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INHERITANCE OF STEM RUST RESISTANCE AT ADULT PLANT STAGE IN SOME EGYPTIAN WHEAT CULTIVARS

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ABSTRACT

Genetic nature of stem rust resistance was studied in seven parental wheat cultivars, i.e. Misr-1, Misr-2, Gemmeiza-11, Gemmeiza-12, Shandaweel-1, Giza-171 and Sakha-94 and their F_1 and F_2 crosses, at Kafr El-Hamam Agricultural Research Station (Sharkyia Governorate), Egypt. Qualitative analysis of the obtained data, showed that the observed ratios, fitted the expected ratios 1:15, 3:13, 9:7, 3:1, 13:3, 1:3 and 7:9 for the aforementioned seven crosses, respectively. Therefore, stem rust resistance in the tested wheat cultivars found to be a simple inherited trait, as it was controlled by only one or two gene pairs in most cases, at adult plant stage. While, quantitative analysis revealed that partial dominance effects being more pronounced in it's genetic expression. Also, the heritability in it's broad-sense was, generally, high (ranged from 79.5 to 96.3%), indicating that the selection for stem rust resistant genotypes in early generations was possible. While, delaying it to the late generations is more effective, due to the importance of dominance effect, in the expression of this trait. Thus, plant breeder should not rely on the host pedigree only, but they should put the pathogen genotype and environment in their considerations, as the two important variables in the pathogen: host: environment systems.

Key words: ***Wheat, Puccinia graminis, Stem rust resistance, Gene action, Heritability, No. of genes.***

INTRODUCTION

Wheat (*Triticum aestivum* L.) is widely cultivated in Egypt and worldwide, as a stable food. Wheat stem rust caused by *Puccinia graminis* f. sp. *tritici* is one of the most important rust diseases of wheat, resulting in high yield losses and reduced grain quality of the susceptible wheat cultivars especially in the late sowing dates (Macharia and Wanyera 2012 and Ashmmawy *et al* 2013). Accordingly, the use of resistant cultivars, offers the most effective and ecologically sustainable method, for controlling this serious disease. Subsequently, incorporating resistance genes to the pathogen into adapted germplasms, is a major goal in most wheat resistance breeding programms.

Breeding for stem rust resistance in wheats is remained a feasible and the most effective method for improving, not only the level of cultivar resistance, but also the yield potentiality of the local wheat cultivars. A fully and good understanding of the mode of inheritance and genetic behavior of the desired characters is of great importance for formulating a successful and an effective breeding program. Genetic analysis has been extensively used to determine gene action and system controlling the quantitatively inherited characters (Abd El-Hamid 2013, Moustaffa 2013 and Khaled and Abd El-Dayem 2014). Host-genetic resistance can be classified into two main categories, *i.e*. qualitative resistance, conferred by a single resistance gene, also termed as a major gene resistance (MGR) and race specific resistance. While, quantitative resistance governed by several numbers of minor genes for resistance, with additive effect. Also called, adult plant resistance (APR), race non-specific, slow-rusting resistance and partial resistance (PR) (Kou and Wang 2010).

The inheritance of stem rust resistance in wheat genotypes defined by some authors, is a simple inherited trait governed by one, two, or few gene paris (Abd El-Latif and Boulot 2000 and Nzuve *et al* 2013). Meanwhile, others suggested that, it is a quantitative triat, controlled by several minor genes with additive effects, as well as the effect of enviromental conditions (Navabi *et al* 2005). Stem rust resistance was dominant over susecptiblity in the majority of host-pathgen interactions, but the reverse was true in some cases (Nzuve *et al* 2013). In addition, high and good progress in selection for disease resistance could be achieved, since genetic control was predominantly additive. Due to the high estimates of heritability in it's broad sense, selection of advanced genotypes, having desired characters in early generations could be possible, but delaying it to the late generations, would be more fruitful. (Shehab El-Dine *et al* 1991 and Hermas and El-Sawi 2015). Moreover, resistance of stem rust was dominant over susceptibility in the majority of host-pathogen interactions, but the reserve was true in the others (Shehab El-Dine *et al* 1991 and Nzuve *et al* 2013). The genetic behavior and mode of inheritance for stem rust resistance in breeding wheat genotypes, is of great impotance, as the main prerequisites for planning a seccessful breeding programm, that aims to maximize the genetic improvement of this resistance.

Accordingly, the main objective of this investigation was to study the inheritance of stem rust resistance in seven parental wheat cultivars. In addition, to give useful information about the genetic behavior, mode of inheritance and number of corresponding gene pairs controlling stem rust resistance in wheat cultivars.

MATERIALS AND METHODS

This investigation was carried out at Kafr El-Hamam Agricultural Research Station (Sharkyia Governorate), Egypt, to study the inheritance of stem rust resistance in seven Egyptian wheat cultivars, *i.e*. Misr-1, Misr-2, Gemmeiza-11, Gemmeiza-12, Shandaweel-1, Giza-171 and Sakha-94. The pedigree and year of release of the parental cultivars, are presented in Table (1). The crosses were represented by seven crosses between the highly susceptible variety; Morocco, and each of the tested cultivars. All cultivars were grown at three different sowing dates in 2013/2014 season. The grains were harvested and kept for growing F_1 plants in the next season (2014/2015). F_1 grains were planted in rows of 4 m long and 30 cm apart and spaced 30 cm, in order to allow production of F_2 seeds.

Table 1. **Pedigree of wheat cultivars, used in genetic analysis, year of release and their stem rust reaction, under field conditions.**

No.	Cultivar	Pedigree	Year of release	Stem rust reaction
1	Misr-1	OASIS/SKAUZ//4*BCN1312*PASTOR.CMSSOOYO1881T-050M-030Y-030M-030WGY-33M-0Y-0S.	2011	Susceptible (S)
2	Misr-2	SKAUZ/BAV92. CMSS96M03611S-1M-010SY-010M-010SY-8M-0Y-0S.	2011	Susceptible (S)
3	Gemmeiza-11	BOW"S" /KVZ"S"// 7C/SERI82/3/GIZA168 /SKHA61. GM7892-2GM-GM-2GM-1GM-0GM.	2011	Resistant (R)
4	Gemmeiza-12	OTUS/3/SARA/THB//VEECMSS97Y00227S-5Y-010M-010Y-010M-2Y-1M-0Y-0GM	2011	Resistant (R)
5	Shandaweel-1	SITE/MO/4NAC/TH.AC//3*PVN/3/MIRLO/BUC/CMSS93B00567S-72Y-010Y-010M-3Y-0M-0HTY-0SH	2011	Moderately resistant (MR)
6	Giza-171	SAKHA 93 / GEMMEIZA 9S.6-1GZ-4GZ-1GZ-2GZ-0S	2013	Moderately susceptible (MS)
7	Sakha-94	OPATA/RAYON//KAUZ. CMBW90Y3180-OTOPM-3Y-010M-010M-010Y-10M-015Y-0Y-0AP-0S.	2004	Moderately susceptible (MS)

In the third season (2015/2016), seeds of the seven parents, F_1 and F_2 plants were sown as single seed for each, inspected individually to estimate distribution frequencies of their disease reaction, under field conditions. All materials were surrounded by 1.5 m belt, served as a spreader of the highly susceptible entries, *i.e*. “Morocco and *Triticum spleta saharences”*. The spreader plants were artificially inoculated, using a mixture of physiological races, in addition to the natural infection. The inocula (urediniospore mixtures) were obtained from stem rust greenhouse in Wheat Diseases Research Department, Plant Pathology Research Institute, ARC, and mixed with talcum powder at the rate of 1:20 (w:w) (Tervet and Cassel 1951). Data were recorded as the percentage of stem rust severity for each plant.

Frequency distributions of stem rust severity (%) were computed for parents, F_1 and F_2 populations, under field conditions. The mode of inheritance, goodness of fit of the observed ratio to the expected ratio of the phenotypic classes, concerning the stem rust severity (%) and infection types, were determined by χ^2 analysis (Steel and Torrie, 1960). Moreover, the minimum number of effective genes, controlling resistance, were detemined by the formula of Wright (1968) as follows:

$N = D^2/8(VF_2 - VF_1)$

Where:

N = Minimum number of effective genes.

$D = \bar{P}_1 - \bar{P}_2$ (the different between the mean response of the two parents).

VF_1 = Variance of F_1.

VF_2 = Variance of F_2.

Degrees of dominance were calculated according to the method suggested by Romero and Frey (1973). In this method, the degree of dominance symbolized as h_1 and h_2 for F_1 and F_2, respectively, were calculated by the following formula:

$h_1 = (\bar{X}\,F_1 - \bar{X}\,MP)/D$ and $h_2 = 2(\bar{X}\,F_2 - \bar{X}MP)/D$

Where:

$D = (\bar{X}\,h_p - \bar{X}\,MP)$

$\bar{X}\,F_1$, $\bar{X}\,F_2$ and $\bar{X}\,h_p$ are the means of F_1, F_2 and high parent, sequently, while $\bar{X}$ MP is the mid-parent value.

In addition, the F_1 and F_2 means were compared with mid-parent value, using t test to determine whether h_1 and h_2 values were significantly different from zero.

Heritability in it's broad-sense was estimated according to the formula of Lush (1949) as follows:

$h^2 = V_G/V_P \times 100$.

Where:

h^2 = broad- sense heritability.

V_G = genotypic variance of F_2 individuals.

V_P = phenotypic variance of F_2 individuals.

V_E = environmental variance estimated from variation with the non-segregating populations, *i.e.* parents and F_1 plants.

RESULTS AND DICUSSION

The present study included seven Egyptian wheat cultivars, having different levels of stem rust severity (%), as well as 7 F_1's and 7 F_2's, obtained from a half diallel crosses between these cultivars and the highly susceptible variety; Morocco. The obtained data are subjected to qualitative and quantitative genetic analysis.

1. Qualitative analysis:

The qualitative analysis of the obtained data was carried out according to the response of the tested parents, F_1 and F_2 populations, against stem rust pathogen at adult plant stage, under field conditions. Data presented in Table (2) and Figs. (1 and 2), indicate that the wheat variety;

Morocco, consistently expressed high susceptibility to stem rust, with disease severity ranged from 60 to 80%. While, the seven wheat parents showed diversity levels of stem rust resistance, as they exhibited different rust severity percentages; ranged from 0 to 80%.

Table 2. Stem rust frequency distribution of seven F_1 and F_2 crosses, among Morocco and each of the tested wheat cultivars, as well as their respective parents, evaluated under artificial inoculation with *P. graminis* f.sp. *tritici*, under field conditions during 2015/2016 season.

Cross name	No. of tested plants		Rust severity (%) classes							
			Resistant (R)			Susceptible (S)				
			0-10%	11-20%	21-30%	31-40%	41-50%	51-60%	61-70%	71-80%
Misr-1 x Morocco	P_1	43							9	34
	P_2	31							14	17
	F_1	46							27	19
	F_2	186	4	10	0	44	24	43	31	30
Misr-2 x Morocco	P_1	40						14	26	
	P_2	39							16	23
	F_1	37							18	19
	F_2	254	8	14	23	12	34	54	42	67
Gemmeiza-11 x Morocco	P_1	36	17	19						
	P_2	44							31	13
	F_1	43	32	11						
	F_2	237	87	43	11	16	20	22	23	15
Gemmeiza-12 x Morocco	P_1	34	12	22						
	P_2	41							17	24
	F_1	53	42	11						
	F_2	222	32	59	78	14	13	7	10	9
Shandaweel-1 x Morocco	P_1	54		31	23					
	P_2	39							23	16
	F_1	51	42	9						
	F_2	229	76	57	48	9	11	8	14	6
Giza-171 x Morocco	P_1	46				17	29			
	P_2	49							34	15
	F_1	39				16	23			
	F_2	204	22	14	12	56	33	43	9	15
Sakha-94 x Morocco	P_1	37				22	15			
	P_2	43							32	11
	F_1	47				15	32			
	F_2	218	36	28	27	32	27	43	18	7

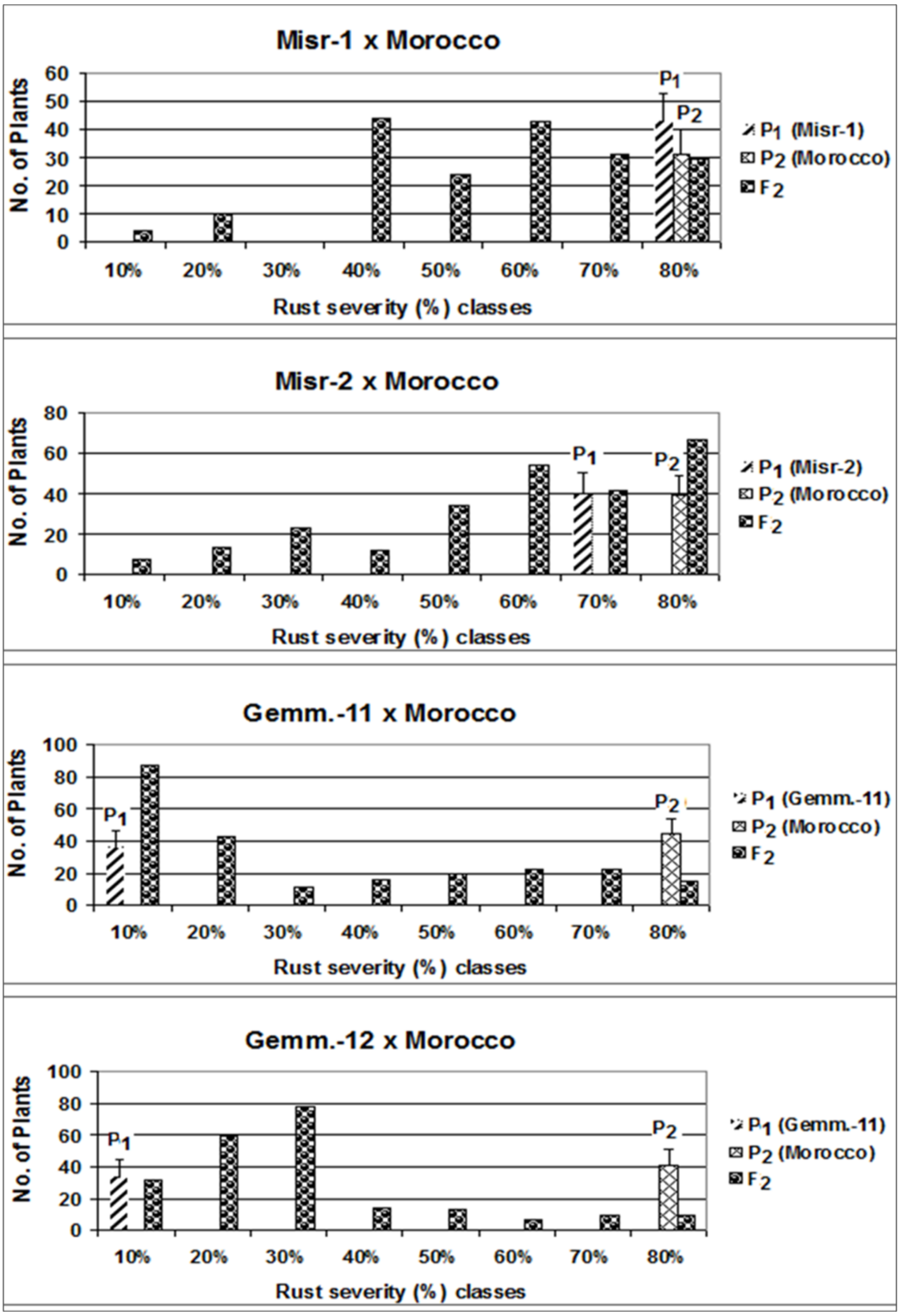

Fig. 1. Frequency distribution of stem rust severity (%), to four wheat crosses (P_1, P_2 and F_2), among Morocco and each of Misr-1, Misr-2, Gemmeiza-11 and Gemmeiza-12, inoculated with *P. graminis* f.sp. *tritici*, under field conditions.

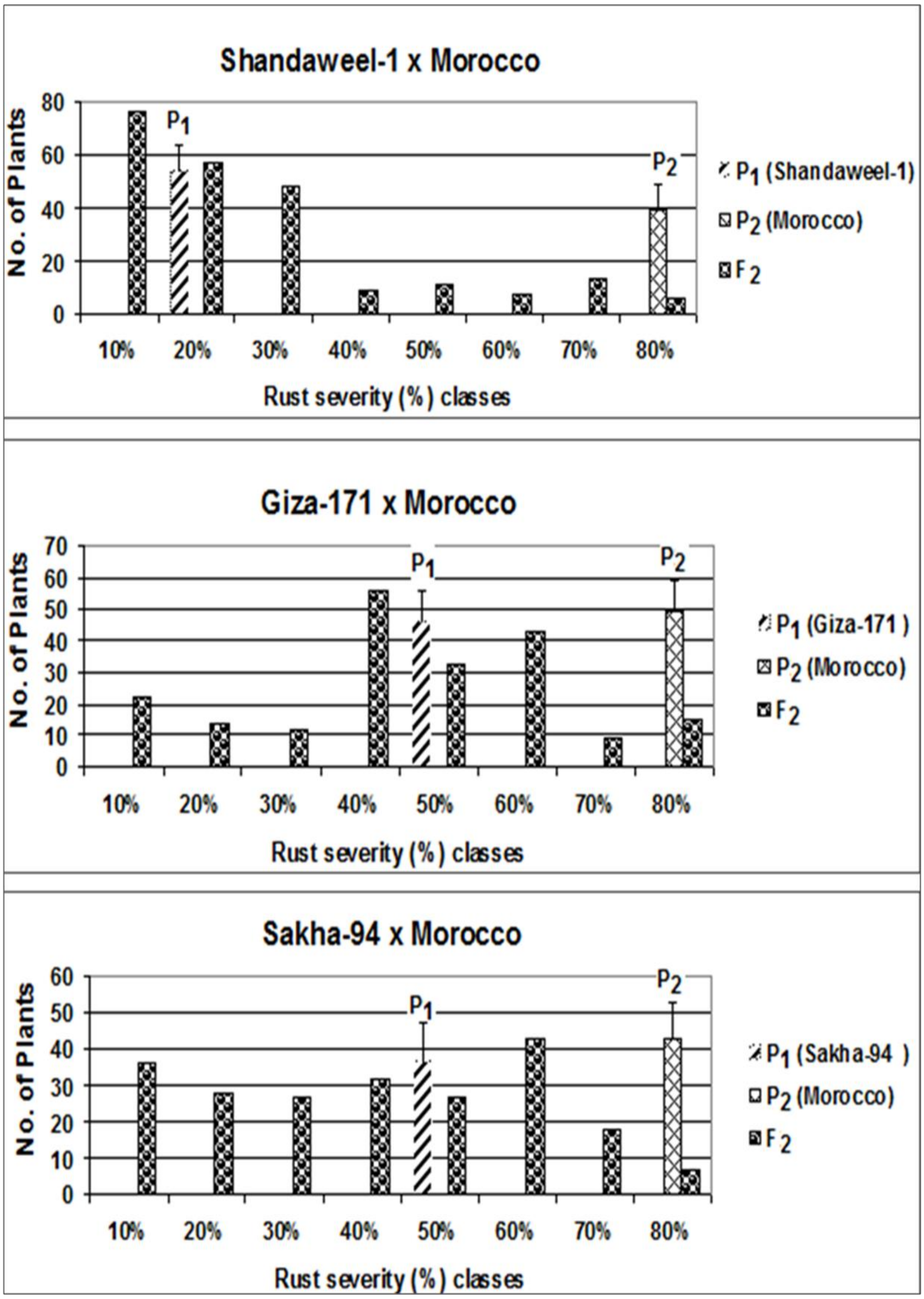

Fig. 2. Frequency distribution of stem rust severity (%), to three wheat crosses (P_1, P_2 and F_2), among Morocco and each of Shandaweel-1, Giza-171 and Sakha-94, inoculated with *P. graminis* f.sp. *tritici*, under field conditions.

In addition, the disease severity (%) of the F_1 plants ranged from 60-80%, for the two crosses, *i.e.* Misr-1 x Morocco and Misr-2 x Morocco, indicating that high disease severity (susceptible reaction) was partially dominant, over low disease severity (resistance). On the other hand, the disease severity (%) of F_1 plants for the other crosses; Gemmeiza-11 x Morocco, Gemmeiza-12 x Morocco, Shandaweel-1 x Morocco, Giza-171 x Morocco and Sakha-94 x Morocco were; 0 to 20%, 0 to 20%, 0 to 20%, 30 to 50% and 30 to 50%, respectively. Accordingly, these results gave an indication to the partial dominant of the low disease severity, *i.e.* resistance over the high disease severity (susceptibility).

The frequency distribution of the disease severity (%) of F_2 plants for the seven crosses, under study, was ranged from 0 to 80%. Similar results were reported by Padidam and Kontt (1988), Ageez and Boulot (1999), Boulot and Gad-Alla (2007) and Nzuve *et al* (2013).

In addition, the observed number of plants with R : S stem rust severity were; 14:172, 45:209, 141:96, 169:53, 181:48, 48:156 and 91:127, for the seven crosses, *i.e.* Misr-1 x Morocco, Misr-2 x Morocco, Gemmeiza-11 x Morocco, Gemmeiza-12 x Morocco, Shandaweel x Morocco, Giza-171 x Morocco and Sakha-94 x Morocco, respectively. These observed ratios, fitted the expected ratios; 1:15, 3:13, 9:7, 3:1, 13:3, 1:3 and 7:9 for the aforementioned seven crosses, respectively (Table, 3).

Table 3. Stem rust severity phenotypic classes of F_2 plants in seven crosses, inoculated with *P. graminis* f.sp. *tritici*, at adult plant stage, under field conditions in 2015/2016 season.

No.	Cross name	Phenotype		Expected ratio	χ 2	P^b
		R	S			
1	Misr-1 x Morocco	14	172	1:15	0.517	0.50 – 0.25
2	Misr-2 x Morocco	45	209	3:13	0.178	0.75 – 0.50
3	Gemmeiza-11 x Morocco	141	96	9:7	1.013	0.50 – 0.25
4	Gemmeiza-12 x Morocco	169	53	3:1	0.254	0.75 – 0.50
5	Shandaweel-1 x Morocco	181	48	13:3	0.436	0.75 – 0.50
6	Giza-171 x Morocco	48	156	1:3	0.235	0.75 – 0.50
7	Sakha-94 x Morocco	91	127	7:9	0.357	0.75 – 0.50

R = Resistant and S = Susceptible

P^b values higher than 0.05 indicated that no significance of χ 2

This result suggested the operation of only one or two interacting gene pairs, governing stem rust resistance in each cross, under study. Therefore, it could be concluded that stem rust resistance in wheat plants is a simple inherited trait, controlled by a few number of stem rust resistance genes. Thus, it can be easily handled by the breeders (Nzuve *et al.*, 2013 and Hermas and El-Sawi 2015).

2. Quantitative analysis:

To determine the genetic parameters of stem rust resistance, quantitatively, the two parents, F_1 and F_2 populations for each of the seven crosses were tested at adult plant stage, under field conditions. Means and variances of the parents and their respective F_1 and F_2 generations, were used to estimate the degree of dominance for F_1 (h_1) and F_2 (h_2). The percentage of heritability in it's broad–sense (h_2) and the number of functioning stem rust resistance genes for each cross were also estimated (Table, 4).

2.1. Degree of dominance:

Data illustrated in Fig. (3) and presented in Table (4), show that F_2 mean values in the seven crosses between Morocco and each of the tested cvs., *i.e.* Misr-1, Misr-2, Gemmeiza-11, Gemmeiza-12, Shandaweel-1, Giza-171 and Sakha-94 were; 23.52, 31.75, 29.63, 27.75, 28.63, 25.50 and 27.25%, respectively. These means were lower than those calculated for their respective mid parents, revealing the presence of partial dominance for low disease severity.

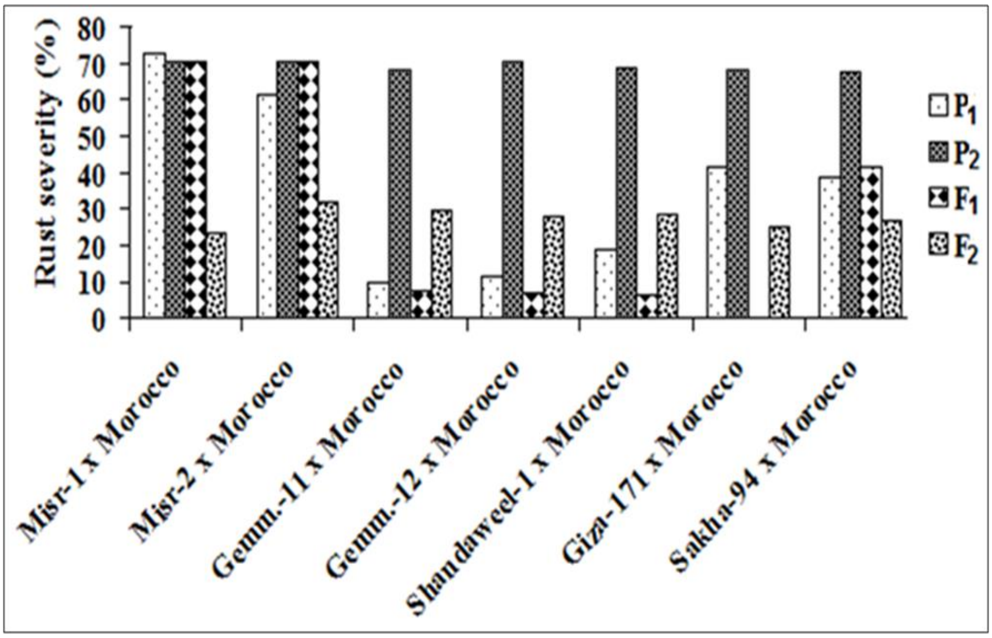

Fig. 3. Mean rust severity (%) for P_1, P_2, F_1 and F_2 populations of seven wheat crosses, among Morocco and each of Misr-1, Misr-2, Gemmeiza-11, Gemmeiza-12, Shandaweel-1, Giza-171 and Sakha-94, inoculated with *P. graminis* f.sp. *tritici*, at adult plant stage under field conditions.

Table 4. Stem rust severity means (%), variances, degrees of dominance, heritability estimates in it's broad sense (%), and number of stem rust resistance genes for seven crosses, under field conditions in 2015/2016 season.

Cross name		$\bar{X}$	S^2	Degree of dominance		Heritability (%)	No. of genes
				h_1	h_2		
Misr-1 x Morocco	P_1	72.90	16.54	0.69	79.62	91.7	0.003
	P_2	70.48	24.76				
	F_1	70.86	24.24				
	F_2	23.52	251.68				
Misr-2 x Morocco	P_1	61.50	22.75	0.84	-14.7	94.1	0.029
	P_2	70.89	24.19				
	F_1	70.13	24.98				
	F_2	31.75	399.18				
Gemmeiza-11 x Morocco	P_1	10.27	24.92	-1.09	-0.66	95.8	0.781
	P_2	67.95	20.81				
	F_1	7.55	19.03				
	F_2	29.63	551.48				
Gemmeiza-12 x Morocco	P_1	11.47	22.83	-1.15	-0.90	96.2	0.721
	P_2	70.85	24.27				
	F_1	7.07	16.44				
	F_2	27.75	627.93				
Shandaweel-1 x Morocco	P_1	19.25	24.45	-1.50	-1.24	96.3	0.482
	P_2	69.10	24.19				
	F_1	6.76	14.53				
	F_2	28.63	658.98				
Giza-171 x Morocco	P_1	41.30	23.29	-1.03	-4.36	91.1	0.396
	P_2	68.06	21.24				
	F_1	40/89	24.19				
	F_2	25.50	250.25				
Sakha-94 x Morocco	P_1	39.05	24.10	-0.81	-3.65	79.5	1.21
	P_2	67.55	19.03				
	F_1	41.80	21.72				
	F_2	27.25	105.43				

The estimated values of F_1 (h_1) were: 0.69, 0.84, -1.09, -1.15, -1.50, -1.03 and -0.81, for the aforementioned seven crosses, in sequence. The significant negative values of F_1 (h_1) revealed the presence of partial dominance for low disease severity (%) (Table 4). Meanwhile, degree of dominance estimates of F_2 (h_2) were; 79.62, -14.7, -0.66, -0.90, -1.24, -4.36 and -3.65, for the seven crosses, respectively. These results supported the existing of partial dominance, for low disease severity (resistance) in most crosses under study. These results are similar to those previously obtained by Shehab El-Din *et al* 1991, Abd El-Latif and Boulot 2000 and Hermas and El-Sawi 2015).

2.2. Variances and heritability estimates:

The values of the F_2 variance were, in general, high for all seven crosses under study. These values were: 251.68, 399.18, 551.48, 627.93, 658.98, 250.25 and 105.43, in respect with the mentioned above crosses. On the other hand, heritability estimates in it's broad sense, calculated from the variance of parents, F_1 and F_2, were found to be high for the seven crosses, under evaluation (Table, 4). Wherein, these values were found to be more than 79%, as they were; 91.7, 94.1, 95.8, 96.2, 96.3, 91.1 and 79.5% for the mentioned above seven crosses, respectively (Fig. 4 and Table, 4). However, high heritability estimates, revealed that most of the phenotypic variability was due to genetic factors or genetic structure of the studied cultivars. This result also considered an indicative for the high possibility to achieve high rates of success in recovering the desired genes in future generations. Also, the selection for stem rust resistance in the early segregating generations was possible, but delaying it to the late generations is more effective and more fruitful, due to the important role of dominance effect in the expression of this trait (Abd El-Latif and Boulot 2000, Menshawy and Youssef 2004 and Hermas and El-Sawi 2015).

2.3. Number of resistance genes:

Few or minimum number of effective genes controlling stem rust resistance was obtained in this study (only one or two gene pairs for the tested seven crosses). Data in Table (4) indicate that one gene pair conditioning stem rust resistance in most of the tested crosses, *i.e.* Misr-1 x Morocco, Misr-2 x Morocco, Gemmeiza-11 x Morocco, Gemmeiza-12 x Morocco, Shandaweel x Morocco and Giza-171 x Morocco. Where, the calculated numbers of resistance genes were; 0.003, 0.029, 0.781, 0.721, 0.482 and 0.396 of these crosses, respectively. Meanwhile, there were two gene pairs (1.21) controlling stem rust resistance in cross between Sakha-94 x Morocco (Fig. 4 and Table, 4).

Actually, the exact number of genes controlling stem rust resistance in wheats, considered to be the subject of much debate and controversy by many investigators. However, conflicting results were obtained from the previous reports relevant to the number of genes controlling such resistance in different wheat genotypes. Numerious numbers of the previous studies reported that wheat stem rust resistane is a simple inherited triat, governed by one, two or few numbers of gene pairs (Abd El-Latif and Boulot 2000, Nzuve *et al* 2013 and Hermas and El-Sawi 2015). In contrast, others emphasized that, it is a quantitative triat, controlled by many gene pairs with additive effects, as well as enviromental conditions (Navabi *et al* 2005). This conclusion was in accordance with the findings of Herrera-Foessel *et al* (2007), as they reported that slow-rusting resistance in durum wheat lines ‘Playero’, ‘Planeta’, and ‘Trile’, was controlled by at least three independently inherited genes, that interacted in an additive manner.

Whereas, this resistance in 'Piquero', 'Amic', 'Bergand', 'Tagua', and 'Knipa' was governed by at least two genes with additive effects.

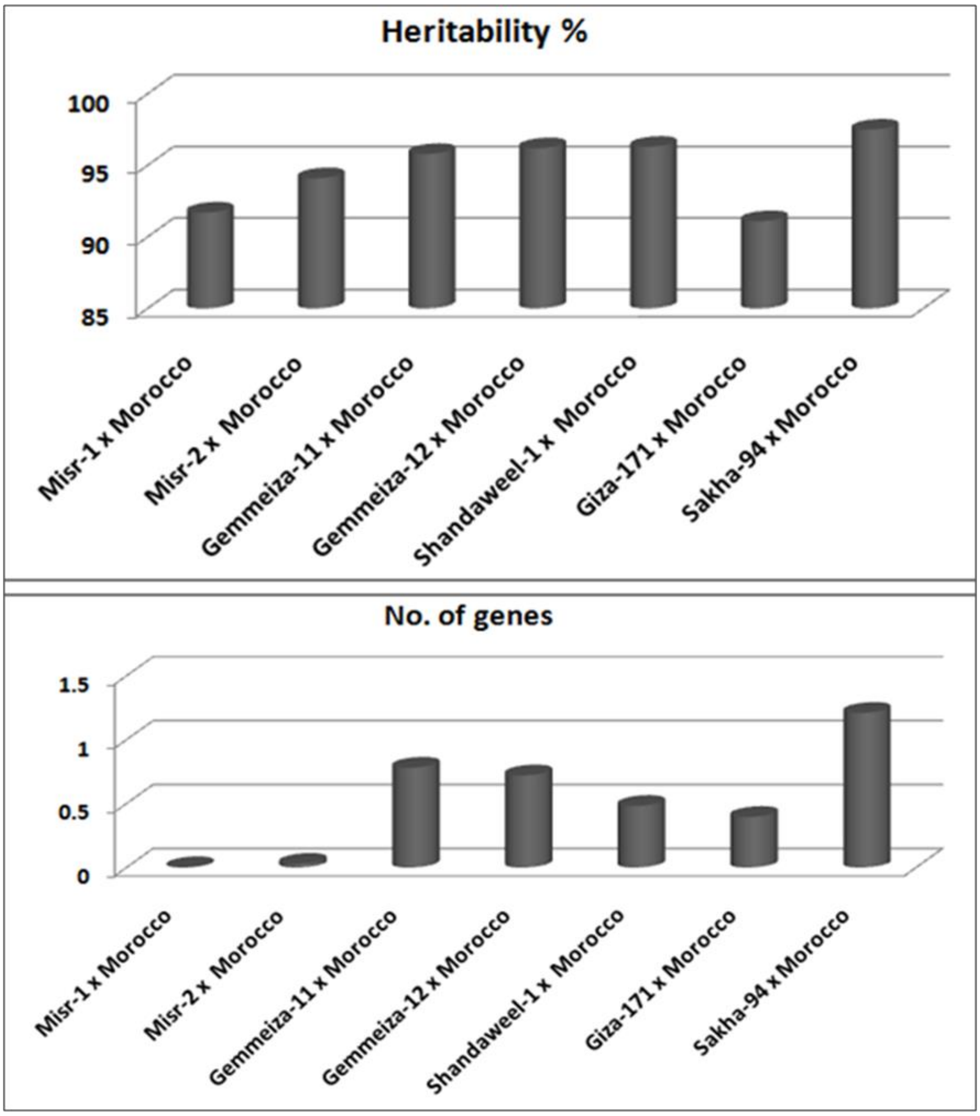

Fig. 4. Heritability (%) and number of resistance genes, in seven crosses between the susceptible variety; Morocco and the tested Egyptian wheat cultivars.

Likewise, Abdul (2011) reported that the crosses between RL6008, Hobbit, Fundin and Tarawith, as well as the susceptible check variety; Armada, segregated in 1:2:1 ratio, in F_3 progenies. While, the cross between cultivar Tara and the susceptible variety; Armada, segregated in F_2 population according to the ratio; 3:1. These results indicated the presence of a single gene for rust resistance. Also, Nzuve *et al.* (2013) suggested that the resistance to stem rust is conditioned by a single dominant gene in the parent line; KSL-2, but it is governed by two genes in other bread wheat lines, under their study. Meanwhile, other authors suggested that resistance to stem rust is a quantitative trait, controlled by several gene pairs, with additive effects and considered to be polygenic inherited character (Padidam and Kontt 1988 and Abd El-Latif and Boulot 2000).

CONCLUSION

Based on the obtained results in this investigation, both qualitative and quantitative analysis revealed that host-genetic response is mainly depends upon both host and pathogen genotypes and environment conditions. Thus, plant breeders should not rely on the host pedigree only, but they should put the pathogen genotype and environment in their considerations as the two important variables in the pathogen: host: environment systems. Also, genetic resistance is the most economic and effective means, not only for reducing the annual yield losses, but also for avoidance the sudden occurrence of severe epidemics. However, breeding rust resistant genotypes is a continuous process, and plant breeders need to add new effective resistance genes to their breeding materials, because of the dynamic nature of stem rust pathogen, which enables it to evolve new virulent races, that can breakdown or overcome the host genetic resistance. Therefore, availability of more information for the genetic nature and inheritance of stem rust resistance is of a major importance to establish an essential primary step, towards the full employment and good exploitation of this resistance in planning and make a correct decision in wheat breeding programms.

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وراثة صفة المقاومة لمرض صدأ الساق في طور النباتات البالغ لبعض أصناف القمح المصرية

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تم دراسة صفة المقاومة لمرض صدأ الساق بإجراء تهجين سبعة أصناف قمح تجارية مصرية وهم مصر ١، مصر ٢، جميزة ١١، جميزة ١٢، شندويل ١، جيزة ١٧١، سخا ٩٤ مع صنف موركو شديد القابلية للإصابة بالمرض وقد تم إختبار نباتات الجيل الأول والجيل الثاني والأباء في محطة بحوث كفر الحمام- شرقية. ثم تم إجراء التحاليل الوراثية الوصفية والكمية لكل التراكيب الوراثية تحت الدراسة. وقد أظهرت النتائج المتحصل عليها أن النسب الأنعزالية المتوقعة في نباتات الجيل الثاني كانت ١:١٥، ٣:١٣، ٧:٩، ١:٣، ٣:١٣، ٣:١، ٩:٧ للتراكيب الوراثية تحت الدراسة بالترتيب. وثبت من الدراسة أن صفة المقاومة في التراكيب الوراثية المختبرة صفة بسيطة يتحكم فيها زوج أو زوجين فقط من العوامل الوراثية (١-٢ زوج) في معظم الحالات مع التأثير الواضح للسيادة الجزئية أتجاة الأب الذي يمتلك صفة المقاومة. وكانت قيم معامل التوريث بمعناه الواسع لكل التراكيب الوراثية تحت الدراسة عالية (تراوحت ما بين ٧٩,٥ – ٩٦,٣%) مما يدل علي أنه من الممكن إجراء الأنتخاب الناجح لصفة المقاومة لمرض صدأ الساق في الأجيال الأنعزالية المبكرة. ولكن تأخير هذا الأنتخاب الي الأجيال الأنعزالية المتأخرة يكون أكثر فاعلية وذلك لما لعامل السيادة من تأثير مهم في التعبير عن هذه الصفة. وبالتالي يجب ألّا يعتمد مربي النباتات اعتمادا كاملاً على التركيب الوراثي للعائل فقط في إجراء عملية الأنتخاب، بل يجب أن يضع النمط الجيني للكائن الممرض والبيئة باعتبارهما متغيرين هامين في التفاعل بين العائل: الكائن الممرض: الظروف البيئية السائدة.

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