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RESISTANCE DEGREE OF SOME SWEET PEPPER GENOTYPES TO POWDERY MILDEW

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ABSTRACT

Resistance degree of some sweet pepper genotypes to powdery mildew caused by Leveillula taurica was studied under artificial conditions. The aim of this study was to determine resistant lines or crosses used as new pepper cultivars or hybrids in commercial production and obtain more information about the mode of inheritance of powdery mildew disease. The evaluated genotypes were nineteen new breeding lines, 10 F_1 crosses with their parental lines and six populations, i.e., the two parents, F_1, F_2, Bc_1 and Bc_2 of only one cross. The experimental work was carried out at Experimental Farm of Faculty of Agriculture, Menoufia University during three seasons. A randomized complete block design (RCBD) with three replicates was used. Data were recorded and statistically analyzed. Some genetical parameters were estimated. The obtained data showed significant differences among the studied lines in average severity of infection. Based on degree of resistance the lines were classified into three groups, i.e., moderate resistance, moderate susceptible and susceptible. The best lines were L-4, L-15, L-19 and L-17, since they showed the lowest average severity of infection (1.9, 2.4, 4.2 and 4.3%) and can be used as resistant cultivars or resistance source in breeding for powdery mildew. Estimated average degree of heterosis for all resulted F_1 crosses indicated that the character is controlled by additive gene actions with slight dominance to the susceptible parent. For the mean generation analysis of the cross (L-9 × L-19) the high estimated additive variance (27.98%) compared with the dominance one (12.62%) and the high estimated broad and narrow sense heritabilities (92.7 % and 63.9%, respectively) showed that a large amount of variance was due to the genetical variance, and additive variance was more important in the inheritance of the trait. These results indicated significant improvement of resistance to powdery mildew can be realized by selection. The high estimated value of genetic advance under selection (ΔG %) support that. In general, it could be concluded that the resistance to powdery mildew may be controlled by a single pair of genes with additive gene action and slight dominance of the susceptible gene.

Key words: ***Leveillula taurica, Capsicum annuum, Gene action, Heritability, Heterosis, Powdery mildew, Severity of infection, Selection.***

INTRODUCTION

The powdery mildew caused by *Leveillula taurica* (Lev) Arn. is the most important and limiting disease for the sweet pepper crop in open field as well as in green houses. It causes leaf abscission, reduction of photosynthetic activity and fruit sun burning (Palti 1988 and Daubeze *et al* 1995). Total losses due powdery mildew disease reported in India was up to 24 – 80% of the crop (Mathur *et al* 1972 and Sharmila *et al* 2006). Significant decline in quantity and quality of pepper yield was also observed in southern Ethiopia by Negash *et al* (2012).

The use of systemic fungicides for control has not been effective, beside this, it causes the development of pathogen resistant strains to the fungicide. Therefore, the best manner of control would be by means of resistant cultivars or hybrids. In *Capsicum annuum* L. partial resistance has not been satisfactory (Shirfriss *et al* 1992). Accordingly, it is very important to breed resistant cultivars coupled with high yields for cultivation by the farmers. Souza and Café-Filho (2003) reported that the best resistance source had been identified in *Capsicum baccatum, capsicum chinese* and *Capsicum fruitecens.* They added that some resistant *Capsicum annuum* materials were identified that may be useful as resistance source for breeding.

Significant differences were observed among pepper genotypes in degree of resistance to powdery mildew (Ullasa *et al* 1981 and Souza and Café-Filho 2003). As large as 162 capsicum genotypes were examined by them. They found that 8.5% were immune or highly resistant, 18% were resistant, 15% were moderately resistant, 15.5% were susceptible and 43% were highly susceptible to powdery mildew.

Farag (2000) in Egypt found three rates of resistance, viz., moderate resistance (MR), moderate susceptible (MS) and susceptible (S). Severity of infection ranged from 15.0 to 48.0% and was lower in resulted F_1 crosses. Significant differences among pepper genotypes were also reported by Blat *et al* (2005b). They added that the intermediate reaction of the (MR) might be able to help the integrated control of powdery mildew using fungicides or alternative control.

Heredity studies of *Capsicum annuum*, L. showed that the results of resistance to powdery mildew were different concerning the mode of inheritance according to the materials used. Van der Plank (1968) reported that the resistance may be controlled by several genes (loci) which demand a greater selection cycles to get homozygosity. According to Blat *et al* (2005a) the character of resistance to powdery mildew in *C. baccatum* was controlled by up to six loci with dominant and epistatic gene action.

Meanwhile it was controlled by single dominant gene according to Todorova and Kunovski (1988) and Mulge and Anand (1997), who suggested the possibility of exploiting heterosis combinations with powdery mildew resistance. Shifress *et al* (1992) and Daubeze *et al* (1995) reported that the resistance was controlled by three pairs of gene with additive, as well as, epistatic effects. Similar results were also previously reported by Anand *et al* (1987) and Daubeze *et al* (1989). In that context, they found that at least three incompletely dominant genes with additive gene actions control this trait. On the other hand, Murthy and Deshpande (1997) reported that the resistance was dominant and under polygenic control and showed allelism differences among the resistant parents.

According to Blat *et al* (2005b) the estimated heritabilities were high, showing that the powdery mildew reaction in general is not much influenced by environmental conditions. In their studies on pepper, the greatest h_b^2 value (76.5%). The estimated gains in selection for F_3 generation was high, indicating prospects for obtaining lines of sweet pepper resistant to powdery mildew. Generally, hot pepper resistance sources to powdery mildew are different with respect to alleles that control the resistance to disease.

Therefore, this work was aimed to evaluate some new pepper lines which were developed by selection and obtain more informations about the inheritance of powdery mildew disease.

MATERIALS AND METHODS

Nineteen homogeneous new sweet pepper lines, which were developed by a selection programme by the first author, 10 F_1 crosses resulted by crossing five lines in a diallel cross mating without reciprocals. In addition, six populations, i.e. (F_1, F_2, Bc_1 and Bc_2 populations of the cross (L-9 × L-19) with their parents) were evaluated for resistance to powdery mildew caused by *Leveillula taurica* (Lev) Arn. The experimental work was conducted at the Faculty of Agriculture, Menoufia University during three seasons, i.e., 1) the summer season of 2016 in open field, 2) in winter season of 2016/2017 into plastic greenhouse and 3) in late summer season of 2017 in cereal greenhouse. The second and third experiments (plantings) were carried out in pots.

In the first season (2016), five lines were grown in an open field and crossed in a diallel cross mating system without reciprocals to produce 10 F_1 crosses. The parental lines were L-3, L-5, L-9, L-17 and L-19. In the second season (2016/2017), pots experiment was carried out into the greenhouse for evaluating 19 breeding line (among them the five parental ones) and the resulted 10 F_1 crosses against powdery mildew disease under artificial infection. A randomized complete blocks design (RCBD) with three replicates was used. Number of plants was 27 for each population arranged on the three replications, three plants per pot. Seedlings were transplanted on the first week of September 2016. All the recommended package were applied, except protection for control of powdery mildew. The severity of infection was measured on a randomly selected three plants from each replicate of each population. A scale of disease scores was used in accordance with the leaf area affected as proposed by Ullasa *et al* (1981) of which: 1) Resistant (R), no symptoms; 2) Moderately resistant (MR) with 1-10% of the leaf area affected; 3) Moderately susceptible (MS) with 11-20% of the leaf area affected; 4) Susceptible (S) with 21-50% of the leaf area affected and 5) Highly susceptible (HS) with 51% or more of the leaf area affected.

In the same season, the F_1 cross (L-9 × L-19) which its parents widely differed in severity of infection was selfed and backcrossed to both parents to produce the required seeds of F_1 and Bc_1 & Bc_2, respectively, for studying the inheritance of resistance to powdery mildew in pepper. The third season (Late summer 2017), the experiment was conducted into greenhouse for studying the inheritance of the disease. The L-9 (P_1), L-19 (P_2), F_1, F_2, Bcp_1 and Bcp_2 populations were grown in pots 25 cm (containing 3 kg of clay-sand mixed soil previously disinfested by 5% formalin) and severity of infection was recorded on the individual plant under artificial infection. Also a (RCBD) was used with three replicates. The total number of plants were 27 (for the non-segregating populations), 108 (for F_2) and 81 (for each of backcross). Populations were arranged on the three replicates.

With regard to the artificial infection for the second and third experiment, powdery mildew spores were collected from diseased leaves. Disease suspension was made using sterilized distilled water, and adjusted to 5×10^4 conidia ml^{-1} using Hemocytometer slides (Souza and Café-Filho 2003). The spore suspension was sprayed directly after preparation of foliage of pepper plants when it was 60 days old and showed vigorous growth. The sprayed plants were kept under plastic bags for 48 hours to maintain high humidity to ensure the infection. The observations were recorded after 7 and 15 days from infection. The examined plants were 10 plants in the second season, but it was measured on the individual plants in the third one.

Statistical analysis

Data were statistically analyzed using the standard method of a (RCBD), illustrated by Singh and Chaudery (1995). Coefficient of variances (c.v. %) and components of variance, i.e., VE, VG, VP, Phenotypic (PCV%) and genotypic (GCV%) coefficients of variability were calculated. Heterosis percentages and potence ratio were determined according to Mather and Jinks (1971). BSH and NSH were estimated according to Allard (1999) and Mather (1949). Genetic advance under selection as percent of F_2 mean (ΔG %) was calculated. Minimum number of genes differentiating in the parents was determined by the formula of Castle and Right (1921).

RESULTS AND DISCUSSION

Reaction of some new lines for resistance to powdery mildew

Nineteen breeding lines were screened under artificial infection for the disease. Data obtained are presented in Table (1).

Table 1. Reaction of some sweet pepper new lines against *Leveillulla taurica* under artificial infection.

Lines	Average of disease severity	Reaction to pathogen	Disease score
L-1	**10.7**	**MS**	**3**
L-2	**7.7**	**MR**	**2**
L-3	**5.1**	**MR**	**2**
L-4	**1.9**	**MR**	**2**
L-5	**19.3**	**MS**	**3**
L-6	**5.3**	**MR**	**2**
L-7	**8.8**	**MR**	**2**
L-8	**7.4**	**MR**	**2**
L-9	**23.0**	**S**	**4**
L-10	**7.9**	**MR**	**2**
L-11	**17.4**	**MS**	**3**
L-12	**18.7**	**MS**	**3**
L-13	**16.8**	**MS**	**3**
L-14	**9.8**	**MR**	**2**
L-15	**2.4**	**MR**	**2**
L-16	**31.0**	**S**	**4**
L-17	**4.3**	**MR**	**2**
L-18	**23.0**	**S**	**4**
L-19	**4.2**	**MR**	**2**

LSD at 5% = 1.16 and at 1% = 1.63. Coefficient of variance (C.V %) = 12.1%

The low estimated coefficient of variance (c.v.%) which was 12.1%, indicated high degree of homogeneity for these lines. Significant differences were observed among the studied lines due to the genetic effects. Three rates of resistance, i.e., moderate resistance (MR), with grade 2, moderate susceptible (MS) with grade 3 and susceptible (S) with grade 4 were observed in eleven lines (L-2, L-3, L-4, L-6, L-7, L-8, L-10, L-14, L-15, L-17 and L-19), in five lines (L-1, L-5, L-11, L-12 and L-13) and in three lines (l-9, L-16 and L-18), respectively. The severity of infection ranged from 1.9 – 9.8% in the first group, 10.7 – 19.3% in the second group and from 23.0 – 31.0% in the third one. This result is agree with Farag (2000) who found three groups of the studied pepper genotypes (MR, MS and R). Five rates of infection, i.e., HR, R, MR, MS and S were found by Wankhade and Mohrir (2015). However, the highest average severity of infection (31%) was reflected by L-16, while the lowest average (1.9%) was reflected by L-4. In general, L-4, L-15, L-19 and L-17 could be considered as the highest resistant lines, since they showed the lowest severity of infection values (1.9, 2.4, 4.2 and 4.3%, respectively). On the other hand, the lines L-16, L-9 and L-18 were susceptible, since they showed the highest values of infection (31.0, 23.0 and 23.0), respectively. Significant differences in degree of resistance were also observed among pepper cultivars or lines by Ullasa *et al* (1981), Farag (2000) and Blat *et al* (2005b). In addition, similar work was also conducted by Wankhade and Mohrir (2015) who reported that none of the studied chilli genotypes they used was found to be immune in reaction to powdery mildew disease.

The estimated broad sense heritability (BSH) was high (96.2%) indicating minor environmental effects and the large portion of variance was mainly genetic. The ratio of genotypic / phenotypic coefficient of variances was also high (0.98) supporting this fact. These results are confirmed with those of Blat *et al* (2005b) who found high heritability and concluded that powdery mildew reaction in general is not much influenced by environmental conditions.

Reaction of F_1 crosses

Five homogeneous breeding lines were chosen as parental genotypes to develop 10 F_1 crosses by a diallel crossing system without reciprocals to study the heterosis effect for resistance to powdery mildew in pepper. This lines were three moderate resistance (L-3, L-17 and L-19), one line (L-5) moderate susceptible and one line (L-9) susceptible. Data in Table (2) showed that three crosses (3 × 17, 3 × 19 and 17 × 19) were moderately resistance (MR) with grade (2) and they were the best combinations for resistance to powdery mildew. Five crosses showed resistance rate of (MS) with grade (3, their severity of infection was ranged from 12.0 to 19.1. Two crosses (5 × 9 and 9 × 17) were susceptible with an average of infection of 22.4 and 20.8%, respectively. However, none of the resulted F_1 crosses were resistant to the disease.

Table 2. Average severity of infection for 10 F_1 and their parental lines.

Lines ♂ ♀		3	MR	5	MS	9	S	17	MR	19	MR
3	MR	5.1	MR	16.9	MS	19.1	MS	5.1	MR	4.9	MR
5	MS			19.3	MS	22.4	S	14.0	MS	15.3	MS
9	S					23.0	S	20.8	S	12.0	MS
17	MR							4.3	MR	4.8	MR
19	MR									4.2	MR

LSD at 5% = 1.14 and at 1% = 1.53. The values of parental lines are underlined.

It is noticed that the parents of the moderate resistant F_1 were also (MR), while the parents of the (MS) F_1 crosses were MR × MS or MR × S. This figure indicated that to realize high degree of resistance, the parents used must be resistant or moderate resistant. The estimated overall means of F_1 crosses and parental lines were very close (13.6 and 12.0%, respectively) suggesting that the character is controlled by mostly additive genes with slight dominance to the susceptible parents. Thus, a selection programme could be effective for improving degree of resistancity in these materials.

With regard to average degree of heterosis, as shown in Table (3), all F_1 crosses except the cross L-9 × L-19, showed positive mid-parent heterosis values ranging from 5.91 in the cross 5 × 9 to 52.38 (in the cross 9 × 17, indicating partial dominance for the susceptible parent, while heterosis in relation to the highest infected parent was high and negative in most crosses, which their parents were widely differ in average severity of infection ranging from -47.83% (in the cross 9 × 19) to -2.61 (in the cross 5 × 9). High positive heterosis values ranging from 16.06% (in the cross 5 × 9) to 383.72 % (in the cross 9 ×17) were estimated in relation to the better (the lowest infected) parent or resistant parent. The positive MP heterosis and negative heterosis in relation to the highest infected parent (susceptible parent) lead to suggest that this trait may be controlled by partial dominance of susceptible genes with mostly additive gene actions. The obtained potence values which ranged from -0.76 to 0.17 support this suggestion. However, none of the resulted crosses showed hybrid vigor or dominance for the highest resistant parent. The additive gene effects were greater than the none-additive ones were also reported by Marchesan *et al* (2009).

Table 3. Average degree of heterosis relative to mid-parent, susceptible and resistant parents of some pepper F_1 crosses*.

Crosses	$H\overline{MP}$	**Heterosis**		**Potence ratio**
		Susceptible parent	**Resistant parent**	
3 × 5	**38.5**	**-12.4**	**231.4**	**-0.66**
3 × 9	**35.9**	**-16.96**	**274.51**	**-0.56**
3 × 17	**–**	**–**	**–**	**–**
3 × 19	**–**	**–**	**–**	**–**
5 × 9	**5.91**	**-2.61**	**16.06**	**-0.68**
5 × 17	**18.64**	**-27.46**	**225.6**	**-0.29**
5 × 19	**30.21**	**-20.73**	**264.3**	**-0.47**
9 × 17	**52.38**	**-9.57**	**383.72**	**-0.76**
9 × 19	**-11.76**	**-47.83**	**185.7**	**0.17**
17 × 19	**–**	**–**	**–**	**–**

*** susceptible parent = (high severity of infection) and resistant parent = (low severity of infection)**

Average degree of heterosis was estimated for the F_1 crosses whose parents widely differed in average severity of infection only.

Inheritance of resistance to powdery mildew

Data in Tables (4 and 5) showed that the two parental lines were widely differed in average severity of infection with an average of 25.1 and 3.8% for P_1 (L-9) and P_2 (L-19), respectively. The resistance rate was susceptible (S) for P_1 and moderate resistant (MR) for P_2 to powdery mildew disease. The disease scores were 4 and 2 for the two parents, respectively. Severity of infection ranged from 21 – 28 (for P_1) and from 2.7 – 6.9 (for P_2). However, none of the plants were found free of infection.

Table 4. Statistics obtained for resistance to powdery mildew in parents, F_1, F_2, Bc_1 and Bc_2 populations in pepper (summer 2017).

Populations	Number of plants	Severity of infection (%)			S^2	C.V.%
		Range	Actual mean ± S.E	Theoretical mean		
L-9 (P_1)	27	21 – 28	25.1 ± 0.44	–	5.4	9.2
L-19 (P_2)	27	2.7 – 6.9	3.8 ± 0.31	–	2.5	42.1
F_1	27	10.5 – 14.8	13.1 ± 0.25	14.25	1.8	9.9
F_2	108	2.3 – 30	16.01 ± 0.64	13.8	43.78	41.4
Bc_1	81	12.0 – 30	18.5 ± 0.63	19.1	32.52	30.8
Bc_2	81	2.1 – 17	10.24 ± 0.57	8.45	27.1	50.9

LSD at 5% = 1.2 and at 1% = 1.7

Table 5. Number of segregating plants of pepper for reaction to *Leveillula taurica* under greenhouse conditions using a disease severity scale of Ullasa *et al* (1981).

Populations	Total number of plants	Number of plants that had average disease of severity of each populations						
		1(R)	2(MR)	3(MS)	4(S)	5(HS)	x^2	P
L-9 (P_1)	27	–	–	–	27	–	0.0	–
L-19 (P_2)	27	–	27	–	–	–	0.0	–
F_1	27	–	–	27	–	–	0.0	–
F_2	108	–	22	61	25	–	1.98	0.10 – 0.50
Bc_1	81	–	–	43	38	–	0.32	0.50 – 0.90
Bc_2	81	–	35	46	–	–	0.95	0.10 – 0.50

**R: resistant, MR: moderately resistant, MS: moderately susceptible,
S: susceptible, HS: highly susceptible.**

All plants of F_1 were led between the two parents with a range of 10.5 to 14.8% and average of 13.1%, indicating that the F_1 population is moderately susceptible (MS) with grade (3), and the character may be controlled by no dominant genes. This suggestion was supported by the estimated low mid-parent heterosis (-9.3%) and low potence ratio. Actual and arithmetic means were close supporting the no-dominance theory postulated. As shown in Table (5), the F_2 plants segregated into three destinct groups. 22 plants have severity of infection ranging from 3 – 7% and similar to those of P_2 (MR). 61 plants were similar to those of F_1 population and ranged from 12 – 18% (MS) and 25 plants were similar to P_1 (S) and ranged from 21.0 – 30.0%.

In other words, the F_2 plants were segregated in a ratio of 22: 61: 25%. This is fit to 1 (MR): 2 (MS): 1 (S) using x^2 test with probability of (0.10 – 0.50) suggesting that the resistance of powdery mildew disease may be controlled by single pair of genes with no-dominance effects. The Bc_1

plants distributed in a ratio of 43 plants similar to the F_1 and 38 plants similar to P_1 (susceptible parent). Also, the plants of Bc_2 were segregated into two classes 46 and 35 plants were similar to F_1 and P_2, respectively. In the two Bc populations the ratio was 1: 1 and fit to x^2 test with a probability of 0.50 – 0.90 in Bc_1 and 0.10 – 0.50 in Bc_2. This ratio in the two backcrosses is expected when the character is controlled by single gene with additive gene actions.

Examination of obtained variances for the studied populations (P_1, P_2, F_2, Bc_1 and Bc_2) showed that they were low in the non-segregating populations, indicating that they were homogenous while it was high in the segregating population (F_2, Bc_1 and Bc_2) as expected because they are heterogeneous i.e., consist of homozygous and heterozygous plants (Table 4).

Heritabilities in broad and narrow senses were estimated as 92.7 and 63.9%, respectively, showing that large amount of the total variance was genetic. The high value of narrow sense relative to broad sense heritabilities suggest that the additive variance is important and significant improvement of resistance to powdery mildew caused by *Leveillula taurica* (Lev.) Arn could be achieved by selection for resistance. The minimum number of gene pairs differentiating the parental lines was estimated as 1.4. ΔG and ΔG% were estimated as 8.73 and 54.5%, respectively. Additive variance ($^1/_2$ D) and dominance variance ($^1/_4$ H) were estimated as 27.98 and 12.62, respectively. The additive variance was calculated by the formula $^1/_2D = 2VF_2 - (VBC_1 + VBC_2)$. The dominance variance was calculated by the formula $^1/_4 H = VF_2 - (^1/_2D + E)$, where E is the environmental variance. All these estimates indicated the importance of selection in improvement pepper genotypes for resistance to powdery mildew in sweet pepper. The high estimated genetic advance under selection as percentage of F_2 mean (ΔG %) and the high estimated $^1/_2$ D (additive variance) compared with $^1/_4$ H (dominance variance) encourage using selection for producing resistant cultivars.

These findings are in agreement with those of Todorova and Kunovski (1988) who found that the resistance is controlled by single gene. The results also are confirmed with those of Blat *et al* (2005), who reported that the estimated gains (ΔG) was high, indicating prospects for obtaining lines of sweet pepper resistant to powdery mildew. On the other hand, it was disagree with Shifress *et al* (1992), Daubeze *et al* (1995), Murthy and Deshpande (1997), who reported that the resistance to powdery mildew in pepper is controlled by more oligogenic and polygenic inherited.

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درجة مُقاومة بعض التراكيب الوراثية للفلفل الحلو لمرض البياض الدقيقي

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تم دراسة بعض التراكيب الوراثية (١٩ سلالة جديدة ، ١٠ هُجن جيل أول ، وعشائر الجيل الأول والثاني والهجين الرجعي الأول لكلا الأبوين لهجين واحد) لصفة مُقاومة مرض البياض الدقيقي تحت ظروف العدوى الصناعية. والغرض من الدراسة هو تحديد السلالات الأعلى في درجة المُقاومة ، وقياس درجة قوة الهجين للصفة وكذلك الحصول على مزيد من المعلومات عن طبيعة وراثة الصفة في الفلفل. أجريت التجارب العملية بمزرعة كلية الزراعة بشبين الكوم جامعة المنوفية خلال ٣ مواسم زراعية بتصميم القطاعات الكاملة العشوائية فيثلاثة مُكررات. وتم تسجيل القراءات وإجراء التحليل الإحصائي والحسابات الوراثية بالطُرق المُناسبة، وأوضحت النتائج المُتحصل عليها الآتي: وجود فروق معنوية بين السُلالات المُختبرة في شدة الإصابة بالمرض. وعلى أساس شدة الإصابة قُسّمت السُلالات إلى ٣ أقسام وهي مُتوسطة المُقاومة، مُتوسطة الإصابة، ومُصابة. أفضل السُلالات كانت L-4 ، L-15 ، L-19 ، L-17 حيث كانت هي الأقل في شدة الإصابة بالمرض (٤,٩ ،٢,١ ، ٣,٥ ،٤,٣%) على التوالي، ويُمكن الاستفادة منها في الزراعة كأصناف جديدة أو كمصدر المُقاومة في التربية لتحسين الفلفل لهذا المرض. أشارت حسابات درجة قوة الهجين بالنسبة للأب الأوسط في عشائر الجيل الأول إلى أن صفة المُقاومة كانت وسط بين الأبوين مع سيادة طفيفةفى اتجاه الأب الأعلى في شدة الإصابة، وهذا يعني أن الصفة محكومة غالباً بعوامل وراثية ذات تأثير إضافي مع سيادة جزئية للأب المُصاب. وهذا الاقتراح يُسانده أن التباين الإضافي المحسوب أعلى من التباين غير الإضافي. تُشير القيم العالية للكفاءة الوراثية على المستوى الواسع والضيق إلى أهمية التباين الوراثي، وكذلك الجزء الإضافي منه- وذلك يجعل الانتخاب فعالاً في تحسين صفة المُقاومة، وخاصةً أن مُعدل التقدم الوراثي المحسوب عند إجراء الانتخاب في الجيل الثاني كان مُرتفعاً (٥٤,٥%). وعموماً يُمكن القول أن صفة المُقاومة لمرض البياض الدقيقي في هذه التراكيب الوراثية محكومة بزوج واحد من العوامل الوراثية (أي بسيطة التوريث) ذات تأثير إضافي مع سيادة جزئية لجين الإصابة وهذا واضح من توزيع نباتات الجيل الثاني، ويُمكن تحسين الصفة بطُرق التربية خاصةً الانتخاب.

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