

COMBINING ABILITY ANALYSIS OF SOME CHARACTERS IN MAIZE

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ABSTRACT: *Combining ability analysis of cultivars is important to exploit the relevant type of gene action for a breeding programme. Half diallel crosses were made among the 7 parental lines, then the resultant 21 F₁'s along with a check white single crosses i.e., SC10 were planted at two locations to estimate both GCA and SCA variances and effects, determine the important types of gene action controlling yield, some agronomic traits and resistance to late wilt disease, and to identify maize genotypes superior in both of high resistance to late wilt disease and high yielding ability to be offered to maize breeding programs.. A randomized complete block design (RCBD) with 4 replicates was used at each location. General (GCA) and specific (SCA) combining ability variances and effects were estimated for all studied traits according to Griffing's (1956) Method III Model I. Highly significant differences were detected between both locations for all studied traits except for late wilt resistance. Combined analysis of variance over the two locations also indicated a large amount of variability among all crosses for all studied agronomic and yield traits, whereas it was insignificant for late wilt resistance. The interaction between genotypes and locations (G X L) was significant for all studied traits except for days to 50% silking and late wilt resistance. Three F₁ crosses i.e., Sd1107 x Sd1179, Sd1179 x Sd1180, and Sd1177 x Sd1180 were significantly surpassed the commercial hybrid check SC10. Both additive and non-additive gene effects played an important role in the inheritance of all studied traits. The magnitude of GCA was greater than that of SCA variance in the inheritance of all studied traits, except for ear diameter. The parental inbred line Sd1179 had the highest significant positive GCA effect for grain yield. The crosses Sd1107 X Sd1179, Sd1179 X Sd1180 and Sd1177 X Sd1180 were the best for grain yield and resistant to late wilt disease and surpassed the commercial hybrid check SC10. Therefore, these crosses could be recommended for hybrid maize program for improving both grain yield and late wilt resistance.*

Key words: *Zea mays, Maize, Corn, Grain yield, Combining ability, Diallel analysis, additive gene action, non-additive gene action.*

INTRODUCTION

Combining ability analysis of cultivars is important to exploit the relevant type of gene action for a breeding program. If specific combining ability is predominant, it could be used in hybrid breeding programs, in other breeding

programme only that segments of total genetic variance which result from additive genes could be used since subsequent inbreeding retains them. Combining ability estimates could be used to evaluate the number of promising lines in F₁ and F₂ generations, which is helpful in selecting the potential parents for hybridization (Iqbal and Chowdhary, 2000).

Diallel mating designs are widely used in plant improvement programs to estimate additive and dominance genetic variances, and to provide a base population for advanced selection. Diallel mating designs provide useful genetic information to breeders, such as general combining ability (GCA) and specific combining ability (SCA), to help them devise appropriate breeding and selection strategies (Hayman, 1954a; Griffing, 1956; Fry, 2004 Zhang *et al.*, 2005). In many studies, GCA effects for parents and SCA effects for crosses were estimated in maize, Dehghanpour *et al.*, 1996; San-Vicente *et al.*, 1998; Konak *et al.*, 1999; Chaudhary *et al.*, 2000; Araujo and Miranda, 2001; Kalla *et al.*, 2001. Non-additive gene effects for grain yield were found to be significant in maize (Dehghanpour *et al.*, 1996; San-Vicente *et al.*, 1998; Kalla *et al.*, 2001).

The main objectives of the present investigation were to estimate both GCA and SCA variances and effects, determine the important types of gene action controlling yield, some agronomic traits and resistance to late wilt disease, and to identify maize genotypes superior in both of high yielding ability and high resistance to late wilt disease to be offered to maize breeding programs.

MATERIALS AND METHODS

The experimental field work of this investigation was carried out at Sakha and Sids Agricultural Research Stations of the Agricultural Research Center during 2007, and 2008 seasons. In 2007 season, seven white inbred lines *i.e.*, Sd1107, Sd1110, Sd1176, Sd1177, Sd1178, Sd1179 and Sd1180 were grown at the field of Sids Research Station of the ARC. All possible crosses (excluding reciprocals) were made among the 7 parental lines, so seeds of 21 direct F₁ crosses were obtained. In 2008 season, two field experiments were conducted. Each experiment included 22 entries *i.e.*, 21 F₁ crosses, along with a check white single crosses *i.e.*, SC10. A randomized complete block design (RCBD) with 4 replicates was used at each location. The experimental plot was one row of 6 m long and 0.8 m wide (4.8m²), with a distance of 0.25m between each two hills. Data were recorded for grain yield and converted to 150.5 g kg⁻¹ water content and then converted to ardabs feddan⁻¹ (ardab=140 kg grains), number of days to 50% silking, plant height (cm), ear height, ear length (cm), ear diameter (cm), and resistance to late wilt disease (%).

PROC GLM of the SAS statistical package (SAS Institute, 1990) was used for data analysis. A separate analysis was done for each location as a randomized complete block design as outlined by Snedecor and Cochran (1989). HOVTEST=BARTLETT option in the MEANS statement of PROC GLM

was used to perform Bartlett's test. After testing the homogeneity of error variances, combined data over two locations was conducted according to McIntosh (1983) with genotypes fixed, and locations random effects. Replication within locations was served as a denominator of F for testing the effect of locations. Least squares means (Lsmeans) were calculated separately for each location and then overall locations. An average LSD was derived by averaging the standard errors of all genotypes comparisons created by the pdiff option of the Lsmeans statement. General (GCA) and specific (SCA) combining ability variances and effects for the resultant 21 F_1 crosses were estimated for all studied traits according to Griffing's (1956) Method IV Model I using SAS program called DIALLEL-SAS05 as introduced by Zhang et al., (2005). Late wilt resistance values for all genotypes were dropped off the combining ability analysis since there was insignificant difference among the evaluated crosses.

RESULTS AND DISCUSSION

1. Analysis of variance.

Highly significant differences were detected between both locations for all studied traits except for late wilt resistance, indicating that these locations differed in their environmental conditions (Table 1). Combined analysis of variance over the two locations also indicated a large amount of variability among all crosses for all studied agronomic and yield traits, whereas it was insignificant for resistance to late wilt disease. Data presented in Table (1) revealed that the interaction between genotypes and locations (G X L) was significant for all studied traits except for days to 50% silking and late wilt resistance. These interactions with locations were indicative of different ranking of the evaluated genotypes of from one location to another. These results are in agreement with the findings of Galal *et al* (1978), Gabr (1997), Abd El Aal (1998) and El-Khishen (2002 and 2006).

2. Mean performance.

Mean performance over the two locations for yield and some other agronomic characters of 21 F_1 diallel crosses, along with the commercial hybrid check SC10 are shown in Table (2). Combined data of Table (2) showed that Sd1177 × Sd1178 produced the lowest mean grain yield (12.8 ardabs feddan⁻¹), whereas the highest mean grain yield was obtained from Sd1107 × Sd1179 (41.3 ardabs feddan⁻¹), with an average of all hybrids 32.3 ardabs feddan⁻¹. Three F_1 crosses *i.e.*, Sd1107 × Sd1179, Sd1179 × Sd1180, and Sd1177 × Sd1180 were significantly surpassed the commercial hybrid check SC10. Sd1176 × Sd1179 and Sd1178 × Sd1180 outyielded but not significantly SC10. Moreover, eleven F_1 crosses, *i.e.*, Sd1107 × Sd1176, Sd1107 × Sd1178, Sd1110 × Sd1176, Sd1110 × Sd1177, Sd1110 × Sd1178, Sd1110 × Sd1179, Sd1110 × Sd1180, Sd1176 × Sd1177, Sd1176 × Sd1180, Sd1177 × Sd1179, and Sd1178 × Sd1179, were not significantly differed than SC10.

Table 1. Analysis of variances for yield, days to 50% silking, plant height, ear height, ear length (cm), ear diameter (cm), and late wilt resistance for 21 diallel F_1 's and 1 check (Data are combined across two locations, in 2008 season).

SOV	df	Mean squares						
		Yield	Days to 50% silking	Plant height	Ear height	Ear length	Ear diameter	Late wilt resistance
Locations (L)	1	2231.59**	696.02**	25368.01**	15827.05**	63.36**	8.73**	0.34
Reps/L	6	8.26	2.57	179.38	96.11	0.74	0.04	1.05
Genotypes (G)	21	255.00**	18.14**	4289.75**	2306.99**	34.27**	0.31**	2.65
G × L	21	35.94*	1.30	148.70*	115.56**	1.05*	0.04**	0.46
Pooled error	126	18.11	1.01	74.40	55.50	0.62	0.02	1.67

*, ** indicate significance at 0.05 and 0.01 levels of probability, respectively.

Table 2. Mean grain yield (ardabs fedaan⁻¹, days to 50% silking (days), plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), and late wilt resistance (%) for 21 diallel F₁'s and 1 check (Data are combined across two locations, in 2008 season).

Genotypes	Yield	Days to 50% silking	Plant height	Ear height	Ear length	Ear diameter	Late wilt resistance
Sd1107 × Sd1110	28.2	60.0	252.3	137.3	17.18	4.75	100.0
Sd1107 × Sd1176	34.3	60.5	267.3	150.3	19.10	4.73	100.0
Sd1107 × Sd1177	28.0	62.0	258.6	140.1	17.95	4.70	100.0
Sd1107 × Sd1178	32.0	62.1	242.9	131.9	17.83	4.83	100.0
Sd1107 × Sd1179	41.3	62.1	297.5	173.8	21.36	4.63	99.5
Sd1107 × Sd1180	27.8	59.3	244.3	132.5	16.40	4.53	97.4
Sd1110 × Sd1176	31.4	60.4	276.6	154.4	19.53	4.60	99.5
Sd1110 × Sd1177	32.5	61.6	282.4	153.5	18.35	4.85	100.0
Sd1110 × Sd1178	30.7	61.3	267.0	146.1	18.58	4.78	100.0
Sd1110 × Sd1179	34.1	61.3	290.9	163.0	20.40	4.95	100.0
Sd1110 × Sd1180	32.2	58.9	256.8	137.0	17.70	4.58	100.0
Sd1176 × Sd1177	31.1	61.4	281.6	158.0	19.13	4.53	100.0
Sd1176 × Sd1178	30.5	61.4	266.6	149.1	19.65	4.60	100.0
Sd1176 × Sd1179	37.1	60.6	288.6	164.3	20.38	4.75	100.0
Sd1176 × Sd1180	34.1	61.3	285.9	163.0	22.40	4.70	99.4
Sd1177 × Sd1178	12.8	65.4	207.8	108.1	15.55	4.00	100.0
Sd1177 × Sd1179	33.9	62.6	285.3	155.8	21.73	4.88	100.0
Sd1177 × Sd1180	38.9	62.4	295.0	170.8	21.23	4.70	100.0
Sd1178 × Sd1179	34.0	62.1	269.4	151.3	21.53	4.88	100.0
Sd1178 × Sd1180	34.9	61.6	286.6	163.8	22.26	4.85	100.0
Sd1179 × Sd1180	39.4	64.3	298.9	170.5	21.30	4.68	100.0
SC10	34.8	63.6	308.4	183.1	23.05	4.85	100.0
Average	32.9	61.6	273.3	152.4	19.66	4.70	99.8
LSD 0.05	4.1	1.0	8.5	7.4	0.78	0.13	1.3

Data presented in Table (2) revealed that the mean values of days to 50 % silking ranged from 58.9 days for Sd1110 × Sd1180 to 65.4 days for Sd1177 × Sd1178 with an average of 61.6 days. All F₁ crosses were in general earlier than the commercial check hybrid SC10, except for Sd1177 × Sd1178 and Sd1179 × Sd1180.

The tallest plant height (298.9 cm) in case of the F₁ crosses was obtained in the cross Sd1179 × Sd1180, whereas the shortest plants (207.8 cm) were obtained from the cross Sd1177 × Sd1178. In general, the mean plant height of the evaluated 21 F₁'s (271.5 cm) was considerably shorter than that of the commercial check hybrid SC10 (308.4 cm).

Regarding mean ear height, combined data over locations showed that ear height means of the evaluated F₁'s crosses ranged from 108.1 cm (Sd1177 × Sd1178) to 173.8 cm (Sd1107 × Sd1179) with an average of 151.2 cm. All F₁'s exhibited significant shorter ear heights compared to the commercial check hybrid SC10 (183.1 cm).

Combined data presented in Table (2) showed that the mean values of ear length for the evaluated 21 F₁'s ranged from 15.6 cm for Sd1177 × Sd1178 to 22.4 cm for Sd1176 × Sd1180 with an average of 19.5 cm.

For mean values of ear diameter, the average was 4.7 cm for the evaluated F₁'s diallel crosses. In addition, the highest mean value of ear diameter was obtained from the cross Sd1110 × Sd1179 (5.0 cm), while the lowest one was exhibited by the cross Sd1177 × Sd1178 (4.0 cm).

All the evaluated F₁'s diallel crosses exhibited resistance to late wilt disease and ranged from 97.4 to 100 %. The cross Sd1107 × Sd1180 (97.4 %) was significantly lower than the commercial hybrid check (100 %), however, it was considerably resistant.

3. Combining ability variances.

Analysis of variance of combining abilities for the F₁ crosses was computed according to Griffing (1956) Method IV Model I and presented in Table (3). Combined analysis showed highly significant mean squares due to general and specific combining ability mean squares for all studied agronomic and yield characters. These results indicated that both additive and non-additive gene effects played an important role in the inheritance of these traits. Moreover, the magnitude of GCA was greater than that of SCA variance in the inheritance of all studied traits except for ear diameter, where the SCA was more important than GCA variance. This was indicated through the ratio of GCA / SCA where it was exceeding the unity for all traits except for ear diameter, where the ratio was below the unity. The present results were in general agreement with those obtained by many investigators such as Dhillon and Singh (1976), Hansen *et al* (1977), El-Zeir (1990), Altinbas (1995), and El-Khishen (2002 and 2006).

Table 3. Combining ability variances computed according to Griffing (1956) Method III Model II for yield, days to 50% silking, plant height, ear height, ear length (cm), ear diameter (cm), and late wilt resistance for resultant 21 diallel F₁'s (Data are combined across two locations, in 2008 season).

SOV	df	Mean squares						
		Yield	Days to 50% silking	Plant height	Ear height	Ear length	Ear diameter	Late wilt resistance
Genotypes	20	5310.18**	347.88**	79714.34**	40641.72**	623.44**	6.28**	55.3
GCA	6	410.15**	35.93**	6880.91**	3377.92**	57.03**	0.23**	3.08
SCA	14	203.52**	9.45**	2744.92**	1455.30**	20.09**	0.35**	2.63
GCA x L	6	65.59**	0.68	119.53	142.45*	0.86	0.04*	0.32
SCA x L	14	25.65	1.64	149.32*	108.87*	0.78	0.03	0.55
Pooled error	120	16.89	0.99	76.42	56.10	0.63	0.02	1.75
GCA/SCA	---	2.02	3.80	2.51	2.32	2.84	0.66	1.17
GCA x L/SCA x L	---	2.56	0.41	0.80	0.72	1.10	1.33	0.58

*, ** indicate significance at 0.05 and 0.01 levels of probability, respectively.

Variances due to the interaction between location and each of GCA, SCA were significant for ear height, for GCA X locations for grain yield and ear diameter, SCA X locations for plant height. In general, the insignificant interaction between locations and each of GCA and SCA for the other studied traits indicated that GCA and SCA variances for these traits did not vary from one location to another. The results showed that the magnitude of mean squares in this concern was higher for the GCA X location interaction than SCA X location interaction for grain yield and ear length and diameter. This indicated that GCA is more affected by location than SCA for these traits. The magnitude of mean squares due to SCA X location in this concern was higher than that of GCA X location for the plant height. These results were in general agreed with the findings of Debnath and Sarkar (1990), El-Khishen (2002), and Gabr *et al.* (2008).

4. Combining ability effects.

Based on the combined data over the two locations, estimates of general combining ability effects of the seven parental inbred lines for grain yield and other studied traits are presented in Table (4). The positive estimates of the GCA effects were desirably considered for all studied traits except for days to 50 % silking, plant and ear heights, where the negative estimates indicating earliness, and shortness, respectively. Estimates of GCA effects either positive or negative may be most desirable and would indicate that a given cultivar is much better than the average of the group involved with it in the diallel crossing system.

Results of the GCA effects (Table 4) showed that the parental inbred line Sd1179 had the highest significant positive GCA effect for grain yield, whereas inbred lines Sd1178 and Sd1177 had the lowest significant negative GCA effect for grain yield. Sd1179 also showed the highest positive (desirable) and significant GCA effect for ear length. The parental line Sd1110 had the lowest significant negative GCA effect (desirable) for number of days to 50 % silking. Sd1178 and Sd1107 were the best general combiners for shortening plant and ear heights.

Specific combining ability effects for the F_1 crosses in the combined data are presented in Table (5). It is worth noting that a good SCA cross may come from two parents possessing good GCA or from one with good GCA and other with poor GCA effect. The best SCA effect for grain yield were obtained from the crosses between poor and good GCA parent, *i.e.* Sd1177 X Sd1180 and Sd1107 X Sd1179, whereas the worst SCA effect for grain yield was obtained from Sd1177 X Sd1178. Similar conclusion was reported by Khristova (1978), Gabr (1997), Abd El Aal (1998) and El-Khishen (2002). The lowest significant and negative (desirable) SCA effects were obtained from the crosses Sd1107 X Sd1180 for days to 50 % silking, Sd1177 X Sd1178, Sd1110 X Sd1180, and Sd1107 X Sd1180 for plant and ear heights. Sd1178 X

Table 4. Estimates of general (GCA) combining ability effects for yield, days to 50% silking, plant height, ear height, ear length (cm), ear diameter (cm), and late wilt resistance for 7 parental inbred lines (Data are combined across two locations, in 2008 season).

Inbred	GCA effects						
	Yield	Days to 50% silking	Plant height	Ear height	Ear length	Ear diameter	Late wilt resistance
Sd1107	-0.50	-0.65	-13.28**	-8.24**	-1.44**	0.01	-0.39
Sd1110	-0.99	-1.18**	-0.65	-3.14	-1.06**	0.07	0.14
Sd1176	0.87	-0.75	7.50*	6.41*	0.64*	-0.05	0.02
Sd1177	-3.36*	1.23**	-3.70	-4.14	-0.62	-0.09	0.24
Sd1178	-3.82*	0.93*	-17.78**	-11.34**	-0.32	-0.04	0.24
Sd1179	5.16**	0.75	20.27**	14.31**	1.94**	0.12	0.14
Sd1180	2.65	-0.33	7.65*	6.11*	0.86**	-0.02	-0.40
S.E. for g_i	1.701	0.414	3.620	3.101	0.329	0.541	0.547
g_i-g_j	2.599	0.632	5.529	4.737	0.503	0.083	0.836

*, ** indicate significance at 0.05 and 0.01 levels of probability, respectively.

Table 5. Estimates of specific (SCA) combining ability effects for yield, days to 50% silking, plant height, ear height, ear length (cm), ear diameter (cm), and late wilt resistance for resultant 21 diallel F₁ crosses (Data are combined across two locations, in 2008 season).

Crosses	GCA effects						
	Yield	Days to 50% silking	Plant height	Ear height	Ear length	Ear diameter	Late wilt resistance
Sd1107 × Sd1110	-2.66	0.28	-5.34	-2.53	0.17	-0.02	0.45
Sd1107 × Sd1176	1.53	0.36	1.51	0.92	0.40	0.08	0.56
Sd1107 × Sd1177	-0.52	-0.12	4.08	1.34	0.50	0.10	0.34
Sd1107 × Sd1178	3.99	0.31	2.41	0.29	0.09	0.17	0.34
Sd1107 × Sd1179	4.31	0.84	18.98**	16.52**	1.36*	-0.18*	-0.05
Sd1107 × Sd1180	-6.65*	-1.52	-21.64**	-16.53**	-2.52**	-0.14	-1.44
Sd1110 × Sd1176	-0.84	0.76	-1.74	-0.06	0.45	-0.12	-0.74
Sd1110 × Sd1177	4.54	0.03	15.21*	9.62	0.52	0.18*	-0.18
Sd1110 × Sd1178	3.19	-0.04	13.91	9.44	0.45	0.05	-0.18
Sd1110 × Sd1179	-2.38	0.13	-0.27	0.67	0.02	0.06	-0.08
Sd1110 × Sd1180	-1.85	-1.27	-21.77**	-17.13**	-1.60*	-0.17	0.46
Sd1176 × Sd1177	1.23	-0.64	6.31	4.57	-0.40	-0.02	-0.06
Sd1176 × Sd1178	1.11	-0.34	5.38	2.89	-0.16	-0.01	-0.06
Sd1176 × Sd1179	-1.26	-0.92	-10.67	-7.63	-1.70**	-0.02	0.04
Sd1176 × Sd1180	-1.76	0.78	-0.79	-0.68	1.41	0.08	0.01
Sd1177 × Sd1178	-12.33**	1.68*	-42.29**	-27.56**	-3.01**	-0.53**	-0.28
Sd1177 × Sd1179	-0.20	-0.89	-2.84	-5.58	0.90	0.16	-0.18
Sd1177 × Sd1180	7.27*	-0.07	19.53**	17.62**	1.48*	0.13	0.36
Sd1178 × Sd1179	0.29	-1.09	-4.64	-2.88	0.41	0.10	-0.18
Sd1178 × Sd1180	3.75	-0.52	25.23**	17.82**	2.23**	0.22*	0.36
Sd1179 × Sd1180	-0.76	2.28**	-0.57	-1.08	-0.99	-0.12	0.46
S.E. for : Sij	3.35	0.81	7.14	6.11	0.64	0.09	1.08
Sij-Sik	5.20	1.26	11.06	9.47	1.01	0.17	1.67
Sij-Skl	4.50	1.09	9.57	8.21	0.87	0.14	1.45

*, ** indicate significance at 0.05 and 0.01 levels of probability, respectively.

Combining ability analysis of some characters in maize

Sd1180 gave the highest positive SCA effects for ear length and diameter. The cross Sd1107 X Sd1179 was the best for grain yield and resistant to late wilt disease expressed in *per se* performance and specific combining ability effects. Also Sd1179 X Sd1180 and Sd Sd1177 X Sd1180 consider superior crosses and surpassed the commercial hybrid check SC10 and also exhibited resistance to late wilt disease. Therefore, these crosses could be recommended for hybrid maize program for improving both grain yield and late wilt resistance.

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تقدير القدرة على الأنتلاف للمحصول والصفات المؤثرة عليه في الذرة الشامية

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الملخص العربي

يعتبر تقدير القدرة على الأنتلاف للتركيب الوراثية من العوامل الهامة لمعرفة فعل الحين في برنامج التربية. فقد تم عمل كل الهجن الممكنة (فيما عدا الهجن العكسية) لـ ٧ سلالات أبوية ثم تم زراعة ٢١ هجين الناتجة من الجيل الأول مع هجين للمقارنة هو هجين فردى ١٠ فى موقعين لحساب القدرة العامة والخاصة على الأنتلاف ومعرفة أهمية فعل الجين المؤثر على المحصول والصفات المدروسة ومعرفة أى التركيب الوراثية عالية المحصول وذات مقاومة. وتم التحليل احصائيا فى تصميم القطاعات الكاملة العشوائية فى اربع مكررات لكل موقع. وتم حساب القدرة العامة والخاصة للأنتلاف لكل الصفات المدروسة. وقد أظهرت النتائج اختلافات عالية المعنوية لكلا الموقعين لكل الصفات المدروسة فيما عدا المقاومة لمرض الذبول المتأخر وكذلك أظهر التفاعل بين التركيب الوراثية والمواقع معنوية للصفات المدروسة فيما عدا صفتى التزهير والمقاومة لمرض الذبول المتأخر.

أعطت ٣ هجن هى $Sd\ 1179 \times Sd\ 1107$ و $Sd\ 1180$ و $Sd\ 1179 \times Sd\ 1177$ و $Sd\ 1180$ تفوق معنوى على هجين المقارنة هجين فردى ١٠ لصفة المحصول. ووجد ان فعل الجين المضيف وغير المضيف لهما دور مهم فى وراثية كل الصفات المدروسة. وكانت القدرة العامة على الأنتلاف اكبر من القدرة الخاصة على الأنتلاف فى وراثية كل الصفات فيما عدا صفة قطر الكوز. ولصفة المحصول أظهرت السلالة الأيوية $Sd\ 1179$ معنوية عالية موجبة للقدرة الخاصة على الأنتلاف. والهجن $Sd\ 1179 \times Sd\ 1107$ و $Sd\ 1180 \times Sd\ 1177$ و $Sd\ 1180 \times Sd\ 1179$ كانت أفضل الهجن للمحصول العالى والمقاومة لمرض الذبول المتأخر عن هجين المقارنة هجين فردى ١٠ مما ينصح بأستخدام هذه الهجن فى برنامج التربية للذرة الشامية