2	2	1	1	2	2	1	5	3	4	1	1	94.4
Yashiro Mochi	Pi-ta	1	5	8	1	1	1	6	5	5	1	1	3	3	6	3	4	5	1	55.5
Pi No.4	Pi-ta2	1	5	1	5	1	2	7	5	5	1	1	5	5	6	5	4	7	1	38.8
Aichi Asahi	Pi-a	1	6	4	6	1	5	6	7	6	4	1	6	6	8	6	1	7	4	22.2
Virulence %		20	30	40	20	0	30	40	60	40	30	0	30	30	50	40	40	60	10	

Table 10. Japanese differential varieties (JDV) reaction under artificial inoculation to 18 rice blast race

Principal components analysis (PCA):

Principal component analysis as main Multivariate technique was utilized to determine relative contribution of each variable in genetic divergence and explain patterns of variation in agronomic attributes with economic importance, in addition to explain variance associated with each variable (Hair *et al.*1987and Sedeek *et al.*, 2012).

The first two principal components were significant and recorded 80.4% of the total variance of all characters (Table 11 and Fig. 1B). While PC1, PC2 and PC3 explained 31.8, 52.5 and 63.6%, of the multivariate variation among genotypes showing the highest values 4.7, 3.1 and 1.6, these values could measure the explained variance associated with variable, (Table11).

Table 11. Principal component (PC) analysis of
characters associated with 15 rice genotypes
showing Eigen values and proportion
variation associated with the first PC axes and
Eigen vector of characters.

Variable	PC1	PC2	PC3	PC4
Eigenvalue	4.7729	3.1055	1.66	1.6128
Proportion	0.318	0.207	0.111	0.108
Cumulative	31.8	52.5	63.6	74.3
Panicle length (PL)	0.382	0.146	-0.018	0.301
Filledgrains panicle ⁻¹ (NFGP)	0.359	0.019	0.091	0.068
Plantheight (PH)	-0.127	0.131	0.644	-0.022
Days to heading (DTH)	0.362	-0.255	0.071	-0.081
No.of panicles plant ⁻¹ (NPP)	0.338	0.027	0.182	0.401
Grain yield plant ⁻¹ (GY)	0.425	-0.023	0.019	-0.101
Hulling (Hul%)	0.157	-0.271	0.245	-0.144
Milling (Mil%)	-0.097	-0.325	-0.369	-0.304
Head rice %	0.007	-0.261	0.336	-0.421
Dead heart %	0.175	0.401	0.01	-0.405
White head %	0.235	0.407	-0.036	-0.283
Blast	0.202	-0.406	-0.077	-0.146
Brown spot	-0.279	-0.09	0.446	0.067
White tip nematode	-0.094	-0.192	-0.104	0.402



A- Rice genotypes

PC1 gave higher loading to grain yield plant⁻¹, panicle length, days to heading, filled grains panicle⁻¹ and No. of panicles plant⁻¹, while PC2 gave higher relative attributes to biotic stress, blast and stem borer (dead heart, white heads).

In addition, PC3 reflected higher values to plant height as an important character of vegetative stage in breeder selection, beside brown spot, milling % and head rice %. On the other side, PC4 was dominated by white tip nematodes, which have a significant direct effect on growth and yield loss of cultivars. Grain yield plant⁻¹, filled grains panicle⁻¹; plant height; panicle length; biotic stress factors such as blast, stem borer and white tip nematode are the most important traits in variation of genotypes. Each genotype was grouped at a principal component score on each axis based on different traits (Brown, 1991). Sakha101and Sakha108 were grouped together based on their grain yield, Milling, head rice %, and low infection of stem borer, whereas, some varieties were grouped based on their reaction to biotic stress (Fig.1A). Each character was an important source of variations(Sedeek et al. 2012).Giza 177, Giza 178, Sakha 108, GZ10590-1-1-3-9-1, GZ10598-9-1-5-5, GZ10101-5-1-1-1 were grouped and clearly allocated to distinctive groups in the PCA separated from all genotypes which suggesting more variance from the other genotypes based on their reaction to blast, brown spot, white tip nematode and desirable agronomic traits (Fig. 1 A and B). Therefore, these genotypes could be used as good sources for improving high yield traits and biotic stress resistance, (Abdel-Salam et al. 2010 and EL-Shafey et al. 2015).



B- Agronomic and biotic stress characters



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التنوع الوراثي والمقاومة للحشرات والامراض لبعض سلالات الأرز المبشرة مرفت محمد عوض الله عثمان' ، أحمد سمير طه' وعبدالعزيز محمد طاحون' 'قسم بحوث الأرز-معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية تقسم بحوث أمراض الأرز – معهد بحوث أمراض النباتات- مركز البحوث الزراعية