SELECTION OF NEW HYBRID COMBINATIONS OF YELLOW MAIZE FOR HIGH YIELD AND RESISTANCE AGAINST LATE WILT DISEASE VIA LINE × TESTER ANALYSES UNDER DIFFERENT ENVIRONMENTAL CONDITIONS

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ABSTRACT

Forty two new inbred lines of yellow maize were top-crossed with two testers at Sakha Agricultural Research Station during 2006 summer season. The resultant 84 top-crosses were divided into two sets where each set included 42 top-crosses with two commercial checks. All genotypes were evaluated under two different experimental conditions in 2007 growing season. The first experiment was conducted at both Sakha and Mallawy Stations to be evaluated for grain yield (GY) and number of days to mid-silking (DS) and the second experiment was cultivated under artificial infection by the pathogen *Cephalosporium maydis* under two levels of nitrogen fertilizer to assess the resistance to late wilt disease (RLW%). The best seven top-crosses for yielding ability with resistance against late wilt disease were selected from the two sets and evaluated at four locations i.e. Sakha, Gemmiza, Sids and Mallawy Stations for GY, DS and RLW% traits during the 2009 growing season.

The mean squares were significant or highly significant due to lines (L) for DS, GY and RLW%. Moreover, mean squares due to testers (T) and L x T interaction were significant or highly significant for RLW% in the two sets except for T in set-2. It appeared that DS and GY in set-2 could be mainly controlled by additive genes, while, GY of set-1 and RLW% of the two sets were mainly controlled by non-additive genes.

Inbred lines Sk10 in set-1 and Sk23 in set-2 were identified to be the best combiners for earliness, grain yield and resistance to late wilt disease simultaneously. Meanwhile, top-crosses Sk3 x SC162 and Sk14 x SC166 in set-1 showed favorable genes for yielding ability with high RLW%. It was noticed that 12 top-crosses in set-1 and two top-crosses in set-2 were significantly increased for grain yield over the best checks and had high resistance to late wilt disease.

Results of evaluation trail for best top crosses across the four locations indicated that the mean performances of the seven crosses i.e. Sk23 x SC162, Sk10 x SC162, Sk11 x SC166, Sk17 x SC166, Sk19 x SC162, Sk17 x SC162 and Sk18 x SC162 significantly surpassed the commercial check in grain yield by 3.15, 2.75, 2.56, 2.54, 2.52, 2.16 and 1.37 ton/ha, respectively. At the same time, they also exhibited high resistance to late wilt disease. This result emphasized the obtained result from top-cross trails, indicating that these promising yellow three way crosses stabilized yield and resistant to late wilt disease in different environments and would be very essential and valuable in maize improvement programs.

Keywords: Yellow Maize, Line x tester, late wilt resistance.

INTRODUCTION

The practical phase of maize breeding is based upon the development of inbred lines and the evaluation of these lines when they are involved in hybrid combinations. Combining ability of inbred lines is the crucial factor in determining their future usefulness for developing maize

hybrids (Vasal *et al.,* 1992). Line x tester mating design provides reliable informations about the general combining ability effects of parents and specific combining ability of their hybrid combinations and provides opportunities to eliminate undesirable inbred lines and select the most desirable ones to constitute various hybrid combinations (Iqbal *et al.* 2007).

Breeding for high yielding ability, early maturity and resistance to main diseases especially late wilt disease are considered among the main targets of national maize breeding program in Egypt to reduce feed and food crisis and also to reduce the amount of imported yellow maize.

Grain yield was reported to be controlled by additive genes (Qadri *et al.* 1983; Zieger, 1989; Faheem *et al.* 1995; Kadlubiec et al. 2000; Motawei and Ibrahim 2005 and Iqbal *et al.* 2007). The same observation was noticed by Rodrigues and Silva (2002); Baoxian et al (2003) and Motawei (2006) for days to mid-silk. However some investigators (Inoue 1984; Anees 1987; Dodiya and Joshi 2003; Motawei *et al.* 2005; Motawei 2006 and Ahsan *et al.* 2007) found that non-additive genetic effects were predominant in the inheritance of grain yield. These differences generally arise due to differences in genetic materials and the environments under which the experiments were performed. In the same way Shehata 1976; El-Itriby *et al.* 1984; Amer *et al.* 1999 and Mosa *et al.* 2004 found that non-additive genetic effects were more important than additive genetic effects in the inheritance of late wilt resistance

The objective of the present investigation were focused on the selection for the most desirable general combiner inbred lines; to generate information on nature and magnitude of gene action for studied traits and to identify candidates of promising yellow hybrid combinations for yielding ability with high resistance to late wilt disease.

MATERIALS AND METHODS

1-Top-cross experiments

The materials in this study were 42 new maize yellow inbred lines (S_5 generation) which isolated from different local and exotic genetic sources. These inbred lines were top-crossed with SC162 and SC166 as yellow male testers at Sakha Agricultural Research Station (SARS) in 2006 growing season. The resulting 84 top-crosses were divided into two sets where each set contained 42 top-crosses along with TWC 351 and TWC 352 as commercial check hybrids and evaluated at two different experiments during 2007 summer season. First experiment was conducted at two locations; Sakha (lower Egypt) and Mallawy (upper Egypt) ARS. A randomized complete blocks design (RCBD), according to Steel and Torrie 1980, with four replications were used. Plot size was one row, 6m long, 0.80m width, 0.25m between hills and one plant was left per hill after thinning. All agricultural practices were done as recommended for the maize cultivation. Data were recorded for number of days to mid-silk (DS) and grain yield t/ha (GY). Each plot was harvested alone where ears were weighed as (kg/plot), shelling percentage and grain moisture% were also recorded. These data were used to calculate grain yield (t/ha) adjusted at 15.5 moisture content.

The second experiment was performed in a disease nursery under artificial soil inoculation by the pathogen *Cephalosporium maydis* which causes late wilt disease under two levels of nitrogen fertilizer 70 and 140kg N/fed. RCBD with three replications was also used where plot size was one row, 2m long, 0.80m apart, 0.20m between hills and one plant was left per hill. After 35 days from days to mid-silk, infected plants from each plot were recorded and adjusted to the percentage of resistance (RLW %). The data were transformed by using arcsine scale according to Snedecor and Cochran (1967).

2- Evaluation trails of best top-crosses

Seven top-crosses chosen on the basis of superiority in grain yield; earliness and high resistance to late wilt disease with simplicity in forming were re-constituted in 2008 season at Sakha station. These seven top-crosses along with check TWC352 were evaluated at Sakha, Gemmiza, Sids and Mallawy in 2009 growing season. RCBD with four replications was used at all locations. Plot size was 4 rows, 6m long, 0.80m width and 0.25m between hills. Data were recorded on the inner two rows for GY, DS and RLW%.

Combined analyses of variance over locations as well as over the two nitrogen levels were done after testing the homogeneity of error mean squares according to Bartlett test (1937). Genotypes and nitrogen levels were considered as fixed effect while, locations were considered random effect. Line x tester analysis was made as outlined by Singh and Chaudhary (1979) to be used to estimate the general and specific combining ability effects.

RESULTS AND DISCUSSION

1-Top cross experiments

Analyses of variance for days to mid-silk (DS) and grain yield (GY) across the two locations and percentage of resistance to late wilt disease across two nitrogen levels for the two sets are presented in Table 1. Highly significant mean squares were detected between locations for the two studied traits (DS and GY) in the two sets, indicating that the presence of differences between the two locations for these traits as a result of the variation in climatic and soil conditions. The mean squares due to nitrogen levels were only significant in set-1, indicating that the dose of nitrogen fertilizer obviously affected the susceptibility to this disease whereas; the resistance was decreased with increasing nitrogen doses.

The mean squares due to genotypes (G) and for the partitioned crosses (C) were detected to be highly significant for all traits analyzed of the two sets indicating the presence of significant differences between genotypes for studied traits in the two sets. It should be indicated that the interaction among G and their partitions i.e. C, CH and C vs. CH with locations were significant or highly significant for grain yield of the two sets. On the other hand, highly significant differences among checks were detected for LWR% in the two sets.

Table 1: Combined analysis for days to mid-silk and grain yield over two locations (Sk and Mal) and percentage of resistance to late wilt disease over two nitrogen levels (70 and 140kg N/fed).

S.O.V.	d.f	Days to mid-silk		grain yield		S.O.V	d.f	Resistance to late wilt %	
		Set-1	Set-2	Set-1	Set-2			Set-1	Set-2
Locations (Loc.)	1	71.82**	112.50**	307.82**	5.27**	Nitrogen (N)	1	902.95*	267.69
R/Loc.	6	7.06	9.07	1.57	0.94	R/N	4	77.73	75.77
Genotypes (G)	43	9.82**	7.33**	12.15**	13.56**	Genotypes (G)	43	510.66**	440.23**
Crosses (C)	41	10.22**	7.64**	12.26**	13.79**	Crosses (C)	41	519.55**	444.52**
Check (Ch)	1	3.06	1.56	0.02	1.41	Check (Ch)	1	618.34**	699.52**
C vs. Ch	1	0.18	0.39	19.77	16.28	C vs. Ch	1	38.49	5.05
G x Loc.	43	2.16	1.89	3.47**	5.67**	G x N	43	43.143	19.45
C x Loc.	41	2.26	1.98	3.50**	5.81**	C x N	41	38.76	17.28
Ch x Loc.	1	0.06	0.06	4.24**	2.84*	Ch x N	1	202.212	104.43
C vs. Ch x Loc.	1	0.33	0.25	3.69**	2.51*	C vs. Ch x N	1	63.78	23.44
Error	258	1.93	2.53	0.51	0.64	Error	172	71.23	44.86
C.V%		2.2	2.5	7.1	7.9	C.V%		10.4	8.07

*, ** significant differences at 0.05 and 0.01 levels of probability, respectively.

Mean performances for days to mid-silk and grain yield t/ha across both locations and resistance to late wilt across two nitrogen levels are presented in Table 2. Days to mid-silk ranged from 59.3 days of top cross (Sk3 x SC162) to 64.0 days of top cross (Sk20 x SC162) with an average of 62.6 days and from 60.8 days of top cross (Sk31 x SC166) to 64.9 days of top cross (Sk38 x SC166) with an average of 62.6 days in set-1 and set-2, respectively. Best top-crosses for earliness were Sk3 x SC162 and Sk3 x SC166 in set-1 and Sk23 x SC162 and Sk31 x SC166 in set-2 where they showed significantly decrease compared to the two checks. Grain yield in set-1 ranged from 7.64 t/ha (Sk3 x SC166) to 12.14 t/ha (Sk19 x SC162) with an average of 10.06 t/ha and in set-2 it ranged from 7.35 t/ha (Sk24 x SC166) to 12.87 t/ha (Sk23 x SC162) with an average of 10.13 t/ha. Twelve top-crosses i.e. Sk19 x SC162 (12.14 t/ha), Sk17 x SC166 (12.11 t/ha), Sk17 x SC162 (12.03 t/ha), Sk11 x SC166 (11.99 t/ha), Sk10 x SC162 (11.83 t/ha), Sk18 x SC162 (11.72 t/ha), Sk16 x SC162 (11.63 t/ha), Sk21 x SC162 (11.50 t/ha), Sk21 x SC166 (11.34 t/ha), Sk16 x SC166 (11.46 t/ha), Sk4 x SC166 (11.33 t/ha) and Sk7 x SC162 (11.09 t/ha) in set-1 and two top-crosses i.e. Sk23 x SC162 (12.87 t/ha) and Sk25 x SC166 (12.16 t/ha) in set-2 were increased significantly for grain yield than the best check TWC352. On the other hand, resistance to late wilt in set-1 ranged from 76.0% for the top cross (Sk12 x SC162) to 100% for the 20 top crosses with an average of 93.8% and from 80.30% for the top cross (Sk23 x SC162) to 100% for the 24 top crosses with an average of 95.6% in set-2. The above results revealed that the top crosses which significantly outyielded the best checks (12 in set-1 and 2 in set-2) also showed high resistance to late wilt disease over 95.5%, this indicated that these new three way crosses would be fruitful in future maize breeding program for high yielding ability with resistance to late wilt disease. In this respect, these promising hybrids still need an extensive testing before releasing them as stable hybrids for yield and important economic traits.

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Line x tester analyses over the two locations for grain yield (GY) and days to mid-silk (DS) and over the two nitrogen levels for RLW% are presented in Table 3. The mean squares due to lines (L) were significant or highly significant for DS, GY and RLW% traits in the two sets, indicating the presence of important differences among lines. Moreover, mean squares due to testers (T) and L x T interaction were significant or highly significant differences for RLW% in the two sets except for testers (T) in set-2. These results reflected the presence of great diversity which was existed among testers and inbred lines in their respective top-crosses, and also the significant of L x T interactions suggested that inbred lines may perform differently in top-crosses according to the type of used tester. Moreover, L x Env. and L x T x Env. interactions were highly significant for GY in the two sets. These results were in harmony with those obtained by Mosa *et al.* (2004), Motawei (2006), Mosa *et al.* (2009) and Rather *et al.* (2009) for grain yield and days to mid-silk.

Table 3: Combined analysis of line x tester across two environmental (Env.) conditions (two locations or nitrogen levels) for the three studied traits.

S.O.V	d.f	MS					
		Set-1			Set-2		
		Days to mid-silk	Grain yield	Resistance to late wilt %	Days to mid-silk	Grain yield	Resistance to late wilt %
Lines (L)	20	18.70**	20.56**	691.78**	13.08**	26.44*	766.95**
Testers (T)	1	1.44	7.97	302.33*	3.44	0.03	94.895
L x T	20	2.18	4.17	358.18**	2.41*	1.83	140.68**
L x Env.	20	2.77	4.93**	51.11	3.01	10.46**	22.39
T x Env.	1	1.44	0.09	0.912	0.58	1.65	0.774
L x T x Env.	20	1.79	2.24**	28.29	1.03	1.37**	13.01

*, ** ♀Significant differences at 0.05 and 0.01 levels of probability, respectively.

Estimates of general combining ability effects for 42 inbred lines in the two sets for the studied traits are shown in Table 4. Five inbred lines in set-1 (Sk3, Sk4, Sk5, Sk10 and Sk21) and three inbred lines in set-2 (Sk23, Sk31 and Sk41) exhibited negative and significant estimates of GCA effects toward earliness. Meanwhile, 6 inbred lines (Sk10, Sk16, Sk17, Sk18, Sk19 and Sk21) in set-1 and 2 inbred lines (Sk23 and Sk25) in set-2 had desirable estimates of GCA effects for high yielding ability. On the other hand, 6 inbred lines i.e. Sk10, Sk11, Sk16, Sk17, Sk18 and Sk19 in set-1 and 10 inbred lines i.e. Sk23, Sk25, Sk28, Sk29, Sk31, Sk36, Sk37, Sk38, Sk41 and Sk42 in set-2 appeared to be the best general combiners for resistance to late wilt disease. In view of the results of GCA effects, it would be noticed that the inbred lines Sk10 in set-1 and Sk23 in set-2 were characterized by good general combiners for earliness, grain yield and resistance to late wilt disease simultaneously. This result indicated that these new inbred lines could be used in future maize breeding programs for improving these traits.

Specific combining ability effects for 84 top-crosses for all studied traits are presented in Table 5. Desirable estimates of SCA effects toward earliness were achieved by Sk4 x SC166, Sk15 x SC166 and Sk17 x SC162

in set-1 and by Sk23 x SC162, Sk28 x SC166, Sk29 x SC166, Sk39 x SC162 and Sk42 x SC162 in set-2. Positive and desirable estimates of SCA effects for grain yield were observed in top crosses Sk3 x SC162, Sk7 x SC162, Sk11 x SC166, Sk14 x SC166 and Sk20 x SC162 in set-1 and Sk22 x SC166, Sk23 x SC162 and Sk41 x SC162 in set-2.

Table 4: Estimates of general combining ability effects for 42 inbred lines and two testers for studied traits at two sets.

Inbred line	Set-1			Inbred line	Set-2		
	Days to mid-silk	grain yield	Resistance to late wilt %		Days to mid-silk	Grain yield	Resistance to late wilt %
Sk-1	0.283	-0.838	-3.978	Sk-22	-0.557	0.899	-2.850
Sk-2	-0.717	-0.159	-5.434*	Sk-23	-0.994*	2.086*	6.986*
Sk-3	-2.655*	-1.414	-3.510	Sk-24	1.631*	-2.601*	-10.30*
Sk-4	-1.155*	0.657	3.345	Sk-25	0.131	1.836*	5.520*
Sk-5	-1.155*	-0.632	-10.934*	Sk-26	-0.432	0.836	2.80
Sk-6	-0.280	-0.794	2.409	Sk-27	0.069	-1.476	-14.73*
Sk-7	0.658	-0.013	0.157	Sk-28	-0.432	0.649	6.986*
Sk-8	0.470	-1.089	-9.995*	Sk-29	-0.682	0.836	6.986*
Sk-9	-0.217	-0.660	2.523	Sk-30	0.006	-1.851*	-8.27*
Sk-10	-1.842*	1.209*	9.020*	Sk-31	-1.619*	1.149	6.986*
Sk-11	0.845	1.061	9.020*	Sk-32	1.506*	-0.914	-11.14
Sk-12	0.408	-1.827	-12.990*	Sk-33	0.569	-0.101	1.310
Sk-13	0.095	-0.629	-0.107	Sk-34	-0.057	-1.726*	-11.113*
Sk-14	0.908*	-0.538	-2.086	Sk-35	0.819	-1.163	-0.617
Sk-15	1.095*	-0.787	-7.442*	Sk-36	0.131	0.399	6.986*
Sk-16	0.783	1.393*	9.020*	Sk-37	0.006	-0.226	6.986*
Sk-17	0.158	1.920*	9.020*	Sk-38	1.881*	1.211	6.986*
Sk-18	0.408	1.272*	9.020*	Sk-39	-0.244	-0.164	-0.982
Sk-19	1.220*	1.648*	9.020*	Sk-40	0.131	-1.164	-12.314*
Sk-20	1.658*	-1.045	-10.727*	Sk-41	-1.307*	0.336	6.986*
Sk-21	-0.967*	1.266*	4.627	Sk-42	-0.557	1.149	6.986*
Tester SC162	0.0655	0.154	-1.095	Tester SC162	0.0804	0.0268	-0.614
Tester SC166	-0.0655	-0.154	1.095	Tester SC166	-0.0804	-0.0268	0.614
L.S.D GCA (Line) at 0.05	0.868	1.158	4.78	L.S.D GCA (L) at 0.05	0.905	1.687	3.79
L.S.D GCA (Tester) at 0.05	1.176	0.294	1.47	L.S.D GCA (T) at 0.05	0.747	1.26	1.17

* Significant difference at 0.05 level of probability.

Concerning the estimates of SCA effects for RLW%, 4 top-crosses i.e. Sk3 x SC162, Sk6 x SC162, Sk13 x SC166 and Sk14 x SC166 in set-1 and 7 top-crosses i.e. Sk24 x SC162, Sk26 x SC166, Sk27 x SC166, Sk33 x SC166, Sk34 x SC162, Sk35 x SC166 and Sk39 x SC162 in set-2 showed positive and significant estimates toward resistance to late wilt disease. Generally, the top-crosses Sk3 x SC162 and Sk14 x SC166 in set-1 had favorable alleles for high yielding ability with resistance to late wilt disease, indicating that these promising yellow hybrids would be effective and valuable in future maize breeding program.

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Additive (K^2GCA) and non-additive (K^2SCA) genetic effects and their magnitudes from total genetic effects for all studied traits are shown in Table 6. Both days to mid-silk of the two sets and GY in set-2 were mainly controlled by additive gene action of about 63.0% and 55.8%, respectively. Meanwhile, GY in set-1 and RLW% in the two sets appeared to be mainly controlled by non-additive gene action of about 69.4% for GY and 96.8% in set-1 and 74.1% in set-2 for RLW%. These results were in good agreements with those obtained by Rodrigues and Silva (2002); Baoxian *et al.* (2003) and Motawei (2006) who reported that days to mid-silk were controlled by additive gene action. The same findings were obtained for grain yield by Qadri *et al.* 1983; Zieger (1989); Faheem *et al.* (1995); Kadlubiec *et al.* (2000); Motawei and Ibrahim (2005); Immanuel *et al.* (2006) and Iqbal *et al.* (2007). Meanwhile, other investigators found that non-additive genetic effects played the main role in the inheritance of grain yield (Inoue, 1984; Anees, 1987, Dodiya and Joshi 2003; Motawei *et al.* 2005, Motawei 2006 and Ahsan *et al.* 2007) and resistance to late wilt disease (Shehata 1976; El-Itriby *et al.* 1984; Amer *et al.* 1999 and Mosa *et al.* 2004).

Table 6: Genetic components for the studied traits in the two sets.

Genetic components	Set-1			Set-2		
	Days to mid-silk	grain yield	Resistance to late wilt %	Days to mid-silk	grain yield	Resistance to late wilt %
Additive genetic effects (K^2GCA)	0.0823	0.1067	1.58	0.295	0.073	5.59
Non-additive genetic effects (K^2SCA)	0.0485	0.242	47.83	0.173	0.0579	15.97
K^2GCA%	62.9	30.6	3.20	63.0	55.8	25.93
K^2SCA%	37.1	69.4	96.8	37.0	44.2	74.1

2- Evaluation trails of best top crosses:

Highly significant mean squares due to locations (L), genotypes (G) and G x L interactions were detected for all studied traits except of G for RLW% and G x L for grain yield which were insignificant as seen in Table 7.

Table 7: Combined analysis of variance for days to mid-silk, grain yield and resistance to late wilt disease of 7 crosses and check variety over four locations.

S.O.V	d.f	Days to mid-silk	Grain yield	RLW%
Location (Loc.)	3	117.77**	47.43**	67.36**
Rep/Loc.	12	4.65	0.77	2.21
Genotypes (G)	7	13.20**	16.07**	10.36
GX Loc.	21	1.80**	1.23	5.18*
Error	84	0.60	0.84	2.96
C.V%		1.30	8.90	1.80

*, ** Significant differences at 0.05 and 0.01 levels of probability, respectively.

The mean performances of 7 top-crosses and the check TWC352 for grain yield, days to mid-silk and resistance to late wilt across the four locations as presented in Table 8, showed that all promising top-crosses were insignificantly different in earliness when compared with the check

variety TWC352 except for the top-cross Sk19 x SC162 which was earlier than the check. On the other hand, the 7 promising top-crosses: Sk23 x SC162 (11.40 ton/ha), Sk10 x SC162 (11.0 ton/ha), Sk11 x SC166 (10.81 ton/ha), Sk17 x SC166 (10.79 ton/ha), Sk19 x SC162 (10.77 ton/ha), Sk17 x SC162 (10.41 ton/ha) and Sk18 x SC162 (9.62 ton/ha) had significant increase in grain yield than the check TWC352 which gave 8.25 ton/ha and surpassed its yield by 3.15, 2.75, 2.56, 2.54, 2.52, 2.16 and 1.37 ton/ha, respectively. Moreover, all previous top-crosses exhibited high resistance to late wilt disease that ranged from 95.1 to 97.4%.

Table 8: Mean performances for 7 crosses and check variety TWC352 for days to mid-silk, grain yield t/ha and resistance to late wilt disease across four locations.

Genotype	Days to mid-silk	Grain yield (t/ha)	RLW%
Sk10 x SC162	61.6	11.00	96.6
Sk11 x SC166	61.6	10.81	96.4
Sk17 x SC162	62.2	10.41	96.7
Sk17 x SC166	63.1	10.79	97.4
Sk18 x SC162	62.2	9.62	97.3
Sk19 x SC162	60.1	10.77	95.0
Sk23 x SC162	62.8	11.40	97.5
TWC352	62.2	8.25	95.9
LSD at 0.05	1.0	0.82	1.7
0.01	1.3	1.09	2.3

In general, the result emphasized that the stability of yield and high resistance to late wilt disease in different environments of these promising three way crosses put them as very essential and fruitful improved germplasm in future maize improvement programs.

REFERENCES

Ahsan M.; H. Hussnain; M. Saleem; T. A. Malik and M. Aslam (2007). Gene action and progeny performance for various traits in maize. Pak. J. Agri. Sci., 44(4):608-613.

Amer, E.A.; S.A. Tolba and H.E. Gado (1999). Genetic analyses of late wilt disease, grain yield and three agronomic traits in maize. Egypt. J. Appl. Sci., 14 (9):133-143.

Anees, M.A. (1987). Combining ability studies in maize (*Zea mays* L.), single crosses, M.Sc. thesis, Dep. Pl. Breed. Genet. Univ. Agric., Faisalabad.

Baoxian, Z.; Z. Han; X. Lei; W. Han; M. Cheng; X. Liang and R. Chen (2003). Analysis and evaluation on combining ability of 9 maize inbred lines. J. Maize Sci.11: 54-58.

Bartlett, M.S. (1937). Properties of Sufficiency and Statistical Tests .Prod. Roy. Soc., London, Series A, 160:268-282.

Dodiya, N.S. and V.N. Joshi (2002). Gene action for grain yield and its attributes in maize (*Zea mays* L.). Indian J. Genet. and Pl. Breed., 62 (3): 253-254.

EL-Itriby H.; M.N. Khamis; R.M. EL-Demerdash and H.A. El-Shafey (1984). Inheritance of resistance to late wilt (*Cephalosporium maydis*) in maize. Proc. 2nd Mediterranean Conf. Genet., Cairo, March (29-44).

Faheem H.; M. Saleem; A. Ahmad and A. Naveed (1995).Combining ability for grain yield and its components in maize (*Zea mays* L.). Pak. J. Agric. Sci., 32(2-3):168-171.

Immanuel S.; P. Nagarajan and L.D. Vijendra (2006). Heterotic expression and combining ability analysis for qualitative and quantitative traits in inbreds of maize (*Zea mays* L.). India Crop Res., 32(1): 77-85.

Inoue, Y. (1984). Specific combining ability between six different types of maize (*Zea mays* L.) obtained from diallel set of 11 open pol1inated varieties. Jap. J. Breed., 34 (1): 17-84.

Iqbal A.M.; F.A. Nehvi; S.A. Wani; Q. Rehana and A.D. Zahoor (2007). Combining ability analysis for yield and yield related traits in maize (*Zea mays* L.). Inter. J. Pl. Breed. and Genet., 1(2): 101-105.

Kadlubiec, W.; C. KarwowSka; Z. Kurczych; R. Kuriata and S. WalczowSka-Kurczych (2000). Combining ability of maize inbred lines. Biuletyn Instytutu Hodowli i Aklimatyzacji Roslin, 216(2): 371-378.

Mosa, H.E.; A.A. Motawei and Afaf A.I. Gabr (2004). Evaluation of new inbred lines of yellow maize via line × tester analysis over three locations. J. Agric. Sci. Mansoura Univ., 29(3): 1023 - 1033.

Mosa, H.E.; A.A. Motawei and A.A. El-Shenawy (2009). Selection of new single crosses of maize for grain yield and resistance to downy mildew disease under different locations and potassium fertilization. J. Agric. Res. Kafr El-Sheikh Univ., 35(2): 522-536.

Motawei, A.A. (2006). Additive and non- additive genetic variances of important quantitative traits in new maize inbred lines via line × tester analysis. J. Agric. Sci. Mansoura Univ., 31:6855-6865.

Motawei, A.A. and M.H. Ibrahim (2005). Useful heterosis and combining ability for grain yield and resistance to downy mildew disease (*Prenosclerospora sorghi*) in some new yellow inbred lines of maize. J. Agric. Res. Tanta Univ., 31(2): 273-292.

Motawei, A.A.; A.A. El-Shenawy and A.E. Nofal (2005). Estimation of combining ability for two sets of yellow maize top-crosses. Assiut J. Agric. Sci., 36(3): 91-107.

Qadri, M.J.; K.N. Garwal and A.K. Sanghi (1983). Combining ability under two populations sizes for ear traits in maize. Indian J. Genet. Pl. Breed., 43(2): 208-211.

Rather, A.G.; S. Najeeb; A.A. Wani; M.A. Bhat and G.A. Parray (2009). Combining ability analysis for *turcicum* leaf blight (TLB) and other agronomic traits in maize (*Zea mays* L.) under high altitude temperate conditions of Kashmir. Maize Genetic Cooperation Newsletter 83: 1-5.

Rodrigues, L.R. and N.D. Silva (2002). Combining ability in baby corn inbred lines (*Zea mays* L.). Crop Breed. and Appl. Biot., 2: 361-368.

Shehata, A.H.(1976). Gene action involved in the manifestation of late wilt (*Cephalosporium maydis*) of maize. Egypt J. Gent. Cytol., 5: 42-47.

Singh, R.K. and D.B. Chaudhary (1979). Biometrical methods in quantitative genetic analysis. Kalyani Publisher, Baharate. Ram Road. Daryagani, New Delhi, India.

Snedecor, G.W. and W.G. Cochran (1967). Statistical Methods. 6th ed. Iowa state Univ. press, Ames., Iowa, USA.

Steel, R.G. and J.H. Torrie (1980). Principles and procedures of statistics. 2nd ed. McGraw- Hill Book Company, New York, USA.

Vasal, S.K.; G. Srinivasan; D.L. Beck; J. Cross; S. Pandey and C. Deleon. (1992). Heterosis and combining ability of Cimmyt's tropical white maize germplasm. Maydica, 37: 217-223.

Zieger, G. (1989). Analysis of combining ability and ecostability of diallel series. Pl. Breed. Abst., 59(12): 10258.

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إنتخاب هجن جديدة من الذرة الصفراء عالية المحصول ومقاومة لمرض الذبول المتأخر باستخدام طريقة الهجن القمية تحت ظروف بيئية مختلفة

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تم التهجين القمى بين 42 سلاله جديدة من الذرة الصفراء مع اثنين من الكشافات بمحطة بحوث سخا فى موسم 2006 ثم قسمت الـ 84 هجين قمى الناتجة الى مجموعتين اضيف لهما اثنين من الهجن التجارية وقيمت فى موسم 2007 فى تجربتين مختلفتين أجريت الأولى فى موقعين بمحطة بحوث سخا وملوى لدراسة صفة محصول الحبوب بالطن/هكتار وكذلك صفة عدد الأيام حتى ظهور 50% من حرائر النورات المؤنثة ، بينما أجريت التجربة الثانية تحت معدلين من التسميد الازوتى بحقل العدوى الصناعي لمرض الذبول المتأخر لدراسة صفة المقاومة لهذا المرض فى محطة بحوث سخا. تم انتخاب أفضل سبعة هجن عالية المحصول ومقاومة لمرض الذبول المتأخر حيث تم تقييمهافي أربع محطات بحثية هى سخا ، الجميزة ، سدس ، ملوى خلال موسم نمو 2009.

أظهرت النتائج وجود اختلافات معنوية إلى عالية المعنوية بين السلالات لصفتي عدد الأيام حتى ظهور 50% من حرائر النورات المؤنثة وصفة محصول الحبوب ومقاومة مرض الذبول المتأخر فى كلا المجموعتين. علاوة على ذلك اظهر تحليل التباين اختلافات معنوية إلى عالية المعنوية لكلا من الكشافات وتفاعل السلالات مع الكشافات لمقاومة مرض الذبول المتأخر فى كلا المجموعتين فيما عدا الكشافات فى المجموعة الثانية. كان الفعل الجيني التجميعي هو المتحكم الرئيسى فى صفات عدد الأيام حتى ظهور 50% من حرائر النورات المؤنثة فى كلا المجموعتين وصفة المحصول فى المجموعة الثانية بينما كان الفعل الجينى الغير تجميعي هو المتحكم الرئيسى فى صفات المحصول فى المجموعة الأولى وصفة المقاومة لمرض الذبول المتأخر فى كلا المجموعتين.

كانت السلالة سخا 10 فى المجموعة الأولى وكذلك السلاله سخا 23 فى المجموعة الثانية من أفضل السلالات لتأثيرات القدرة العامة على التآلف لصفات التبكير والمحصول ومقاومة مرض الذبول المتأخر معا. بينما أظهرت الهجن القمية سخا 3هـ × .ف 162 و سخا 14هـ.ف166 جينات مرغوبة للقدرة المحصولية العالية مع مقاومة مرض الذبول المتأخر ومن الملاحظ انه ازدادت متوسطات 12 هجين قمى فى المجموعة الاولى وإثنان فى المجموعة الثانية زيادة معنوية عن أفضل هجن المقارنة لصفة محصول الحبوب وكانت أيضا عالية المقاومة لمرض الذبول المتأخر.

أظهرت نتائج تجربة التقييم لأفضل الهجن القمية على مستوى الأربع مواقع أن متوسطات السبعة هجن الثلاثية المنتخبة من تجارب الهجن القمية وهى:- سخا23هـ× .ف 162 ، سخا10هـ× .ف 162، سخا 11هـ × .ف 166، سخا 17هـ × .ف 166، سخا 19هـ× .ف 162، سخا 17هـ× .ف 162، سخا 18هـ× .ف 162 ازدادت معنويا فى محصول الحبوب عن هجين المقارنة التجاري وتفوقت عليه بمقدار 3.15، 2.75، 2.56، 2.54، 2.52، 2.16، 1.37 طن / هكتار على التوالي وفى نفس الوقت أظهرت هذه الهجن القمية مقاومة عالية لمرض الذبول المتأخر. وهذه النتيجة تؤكد ما تحصل عليه من تجارب الهجن القمية مما يشير إلى أن هذه الهجن الثلاثية الجديدة ثابتة محصولياً ومقاومة لمرض الذبول المتأخر في البيئات المختلفة وترشحها بقوة لتكون مهمة وذات قيمة فى برامج تحسين الذرة الشامية.

قام بتحكيم البحث

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Table 2: Mean performances for 84 top-crosses in the two sets for days to mid-silk and grain yield over two locations and resistance to late wilt % across two nitrogen levels.

	Set-1							Set-2					
Inbred lines	Days to mid-silk		grain yield (t/ha)		Resistance to late wilt %		Inbred lines	Days to mid-silk		grain yield (t/ha)		Resistance to late wilt %	
	SC162	SC166	SC162	SC166	SC162	SC166		SC162	SC166	SC162	SC166	SC162	SC166
Sk-1	62.3	62.9	8.93	9.7	92.4	89.9	Sk-22	62.4	61.8	10.38	11.76	95.5	93.9
Sk-2	62.0	61.1	9.7	10.3	87.9	95.6	Sk-23	61.0	62.2	12.87	11.73	100	100
Sk-3	59.3	60.0	9.84	7.64	100	81.4	Sk-24	64.9	63.6	7.79	7.35	92.3	86.4
Sk-4	62.0	60.3	10.28	11.33	92.4	100	Sk-25	62.5	63.0	11.80	12.16	98.5	100
Sk-5	61.3	61.3	9.85	9.19	87.9	83.8	Sk-26	62.0	62.4	10.71	11.18	95.5	100
Sk-6	62.3	61.8	9.81	8.9	100	89.6	Sk-27	62.6	62.8	8.85	8.47	80.3	89.4
Sk-7	62.8	63.1	11.09	9.22	96.9	91.9	Sk-28	63.0	61.4	10.75	10.85	100	100
Sk-8	62.5	63.0	9.42	8.7	85.3	88.8	Sk-29	62.6	61.3	11.12	11.01	100	100
Sk-9	62.3	61.9	10.2	8.79	92.4	100	Sk-30	63.0	62.3	8.04	8.55	87.2	92.1
Sk-10	60.5	60.4	11.83	10.89	100	100	Sk-31	61.3	60.8	10.90	11.68	100	100
Sk-11	63.1	63.1	10.44	11.99	100	100	Sk-32	64.3	64.0	8.97	9.93	89.4	89.1
Sk-12	63.1	62.3	8.38	8.27	76.0	89.6	Sk-33	63.6	62.8	10.01	9.96	92.4	100
Sk-13	62.8	62.0	9.43	9.61	85.4	100	Sk-34	62.8	62.4	8.70	8.20	90.3	86.4
Sk-14	62.8	63.6	9.06	10.17	85.2	100	Sk-35	63.6	63.3	8.94	9.07	91.5	100
Sk-15	64.0	62.8	9.16	9.57	88.5	86.6	Sk-36	62.9	62.6	10.52	10.41	100	100
Sk-16	63.3	62.9	11.63	11.46	100	100	Sk-37	62.8	62.5	9.62	10.35	100	100
Sk-17	61.9	63.0	12.03	12.11	100	100	Sk-38	64.6	64.4	11.17	11.41	100	100
Sk-18	62.5	62.9	11.72	11.13	100	100	Sk-39	61.8	63.0	10.13	9.74	100	90.9
Sk-19	63.4	63.6	12.14	11.46	100	100	Sk-40	62.8	62.8	9.54	8.61	86.4	89.2
Sk-20	64.0	63.9	10.0	8.21	87.7	84.4	Sk-41	61.3	61.4	11.22	9.80	100	100
Sk-21	61.6	61.0	11.5	11.34	95.5	100	Sk-42	61.6	62.5	11.28	11.03	100	100
TWC351	61.8		8.97		90.8		TWC351	63.1		8.82		89.6	
TWC352	62.6		9.04		100		TWC352	62.5		9.42		100	
L.S.D at 0.05	1.48		1.88		9.55		L.S.D at 0.05	1.39		2.41		7.58	

Table 5: Specific combining ability effects for 84 top-crosses of the two sets for studied traits.

	Set-1							Set-2					
Inbred lines	Days to mid-silk		grain yield		Resistance to late wilt %		Inbred lines	Days to mid-silk		grain yield		Resistance to late wilt %	
	SC162	SC166	SC162	SC166	SC162	SC166		SC162	SC166	SC162	SC166	SC162	SC166
Sk-1	-0.378	0.378	-0.535	0.535	1.101	-1.101	Sk-22	0.211	-0.211	-0.589	0.589	0.838	-0.838
Sk-2	0.372	-0.372	-0.446	0.446	-4.58	4.58	Sk-23	-0.73*	0.726*	0.598	-0.598	0.614	-0.614
Sk-3	-0.441	0.441	0.947	-0.947	13.58*	-13.6*	Sk-24	0.524	-0.524	0.285	-0.285	4.75*	-4.75*
Sk-4	0.810	-0.81	-0.678	0.678	-4.58	4.58	Sk-25	-0.351	0.351	-0.152	0.152	-0.850	0.850
Sk-5	-0.065	0.065	0.180	-0.180	2.57	-2.57	Sk-26	-0.289	0.289	-0.402	0.402	-3.78*	3.78*
Sk-6	0.185	-0.185	0.303	-0.303	7.70*	-7.70*	Sk-27	-0.164	0.164	0.161	-0.161	-3.91*	3.91*
Sk-7	-0.253	0.253	0.767	-0.767	5.75	-5.75	Sk-28	0.711	-0.711	-0.089	0.089	0.61	-0.61
Sk-8	-0.315	0.315	0.205	-0.205	-2.07	2.07	Sk-29	0.586	-0.586	0.098	-0.098	0.61	-0.61
Sk-9	0.122	-0.122	0.552	-0.552	-5.39	5.39	Sk-30	0.274	-0.274	-0.089	0.089	-3.08	3.08
Sk-10	-0.003	0.003	0.320	-0.320	1.10	-1.10	Sk-31	0.149	-0.149	-0.464	0.464	0.61	-0.61
Sk-11	-0.065	0.065	-0.930	0.930	1.10	-1.10	Sk-32	0.024	-0.024	-0.402	0.402	1.55	-1.55
Sk-12	0.372	-0.372	-0.099	0.099	-5.7	5.7	Sk-33	0.336	-0.336	-0.089	0.089	-5.06*	5.06*
Sk-13	0.310	-0.310	-0.246	0.246	-8.03*	8.03*	Sk-34	0.086	-0.086	0.286	-0.286	3.92*	-3.92*
Sk-14	-0.503	0.503	-0.707	0.707	-10.0*	10.01*	Sk-35	0.086	-0.086	-0.027	0.027	-6.99*	6.99*
Sk-15	0.560	-0.560	-0.357	0.357	4.05	-4.05	Sk-36	0.024	-0.024	0.036	-0.036	0.61	-0.61
Sk-16	0.122	-0.122	-0.070	0.070	1.10	-1.10	Sk-37	-0.024	0.024	-0.339	0.339	0.61	-0.61
Sk-17	-0.628	0.628	-0.196	0.196	1.10	-1.10	Sk-38	0.024	-0.024	-0.027	0.027	0.61	-0.61
Sk-18	-0.253	0.253	0.138	-0.138	1.10	-1.10	Sk-39	-0.73*	0.726*	0.223	-0.223	8.58*	-8.58*
Sk-19	-0.191	0.191	0.185	-0.185	1.10	-1.10	Sk-40	-0.101	0.101	0.223	-0.223	-1.49	1.49
Sk-20	-0.003	0.003	0.739	-0.739	2.33	-2.33	Sk-41	-0.164	0.164	0.598	-0.598	0.61	-0.61
Sk-21	0.247	-0.247	-0.073	0.073	-3.29	3.29	Sk-42	-0.539	0.539	0.161	-0.161	0.61	-0.61
L.S.D S$_{ij}$ at 0.05	0.987		1.104		6.75		L.S.D S$_{ij}$ at 0.05	0.748		0.863		3.072	

* Significant difference at 0.05 level of probability.