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INHERITANCE OF MAIZE COMMON SMUT RESISTANCE

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ABSTRACT

Eight white maize inbreds, namely L 120, L74, L 144, L56, L 82, L 71, L 85 and L 173 and 28 F_1 maize crosses derived from a half diallel cross among these white inbreds, in addition to S.C. 10 check hybrid were evaluated for their resistance to the common smut disease and also for their grain yield (ardab/feddan) in two seasons. Artificial infection was applied using *Ustilago maydis* spore suspension (at 5 x 10^5 sporidia /ml. which was injected into the ear heads (2 ml per ear head) 4 to 7 days after the silking stage). Also, two sowing dates were applied. The results indicated that there were significant differences among the genotypes, parents, crosses and parent *vs.* crosses for disease incidence (DI), disease severity (DS), total soluble solids (T.S.S.), percent yield reduction and grain yield (ardab/feddan). The parental inbred lines L3 and L4 and their F1 crosses L3 x L4, L3 x L6, L1 x L3, L2 x L4 and L3 x L5 exhibited the lowest values of DI, DS and percent yield reduction with higher values of T.S.S. and grain yield and classified as more resistant to common smut disease than other lines and therefore considered the promising ones. Disease incidence and DS were lower in early sowing than late one. Variances due to general combining ability (GCA) and specific combining ability (SCA) was highly significant for all the studied characters under the two sowing dates. The additive gene action was more important than the dominance one in the inheritance of common smut resistance measurements, but the non-additive gene action was adequate in the inheritance of grain yield in both sowing dates. Inbred lines (L1), (L2), (L3) and (L4) significantly exhibited negative GCA effects. Hereby these inbreds were the best general combiners for common smut resistance characters, while the inbred lines (L2), (L3), (L5) and (L6) were the best for grain yield. The single crosses (L_1 x L_8), (L_2 x L_3), (L_3 x L_4), (L_4 x L_6), (L_4 x L_8) and (L_6 x L_8) could be recommended to be used in maize breeding program for resistance to common smut disease and high grain yield. Heritability in narrow sense was high (> 50%) for DI, DS and percent yield reduction; moderate (30-50%) for T.S.S. and low (< 30%) for grain yield.

Keywords: Corn, common smut, *Ustilago maydis,* breeding.

INTRODUCTION

Common smut of maize, caused by *Ustilago maydis* (C.D.) Corda [= *U. zeae* (Beckm.) Unger], is a prevalent disease worldwide (Ullstrup, 1978). Yield losses associated with this disease vary but are usually less than 10% over large areas (Shurtleff, 1986), and it ranges from a trace up to 15% in individual fields (Patrick *et al.,* 1981). Smut can lead to substantial losses in grain yield within the infected plants (Bojanowski, 1969) and might cause severe yield losses to agriculture when environmental conditions are suitable to the pathogen (Christensen, 1963 and Abbas *et al.* 2002). Losses due to common smut are associated mainly with ear galls. *U. maydis* infects young meristematic tissue aboveground and triggers the formation of tumors on all

aerial parts of infected plants (Christensen 1963) and causes stunting (Banuett, 1995).

U. maydis can't be controlled chemically. Thus, for economic and ecological reasons, cultivation of resistant varieties is the preferred control strategy for this disease. Breeding for resistance against smut fungi is promising in view of the large genetic variation present in maize germ-plasm and the preponderance of additive gene action underlying these traits (Ali and Baggett, 1990 and Bojanowski, J. 1969).

Host resistance is the most efficient method of controlling common smut, but resistance and the nature of the host-pathogen interaction are poorly understood, partly due to the lack of an efficient and reliable method of inoculation with *U. maydis*. Maize ears are infected by *U. maydis* through silks, which extend from the ovaries and emerge through a silk channel formed by husk leaves at the tip of the ear. Sporidia disseminated by wind or rain are deposited onto newly emerged silks (Shurtleff, 1980).

Precise timing of ear inoculation with *U. maydis* is relative to silk maturity and pollination and therefore, might improve the ability to screen maize germ-plasm for disease resistance (du Toit**,** *et al.* 1999). The susceptibility of maize to pathogens that infect ears through silks varies with silk development (Enerson and Hunter, 1980 and Reid, *et al.,* 1982). Snetselaar and Mims (1993) hypothesized that ears remain susceptible to infection by *U. maydis* for a longer time when silks aren't pollinated than when silks are pollinated, because *U. maydis*, an obligate bio-trophic in its dikaryotic form, is not able to grow across the layer of dead cells in the abscission zone of pollinated silks.

Agronomic and chemical approaches to control the disease are often ineffective and increase the cost of production. In contrast, host resistance breeding is a durable and eco-friendly approach to alleviate the losses caused by common smut in maize. A better understanding of the genetic basis of common smut resistance might help to accelerate resistance breeding efforts. Many investigators found that the additive gene effects were responsible for inheritance of common smut resistance (Odiemah and Kovacs, 1990; Fahmi *et al.* 2004; Chougan *et al*. 2008). El-Shenawy *et al.* (2009), Ali *et al.* (2010) and Bocanski *et al.* (2010) found that variance of SCA was more than that of GCA for grain yield.

The main objective of the present study was to estimate the type and magnitude of gene action controlling common smut resistance and yield of maize.

MATERIALS AND METHODS

A field experiment was conducted during two successive summer growing seasons, viz, 2008 and 2009 at two sowing dates at the Faculty of Agriculture Research Station, Zagazig, Egypt, to assess and quantify mean performance; general and specific combining abilities, as well as heritability for resistance to common smut disease and grain yield. The origin and pedigree of the used maize inbred lines are given in Table (1).

Table (1): The origin and pedigree of the maize inbred lines used in the present study

Code No.	Inbred lines	Origen	Pedigree
1	**L 120**	Locally developed	L. 57-B
2	**L 74**	(PI 221866 x 307) (Sc.14)	Rg. 31
3	**L 144**	Locally developed	L. 226 -A
4	**L 173**	Locally developed	C. M. 400
5	**L 56**	g.s (Beida x ci .64) (Sc. 14)	Rg – 11
6	**L 82**	(Sanjuan x 307) (Sc. 14)	Rg – 39
7	**L 71**	g.s. (sun. Laposta x 303) (G216 x Mo2)	Rg – 27
8	**L 85**	(Sanjuan x 307) (Sc. 14)	Rg - 42

In 2008 summer growing season, 8 inbred lines were grown and crossed to obtain 36 F_1's crosses in a half diallel fashion. In 2009 summer growing season, the inbred lines and their F_1 crosses were sown in rows (6 m long and 70 cm apart, the distance between hills was 25 cm). Randomized complete block design with three replicates was used.

Plants were artificially infected with a spore suspension of *U. maydis* by injecting 2 ml of inoculum (5 x 10^5 sporidia/ ml.) into ear heads 4 to 7 days after the silking stage (Lana and Xiaoyang, 2005).

The field plots received 15 kg of P_2O_5 per feddan before seeding, which took place on May 29, at the 1st sowing date and June 19, at the 2nd sowing date. Nitrogen fertilizer was applied at the rate of 120 kg N per feddan and splitted in two equal doses with the 1st and 2nd irrigations.

Collected data for the common smut disease resistance:

The following data were recorded on ten guarded and competitive plants from each replicate for parents and their F_1 crosses.

1- Disease incidence based on the infection rate in each genotype.
2- Disease severity based on disease percentage in each ear.
3- Total soluble solids (T.S.S.) in stalks.
4- Yield reduction (%), which was calculated using the following formula: Reduction (%) = (yield of un-inoculated plants - yield of inoculated plants) / yield of un-inoculated plants x 100.
5- Grain yield (Ardab / feddan).

The data were statistically analyzed using conventional two way analysis of variance according to Steel and Torrie (1980). Genotype mean squares were partitioned into its main components. General combining ability (GCA) and specific combining ability (SCA) were estimated using model 1; method 2 for parents and their F_1 crosses (Griffing, 1956).

Variance components were estimated as follows:

σ^2 GCA = (Mg – Me) / (n + 2)

σ^2 SCA = MS – Me

σ^2 e = Me

These components may be translated into genetic components using the following equations:

σ^2 A = 2 σ^2 GCA

σ^2 D = σ^2 SCA

σ^2 e = Me

Where:

σ^2 A = Additive genetic variance

σ^2 D = Dominance genetic variance

σ^2 e = Environmental variance.

A test of significance was estimated using the following formula:

$$+ t = \frac{Effect}{\sqrt{Variance\ of\ effect}}$$

Heritability in narrow sense was estimated according to Hallauer, (1989).

$$h^2_{(n)} = \frac{\frac{1}{2}\sigma^2 A}{\frac{1}{2}\sigma^2 A + \frac{1}{4}\sigma^2 D + \sigma^2 E} x100$$

RESULTS AND DISCUSSION

Mean performance:

Data presented in Table (2) show mean squares of common smut resistance measurements *i.e.* DI (%, DS (%), T.S.S (%),yield reduction (%) and grain yield (ardab/feddan) for half F1 diallel crosses at two sowing dates.

The results indicated that mean squares due to genotypes, parents and their F1 crosses were highly significant at both sowing dates. These results revealed the presence of adequate amount of genetic variability that are valid for further biometric assessments.

Mean square of parent versus crosses was also highly significant for all common smut resistance measurements and grain yield at both sowing dates, indicating average heterosis for these characters.

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Mean performance of common smut resistance measurements and grain yield presented in Table (3) show significant differences among the eight maize parental inbred lines and their F1 crosses at both sowing dates, suggesting that the studied genotypes differed in genes controlling common smut resistance and grain yield.

It is interest to mention that, the parental maize inbred lines L3 and L4 and F1 crosses (L3 x L6), (L3 x L4), (L1 x L3), (L3 x L6), (L1 x L2), (L2 x L4), and (L3 x L5) gave the lowest values of DI, DS, and percent yield reduction as they exhibited desirable values for T.S.S compared to the S.C. 10 check hybrid.

The lowest DI for early and late sowing dates were: 33.33 and 50.00 for L3; 50.00 and 63.33 for L4; 16.67 and 40.00 for (L3 x L4); 30.00 and 53.33 for (L3 x L6); 30.00 and 53.33 for (L1 x L3); 33.33 and 56.67 for (L1 x L2); 33.33 and 56.67 for (L2 x L4) and 36.67 and 60.00 for (L3 x L5), respectively, compared to 36.67 and 60.00 for the S.C. 10 check hybrid. The DS was also lower in early sowing date than the late one. The lowest values of DS for early and late sowing dates were: 13.33 and 20.00 for L3; 20.00 and 33.33 for L4; 18.33 and 25.00 for (L3 x L6); 8.63 and 13.33 for (L3 x L4); 16.67 and 23.33 for (L1 x L3); 21.33 and 24.13 for (L1 x L2); 20.00 and 26.67 for (L2 x L4) and 29.00 and 30.00 for (L3 x L5), respectively, compared to 23.33 and 29.11 for the S.C. 10 check hybrid.

Values of T.S.S for early and late sowing dates were: 12.77 and 10.00 for L3; 10.17 and 8.50 for L4; 11.20 and 4.97 for (L3 x L6); 12.13 and 4.33 for (L3 x L4); 12.20 and 8.00 for (L1 x L3); 12.23 and 10.37 for (L1 x L2); 9.97 and 7.30 for (L2 x L4) and 11.63 and 8.70 for (L3 x L5), respectively, compared to 10.77 and 9.60 for the S.C. 10 check hybrid (Table 3).

These results indicate that maize crosses (L3 x L4), (L3 x L6), (L1 x L3), (L1 x L2), (L2 x L4) and (L3 x L5) were more resistant to common smut disease and could be promising in this regard (Table 3).

On the other hand, the inbred lines L5, L8, L6 and L7 as well as the F1 crosses (L5 x L8), (L5 x L6), (L5 x L7), (L6 x L8), and (L2 x L8) were classified as highly susceptible to common smut disease. They attained the highest DI, DS and yield reduction and the least T.S.S. (Table 3). In this connection, significant amount of genetic variability among parents and their F1 crosses for DS were reported by Jalali and Sabzi (2004), Michalski and Bartos (2004) and Zamani and Dehghanpour (2008).

For grain yield, the following maize inbred lines exhibited the highest values of grain yield at both early and late sowing: L1 (11. 65 and 10.43), L2 (13.12 and 11.42) and L3 (11.27 and 9.82), respectively (Table 3). However, inbred line L7 produced the lowest grain yield at both sowing dates (9.04 and 7.39, respectively), while the remaining inbred lines L4, L5, L6, and L8 exhibited different magnitudes for grain yield (ardab/feddan) (Table 3).

Concerning F1 crosses, the (L3 x L6), (L2 x L3), (L2 x L6), (L4 x L6), (L6 x L8), and (L5x L8) produced the highest grain yield at both early and late sowing dates, but not surpassed the check cultivar S.C.10 except for (L3 x L6) and (L4 x L6) at the late sowing date only (Table 3).

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On the other hand, maize single crosses (L3 x L5) and (L7 x L8) produced the lowest grain yield while the remaining single crosses exhibited different magnitudes for grain yield (Table 3). The variation among maize inbred lines and their F1 crosses might be due to the differences in genetic makeup and characters correlated to this genetic structure of the studied genotypes (Walker, 1975). In this connection, significant differences in grain yield by Habliza *et al.* (2008) and Abd El-Azeem *et al.* (2009).

Combining ability:

Data in Table (4) show mean squares due to GCA, SCA, and GCA/SCA ratio for common smut resistance measurements including. DI, DS, T.S.S., yield reduction, and grain yield at the first and second sowing dates.

The results indicated that, both GCA and SCA variances were highly significant for all common smut resistance measurements and grain yield at both sowing dates. The ratio of σ^2 GCA / σ^2 SCA was more than unity for common smut resistance measurements, indicating that GCA variance was more important than that of SCA in heritability of these characters. Therefore, additive genetic variance was the predominant type controlling common smut resistance characters. These results are in agreement with the results obtained by Odiemah and Kovacs (1990) and Jun *et al.* (2008) who found that GCA mean square was higher in its magnitude than the corresponding SCA ones for common smut resistance. Whereas, for grain yield, SCA variance was larger in magnitude than GCA, resulting in GCA/SCA ratio less than the unity, indicating that dominance gene action was more important in the inheritance of grain yield character. In this respect, El-Shenawy *et al.* (2009), Ali *et al.* (2010), and Bocanski *et al.* (2010) found that SCA variance was more effective than that of GCA for grain yield, which confirms the obtained results.

Estimates of GCA effects on individual parental inbred lines for common smut resistance characters and grain yield at two sowing dates are presented in Table (5). The results revealed that, the inbred lines (L1), (L2), (L3) and (L4) exhibited negative and significant GCA effects. Therefore, these inbreds were the best general combiners and possessed more desired genes for increasing resistance to the common smut disease at both sowing dates. Thus, hybrid breeding program involving these inbred lines, and in particular (L3) and (L4) in single, triple, or double crosses might be useful for building up high resistant hybrids. Similarly, negative and significant GCA effects for common smut resistance were obtained by Fahmi *et al.* (2004) and Chougan *et al.* (2008).Whereas, inbred lines L6 at the two sowing dates, L_2 and L_5 at the first sowing date and L_3 and L_8 at the second sowing date were the best general combiners for grain yield. Thus, hybrid breeding program involving these lines might be useful for producing high yielding hybrids. In this respect, Singh *et al.* (2010) reported that GCA effects were positive and significant for grain yield.

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Data in Table (6) show SCA effects for F1 crosses of some characters related to common smut resistance and grain yield at two sowing dates. These results indicated that negative and highly significant SCA effects were recorded in the single cross (L7 x L8) for DI, DS, and yield reduction, and in the single crosses (L1 x L2), and (L6 x L8) for DI only and single cross (L1 x L8) for yield reduction only at both sowing dates (Table 6). While negative and highly significant SCA effects were recorded in the single cross (L4 x L6) for DI, DS, and yield reduction, and in the single cross (L1 x L8) for DI only, and in the single cross (L1 x L2) for DS and yield reduction at the second sowing date only (Table 6). Moreover, positive and significant SCA effects for T.S.S. in favor of common smut resistance were recorded in the single crosses (L1 x L5), (L3x L5), (L4 x L6), and (L6 x L7) at both sowing dates; while they were recorded in the single crosses (L1 x L2), (L3 x L4), and (L3 x L8) at the first sowing date only (Table 6). However, in the single crosses (L1 x L6), (L2 x L3),(L2 x L5), (L2 x L7), (L4 x L5), (L4 x L7), and (L4 x L8) positive and significant SCA effects for T.S.S. were recorded at the second sowing date only (Table 6). These single crosses could be used to improve common smut resistance. In contrast, negative and significant SCA effects were obtained by Fahmi *et al.* (2004) and Chougan *et al.* (2008).

For grain yield, the results revealed positive and significant SCA effects in most single crosses at the two sowing dates (Table 6). Thus, these single crosses could be used to improve high yielding maize hybrids. These results are in line with those of Abdel-Moneam *et al.* (2009) who reported positive and significant SCA effects for grain yield.

Components of variance and heritability

Data presented in Table (7) show additive, dominance, and environmental variances along with heritability in a narrow sense for some characters related to common smut resistance and grain yield at the two sowing dates. The results indicated that both additive and dominance genetic variances were highly significant and involved in the inheritance of the DI, DS, and yield reduction. The additive genetic variance was larger in its magnitudes than the corresponding dominance one, resulting in σ^2_A/σ^2_D more than unity and confirmed with the results of the GCA and SCA. Therefore, these characters could effectively be improved through the phenotypic selection procedure. On the other hand, the dominance genetic variance represented a major part in the inheritance of TSS and grain yield.

Environmental variance was significant, suggesting that common smut resistance characters are influenced by the environmental changes.

The ratio of additive genetic variance to the total genetic variance as indicated by heritability in narrow sense was high (> 50%) for DI, DS, and yield reduction. These results suggest that selection based on phenotype might be effective for improving common smut resistance. In this connection, Jun *et al.* (2008) recorded high values of narrow sense heritability for common smut disease resistance. Whereas, narrow sense heritability was moderate (30 - 50%) for T.S.S. and low (< 30%) for grain yield. Therefore, selection for such characters might be delayed to later segregated generations.

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Conclusion

It could be concluded that early sowing of maize suppressed the infection of common smut disease, which may be due to increasing T.S.S. and consequently increasing grain yield when compared to late sowing. Inbred lines L1, L2, L3, and L4 were the best general combiners for common smut resistance, while, L2, L3, L5, and L6 were the best for grain yield. The additive genetic variance was the predominant type controlling common smut resistance, while the dominance gene action was more important in the inheritance of grain yield. High values of narrow sense heritability for common smut disease resistance, moderate for T.S.S. % and low for grain yield. Grain yield of the crosses (L3 x L6) (28.46 ardab/feddan) and (L4 x L6) (27.40 ardab/feddan) has surpassed the check hybrid S.C.10 (26.81 ardab/feddan) at the second sowing date.

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وراثة مقاومة مرض التفحم العادي في الذرة الشامية

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***قسم وقاية النبات - كلية الزراعة - جامعة الزقازيق**

أجريت هذه الدراسة فى محطة البحوث الزراعية، كلية الزراعة، جامعة الزقازيق، خلال الموسم الصيفي لعامى ٢٠٠٧ و ٢٠٠٨ باستخدام نظام التهجين الدائري بين ٨ سلالات من الذرة الشامية البيضاء هي L120 و L74 و L144 و L173 و L56 و L82 و L71 و L85 بهدف دراسة متوسط السلوك وتحديد طبيعة الفعل الجيني المتحكم في وراثة المقاومة لمرض التفحم العادي ومحصول الحبوب في الذرة الشامية.

أظهرت النتائج وجود اختلافات معنوية بين التراكيب الوراثية لجميع الصفات تحت الدراسة والتى اشتملت على: نسبة الإصابة ، نسبة المواد الصلبة الذائبة الكلية (TSS) ، شدة الإصابة ، وكذا محصول الحبوب (أردب/فدان). وكان التباين الراجع إلى كل من القدرة العامة والخاصة على الائتلاف معنوياً لجميع الصفات تحت الدراسة كلا الموعدين وكان الفعل الجيني المضيف (ممثلاً في القدرة العامة على الائتلاف) أكثر فعالية من الفعل الجيني غير المضيف (ممثلاً في القدرة الخاصة على الائتلاف) في وراثة صفات المقاومة للمرض، ونسبة المواد الصلبة الذائبة الكلية، و نسبة النقص في المحصول ، بينما كان الفعل الجيني غير المضيف هو المتحكم في وراثة صفة محصول الحبوب (أردب/ فدان). تميزت السلالات (L120)و (L74)و (L144) و(L173) بقدرة عامة على الائتلاف سالبة ومعنوية للصفات المرتبطة بالمقاومة، بينما أظهرت السلالات (L74)و (L144)و (L56) و(L82) قدرة عامة على الائتلاف موجبة ومعنوية لمحصول الحبوب (أردب/فدان). كانت الهجن (L_{120} x L_{85})و (L_{74}x L_{14})و (L_{144} x L_{173})و (L_{173} x L_{82}) و (L_{173}x L_{85}) و (L_{82} x L_{85}) هي الأفضل من حيث المقاومة لمرض التفحم العادي ومحصول الحبوب (أردب/فدان). وقد كانت كفاءة التوريث في المعنى الضيق مرتفعة(أكبر من ٥٠%) لكل من نسبة الإصابة، شدة الإصابة و نسبة النقص في المحصول؛ وكانت متوسطة (٣٠ – ٥٠%) لنسبة المواد الصلبة الذائبة الكلية بينما كانت منخفضة (أقل من ٣٠%) لمحصول الحبوب (أردب/فدان).

قام بتحكيم البحث

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Table (2): Mean squares for disease incidence (DI), disease severity (DS), T.S.S, yield reduction, and grain yield.

Source of variation	df	DI (%)		DS (%)		T.S.S (%)		Yield reduction (%)		Grain yield (ardab/feddan)	
		1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing	1st Sowing date	2nd Sowing date
Replicates	**2**	14.81	136.11	31.55	5.54	9.75	2.23	27.84	6.42	1.40	0.41
Genotypes	**35**	689.4**	606.43**	741.23**	538.62**	11.70**	15.50**	785.22**	639.32**	143.09**	104.10**
Parents	**7**	969.1**	1013.7**	1173.68**	810.95**	4.48**	2.51**	1200.99**	843.39**	4.95**	4.46*
Crosses	**27**	419.1**	430.16**	644.96**	425.91**	13.35**	18.95**	645.11**	444.66**	40.49**	35.82**
P. vs. C.	**1**	6032.1**	2514.9**	313.51**	1675.52**	17.83**	13.15**	1657.69**	4466.77**	3880.28**	2645.32**
Error	**70**	43.39	22.78	36.18	26.00	0.27	0.06	35.90	26.91	0.90	1.70

Table (3): Mean performance of eight maize parents and their F1 crosses for disease incidence (DI), disease severity (DS), T.S.S , yield reduction, and grain yield.

Genotypes	DI (%)		DS (%)		T.S.S. (%)		Yield reduction (%)		Grain yield (ardab/feddan)	
	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date
L1	53.33	70.00	23.33	40.00	11.33	8.73	31.94	49.61	11.65	10.43
L2	60.00	76.67	36.67	46.67	12.07	10.10	44.31	55.56	13.12	11.42
L3	33.33	50.00	13.33	20.00	12.77	10.00	22.21	30.25	11.27	9.82
L4	50.00	63.33	20.00	33.33	10.17	8.50	30.44	45.04	9.59	8.57
L5	83.33	100.00	60.00	68.00	9.53	7.63	69.53	78.80	10.50	9.28
L6	76.67	93.33	51.30	60.67	10.37	8.80	61.19	72.00	10.15	8.83
L7	73.33	90.00	50.00	57.00	9.23	7.97	61.10	67.24	9.04	7.39
L8	83.33	100.00	66.67	63.33	10.53	8.00	75.69	73.76	11.14	9.60
L1 x L2	33.33	56.67	21.33	24.13	12.23	10.37	26.59	29.71	19.01	13.31
L1 x L3	30.00	53.33	16.67	23.33	12.20	8.00	20.48	28.13	26.24	20.86
L1 x L4	36.67	60.00	20.00	31.00	10.97	8.10	24.36	35.89	22.93	14.48
L1 x L5	56.67	80.00	46.67	50.43	13.13	10.30	50.89	55.69	23.70	19.01
L1 x L6	46.67	76.67	36.67	47.14	10.20	10.43	40.59	52.81	25.48	17.66
L1 x L7	46.67	66.67	34.00	37.50	10.53	7.47	38.32	42.11	23.15	21.67
L1 x L8	53.33	70.00	38.67	40.33	8.27	7.17	42.35	44.59	27.29	23.49
L2 x L3	36.67	53.33	16.67	20.00	9.97	9.97	20.06	23.88	29.53	25.82
L2 x L4	33.33	56.67	20.00	26.67	9.97	7.30	24.43	32.01	22.58	18.75
L2 x L5	53.33	76.67	40.67	47.67	10.33	13.10	44.21	53.61	28.26	16.83
L2 x L6	46.67	70.00	30.00	40.33	9.40	9.33	33.30	44.45	30.36	24.29
L2 x L7	46.67	70.00	33.67	39.33	9.60	9.97	37.54	43.61	25.86	23.39
L2 x L8	56.67	80.00	56.67	51.00	7.63	7.53	60.59	55.64	25.54	21.57
L3 x L4	16.67	40.00	8.63	13.33	12.13	4.33	12.15	17.67	28.47	23.08
L3 x L5	36.67	60.00	29.00	30.00	11.63	8.70	34.58	35.26	17.92	19.04
L3 x L6	30.00	53.33	18.33	25.00	11.20	4.97	21.74	28.51	29.34	28.46
L3 x L7	43.33	66.67	47.83	35.70	5.33	5.37	52.72	40.37	20.48	21.77
L3 x L8	50.00	70.00	50.00	40.00	9.80	5.03	54.16	44.25	24.07	23.90
L4 x L5	46.67	70.00	38.00	40.73	10.60	9.73	41.69	45.29	27.16	22.13
L4 x L6	40.00	60.00	26.67	30.33	13.33	10.20	30.21	34.00	28.26	27.40
L4 x L7	43.33	66.67	32.67	36.67	8.83	8.17	36.65	43.16	25.10	15.61
L4 x L8	50.00	73.33	34.33	38.33	8.37	12.27	38.16	42.45	26.16	24.30
L5 x L6	63.33	86.67	63.33	56.67	8.47	5.90	67.11	61.44	26.46	20.97
L5 x L7	63.33	83.33	48.33	53.33	9.67	2.80	51.78	57.84	29.06	22.35
L5 x L8	70.00	93.33	62.67	63.49	4.77	5.00	66.00	69.21	30.08	17.50
L6 x L7	53.33	76.67	36.67	46.11	10.43	7.33	41.56	52.67	20.42	15.24
L6 x L8	56.67	80.00	58.33	50.00	6.60	6.87	62.15	53.93	26.22	25.48
L7 x L8	53.33	76.67	43.33	46.00	8.03	4.87	49.21	51.57	17.19	17.96
S.C.10	36.67	60.00	23.33	29.11	10.77	9.60	26.49	32.88	31.75	26.81
L.S.D 0.05	10.70	12.55	9.77	10.44	0.85	0.39	9.74	8.43	1.54	2.15

Table (4): Mean squares for general combining ability (GCA) and specific combining ability (SCA) for disease incidence (DI), disease severity (DS), T.S.S., yield reduction, and grain yield.

Source of variation	df	DI (%)		DS (%)		T.S.S. (%)		Yield reduction (%)		Grain yield (ardab/feddan)	
		1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date
Genotypes	**35**	689.42**	606.43**	741.23**	538.62**	11.70**	15.50**	785.22**	639.32**	143.09**	107.49**
GCA	**7**	2760.00**	2867.50**	3062.86**	2233.92**	22.44**	22.01**	3088.52**	2318.99**	25.62**	40.44**
SCA	**28**	270.34**	143.57**	160.83**	114.80**	9.02**	13.87**	209.39**	219.41**	172.45**	124.26**
Error	**70**	43.39	22.78	36.18	26.00	0.27	0.06	35.90	26.91	0.90	1.75
σ2 GCA/ σ2 SCA		10.21	19.97	19.04	19.46	2.49	1.59	14.75	10.57	0.15	0.33

Table (5): Effect of general combining ability on disease incidence (DI), disease severity (DS), T.S.S.,yield reduction, and grain yield.

Lines	DI (%)		DS (%)		T.S.S. (%)		Yield reduction (%)		Grain yield (ardab/feddan)	
	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date
L1	-4.17**	-3.92**	-7.21**	-3.45**	1.03**	0.67**	-7.25**	-3.48**	-0.71**	-1.41**
L2	-2.50*	-2.58**	-4.04**	-2.59	0.34**	1.52**	-4.47**	-2.90*	0.92**	0.14
L3	-14.17**	-14.58**	-11.90**	-14.10**	0.79**	-0.62**	-11.97**	-14.44**	0.04	1.72**
L4	-8.50**	-8.92**	-11.25**	-8.47**	0.46**	0.45**	-11.15**	-8.25**	0.16	-0.25
L5	10.50**	10.75**	11.59**	10.99**	-0.22*	-0.18**	11.53**	11.29**	0.54**	-0.90**
L6	3.83**	4.75**	3.98**	4.85**	0.05	0.01	3.91**	4.88**	0.86**	1.17**
L7	4.50**	4.42**	4.37**	4.02*	-0.90**	-1.07**	5.00**	4.28**	-1.89**	-1.26**
L8	10.50**	10.08**	14.46**	8.74**	-1.54**	-0.78**	14.40**	8.62**	0.06	0.80**
S.E.(gi-gj)	1.125	0.815	1.027	1.097	0.089	0.041	1.023	0.886	0.162	0.226

Table (6): Effect of specific combining ability (SCA) on disease incidence (DI), disease severity (DS), T.S.S., yield reduction, and grain yield.

Genotypes	DI (%)		DS (%)		T.S.S. (%)		Yield reduction (%)		Grain yield (ardab/feddan)	
	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date
L1 x L2	-10.2** [b]	-8.22* [c]	-4.39	-10.8**	0.88**	0.11	-3.91	-10.9**	-3.22**	-3.80**
L1 x L3	-1.85	0.44	-1.20	-0.04	0.39	-0.12	-2.52	-0.94	4.89**	2.17**
L1 x L4	-0.85	1.44	1.48	1.99	-0.51	-1.09**	0.54	0.62	1.45*	-2.24**
L1 x L5	0.15	1.78	5.31	1.95	2.34**	1.74**	4.38	0.88	1.85**	2.94**
L1 x L6	-3.19	4.44	2.92	4.81	-0.86**	1.69**	1.72	4.41	3.30**	-0.48
L1 x L7	-3.85	-5.22*	-0.14	-4.00	0.42	-0.20	-1.65	-5.68	3.72**	5.97**
L1 x L8	-3.19	-7.56**	-5.55	-5.89	-1.21**	-0.79**	-7.02*	-7.54*	5.92**	5.72**
L2 x L3	3.15	-0.89	-4.37	-4.24	-1.15**	1.00**	-5.73	-5.78	6.55**	5.59**
L2 x L4	-5.85	-3.22	-1.68	-3.21	-0.82**	-2.74**	-2.17	-3.85	-0.52	0.49
L2 x L5	-4.85	-2.89	-3.85	-1.67	0.23	3.69**	-5.08	-1.78	4.77**	-0.78
L2 x L6	-4.85	-3.56	-6.91*	-2.86	-0.97**	-0.26*	-8.36**	-4.53	6.56**	4.60**
L2 x L7	-5.52	-3.22	-3.64	-3.03	0.18	1.45**	-5.22	-4.77	4.80**	6.14**
L2 x L8	-1.52	1.11	9.28**	3.92	-1.15**	-1.27**	8.43**	2.92	2.53**	2.25**
L3 x L4	-10.8**	-7.89**	-5.20	-5.03	0.89**	-3.56**	-6.96*	-6.64*	6.25**	3.24**
L3 x L5	-9.85**	-7.56**	-7.67	-7.82*	1.08**	1.43**	-7.20*	-8.6**	-4.69**	-0.16
L3 x L6	-9.85**	-8.22**	-10.7**	-6.68*	0.38	-2.48**	-12.4**	-8.9**	6.41**	7.19**
L3 x L7	2.81	5.44*	18.4 **	4.84	-4.54**	-1.01**	17.5**	3.53	0.30	2.94**
L3 x L8	3.48	3.11	10.5**	4.43	0.56*	-1.63**	9.51**	3.07	1.95**	3.01**
L4 x L5	-5.52	-3.22	0.68	-2.73	0.37	1.39**	-0.92	-4.76	4.43**	4.90**
L4 x L6	-5.52	-7.22**	-3.04	-6.99*	2.84**	1.68**	-4.77	-9.6**	5.21**	8.10**
L4 x L7	-2.85	-0.22	2.57	0.18	-0.72*	0.72**	0.58	0.12	4.80**	-1.25
L4 x L8	-2.19	0.78	-5.85	-2.88	-0.55*	4.53**	-7.31*	-4.92	3.91**	5.38**
L5 x L6	-1.19	-0.22	10.8**	-0.11	-1.34**	-1.99**	9.45**	-1.73	3.03**	2.31**
L5 x L7	-1.85	-3.22	-4.60	-2.62	0.80*	-4.02**	-6.98*	-4.73	8.38**	6.14**
L5 x L8	-1.19	1.11	-0.35	2.82	-3.46**	-2.10**	-2.16	2.30	7.45**	-0.77
L6 x L7	-5.19	-3.89	-8.66**	-3.70	1.30*	0.33**	-9.56**	-3.49	-0.58	-3.05**
L6 x L8	-7.85*	-6.22*	2.92	-4.53	-1.90*	-0.42**	1.62	-6.57*	3.27**	5.12**
L7 x L8	-11.9**	-9.22**	-12.5**	-7.70*	0.48	-1.35**	-12.4**	-8.33*	-3.01**	0.05
S.E.(sij)	3.448	2.499	3.149	3.252	0.273	0.127	3.137	3.252	0.498	0.703

[a] **Yield reduction (%) = (yield of un-inoculated plants - yield of inoculated plants) / yield of un-inoculated plants x 100**
[b] **** significant at 0.01 %**
[c] ***significant at 0.05 %**

Table (7): Components of variances and heritability for some related characters to common smut resistance and grain yield.

Genetic components	Disease incidence (%)		Disease severity (%)		T.S.S (%)		Yield reduction (%)		Grain yield (ardab/feddan)	
	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date	1st Sowing date	2nd Sowing date
σ^2 A	543.3**±6.01	568.9**±6.15	605.3**±6.35	441.6**±5.42	4.43**±0.543	4.4**±0.541	610.5**±6.37	458.4**±5.52	4.9**±0.57	6.0**±0.632
σ^2 D	226.96**±3.88	120.8**±2.83	124.6**±2.88	88.8**±2.43	8.75**±0.763	13.8**±0.959	173.5**±3.40	192.5**±3.58	171.6**±3.38	120.5**±2.83
σ^2 E	43.4**±1.7	22.8**±1.23	36.2**±1.55	26.0**±1.31	0.27*±0.134	0.06±0.063	35.90**±1.54	26.9**±1.33	0.90**±0.24	1.7**±0.336
h^2 (n)	73.06	84.30	81.79	82.08	47.40	38.47	79.38	75.33	5.34	8.62
σ^2 A/ σ^2 D	2.39	4.70	4.85	4.97	0.50	0.32	3.01	2.38	0.02	0.04