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Efficiency of Yellow Rust Resistance Genes *Yr5, Yr10, Yr15* and *YrSp* in Improving the Two Egyptian Bread Wheat Cultivars Sids 12 and Gemmeiza 11

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A FIELD and greenhouse study was conducted at Sakha Agricultural Research Station during 2015-2020 wheat seasons to enhance stripe rust resistance of the two Egyptian bread wheat cultivars Sids 12 and Gemmeiza 11 using the four monogenic lines *Yr5*, *10*, *15* and *Sp*. The two wheat cultivars were crossed to the four monogenic lines to obtain eight F_1 hybrids then selfed to produce F_2 populations and selected F_3 families. In the field, parents, F_1, F_2, F_3, and differential genotypes were inoculated with a mixture of predominating pathotypes of the wheat stripe rust pathogen *Puccinia striiformis* f. sp *tritici* (*Pst*). Evaluation of the monogenic lines indicated that wheat genotypes carrying *Yr5* and *Yr15*, at both seedling and adult plant stages exhibited high resistance to the *Pst* races. F_1 field response confirmed that the four tested *Yr* genes are effective against the tested stripe rust races and resistant reaction is dominating over susceptibility. Segregation ratios of the eight F_2 crosses indicated that the cultivars differ in three, two, or one genes with the monogenic lines. Average coefficient of infection recorded the lowest mean values for F_2 crosses with *Yr5* and *Yr15* in both cultivars indicating that the two genes shifted the F_2 population means toward resistance more than *Yr10* and *YrSp*. Efficacy of the four genes can be arranged in the following order *Yr5 >Yr15 >YrSp >Yr10* with the Sids 12 background and *Yr5 >Yr15 >Yr10 >YrSp* with the Gemmeiza 11 background. Out of the tested 63 F_3 families, the highest percentage of completely resistant plants were recorded with the *Yr5* crosses (35-40%) followed by *Yr10* cross (34%) with Gemmeiza 11 and then the *Yr15* cross (26%) with Sids 12. Two of the F_3 families from *Yr5* crosses were phenotypically closer to the recipient cultivars that were completely resistant and hence may have *Yr5* gene in homozygous state. The promising resistant lines derived from both cultivars will be evaluated for yield and quality characteristics during the next season. Based on our results, pyramiding combinations of the three effective genes *Yr5*, *Yr10* and *Yr15* in one wheat background is expected to enhance resistance for the dominating stripe rust races in Egypt.

Keywords: Wheat, Breeding, Stripe rust, *Yr5*, *Yr10*, *Yr15* and *YrSp* genes, Resistance.

Introduction

Wheat (*Triticum aestivum* L.) is the most widely grown and consumed cereal food crop over all the world as well as Egypt. The Egyptian wheat production is not enough for domestic consumption and the gap between production and consumption reached to 50% (Kishk et al., 2019). Egypt's wheat production for the marketing year 2020-21 is 8.9 million tons while, the country's consumption of wheat is 20.1 million tons. Therefore, Egypt's wheat imports for the 2020-21 market year are forecast at 12.85 million tons (USDA Economics, Statistics

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and Market Information System). Increasing total wheat production could be possible via increasing the wheat cultivated area but there are many challenges specially water shortages. Therefore, developing new cultivars having high yield potential is the best and available option to decrease the gap. Releasing new high yielding and stress resistant wheat cultivars is the main goal of the national breeding program. Biotic and abiotic stresses are becoming more and more challenges to wheat production due to narrow genetic base and climate changes (Muleta et al., 2017; Prank et al., 2019). Therefore, a need to develop more stress tolerant cultivars has become crucial to sustain wheat production or even to increase stagnant yields.

Rusts are the most damaging fungal diseases affecting wheat worldwide. Yellow (or stripe) rust caused by *Puccinia striiformis* Westend f. *sp. tritici* (*Pst*) is the major foliar disease of wheat, resulting in yield loss all over the world (Chen, 2014). The seriousness of stripe rust pathogen is in the ability of the pathogen for mutation, rapid generation turnover accelerating the development of races and ability to spread over distance of hundreds of kilometers. In recent years, severe stripe rust epidemics have occurred in major wheat producing countries causing significant yield losses (Wellings, 2011; Hu et al., 2020). Yield losses due to stripe rust have been reported ranging from 10% to 70% and up to 100% in extreme conditions. The calculated yield loss due to stripe rust varied among genotypes and locations with an overall range from 12.7-87% (Bolat & Altay, 2007). In Egypt, stripe rust attacked many commercial wheat cultivars causing severe infection in North Delta Area (El-Daoudi et al., 1996). The distribution of rust resistant cultivars has been the most economical and environmentally cautious strategy to control rust diseases. Genetic resistance is the most economic and environmentally friendly methodology to protect crops from damage due to biotic factors such as stripe rust (Chen, 2005). Identifying new sources of resistance to the disease is necessary (Singh et al., 2005; Shahin et al., 2018). A significant step toward a better control of the strip rust is the identification of genes controlling this disease (Hussain et al., 1999). Studying inheritance of rust resistance is very important for improving wheat rust resistance. In terms of its genetic basis, resistance can be single or major gene, oligogene (i.e. controlled by a few genes with large effects), or polygene (multiple minor gene), where resistance is controlled by a larger number of genes, each with a small effect (McIntosh et al., 1995; Zakeri et al., 2016). Hussain et al. (2011) and Shahin & Ragab (2015) reported that additive, dominance and epistasis were involved in the expression of genes for yellow rust resistance in wheat. Kaur & Bariana (2010) reported three genetically independent genes for adult plant resistance to stripe rust in some Australian wheat cultivars.

The two bread wheat cultivars Sids 12 and Gemmeiza 11 are the most popular cultivars in Egypt, especially for small farms. The reason for farmers preference for those cultivars is due to its good bread making quality (Mahrous et al., 2009, Sadek et al., 2013; Ragab, & Mohamed, 2014). Area cultivated with both cultivars reached 25% of total wheat area in the 2015/2016 season (Economic Affairs Section, Ministry of Agriculture and Land Reclamation, Egypt, 2016). Unfortunately, both Sids 12 and Gemmeiza 11 became susceptible to stripe rust disease and great yield loss occurs every year if infection discovered late and chemical control is not applied in the proper time. Incorporating yellow rust effective genes into the two cultivars is the most efficient method to control the disease and reduce yield losses (Singh et al., 2005). *Yr5*, *Yr10*, *Yr15*, and *YrSp* are the most effective resistance genes against predominating races of *Pst* in Egypt (Shahin, 2017, 2020). The objective of this study was to examine the efficiency of incorporating the four stripe rust resistance genes *Yr5*, *Yr10*, *Yr15* and *YrSp* in improving resistance of the two rust susceptible bread wheat cultivars Sids 12 and Gemmeiza 11.

Materials and Methods

Experimental site and plant materials

This investigation was carried out at the experimental farm of Sakha Agricultural Research Station, Egypt, during five wheat growing seasons from 2015 to 2020. Two Egyptian bread wheat cultivars; Sids 12 and Gemmeiza 11 were provided by Wheat Research Department, Field Crops Research Iinstitute, Agricultural Research Center (ARC), Egypt. Both Avocet S and four stripe rust monogenic lines (*Yr5*, *Yr10*, *Yr15* and *YrSp)* were provided by the International Center of Agricultural Research in Dry Areas (ICARDA). The identification of *Pst* races was done in the greenhouse of Wheat Diseases Research Department, Plant Pathology Research Institute (PPRI), Agricultural Research Center (ARC), Egypt.

Production of inbred lines

Two *Yr* inbred lines populations of the two cultivars were produced to evaluate them through individualizing its genes in *Yr* susceptible background (Avoset S). The two Egyptian bread wheat cultivars Sids12 and Gemmeiza11 were crossed to the wheat line Avocet S, a strip rust susceptible selection from Australia (McIntosh et al., 1995), during the winter season of 2015 to produce two F_1 hybrids. During summer of 2015 (off season), the two F_1 hybrids were sown to produce F_2 seeds. Single seed dissent procedure was used during the following seasons, 2016-2018, to have two inbred line populations for the two crosses (Sids 12/Avocet S and Gemmeiza 11/Avocet S), 85 F_5 lines for the first cross and 118 F5 lines for the second, respectively. In 2018/2019 season each F_5 line was presented by one row, 2m long. The two populations were surrounded by the highly susceptible spreader wheat cultivar (Morocco) to get a uniform spread of stripe rust inoculum of the pathogen (*Pst*).

Crossing and field evaluation

During the 2016/2017 season, the two Egyptian bread wheat cultivars and the four *Yr* monogenic lines were sown in three planting dates to synchronize flowering. Each parent was planted in two rows; 2.5m long in each planting date. The two wheat cultivars (stripe rust susceptible parents) were crossed to the four resistant parents carrying the genes *Yr5*, *Yr10*, *Yr15*, and *YrSp* to generate F_1 seeds. In the 2017/2018 season, the F_1 seeds of each cross were sown in rows of 2.5m long and 30 cm apart and spaced widely at 30 cm apart in order to allow for the production of the large number of F_2 seeds and the F_1 seeds were reproduced by crossing the parents.

In the 2018/2019 season all materials were collected and sown in a field experiment. The eight F_1's, F_2's and their six parents were arranged in randomized complete block design with three replications. The two parents, F_1 and F_2 of each cross were planted in rows 4 m long, 30 cm apart and 20 cm between plants. Each plot consisted of 19 rows (one for each for P_1, P_2 and F_1 and 16 for F_2). The experimental field was surrounded by the highly susceptible spreader wheat cultivar (Morocco) to get a uniform spread of *Pst* inoculum. The stripe rust responses of all F_2 plants, were recorded at the adult plant stage using a Modified Cobb's scale (Peterson et al., 1948). Resistant F_2 plants that are closer in phenotype to the commercial cultivars Sids12 and Gemmeiza11 from each corresponding cross were tagged and seed samples were harvested. In the 2019/2020 season, a total of 63 F_3 families were sown in the field. Each F_3 family was planted one row (15 plants). The field was surrounded by the highly susceptible spreader wheat cultivar (Morocco) to get a uniform spread of *Pst* inoculum.

Inoculation and field response to stripe rust

Twenty five *Pst* pathotypes were identified in Egypt during 2016 to 2020 (Table 1). Virulence of these *Pst* pathotypeson *Yr* genes ranged from zero 0E0 to 13 genes (159E255) at seedling stage in the greenhouse test (Table 1). A mixture predominating *Pst* pathotypeswas used to inoculate the plants in the field of F_1, F_2 and F_3, including the parents, *Yr* differential and near-isogenic lines, and susceptible check Avocet S.

The inoculation of spreader row plants was carried out at wheat booting stage according to the method of Tervet & Cassel (1951). The responses of all the tested wheat genotypes to the *Pst* pathotypes, were recorded at the adult plant stage using a Modified Cobb's scale (Peterson et al., 1948; Roelfs et al., 1992) methods. In this method, immune, resistance, moderately resistance, moderately susceptible and susceptible infection types (IT) were symbolized as 0, R, MR, MS and S, respectively. Plants having 0, R, and MR infection types were pooled together and considered as resistant, while plants with MS and S infection types were considered as susceptible ones. The yellow rust reaction (severity and infection type) was recorded at the adult stage of the tested plants when the flag leaf reaction of the susceptible control rust severity reached 100S. For quantitative analysis, field response was converted into an average coefficient of infection (ACI) following the method proposed by (Saari & Wilcoxson, 1974). ACI obtained by multiplying infection severity by an assigned constant values namely, 0.0, 0.2, 0.4, 0.8 and 1 for 0, R, MR, MS, and S infection types, respectively.

TABLE 1. Virulence patterns of *Puccinia striiformis* f. sp. tritici races detected in Egypt from 2016 to 2019

Pathotype†	Virulence on *Yr* genes	Percentage of *Yr* genes		Frequency %			
		R‡	S	2016	2017	2018	2019
0E0	-	100.0	00.00	24.44	20.00	16.66	26.67
0E16	*8*	94.12	05.88	0	0	5.00	0
2E16	*7,8*	88.24	11.76	6.67	0	3.33	6.67
4E130	*6,(7),2*	82.35	17.65	0	0	6.67	0
6E4	*7,6,(6)*	82.35	17.65	15.55	10.90	0	0
34E16	*7,Sd,8*	82.35	17.65	0	7.27	0	0
64E0	*Su*	94.12	05.88	0	0	13.33	11.11
64E16	*Su,8*	88.24	11.76	6.67	0	11.67	0
66E0	*7,Su*	88.24	11.76	0	0	6.67	0
70E20	*7,6,Su,(6),8*	70.59	29.41	6.67	0	0	0
70E32	*6,7,Su,Cv*	76.47	23.53	0	0	10.00	0
70E182	*7,6,Su,(7),(6),8,Cv,2*	52.94	47.06	0	9.10	6.67	0
70E214	*7,6,Su,(7),(6),8,Sp,2*	52.94	47.06	0	5.45	0	11.11
74E16	*7,3,Su,8*	76.47	23.53	0	3.64	0	0
78E16	*7,6,3,Su,8*	70.59	29.41	0	5.45	0	0
104E137	*3,Sd,Su,4,(3),2*	64.71	35.29	0	9.10	0	0
106E139	*7,3,Sd,Su,4,(7),(3),2*	52.94	47.06	0	9.10	0	0
106E166	*7,3,Sd,Su,(7),(6),Cv,2*	52.94	47.06	6.67	0	0	0
128E28	*9,(6),(3),8*	76.47	23.53	11.10	0	0	13.33
130E20	*7,9,(6),8*	76.47	23.53	0	7.27	0	0
134E242	*7,6, 9, (7),8,Cv, Sp, 2*	52.94	47.06	**0**	**0**	**0**	13.33
150E244	*7,6,10,9,(6),8,Cv,Sp,2*	47.05	52.94	6.67	0	0	0
151E244	*1,7,6,10,9,(6),8,Cv,Sp,2*	41.17	58.83	6.67	0	0	0
159E255	*1,7,6,3,10,9,4,(7),(6),(3),8,Cv,Sp,2*	17.65	82.35	2.22	5.45	5.00	0
250E254	*7,3,10,Sd,Su,9,(7),(6),(3),8,Cv,Sp,2*	23.53	76.47	6.67	0	6.67	17.78
450E214	*7,Su,9,5,(7),(6),8,Sp,2*	47.05	52.95	0	7.27	8.33	0

† Refer to Johnson et al. (1972) for pathotype nomenclature, and ‡R= resistance, S= susceptible.

Genetic and statistical analysis

Genetic analysis based on the reaction data of F_1's, F_2's plants and the parents to infection was used for determining the number of genes for resistance. Chi-squire test (χ^2) was used to test significance of difference between observed and expected ratios in F_2 populations for yellow rust reaction according to Little & Hills (1978). The ratio of resistant versus susceptible plants in segregating populations was used to determine the mode of inheritance and the number of resistance genes each two parents differ in. The frequency distributions values were computed for parental, F_1 and F_2 plant populations for stripe rust infection type and severity under field conditions. Field response of F_2 plants were divided into 9 classes, i.e. 0, 10R, 10MR, 40MR, 10MS, 40MS, 10S, 40S, and 100S. Some genetic parameters were estimated based on ACI, i.e. means (of parents, F_1 and F_2), environmental variance VE= [(VP1 + VP_2 + VF_1)/3], phenotypic variance VP= V F_2 and genotypic variance VG= VP – VE (Allard 1960). In addition, broad sense heritability (h^2b)= VG/VP × 100 (Falconer & Mackay, 1996), the expected genetic advance at 5% selection intensity (Δg%) = (k × $(VP)^{0.5}$ × h^2b)/×¯) (Allard, 1960) and genotypic coefficient of variation (GCV)= [$(VG)^{0.5}$/F_2 mean) × 100] (Singh & Naraynan, 2000) were estimated.

Results and Discussion

Responses of wheat genotypes carrying stripe rust resistance genes

The wheat genotypes (48) including differential hosts and near-isogenic lines to *Pst* pathotypes showed a wide range of rust responses during 2017 to 2019 growing seasons (Table 2). In most cases, the adult plant reaction was different from the seedling reaction. While, wheat genotypes carrying *Yr5* and *Yr15*, at both seedling, and adult plant stages exhibited high resistance to *Pst* pathotypes (Table 2). *Yr1*, *Yr17*, *Yr32* and *YrSp* became ineffective to the new race, 159E255. These genes were known to be resistant to the previously characterized races. The genotypes with *Yr5*, *Yr10* and *Yr15* had 0-type or R-type reaction, showing immune or resistant against the pathogen populations at the three growing seasons under field conditions. The genotypes with *Yr2*, *Yr6*, *Yr7*, *Yr9*, *YrSu* and *YrA* were susceptible. On the other hand, the genotypes with *Yr29*, *Yr18* and Anza (*YrA+Yr18*) were moderately susceptible.

Filed response of inbred line populations

The data of evaluated two inbred line populations under field condition were arranged in 9 categories starting from zero to 100S reaction (Fig. 1). Both populaions showed high infection for stripe rust at adult plant stage indicating that both cultivars have no effective resistance genes against the stripe rust races in the used inoculm. More than 75% of lines in both poplations showed susceptability reaction. Sids12/Avocet S inbred lines population tested lines showed a percentage of 77% suceptible: 23% resistant while Gemmeiza 11/Avocet population showed a percentage of 80% suceptible: 20% resistant. This result indicate that both cultivars (Sids 12 and Gemmeiza 11) having simillar genetic constitution against the tested stripe rust races. The percentage of resistant lines may be attributed to a type of gene interaction. In addition, DNA characterization by specific markers indicated the presence of *Yr9, Yr18* and absence of *Yr 17* in Sids 12 and Gemmeiza11 cultivars (Abu Aly et al., 2014).

Field responses of the parents and F_1

Adult plant field response to stripe rust for Sids12 and Gemmeiza11 cultivars, the four *Yr* monogenic lines and their eight F_1 crosses during 2017/2018 season are presented in Table 3. Both cultivars showed susceptibility in the field while the three *Yr* monogenic lines *Yr5*, *Yr10* and *Yr15* showed resistance reaction and *YrSp* monogenic line showed moderate type (MR-MS). All the eight F_1`s showed resistant type field reaction even the cross between Sids 12 and *YrSp*. Whereas, F_1 cross between Gemmeiza 11 and *YrSp* showed moderate resistant type. These results indicated that the four tested genes are effective against the tested stripe rust races and resistant reaction is dominating over susceptibility one.

F_2 populations field response

Over 200 F_2 plants from each cross were scored for stripe rust (Table 4). F_2 populations segregated for stripe rust resistance. The Chi-squared tests revealed that the segregation data gave a good fit for segregation at three, two or one independent loci (Table 4). The test confirmed the previous result from F_1 of dominating resistant reaction over susceptibility in all crosses except the cross Gemmeiza 11//*YrSp*/6* Avocet S, it was the opposite. Segregation ratios of the Sids12 crosses indicated that the cultivar differ in two genes with the monogenic lines carrying *Yr5, 10* and *Sp* while it differ in three genes with the line carrying *Yr15* gene. The observed ratios fitted the theoretical expected ratios, 15:1, 11:5, 11:5 and 57:7, respectively (Table 4). On the other hand, the segregation ratio of Gemmeiza 11 crosses indicated that the cultivar differ in two genes with the monogenic lines carrying *Yr15* or *YrSp* and in three genes and one gene with lines carrying *Yr5* (57:7) or *Yr10* genes (3:1), respectively. The difference of segregation ratios indicate that there were different types of epistatic interactions (Table 4). Resistance to stripe rust is controlled by partial dominance or recessive with certain crosses (Anpilogova, 1983), or by complementary genes (Chen, 2007; Dracatos et al., 2016). Moreover, Xianming & Roland (1992) indicated that some cultivars may include two genes for resistance to stripe rust, one was dominant and the other was recessive gene, while Kaur & Bariana (2010) reported three genetically independent genes for adult plant resistance.

Parents, F_1's and F_2's Population mean and variance based on ACI values were used to estimate some genetic parameters (Table 5). The F_2 ACI mean values for the crosses between each cultivars with both *Yr5* and *Yr15* recorded the lowest values indicating the two genes (*Yr5* and *Yr15*) shifted the F_2 population mean toward resistant more than the other two genes (*Yr10* and *YrSp*). These results indicate that both *Yr5* and *Yr15* are more effective for improving resistance to the dominating stripe rust races under this study (Tables 1, 5). Variance estimates; environmental (VE), phenotypic (VP) and genotypic (VG) variances ranged from 3.0, 217.2 and 208.7 to 11.1, 1285.7 and 1274.6, respectively. Broad sense heritability (h^2b) estimates ranged from 95.8 for the cross Gemmeiza 11//*Yr5*/6*Avocet S to 99.6 for the cross Sids 12//*Yr10*/6*Avocet S. The genetic advance from selection (Δg%) ranged from 2.8 for cross Gemmeiza 11//*YrSp*/6*Avocet S to 7.9 for cross Sids 12//*Yr15*/6*Avocet S. The highest genetic coefficient of variation estimates were recorded for the crosses with both *Yr5* and *Yr15* monogenic lines. The variance and its components and related parameters were investigated by many researchers and their results were in line with obtained here (Ragab, 2005, 2010; Shahin & Ragab, 2015; Aglan et al., 2020).

Efficiency of the Yr genes

Frequency distribution of yellow rust reaction as infection type and severity in the F_2 populations of the studied crosses are illustrated in Fig. 2. Out of the four used genes, the frequency distribution indicated that the two genes *Yr5* and *Yr15* were the most effective genes. Percentage of resistant plants of Sids 12 and Gemmeiza 11 F_2 populations were 92% and 89% for *Yr5* and 90% and 84% for *Yr15*, respectively. Efficiency of the gene *Yr10* came in the second order where it produced 76% and 65% resistant plants of the F_2 populations with the two cultivars Sids12 and Gemmeiza11, respectively. Meanwhile, the efficiency of *YrSp* gene differed with the background where it was more effective in the F_2 population of the cross with Sids12 than with Gemmeiza11, percentages of resistant plants were 71% and 47%, respectively. Efficiency of the four genes can be arranged in the following order *Yr5 >Yr15 >YrSp >Yr10* with Sids12 background and *Yr5 >Yr15 >Yr10 >YrSp* with Gemmeiza11 background. Abu Aly et al. (2014) in Egypt, reported that the seven monogenic lines *Yr1, Yr5, Yr10, Yr15, Yr17, Yr32* and *YrSp* exhibited high levels of resistance to both 198E56 and 128E28 races at seedling stage and showed adult plant resistance under field condition. Whereas, those with *Yr17* and *YrSP* showed a disease severity ranged between 5MR to 10MR. On the other hand, the first report of *Pst* virulence to *YrSp*, *Yr1* and *Yr3* was reported in North Africa (Hovmoller et al., 2016) and some Asian countries (Hovmoller et al., 2017; Mert et al., 2016).

Out of the three monogenic lines (*Yr5*, *Yr10* and *Yr15*), *Yr5* was more effective to produce plants having zero infection type, about 60% of the F_2 population of both Sids 12 and Gemmeiza 11. On the other hand, *Yr15* was more effective to produce such plants with Sids12 than Gemmeiza 11; 54% and 42%, respectively. Only about 35% of the F_2 populations with *Yr10* produced plants with zero infection type. These findings are in agreement with those reported by (Zhang et al., 2001; Shahin & Ragab, 2015; Kokhmetova et al., 2010, 2017).

F_3 families field response

A total of 63 resistant F_2 plants that are closer in phenotype to the commercial cultivars Sids 12 and Gemmeiza 11 were selected (Table 6). In 2019/2020 season, the F_3 families were presented by 815 plants in the field, out of them 227 plants were scored to have zero infection type (27%). Fortunately, one family from each cross of both cultivars with *Yr5* showed no segregation (all plants are resistant). Both families are considered promising as expecting to have *Yr5* (have zero infection type) and phenotypically closer to the commercial cultivar. Out of the tested F_3 plants, the highest percentage of zero infection type plants were recorded with *Yr5* crosses in both cultivars (35.4-40.4%) followed by *Y10* then *Yr15* crosses for Gemmeiza11and Sids12, 33.8% and 25.6%, respectively. Continues selection and evaluation for stripe rust and grain yield for the selected resistant F_4 plants will be conducted during the 2020/2021 season to identify resistant homozygous lines for each of *Yr10* and *YrSp* genes.

Conclusion

The four strip rust resistant genes *Yr5, Yr10, Yr15* and *YrSp* were effective against the dominating *Pst* races in Egypt. Moreover, the two genes *Yr5* and *Yr15* showed complete resistance at both seedling and adult plant stages. Therefore, pyramiding combinations of these genes in one wheat background is expected to enhance resistance for stripe rust in Egypt.

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TABLE 2. Wheat genotypes used in trap nursery, their resistance genes, severity and IT's produced by yellow rust from 2017 to 2019

No.	Host genotype	Yr gene(s)[a]	Response to Pst pathotypes[b]				
			Seedling		Adult		
			Old pst (6E4)	New pst (159E255)	2017	2018	2019
1	Avocet 'S'	-	9	9	40S	50S	80S
2	Avocet 'R'	YrA	3	8	30S	40S	60S
3	Yr1/6*Avocet S	Yr1	0;	8	0	0	TrR
4	Yr5/6*Avocet S	Yr5	0	2	0	0	0
5	Yr6/6*Avocet S	Yr6	9	9	60S	70S	70S
6	Yr7/6*Avocet S	Yr7	9	9	50S	70S	80S
7	Yr8/6*Avocet S	Yr8	2	9	10MSS	40MSS	40MSS
8	Yr9/6*Avocet S	Yr9	3	8	50S	70S	60S
9	Yr10/6*Avocet S	Yr10	0	7	0	0	0
10	Yr15/6*Avocet S	Yr15	0	0	0	0	0
11	Yr17/6*Avocet S	Yr17	2	6	40MSS	50MSS	60MSS
12	Yr18/6*Avocet S	Yr18	3	7	5MSS	30MSS	50MSS
13	Yr27/6*Avocet S	Yr27	3	7	10MSS	20MSS	20MS
14	Yr32/6*Avocet S	Yr32	2	6	5S	10S	20S
15	YrSP/6*Avocet S	YrSp	0;	7	0	TrS	5S
16	Chinese 166	Yr1	0	7	0	0	5S
17	Lee	Yr7	9	9	20S	50S	60S
18	Heine's Kolben	Yr6+1	7	9	10MSS	20MSS	20S
19	Vilmorin 23	Yr3a,4a	3	5	5R	20MR	30S
20	Moro	Yr10,	0	2	0	0	0
21	Strubes Dickopf	YrSd	1	4	TrR	5R	20MS
22	Suwon 92/Omar	YrSu	2	6	TS	10S	20S
23	Clement	Yr9,2+?	3	8	5MR	20MR	20MS
24	Hybrid 46	Yr4	2	9	0	0	30MR
25	Reichersberg 42	Yr7+?	9	9	0	20MS	20MS
26	Heine's Peko	Yr6+?	9	9	5R	10MSS	20MSS
27	Nord Desprez	YrNd	2	6	0	5MR	30MR
28	Compare	Yr8	1	7	5MS	10MS	20MS
29	Carstens V	Yr32	0;	8	TrR	TrR	TrS
30	Spalding Prolific	YrSp	0	8	5S	5S	5S
31	Heines VII	Yr2+?	1	8	TR	TR	30MR
32	Spaldings Prolific	YrSp	2	7	TS	TS	TS
33	Federation4/Kavkaz	Yr9	3	9	10MS	20MSS	20S
34	Trident	Yr17	5	9	50MS	30MSS	10S
35	Anza	YrA,18	3	7	10MS	10MS	20MS
36	Kalyansona	Yr2	2	9	20MSS	20MSS	10MSS
37	Triticum spelta album	Yr5	0	2	0	0	0
38	TP1295	Yr25	0	9	20S	20S	30S
39	Jupateco 'R'	Yr18+	3	8	5MS	50MS	80MSS
40	Fielder	Yr6,Yr20	9	9	30S	40S	40S
41	Lemhi	Yr21	3	8	20S	50S	50S
42	LalBahadur/Pavon BL	Yr29	3	8	TMS	20MS	30MS
43	Opata 85	Yr27,Yr18	3	7	10MSS	30MSS	30MSS
44	Ciano 79	Yr27	3	7	20MSS	50MSS	40MS
45	Yr28/Avocet	Yr28	2	9	30S	50S	60S
46	Pavon 76	Yr29,Yr30	2	7	10MS	30MS	30MS
47	Pastor	Yr31,APR	1	8	5MS	20MS	30MS
48	Morocco	-	9	9	80S	90S	90S

[a]Resistance genes based on the studies of Chen (2005).; [b]ITs based on Roelfs et al. (1992)., 0= Immune. R= Resistant (necrosis with few uredinia); MR= Moderately resistant (necrosis with small to moderate number of uredinia); MS= Moderately susceptible (moderate number of uredinia with chlorotic areas); and S= Susceptible (large number of uredinia, no necrosis but chlorosis may be evident).

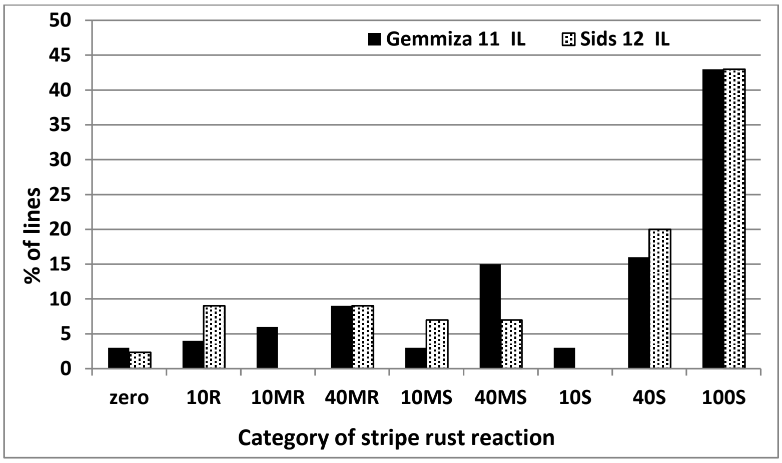

Fig. 1. Yellow rust reaction during 2018/2019 growing season for the two inbred line (IL) populations Gemmeiza 11/Avocet S and Sids 12/Avocet S developed by wheat research section at Sakha Agricultural Research Station

TABLE 3. The adult plant field response to stripe rust under field condition for the two Egyptian bread wheat cultivars Sids 12 and Gemmeiza 11, four monogenic lines and their eight F_1 crosses in 2017/2018 season

Cross name	Adult plant field response to stripe rust‡		
	P_1	P_2	F_1
Sids12//*Yr5*/6* Avocet S	S	R	R
Sids12//*Yr10*/6* Avocet S	S	R	R
Sids12//l*Yr15*/6* Avocet S	S	R	R
Sids12//*YrSp*/6* Avocet S	S	MRMS	R
Gemmeiza11//*Yr5*/6* Avocet S	S	R	R
Gemmeiza11//*Yr10*/6* Avocet S	S	R	R
Gemmeiza11//*Yr15*/6* Avocet S	S	R	R
Gemmeiza11//*YrSp*/6* Avocet S	S	MRMS	MR

‡ R= resistance, MR= Moderately resistance, MS= Moderately susceptible and S= Susceptible.

TABLE 4. Adult plant response for stripe rust, observed hypothetical ratios, Chi-square and probability values for nine wheat F_2 populations inoculated with *Pst* under field conditions during 2018/2019

Cross	No. of plants			Ratio	χ^2	P value	Number of genes and mode of inheritance†
	Resistant	Susceptible	Total				
Sids12//*Yr5*/6* Avocet S	214	19	233	15 : 1	1.44	0.23	2D
Sids12//*Yr10*/6* Avocet S	170	93	263	11 : 5	2.07	0.15	1R, 1D
Sids12//*Yr15*/6* Avocet S	266	30	296	57 : 7	0.20	0.66	3D
Sids12//*YrSp*/6* Avocet S	226	92	318	11 : 5	0.80	0.37	1R, 1D
Gemmeiza11//*Yr5*/6* Avocet S	218	28	246	57 : 7	0.02	0.89	3D
Gemmeiza11//*Yr10*/6* Avocet S	172	54	226	3 : 1	0.15	0.70	1D
Gemmeiza11//*Yr15*/6* Avocet S	178	35	213	13 : 3	0.75	0.39	1R, 1D
Gemmeiza11//*YrSp*/6* Avocet S	110	122	232	7 : 9	1.27	0.30	2R

†D = dominant and R = recessive. Interpretation for some ratios can be found in Fasoulas (1980).

TABLE 5. Genetic parameters based on average coefficient of infection (ACI) for yellow rust of eight wheat crosses

Cross	ACI Mean				Variance			h^2b%	Δg%	GCV
	P_1	P_2	F_1	F_2	VP	VE	VG			
Sids12//Yr5/6* Avocet S	50	0.05	0.4	3.68	217.2	8.4	208.8	96.1	7.9	393.0
Sids12//Yr10/6* Avocet S	50	0.05	0.05	14.53	717.8	3.0	714.8	99.6	3.8	184.1
Sids12//lYr15/6* Avocet S	50	0.05	0.05	5.49	345.6	3.0	342.6	99.1	6.9	336.9
Sids12//YrSp/6* Avocet S	50	4.00	2.00	12.91	648.1	8.1	640.0	98.8	4.0	196.0
Gemmeiza11//Yr5/6* Avocet S	40	0.05	0.05	5.34	247.0	10.3	236.6	95.8	5.8	287.9
Gemmeiza11//Yr10/6* Avocet S	40	0.05	1.00	9.4	526.5	10.5	516.0	98.0	4.9	241.7
Gemmeiza11//Yr15/6* Avocet S	40	0.05	0.05	5.65	252.4	10.3	242.0	95.9	5.6	275.4
Gemmeiza11//YrSp/6* Avocet S	40	4.00	2.00	26.33	1285.7	11.1	1274.6	99.1	2.8	135.6

† P_1= Susceptible cultivar P_2= Yr monogenic line, VP, VE and VG= Phenotypic, environment and genetic variance, respectively, h^2b = Broad sense heritability, Δg% = The expected genetic advance under selection, GCV = Genotypic coefficient of variation.

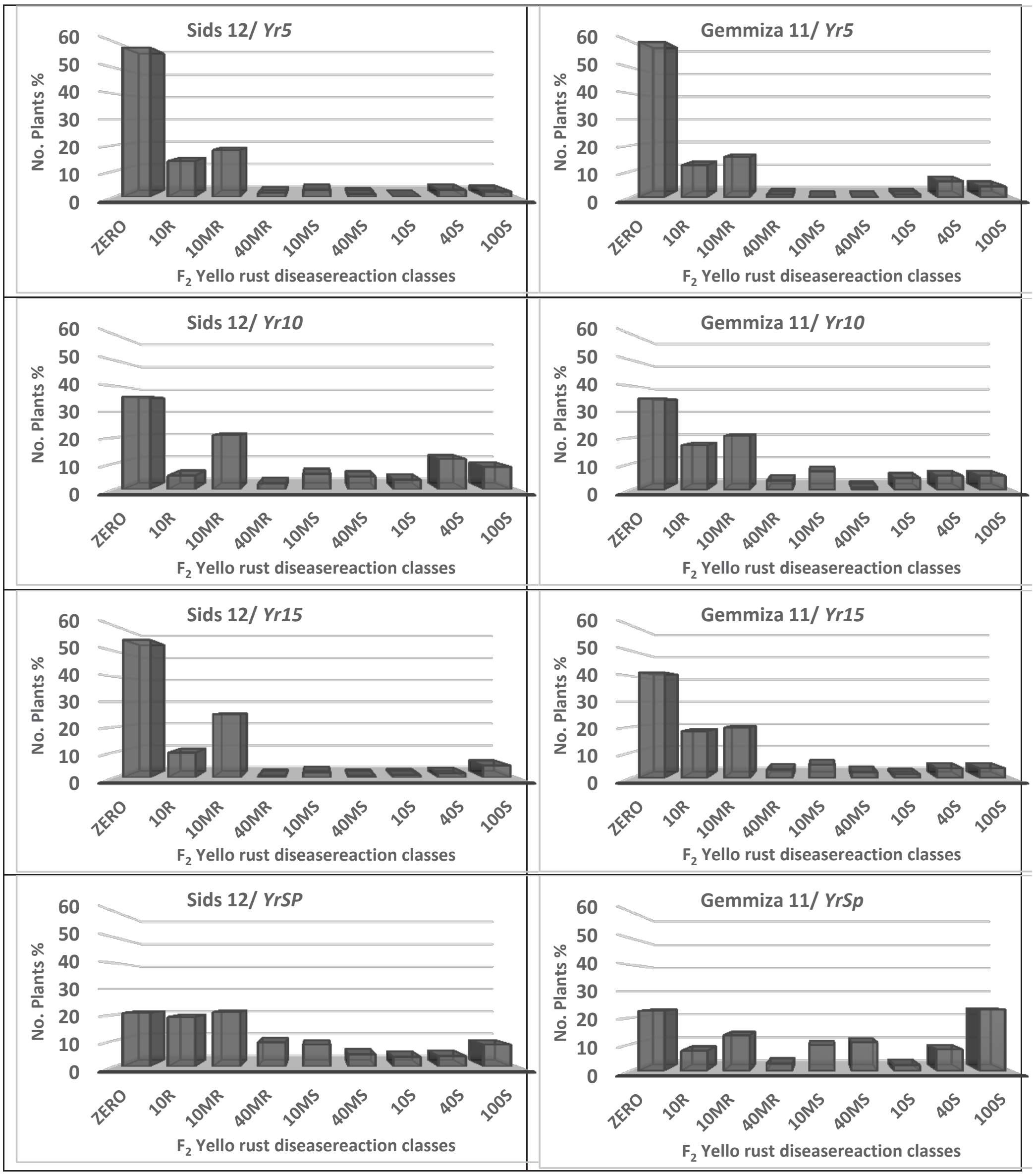

Fig. 2. Yellow rust reaction of the four F_2 crosses for both Sids 12 and Gemmeiza 11 wheat cultivars with the four monogenic lines *Yr5, Yr10, Yr15*, and *YrSp* during 2018/2019 growing season

TABLE 6. Number of selected resistant plants from F_3 families of the crosses between Sids12 and Gemmeiza11 with four monogenic lines during the wheat growing season 2019/2020

Cross name	No. of planted F_3 families+	Total no. of plants	No. of selected zero type plants++	No. of non-segregating zero type families	Percentage of zero type plants/cross (%)	Percentage of zero type plants/ cultivar (%)
Sids12//*Yr5*/6* Avocet S	10	141	57	1	40.4	29.1
Sids12//*Yr10*/6* Avocet S	3	47	10	0	21.3	
Sids12//l*Yr15*/6* Avocet S	5	78	20	0	25.6	
Sids12//*YrSp*/6* Avocet S	10	115	24	0	20.9	
Gemmeiza11//*Yr5*/6* Avocet S	10	99	35	1	35.4	26.7
Gemmeiza11//*Yr10*/6* Avocet S	5	71	24	0	33.8	
Gemmeiza11//*Yr15*/6* Avocet S	10	136	29	0	21.3	
Gemmeiza11//*YrSp*/6* Avocet S	10	128	28	0	21.9	
Total	63	815	227	2	-	

+ Selected F_2 plants are resistant to strip rust and phenotypically similar to the commercial cultivar; ++The selected F_3 plants have the same reaction like the monogenic line (zero type).

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كفاءة جينات المقاومة للصدأ الاصفر *Yr5* و *Yr10* و *Yr15* و *YrSp* فى تحسين صنفي قمح الخبز المصرى سدس 12 وجميزة 11

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أجريت هذه الدراسة في صوبة الصدأ الأصفر والمزرعة البحثية لمحطة البحوث الزراعية بسخا خلال الفترة من عام 2015 إلى 2020 وذلك لتحسين صفة المقاومة للصدأ الأصفر في صنفي قمح الخبز المصريين سدس 12 وجميزة 11. حيث استخدمت السلالات أحادية الجين التي تحتوي على جينات المقاومة للصدأ الأصفر *Yr5* و *Yr10* و*Yr15* و *YrSp*. تم إجراء التهجين بين صنفي القمح والأربعة سلالات أحادية الجين للحصول على الحبوب الهجينية للجيل الأول لثمانية هجن ومن ثم إنتاج حبوب الجيل الثاني ثم الانتخاب لعائلات الجيل الثالث. تم إجراء العدوي للتراكيب الوراثية المدروسة بسلالات المسبب المرضي السائدة فى مصر. أوضحت نتائج تقييم السلالات الأحادية الجين كفاءة كلا من *Yr5* و*Yr15* فى مقاومة سلالات المسبب المرضي السائدة بمصر وذلك في مرحلتي البادرة والنبات البالغ . أكدت استجابة هجن الجيل الأول أن الجينات الأربعة المختبرة فعالة ضد السلالات السائدة لمرض الصدأ الأصفر بمصر وأن المقاومة سائدة على القابلية للإصابة. أوضحت نسب الانعزال في الجيل الثاني إلى أن الأصناف والسلالات أحادية الجين تختلف في جين أو جينين أو ثلاثة جينات ، كما سجلت هجن الجيل الثاني مع كل من *Yr5* و *Yr15* مع كلا الصنفين اقل قيم لمتوسط معامل الإصابة (ACI) مما يشير إلى أن كلا الجينين قد أحدثا إزاحة لمتوسط العشيرة تجاه المقاومة أكثر من كل من الجين *Yr10* والجين *YrSp*. ويمكن ترتيب كفاءة الجينات الأربعة في خلفية الصنف سدس 12 بالترتيب *Yr5>Yr15>YrSp>Yr10* وفى خلفية الصنف جميزة 11 بالترتيب *Yr5>Yr15>Yr10>YrSp*. من بين نباتات الـ 63 عائلة من عائلات الجيل الثالث التي تم اختبارها كانت أعلى نسبة من النباتات التي أظهرت مقاومة (صفر إصابة) لهجن *Yr5* (35-40%) تليها هجن Yr10 (34%) مع الصنف جميزة 11 ثم *Yr15* (26%) مع الصنف سدس 12 والتي يمكن استخدامها فيما بعد في برنامج التربية. تم الحصول على عائلتين من عائلات الجيل الثالث لهجن *Yr5* مع كلا الصنفين والتي كانت أقرب في مظهرها للصنف ، مع عدم وجود انعزال بها (جميع النباتات مقاومة) والتي من المحتمل أن تكون حاملة لجين المقاومة *Yr5* بحالة أصيلة وبالتالي يمكن استخدامها كسلالات محسنة من الصنفين. وسوف يتم تقييم هاتان العائلتان في موسم القمح القادم لصفات المحصول والجودة. استنادًا إلى نتائج الدراسة فان من المتوقع أن تجميع الجينات الثلاثة الفعالة *Yr5* و *Yr10* و *Yr15* في خلفية قمح واحدة يؤدي إلى تحسين مقاومة القمح لسلالات الصدأ الأصفر السائدة في مصر.