

## EXPLOITING MODIFIED SINGLE CROSSES IN MAIZE (*ZEA MAYS* L.) TO FACILITATE HYBRID USE IN DEVELOPING COUNTRIES\*

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Received June 10, 2009

**ABSTRACT** - A three-phase study was led by CIMMYT during 1996-99 to assess the usefulness of modified single-cross hybrids to accelerate the adoption of maize hybrids by farmers in developing countries. During Phase I, we evaluated and selected elite, conventional, single-cross hybrids. Based on the information from Phase I, different versions of related crosses between sister lines used in the elite single crosses identified in Phase I were formed and tested during Phase II. Finally, in Phase III we used the results of Phase II to form different versions of modified single crosses and tested them with the original conventional single crosses. From Phase I, 13 conventional single-cross hybrids selected averaged 11.2 t ha<sup>-1</sup> and the best three averaged 11.9 t ha<sup>-1</sup>, outyielding the best check, A-7545 (11.5 t ha<sup>-1</sup>). From Phase II, the 18 related crosses averaged 6.7 t ha<sup>-1</sup>, while the 25 lines per se involved in these crosses yielded 4.5 t ha<sup>-1</sup>, an average difference of 50%. The related crosses selected expressed a 37% high parent heterosis on average. Finally, in Phase III we found non-significant differences in yield between the original conventional single crosses and the corresponding modified single crosses (both averaged 9.6 t ha<sup>-1</sup>). These results confirm that modified single crosses can produce grain yields comparable to their corresponding conventional crosses. Thus, modified single-cross hybrids represent a possible option for exploiting the high yield performance of elite conventional single crosses, where this type of cultivars cannot be adopted by resource-poor farmers in developing countries because expensive price of certified seed.

**KEY WORDS:** *Zea mays* L.; Maize; Modified Single Crosses; Maize Hybrid Technology; Maize Related Crosses; Sister Lines, Heterosis.

## INTRODUCTION

The development and dissemination of maize (*Zea mays* L.) hybrids has been an important factor in meeting the increasing demand for this cereal worldwide during the past 30 years. Although there are countries in which hybrids are not the main type of maize cultivar used, national and private breeding programs nearly every where are investing in hybrid development to increase domestic maize production, both for domestic consumption and export (CASTELLANOS *et al.*, 1998).

One of the main problems facing breeders who develop maize hybrids is the inbreeding depression usually expressed in the inbred lines used as parents. Different alternatives have been proposed through the time to alleviate this problem. Modified single-cross hybrids, in which either one or both parents are crosses of related lines (HALLAUER and MIRANDA, 1988), offer a potentially attractive alternative to lower the costs of hybrid seed production and provide a good steppingstone between three-way hybrids and conventional single-cross hybrids.

One of the main reasons for using modified single crosses in maize is to increase the amount of seed produced. Modified single crosses were used extensively in hybrid seed maize production in the USA in the 1960s and early 1970s. Today, modified single crosses and three-way crosses account for about 10% of the North American market (WYCH, 1988). But modified single crosses have been exploited on a much smaller scale in developing countries (CASTELLANOS *et al.*, 1999). MWALE *et al.* (1994) stated that maize seed yields and kernel size were increased by using sister line crosses in hybrid seed production. CHEN *et al.* (1994) reported non-significant differences in grain yield and main agronomic traits between modified single crosses and their corresponding conventional single crosses in maize.

\* Data from this study were used partially by J. L. Quemé for writing his Ph D Theses in Plant Breeding at the Universidad Autónoma Agraria Antonio Narro, Saltillo, Coahuila, México.

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They recommended the  $S_3$  or  $S_4$  inbred generation as the suitable time to separate sister lines. LIU *et al.* (1994) concluded that early generation sister crosses were better than later generation sister crosses. LUO *et al.* (1993) found that the yield of sister crosses was significantly higher than their parental inbreds and suggested that use of modified single crosses could significantly increase hybrid seed production. CORDOVA *et al.* (2000) tested crosses of tropical sister lines separated at  $S_3$  inbred generation and reported yields similar to those crosses using parental elite lines. They concluded that this breeding technique is useful to increase yield and reduce the cost of maize hybrid seed in developing countries.

Seed industry reports from Mexico, Thailand, Vietnam, and Brazil indicate a tendency to shift from three-way cross hybrid to modified single and single cross hybrids for enhancing maize yields and seed production in developing countries (personal communication).

STRINGFIELD (1972) suggested the formation of broad partially-inbred parent lines, using a slow inbreeding process in assortative mating instead of selfing. In line development using a pool of hybrids as a source populations, this system will provide more time for applying selection within broad based lines, and the resulting partially-inbred lines will possess more defensive traits, plasticity and heterozygosity than homozygous inbred lines derived by conventional pedigree breeding. On the other hand, it will be more difficult to eliminate recessive deleterious genes by this method, and it is a time

consuming method, requiring three times as long as conventional pedigree breeding using repeated self pollinations.

To form a line with adequate defensive traits in one-third of the time used to develop a broad line, a good breeder can use the selfing procedure starting with a source  $F_2$  population derived from a cross between two elite lines that possess the required defensive traits. Nevertheless, in breeding programs that must produce inexpensive hybrid seed, a broad line can be formed using two to four sister lines derived from a project similar to the one proposed here. Such broad lines can be effectively used as seed parents, reducing the cost of hybrid seed relative to conventional hybrids.

As part of the maize research conducted by the International Maize and Wheat Improvement Center (CIMMYT), the main objective of this study was to generate information about the application of the modified single-cross hybrids concept, mainly for developing countries, as a less costly alternative to conventional single-cross hybrids to help accelerate the use of maize hybrid technology.

## MATERIALS AND METHODS

Research was conducted in three phases during 1996-99 in seven subtropical environments in Mexico. Phase I (1996-97) was a North Carolina Mating Design II trial (SSCW964) between two sets of elite maize inbred lines from the subtropical intermediate white heterotic pattern, CIMMYT Populations 501(A) and 502 (B) (Table 1). The 130 conventional single crosses and 5 checks,

TABLE 1 - Pedigrees of lines from CIMMYT maize Populations 501 (heterotic group A) and 502 (heterotic group B) used to form conventional single-cross hybrids included in trial SSCW964, México, 1996.

Progenitor	Population 501 (A)	Progenitor	Population 502 (B)
	Pedigree		Pedigree
1	P501 C <sub>1</sub> #-77-3-3-3-3	13	P502 C <sub>1</sub> #-28-3-1-2-B
2	P501 C <sub>1</sub> #-77-3-4-4-1	14	P502 C <sub>1</sub> #-325-2-4-1-B
3	P501 C <sub>1</sub> #-92-2-3-1-4	15	P502 C <sub>1</sub> #-325-4-1-1-B
4	P501 C <sub>1</sub> #-140-1-1-3-3	16	P502 C <sub>1</sub> #-421-2-2-1-B
5	P501 C <sub>1</sub> #-140-3-1-1-B	17	P502 C <sub>1</sub> #-480-3-4-1-1
6	P501 C <sub>1</sub> #-284-1-1-3-B	18	P502 C <sub>1</sub> #-488-2-2-1-B
7	P501 C <sub>1</sub> #-286-4-1-2-2	19	P502 C <sub>1</sub> #-668-2-2-2-3
8	P501 C <sub>1</sub> #-303-1-1-1-2	20	P502 C <sub>1</sub> #-731-2-4-1-B
9	P501 C <sub>1</sub> #-303-1-1-2-2	21	P502 C <sub>1</sub> #-771-1-1-1-B
10	P501 C <sub>1</sub> #-401-3-1-2-B	22	P502 C <sub>1</sub> #-771-2-2-1-1
11	P501 C <sub>1</sub> #-441-1-1-1-B	23	P502 C <sub>1</sub> #-771-2-2-1-3
12	P501 C <sub>1</sub> #-886-3-1-1-B		

Note: Lines 1 to 12 were crossed with 13 to 23 to form 132 hybrids; however, two crosses failed (12 x 19 and 12 x 21) and hence 130 hybrids were included in the trial.

TABLE 2 - Groups of sister lines from CIMMYT maize Populations 501 and 502 included in the Line Evaluation Trial (SLET981), México, 1998.

Entry	Line†	Sister lines‡	Entry	Line	Sister lines	Entry	Line	Sister lines
1	P4	P501c1#-140-1-1-3-3-B	21		P501c1#-303-1-1-1-1-B-B	41		P502c1#-488-2-2-1-B-3-B-B
2		P501c1#-140-3-1-1-B-B-B	22		P501c1#-303-1-1-1-2-1-3-B-B	42	P21	P502c1#-771-1-1-1-B-B-B
3		P501c1#-140-1-1-3-3-1-1-B-B	23		P501c1#-303-1-1-2-2-1-3-B-B	43		P502c1#-771-1-1-3-B-B
4		P501c1#-140-1-1-3-3-1-2-B-B	24		P501c1#-303-1-1-2-2-1-5-B-B	44		P502c1#-771-1-1-1-B-1-1-B-B
5	P5	P501c1#-140-3-1-1-B-B-B	25	P10	P501c1#-401-3-1-2-B-B-B	45	P22	P502c1#-771-2-2-1-1-B-B
6		P501c1#-140-3-1-1-B-1-B-B	26		P501c1#-401-3-1-3-B-B	46		P502c1#-771-2-2-1-2-B-B
7		P501c1#-140-3-1-1-B-4-B-B	27		P501c1#-401-3-1-2-B-2-B-B	47		P502c1#-771-2-2-3-B-1-1-B-B
8	P6	P501c1#-284-1-1-3-B-B-B	28		P501c1#-401-3-1-2-B-3-B-B	48		P502c1#-771-2-2-1-1-1-2-B-B
9		P501c1#-284-1-1-3-B-1-B-B	29	P11	P501c1#-441-1-1-1-B-B	49		P502c1#-771-2-2-1-1-1-3-B-B
10		P501c1#-284-1-1-3-B-1-2-B-B	30		P501c1#-441-1-1-1-B-1-1-B-B	50	P23	P502c1#-771-2-2-1-3-B-B
11	P7	P501c1#-286-4-1-2-2-B-B	31		P501c1#-441-1-1-1-B-1-2-B-B	51		P502c1#-771-2-2-1-B-B
12		P501c1#-286-4-1-2-1-B-B	32	P12	P501c1#-886-3-1-1-B-B-B	52		P502c1#-771-2-2-1-3-7-B-B
13		P501c1#-286-4-1-2-3-B-B	33		P501c1#-886-3-1-1-B-3-B-B	53		P502c1#-771-2-2-1-3-1-6-B-B
14		P501c1#-286-4-1-2-2-2-B-B	34		P501c1#-886-3-1-1-B-1-1-B-B	54		P502c1#-771-2-2-3-B-1-3-B-B
15	P8	P501c1#-303-1-1-1-2-B-B	35	P17	P502c1#-480-3-4-1-1-B-B	55	Check	CML-311 = S89500 F2-2-2-2-B*5
16		P501c1#-303-1-1-1-2-1-1-B-B	36		P502c1#-480-3-4-1-2-B-B	56	Check	CML-312 = S89500 F2-2-2-1-1-B*5
17		P501c1#-303-1-1-1-2-1-3-B-B	37		P502c1#-480-3-4-1-1-4-2-B-B	57	Check	CML-321 = P502c0F1-1-3-1-B*4
18		P501c1#-303-1-1-2-2-1-4-B-B	38	P18	P502c1#-488-2-2-1-B-B-B	58	Check	CML-78 = G32C19MH32-1-#2-B-###-3-B
19		P501c1#-303-1-1-2-2-1-5-B-B	39		P502c1#-488-2-4-1-2-B	59	Check	P43SR-4-1-1-2-1-B-B-1-B
20	P9	P501c1#-303-1-1-2-2-B-B	40		P502c1#-488-2-2-1-B-2-B-B	60	Check	(SIWHG88*A*c1#-B-140-1-1-3-B x SIWHG88*A*c1#-B-361-1-2-1-B)

† Line = the original lines from the conventional single cross hybrids selected in Phase I.

‡ Sister lines used to form related single crosses that comprised the SSCW9810 trial.

were tested at 7 locations in a 15 x 9 Alpha lattice (0,1) design with 2 replications of a 5 m long row as the experimental unit. From the 132 possible crosses between the 2 sets of lines, 2 crosses (P501 C1#-886-3-1-1-B x P502 C1#-668-2-2-2-3 and P501 C1#-886-3-1-1-B x P502 C1#-771-1-1-1-B) did not produce enough seed for testing, so yield data for these crosses were estimated using a modification of the formula proposed by ECKHARDT (1952). Information on grain yield and other agronomic traits were recorded and used to identify superior crosses.

The testing locations were (institution-location): 1) INIFAP-Celaya, Guanajuato, 1996B; 2) ASGROW-Tlajomulco, Jalisco, 1996B; 3) INIFAP-Aguascalientes, Aguascalientes, 1996B; 4) INIFAP-Cd. Obregón, Sonora, 1997A; 5) CERES-Los Mochis, Sinaloa, 1997A; 6) CIMMYT-Tlaltizapán, Morelos, 1996B; and 7) GENOTEC-Ameca, Jalisco, 1996B. All locations are between 18° 41'N (Tlaltizapán) and 26° 40'N (Cd. Obregón) of latitude; 99° 08'W (Tlaltizapán) and 109° 25'W (Cd. Obregón) of longitude; 14 masl (Los Mochis) and 1870 masl (Aguascalientes) of altitude. All sites received adequate moisture for crop development. Near optimum, high-input agronomic management practices were applied at all sites. CIMMYT coordinated the work. Partners included INIFAP, and several Mexican seed companies.

Information of the superior conventional single crosses identified in Phase I was used in 1997 to form different versions of related single crosses (crosses between sister lines separated at different stage of inbreeding), using parental sister lines from the

selected conventional crosses. At the same time, we increased seed of all lines involved in the formation of these related single crosses.

During cycle 1998A, two types of trials were included in Phase II. The first, SLET981, included the set of 54 lines involved in the related single crosses, and 6 checks (5 lines and 1 related cross) (Table 2). Entries were arranged in a 10 x 6 Alpha lattice (0,1), with two replications, and three 5-m rows as the experimental plot. The second trial, SSCW9810, included 51 related single crosses, plus 4 checks (related single crosses involving lines that were not sisters, but from the same population) (Table 3). This trial was arranged as a 11 x 5 Alpha lattice (0,1), with two replications, and two 5 m rows as the experimental plot. These two trials were grown in pairs at four different locations, except for location 2, where they were grown about 10 km apart. The 4 locations were (institution-location): 1) CIMMYT-Tlaltizapán, Morelos, 1998A; 2) Cargill-Vallarta, Jalisco, 1998A, and ASGROW-Nayarit, Nayarit, 1998A; 3) CERES-Los Mochis, Sinaloa, 1998A; and 4) DEKALB-Culiacán, Sinaloa, 1998A. Trials were grown during the winter cycle (A) because this is when seed is normally produced and when lines and related single crosses should be expected to be planted for certified seed production.

The choice of modified single crosses for evaluation in Phase III was based on the yield performance of the lines per se from trial SLET981, and on related crosses from SSCW9810 trial that outyielded (at least 15% high parent heterosis) their parental sis-

<sup>1</sup> The Mexican National Institute of Forestry, Livestock, and Agriculture Research.

TABLE 3 - Groups of related single crosses sown in trial SSCW9810, México, 1998.

Entry	Line†	Pedigree	Entry	Line	Pedigree
1	P4	P501c1#-140-1-1-3-3-B x P501c1#-140-1-1-3-3-1-2-B	29		P502c1#-480-3-4-1-2-B x P502c1#-480-3-4-1-1-4-2-B
2		P501c1#-140-3-1-1-B-B x P501c1#-140-1-1-3-3-1-2-B	30	P18	P502c1#-488-2-2-1-B-B x P502c1#-488-2-2-1-B-2-B
3		P501c1#-140-1-1-3-3-1-1-B x P501c1#-140-1-1-3-3-1-2-B	31		P502c1#-488-2-4-1-2 x P502c1#-488-2-2-1-B-2-B
4	P5	P501c1#-140-3-1-1-B-B x P501c1#-140-3-1-1-B-1-B	32		P502c1#-488-2-2-1-B-3-B x P502c1#-488-2-2-1-B-2-B
5		P501c1#-140-3-1-1-B-4-B x P501c1#-140-3-1-1-B-1-B	33	P21	P502c1#-771-1-1-1-B-B x P502c1#-771-1-1-1-B-1-1-B
6	P6	P501c1#-284-1-1-3-B-B x P501c1#-284-1-1-3-B-1-2-B	34		P502c1#-771-1-1-3-B x P502c1#-771-1-1-1-B-1-1-B
7		P501c1#-284-1-1-3-B-1-B x P501c1#-284-1-1-3-B-1-2-B	35	P22	P502c1#-771-2-2-1-1-B x P502c1#-771-2-2-1-1-1-2-B
8	P7	P501c1#-286-4-1-2-2-B x P501c1#-286-4-1-2-2-2-2-B	36		P502c1#-771-2-2-1-2-B x P502c1#-771-2-2-1-1-1-2-B
9		P501c1#-286-4-1-2-1-B x P501c1#-286-4-1-2-2-2-2-B	37		P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-1-1-2-B
10		P501c1#-286-4-1-2-3-B x P501c1#-286-4-1-2-2-2-2-B	38		P502c1#-771-2-2-1-1-1-3-B x P502c1#-771-2-2-1-1-1-2-B
11		P501c1#-286-4-1-2-2-1-2 x P501c1#-286-4-1-2-2-2-2-B	39		P502c1#-771-2-2-1-3-7-B x P502c1#-771-2-2-1-1-1-2-B
12	P8	P501c1#-303-1-1-1-2-B x P501c1#-303-1-1-1-2-1-1-B	40	P23	P502c1#-771-2-2-1-3-B x P502c1#-771-2-2-1-3-1-6-B
13		P501c1#-303-1-1-1-2-1-3-B x P501c1#-303-1-1-1-2-1-1-B	41		P502c1#-771-2-2-1-B x P502c1#-771-2-2-1-3-1-6-B
14		P501c1#-303-1-1-2-2-1-4-B x P501c1#-303-1-1-1-2-1-1-B	42		P502c1#-771-2-2-1-3-7-B x P502c1#-771-2-2-1-3-1-6-B
15		P501c1#-303-1-1-2-2-1-5-B x P501c1#-303-1-1-1-2-1-1-B	43		P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B
16	P9	P501c1#-303-1-1-2-2-B x P501c1#-303-1-1-2-2-1-3-B	44		P502c1#-771-2-2-3-B-1-3-B x P502c1#-771-2-2-1-3-1-6-B
17		P501c1#-303-1-1-1-1-B x P501c1#-303-1-1-2-2-1-3-B	45		P502c1#-771-2-2-1-1-1-3-B x P502c1#-771-2-2-1-3-1-6-B
18		P501c1#-303-1-1-1-2-1-3-B x P501c1#-303-1-1-2-2-1-3-B	46		P502c1#-771-1-1-1-B-1-1-B x P502c1#-771-2-2-1-1-1-2-B
19		P501c1#-303-1-1-2-2-1-5-B x P501c1#-303-1-1-2-2-1-3-B	47		P502c1#-771-1-1-1-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B
20		P501c1#-303-1-1-1-2-1-1-B x P501c1#-303-1-1-2-2-1-3-B	48		P502c1#-771-2-2-1-1-1-2-B x P502c1#-771-2-2-1-3-1-6-B
21	P10	P501c1#-401-3-1-2-B-B x P501c1#-401-3-1-2-B-3-B	49	P21xP22	P502c1#-771-1-1-1-B-B x P502c1#-771-2-2-1-1-B
22		P501c1#-401-3-1-3-B x P501c1#-401-3-1-2-B-3-B	50	P21xP23	P502c1#-771-1-1-1-B-B x P502c1#-771-2-2-1-3-B
23		P501c1#-401-3-1-2-B-2-B x P501c1#-401-3-1-2-B-3-B	51	P22xP23	P502c1#-771-2-2-1-1-B x P502c1#-771-2-2-1-3-B
24	P11	P501c1#-441-1-1-1-B x P501c1#-441-1-1-1-B-1-1-B	52	Check	SIWHG88°A°c1#-B-140-1-1-3-B x SIWHG88°A°c1#-B-361-1-2-1-B
25		P501c1#-441-1-1-1-B-1-2-B x P501c1#-441-1-1-1-B-1-1-B	53	Check	P501c1#-284-1-1-3-B-1-2-B x P501c1#-286-4-1-2-2-2-2-B
26	P12	P501c1#-886-3-1-1-B-B x P501c1#-886-3-1-1-B-1-1-B	54	Check	P502c1#-488-2-2-1-B-2-B x P502c1#-480-3-4-1-1-4-2-B
27		P501c1#-886-3-1-1-B-3-B x P501c1#-886-3-1-1-B-1-1-B	55	Check	P501c1#-401-3-1-2-B-3-B x P501c1#-886-3-1-1-B-1-1-B
28	P17	P502c1#-480-3-4-1-1-B x P502c1#-480-3-4-1-1-4-2-B			

† Line = the original lines from the conventional single crosses selected in Phase I.

ter lines. These selected related crosses were used to form different versions of modified single crosses (AxA' x B) during 1999A, following the same pedigree of the selected conventional single crosses identified in Phase I. We also formed the best conventional single crosses identified in Phase I to have fresh seed for testing. The modified single crosses (MSC) trial (SSCW9921) tested during 1999 included the best conventional single crosses from Phase I and different versions of modified single crosses of the same, based on Phase II results (Table 4).

The 6 locations for testing the MSC trial (SSCW9921) were (institution-location): 1) CIMMYT-Tlaltizapán, Morelos, 1999A; 2) CIMMYT-Tlaltizapán, Morelos, 1999B; 3) INIFAP-Celaya, Guanajuato, 1999B; 4) ASGROW-Tlajomulco, Jalisco, 1999B; 5) ASPROS-Roque, Guanajuato, 1999B; 6) PIONEER-Guasave, Sinaloa, 1999B.

For all trials conducted during the three phases of this study, we recorded data for grain yield and selected agronomic traits: days to 50% silking, plant and ear height (cm), plant and ear aspect (on a 1-to-5 scale, where 1 = good, 5 = poor), grain moisture at harvest, stem and root lodging (%), and important foliar

and ear diseases. Analysis of variance (ANOVA) was performed for grain yield (adjusted to 15% moisture) and the least significant differences test (LSD with an  $\alpha = 0.05$ ) was used to check differences between means. Genotype selection was based mainly on grain yield, but undesirable traits, such as, ear diseases were also considered.

## RESULTS AND DISCUSSION

### Phase I: conventional single cross test (DII trial, SSCW964)

The main goal of Phase I was to identify superior, conventional single crosses involving two sets of elite lines developed from two heterotic groups of CIMMYT maize. Average yields of the conventional single crosses varied across seven locations from 7.6 t ha<sup>-1</sup> (location 4) to 12.7 t ha<sup>-1</sup> (location 1), re-

TABLE 4 - Groups of conventional and modified single-cross maize hybrids included in CIMMYT trial SSCW9921, México, 1999.

Entry	Pedigree
1	<b>P501c1#-401-3-1-2-B-B-B x P502c1#-771-2-2-1-1-B-B</b>
2	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-401-3-1-2-B-3-B-B
3	(P501c1#-401-3-1-3-B x P501c1#-401-3-1-2-B-3-B) x P502c1#-771-2-2-1-1-2-B-B
4	(P501c1#-401-3-1-3-B x P501c1#-401-3-1-2-B-3-B) x P502c1#-771-2-2-1-3-1-6-B-B
5	<b>P501c1#-886-3-1-1-B-B-B x P502c1#-771-2-2-1-3-B-B</b>
6	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-886-3-1-1-B-1-1-B-B
7	(P502c1#-771-2-2-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-886-3-1-1-B-1-1-B-B
8	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-1-2-B) x P501c1#-886-3-1-1-B-1-1-B-B
9	(P501c1#-886-3-1-1-B-B x P501c1#-886-3-1-1-B-1-1-B) x P502c1#-771-2-2-1-1-2-B-B
10	<b>P501c1#-140-3-1-1-B-B-B x P502c1#-488-2-2-1-B-B-B</b>
11	(P502c1#-488-2-2-1-B-B x P502c1#-488-2-2-1-B-2-B) x P501c1#-140-3-1-1-B-1-B-B
12	(P502c1#-488-2-4-1-2 x P502c1#-488-2-2-1-B-2-B) x P501c1#-140-3-1-1-B-1-B-B
13	(P502c1#-488-2-2-1-B-3-B x P502c1#-488-2-2-1-B-2-B) x P501c1#-140-3-1-1-B-1-B-B
14	<b>P501c1#-303-1-1-2-2-B-B x P502c1#-771-2-2-1-3-B-B</b>
15	<b>P501c1#-303-1-1-1-2-B-B x P502c1#-771-2-2-1-3-B-B</b>
16	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-303-1-1-1-2-1-1-B-B
17	(P502c1#-771-2-2-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-303-1-1-1-2-1-1-B-B
18	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-303-1-1-2-2-1-3-B-B
19	(P502c1#-771-2-2-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-303-1-1-2-2-1-3-B-B
20	(P501c1#-303-1-1-1-1-B x P501c1#-303-1-1-2-2-1-3-B) x P502c1#-771-2-2-1-3-1-6-B-B
21	(P501c1#-303-1-1-1-2-1-3-B x P501c1#-303-1-1-2-2-1-3-B) x P502c1#-771-2-2-1-3-1-6-B-B
22	(P501c1#-303-1-1-1-2-1-3-B x P501c1#-303-1-1-2-2-1-3-B) x P502c1#-771-2-2-1-1-1-2-B-B
23	(P501c1#-303-1-1-1-2-1-3-B x P501c1#-303-1-1-1-2-1-1-B) x P502c1#-771-2-2-1-3-1-6-B-B
24	(P501c1#-303-1-1-2-2-1-4-B x P501c1#-303-1-1-1-2-1-1-B) x P502c1#-771-2-2-1-3-1-6-B-B
25	(P501c1#-303-1-1-1-2-B x P501c1#-303-1-1-1-2-1-1-B) x P502c1#-771-2-2-1-1-1-2-B-B
26	<b>P501c1#-401-3-1-2-B-B-B x P502c1#-771-1-1-1-B-B-B</b>
27	(P502c1#-771-1-1-3-B x P502c1#-771-1-1-1-B-1-1-B) x P501c1#-401-3-1-2-B-3-B-B
28	(P501c1#-401-3-1-3-B x P501c1#-401-3-1-2-B-3-B) x P502c1#-771-1-1-1-B-1-1-B-B
29	<b>P501c1#-284-1-1-3-B-B-B x P502c1#-771-2-2-1-3-B-B</b>
30	(P502c1#-771-2-2-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-284-1-1-3-B-1-2-B-B
31	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-284-1-1-3-B-1-2-B-B
32	<b>P501c1#-303-1-1-2-2-B-B x P502c1#-480-3-4-1-1-B-B</b>
33	(P502c1#-480-3-4-1-1-B x P502c1#-480-3-4-1-1-4-2-B) x P501c1#-303-1-1-1-2-1-1-B-B
34	(P502c1#-480-3-4-1-1-B x P502c1#-480-3-4-1-1-4-2-B) x P501c1#-303-1-1-2-2-1-3-B-B
35	(P501c1#-303-1-1-1-2-1-3-B x P501c1#-303-1-1-1-2-1-1-B) x P502c1#-480-3-4-1-1-4-2-B-B
36	(P501c1#-303-1-1-2-2-1-4-B x P501c1#-303-1-1-1-2-1-1-B) x P502c1#-480-3-4-1-1-4-2-B-B
37	(P501c1#-303-1-1-1-1-B x P501c1#-303-1-1-2-2-1-3-B) x P502c1#-480-3-4-1-1-4-2-B-B
38	(P501c1#-303-1-1-1-2-1-3-B x P501c1#-303-1-1-2-2-1-3-B) x P502c1#-480-3-4-1-1-4-2-B-B
39	<b>P501c1#-140-1-1-3-3-B x P502c1#-771-2-2-1-1-B-B</b>
40	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-1-1-2-B) x P501c1#-140-1-1-3-3-1-2-B-B
41	<b>P501c1#-140-3-1-1-B-B-B x P502c1#-771-2-2-1-3-B-B</b>
42	(P502c1#-771-2-2-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-140-3-1-1-B-1-B-B
43	<b>P501c1#-303-1-1-1-2-B-B x P502c1#-488-2-2-1-B-B-B</b>
44	(P502c1#-488-2-4-1-2 x P502c1#-488-2-2-1-B-2-B) x P501c1#-303-1-1-1-2-1-1-B-B
45	(P502c1#-488-2-2-1-B-3-B x P502c1#-488-2-2-1-B-2-B) x P501c1#-303-1-1-1-2-1-1-B-B
46	(P501c1#-303-1-1-1-2-1-3-B x P501c1#-303-1-1-1-2-1-1-B) x P502c1#-488-2-2-1-B-2-B-B
47	(P501c1#-303-1-1-2-2-1-4-B x P501c1#-303-1-1-1-2-1-1-B) x P502c1#-488-2-2-1-B-2-B-B
48	<b>P501c1#-284-1-1-3-B-B-B x P502c1#-771-1-1-1-B-B-B</b>
49	(P502c1#-771-1-1-3-B x P502c1#-771-1-1-1-B-1-1-B) x P501c1#-284-1-1-3-B-1-2-B-B

TABLE 4 - *Continued*

Entry	Pedigree
50	<b>P501c1#-441-1-1-1-B-B x P502c1#-771-2-2-1-3-B-B</b>
51	(P502c1#-771-2-2-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-441-1-1-1-B-1-1-B-B
52	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-441-1-1-1-B-1-1-B-B
53	(P501c1#-441-1-1-1-B-1-2-B x P501c1#-441-1-1-1-B-1-1-B) x P502c1#-771-2-2-1-3-1-6-B-B
54	(P502c1#-488-2-2-1-B-2-B x 502c1#-480-3-4-1-1-4-2-B) x P501c1#-140-1-1-3-3-1-2-B-B
55	(P501c1#-401-3-1-2-B-3-B x P501c1#-886-3-1-1-B-1-1-B) x P502c1#-771-2-2-1-3-1-6-B-B
56	(P502c1#-771-1-1-1-B-1-1-B x P502c1#-771-2-2-1-1-1-2-B) x P501c1#-401-3-1-2-B-3-B-B
57	(P502c1#-771-1-1-1-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-303-1-1-2-2-1-3-B-B
58	CML 78 x CML 321
59	CML 78 x CML 373
60	Local Check

Entries typed in boldface refer to the conventional single crosses selected from phase I (SSCW964 Trial).

TABLE 5 - ANOVA for grain yield ( $t\ ha^{-1}$ ) for CIMMYT trial SSCW964 involving conventional single-cross maize hybrids tested at seven locations in the subtropics of Mexico, 1996.

Source of variation	DF†	SS‡	MS§	F significance
Locations	6	5161.41	860.23	75.99**
Replications (locations)	7	79.21	11.32	
Block (replication x location)	112	422.58	3.77	
Entries (adjusted)	134	1998.14	14.91	12.12**
Checks	2	2.73	1.36	0.89ns
Crosses	131	2022.56	15.44	5.20**
GCA (L- 501)+	11	786.07	71.46	12.30**
GCA (L- 502)++	10	642.62	64.26	7.12**
SCA (L-501xL-502)	110	593.87	5.39	2.52**
Checks vr. Crosses	1	79.35	79.35	9.67*
Genotype x environment interaction	804	2404.52	2.99	2.43**
Locations x Checks	12	18.35	1.53	1.24ns
Locations x Crosses	786	2336.89	2.97	2.41**
GCA(L-501) x Locations	66	383.57	5.81	4.72**
GCA(L-502) x Locations	60	541.64	9.03	7.34**
SCA(L-501xL-502) x Locations	660	1411.68	2.14	1.74**
Loc x (checks vr. crosses)	6	49.28	8.21	6.67**
Error				
Residual	826	932.99	1.13	
Effective	826	1015.98	1.23	
Total	1889	11105.35		
Mean ( $t\ ha^{-1}$ )		9.73		
C.V. (%) †		11.00		
R.E. ††		1.18		
Standard error average		0.29		
LSD ( $\alpha = 0.05$ ) $t\ ha^{-1}$		0.82		

† DF = degree of freedom. ‡ SS = sum of squares. § MS = mean square. # C.V. (%) = coefficient of variation.

†† R.E. = lattice efficiency, compared with a randomized complete block. \*\*, \* and ns = significant with an  $\alpha$  of 0.01, 0.05, and not significant. + Lines from Population 501. ++ Lines from Population 502.

flecting the contrasts in testing environments. Coefficients of variation ranged from 8 to 13% acceptable for this type of trial. From the analysis of variance for grain yield at each location, no significant differences were found for replications at any site, with the exception of location 2. At all locations, highly significant differences ( $\alpha = 0.01$ ) were observed for entries, as well as for the general and specific combining ability (GCA and SCA) sources (ANOVA data for each location not shown).

The combined ANOVA across locations for grain yield, exhibited highly significant differences for locations, entries, and genotype x environment interaction (G x E), accounting for 46.5, 18, and 21.6% of the total variation, respectively (Table 5). The significant differences for entries and G x E indicates that at least one entry is different from the others and that yield differences among entries differed either in ranking or relative yields across the environments. From the breakdown of the variance among

crosses, specific combining ability (SCA) accounted for 29.4% and general combining ability (GCA) for 70.7%, which suggests yield was determined mainly by additive genetic effects. Both GCA and SCA effects were important ( $P < 0.01$ ) in determining grain yield in crosses among these lines.

In the D II trial (SSCW964), average yield across locations for the 13 selected crosses was 11.20 t ha<sup>-1</sup>. Three entries (132, 109, and 66) yielded more (average 11.90 t ha<sup>-1</sup>) than the best check, A-7545 (11.50 t ha<sup>-1</sup>), and significantly more than the trial mean of 9.73 t ha<sup>-1</sup> (Table 6). Eight lines from Population 501 and 5 lines from Population 502 are involved in the 13 crosses selected, and the 3 sister lines from Population 502 (lines 21, 22, and line 23) were involved in 10 of the 13 crosses.

Lines 10, 12, and 5 from Population 501 and lines 22 and 23 from Population 502 showed the highest GCA effects (0.831, 0.736, 0.657, 1.156, and 0.943 t ha<sup>-1</sup>, respectively) and were included in 10

TABLE 6 - Yield (t ha<sup>-1</sup>) of conventional, subtropical (parental lines from Populations 501 and 502), single-cross maize hybrids selected from CIMMYT trial SSCW964 grown at seven locations, Mexico, 1996.

Entry	Cross	Site 1 <sup>‡</sup>	Site 2	Site 3	Site 4	Site 5	Site 6	Site 7	Mean
<b>132</b>	12 x 23	17.80	11.27	12.93	8.41	12.69	11.21	9.95	12.04
<b>109</b>	10 x 22	15.81	9.88	11.77	9.24	11.27	13.83	12.22	12.00
<b>66</b>	6 x 23	18.14	10.00	11.41	9.57	11.24	11.81	9.54	11.67
<b>50</b>	5 x 18	15.68	10.53	12.13	8.19	11.13	13.08	9.03	11.39
<b>93</b>	9 x 17	15.36	10.15	12.12	9.40	11.19	11.94	9.35	11.36
<b>108</b>	10x 21	15.12	9.09	10.51	5.55	10.98	12.50	12.20	11.28
<b>88</b>	8 x 23	15.85	7.77	11.55	8.96	13.01	11.37	9.85	11.20
<b>43</b>	4 x 22	15.30	7.05	13.09	8.68	11.31	11.20	9.73	11.18
<b>83</b>	8 x 18	12.82	10.25	12.14	9.56	9.76	11.51	9.59	10.81
<b>55</b>	5 x 23	15.18	9.61	12.67	6.57	10.47	11.29	9.87	10.81
<b>64</b>	6 x 21	14.66	9.42	9.60	8.93	10.56	12.19	9.49	10.69
<b>99</b>	9 x 23	15.26	10.58	12.25	8.40	7.47	10.22	10.00	10.60
<b>120</b>	11 x 22	14.31	7.59	11.03	7.63	11.56	11.10	10.07	10.47
<b>133</b>	A-7545	14.59	8.71	12.01	9.18	14.41	11.47	10.20	11.51
<b>134</b>	CML78 x CML 322	12.75	8.44	11.98	8.80	13.20	10.00	8.89	10.58
<b>135</b>	Local check	16.21	9.26	11.96	7.39	14.66	10.20	9.71	(11.34)
<b>LSD<sup>¶</sup></b>		3.13	2.10	2.27	1.94	2.10	1.65	1.86	0.82
<b>Max<sup>††</sup></b>		18.14	11.27	13.75	10.51	14.65	14.38	12.56	12.04
<b>Mean</b>		12.71	7.67	10.45	7.63	10.18	10.45	9.13	9.73
<b>Min</b>		7.52	2.96	2.69	3.54	4.67	7.46	6.25	6.16

<sup>‡</sup> Site 1= Celaya, Gto.; Site 2 =Tlajomulco, Jalisco; Site 3 = Aguascalientes, Aguascalientes; Site 4 = CD.Obregón, Sonora; Site 5 = Mochis, Sinaloa; Site 6 =Tlaltizapán, Morelos; Site 7 = Ameca, Jalisco. <sup>¶</sup> LSD = least significant difference ( $\alpha = 0.05$ ). <sup>††</sup> The values maximum (Max), minimum (Min) and mean, considers the 135 entries by location and 134 in the combined (local check not included).

TABLE 7 - Combined ANOVA for yield ( $t\ ha^{-1}$ ) of the trial SLET981, involving subtropical, white CIMMYT maize inbred lines, and the trial SSCW9810, of related crosses, sown at four locations, Mexico, 1998.

Source of variation	SLET981 trial			SSCW9810 trial		
	DF†	SS‡	MS§	DF†	SS‡	MS§
Locations	3	325.31	108.44**	3	445.83	148.61**
Replications/locations	4	25.90	5.42	4	15.52	3.88
Blocks (locations x replications)	40	47.82	1.37	32	75.65	2.36
Entries (adjusted)	59	503.71	8.54**	54	767.58	14.21**
Genotype x environment interaction	177	268.30	1.52**	162	267.06	1.65**
<i>Error</i>						
Residual	196	170.75	0.87	184	160.23	0.87
Effective	196	6.51	0.15	184	184.70	1.00
Total	479	1341.79		439	1756.34	
Mean ( $t\ ha^{-1}$ )	4.420			6.119		
Coefficient of variation (%)	21.0			16.0		
R.E.¶	1.17			1.09		
Standard error	0.478			0.354		
MDS ( $\alpha = 0.05$ )	0.910			0.989		

† G.L. = degree of freedom. ‡ SS = sum of squares. § MS = Mean square. \*\* and \* = significance with an  $\alpha$  of 0.01 and 0.05, respectively. R.E. = relative efficiency of the lattice design compared to randomized complete blocks.

of the 13 selected crosses. The crosses 1 x 15, 9 x 17, and 2 x 14 showed the highest SCA effects (1.444, 1.288, and 1.115  $t\ ha^{-1}$ , respectively), but none of the lines involved in these crosses expressed good GCA, and only cross 9 x 17 was among the selected crosses. The cross 10 x 22, whose lines showed the highest GCA, exhibited just 0.300  $t\ ha^{-1}$  SCA. The best selected cross, 12 x 23, showed an SCA of 0.645 and involved two of the lines with highest GCA effects. The 13 conventional single crosses selected from the DII trial of Phase I (SSCW964) were used as base pedigrees to form the crosses developed for Phase II of this study.

### **Phase II: related single crosses (SSCW9810 trial) and sister lines (SLET981 trial) test**

We selected 13 superior conventional single crosses based on Phase I results. The idea for Phase II was to form different versions of related crosses (crosses between sister lines) using the lines from the 13 superior crosses, and test these together with all the sister lines involved in them. The main objective of Phase II was to identify those related single crosses that expressed higher yield potential than the sister lines involved in the cross. In other words, we sought to identify the related crosses that expressed useful high parent heterosis, for use as female parents in assembling modified single-cross

versions of the original 13 conventional single crosses selected in Phase I.

For the sister line trial (SLET981), highly significant differences were detected for locations, entries, and the G x E (Table 7). Entries accounted for 37.5% of the total variation, locations 24.2%, and G x E 20.0%. The ANOVA for the related crosses trial (SSCW9810) also revealed highly significant differences for locations, entries, and G x E. These results reflect the differential expression of the genotypes in the contrasting environmental conditions of testing.

Data of some agronomic characteristics and grain yields of the best lines and related crosses selected from the SLET981 and SSCW9810 trials are shown in Table 8. These genotypes were selected mostly for expression of high parent heterosis for yield of the two sister lines involved in each cross. High parent heterosis was estimated as:  $H = [(F_1 - BP)/BP] * 100$ , where BP is the yield of the best parental line. Grain yield for the selected sister lines ranged from 2.70  $t\ ha^{-1}$  (line 28) to 5.70  $t\ ha^{-1}$  (line 53), with an average of 4.50  $t\ ha^{-1}$ . For the selected related crosses the yield ranged from 5.00  $t\ ha^{-1}$  (cross 26) to 8.70  $t\ ha^{-1}$  (cross 46), with an average of 6.70  $t\ ha^{-1}$ . Average yield for the selected related crosses was 50% higher than that of the selected sister lines. The selected lines from Population 501



TABLE 8 - Yield (t ha<sup>-1</sup>) and agronomic traits of the selected entries from the lines trial (SLET981) and related crosses trial (SSCW9810) tested at four subtropical locations, Mexico, 1998.

SLET981 trial						SSCW9810 trial					
Entry	Yield (t ha <sup>-1</sup> )	Days to 50% silk	Plant height (cm)	PA (1-5)	EA (1-5)	Entry	Yield (t ha <sup>-1</sup> )	Days to 50% silk	Plant height (cm)	PA (1-5)	EA (1-5)
15	4.02	112	149	2.3	2.8	Pob. 501					
16	4.31	114	152	2.3	3.4	14	6.73	114	172	2.5	2.0
17	4.77	112	147	2.4	2.7	17	5.88	118	176	2.5	2.9
18	4.28	112	144	2.5	2.7	18	6.21	119	174	2.5	1.9
21	4.57	112	139	2.4	3.3	22	6.67	114	157	2.8	2.6
22	4.35	112	142	2.4	2.9	12	5.50	116	159	2.8	3.0
23	4.19	116	151	2.5	3.5	26	4.98	103	133	4.0	3.8
26	3.77	116	127	2.9	3.0	13	5.80	116	169	3.0	3.0
28	2.74	116	119	2.9	3.4	25	5.53	115	129	3.3	3.1
30	4.28	109	119	2.3	3.5	Pob. 502					
31	4.71	109	120	2.8	3.1	46	8.73	110	174	2.8	2.4
32	4.20	105	127	2.4	3.3	47	8.49	111	169	2.5	2.4
34 Pop. 501	4.09	102	141	2.3	3.1	31	7.62	110	166	2.5	2.1
35 Pop. 502	4.65	110	125	2.4	3.2	34	7.62	113	162	2.5	2.6
37	4.31	116	141	2.1	3.8	37	7.26	111	151	2.5	2.4
38	4.40	109	129	2.5	2.3	43	7.40	111	159	2.5	2.9
39	4.25	108	120	2.8	3.1	41	6.78	110	163	3.0	2.5
40	4.32	107	132	2.5	2.8	28	6.02	117	147	3.0	3.5
41	4.54	109	137	2.1	2.6	30	5.39	113	142	3.5	2.6
43	4.55	112	138	2.6	3.0	32	5.56	112	148	2.8	2.9
44	3.60	112	131	2.6	3.9	53 ‡	9.17	104	185	2.0	2.3
47	5.27	111	146	2.5	2.6	54	9.68	107	203	1.8	1.8
48	6.14	107	141	2.1	2.2	55	10.62	105	194	1.5	1.6
51	5.33	108	140	2.3	2.8						
53	5.66	110	137	2.1	2.2						
CML-311	4.57	102	138	2.6	3.3						
CML-312	4.19	105	161	2.5	2.9						
CML-321	4.82	108	146	2.4	2.1						
CML-78	3.63	103	128	2.9	3.4						
P43SRS <sub>10</sub>	5.18	106	139	2.1	2.3						
LSD ‡	0.91	3.0	12.0	0.4	0.7	LSD ‡	0.92	2.1	12.3	0.4	0.6
Máximo §	6.60	116	161	4.0	4.0	Máximo §	10.62	120	203	4.3	3.9
Mean	4.24	109	134	2.5	3.1	Mean	6.12	112	155	3.0	2.8
Mínimo	2.43	102	105	2.0	2.0	Mínimo	3.39	103	108	1.5	1.6
No. Locs. ¶	4	2	4	2	3	No.Locs. ¶	4	2	4	1	2

PA = plant aspect (1 = good, 5 = bad). EA = ear aspect (1 = good, 5 = bad). ‡ Entries 53, 54, and 55, are single crosses between non-related lines from CIMMYT maize Populations 501, 502, and 501. § The values maximum, mean, and minimum are estimated for the 55 entries of the SSCW9810 trial and the 59 line-entries of the SLET981 trial. ¶ No. Locs. = number of locations that were accounted to calculate the mean.

had an average yield of 4.24 t ha<sup>-1</sup> and the selected lines from Population 502 had average yield of 4.80 t ha<sup>-1</sup>, whereas the selected related crosses of Population 501 yielded an average 5.90 t ha<sup>-1</sup> and the selected related crosses of Population 502 had an average yield of 7.10 t ha<sup>-1</sup>. These results are similar to those reported by LUO *et al.* (1993). Comparing these two trials for other agronomic characteristics, there were significant differences for plant height (the related crosses were 16% taller on average than the lines).

High parent heterosis of the selected related crosses ranged from 17% for cross 25 to 77% for

cross 22, with an average of 32% (Table 9). Cross 22 involved two lines separated in the fourth generation of inbreeding, whereas cross 25 included lines separated in the seventh generation. Considering the inbreeding generation of separation of the sister lines involved in the 54 related crosses tested in this trial, we evaluated the following materials (average high-parent heterosis in parentheses): 3 crosses from lines separated in the S<sub>1</sub> generation (174%), 5 crosses from lines separated at S<sub>2</sub> (43.4%), 1 cross from lines separated at S<sub>3</sub> (76.5%), 10 crosses from lines separated at S<sub>4</sub> (40.0%), 9 crosses from lines separated at S<sub>5</sub> (12.5%), 20 crosses from lines sepa-

TABLE 9 - Mean yield (t ha<sup>-1</sup>) and heterosis of selected lines per se and related crosses from trials SLET981 and SSCW9810 tested at four locations, Mexico, 1998.

Entry SSCW9810	Crosses†	Pedigree	GS ‡	Yield, parent 1	Yield, parent 2	Yield, of cross	High parent heterosis (%)
Pop. 501							
14	18 x 16	P501c1#-303-1-1-2-2-1-4-B x P501c1#-303-1-1-1-2-1-1-B	4	4.29	4.39	6.73	56
17	21 x 23	P501c1#-303-1-1-1-1-B x P501c1#-303-1-1-2-2-1-3-B	4	4.57	4.19	5.88	29
18	22 x 23	P501c1#-303-1-1-1-2-1-3-B x P501c1#-303-1-1-2-2-1-3-B	4	4.35	4.19	6.21	43
22	26 x 28	P501c1#-401-3-1-3-B x P501c1#-401-3-1-2-B-3-B	4	3.77	2.74	6.67	77
12	15 x 16	P501c1#-303-1-1-1-2-B x P501c1#-303-1-1-1-2-1-1-B	6	4.02	4.31	5.50	28
26	32 x 34	P501c1#-886-3-1-1-B-B x P501c1#-886-3-1-1-B-1-1-B	6	4.20	4.09	4.98	19
13	17 x 16	P501c1#-303-1-1-1-2-1-3-B x P501c1#-303-1-1-1-2-1-1-B	7	4.78	4.31	5.78	21
25	31 x 30	P501c1#-441-1-1-1-B-1-2-B x P501c1#-441-1-1-1-B-1-1-B	7	4.71	4.28	5.53	17
Pop. 502							
46	44 x 48	P502c1#-771-1-1-1-B-1-1-B x P502c1#-771-2-2-1-1-1-2-B	2	3.60	6.14	8.73	42
47	44 x 53	P502c1#-771-1-1-1-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B	2	3.60	5.66	8.49	50
31	39 x 40	P502c1#-488-2-4-1-2 x P502c1#-488-2-2-1-B-2-B	3	4.25	4.32	7.62	76
34	43 x 44	P502c1#-771-1-1-3-B x P502c1#-771-1-1-1-B-1-1-B	4	4.55	3.60	7.61	67
37	47 x 48	P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-1-1-2-B	4	5.27	6.14	7.25	18
43	47 x 53	P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B	4	5.27	5.66	7.40	31
41	51 x 53	P502c1#-771-2-2-1-B x P502c1#-771-2-2-1-3-1-6-B	5	5.33	5.66	6.78	20
28	35 x 37	P502c1#-480-3-4-1-1-B x P502c1#-480-3-4-1-1-4-2-B	6	4.65	4.31	6.02	29
30	38 x 40	P502c1#-488-2-2-1-B-B x P502c1#-488-2-2-1-B-2-B	6	4.40	4.32	5.40	23
32	41 x 40	P502c1#-488-2-2-1-B-3-B x P502c1#-488-2-2-1-B-2-B	6	4.54	4.32	5.56	22
53§	10 x 14	P501c1#-284-1-1-3-B-1-2-B x P501c1#-286-4-1-2-2-2-2-B	1	2.71	2.43	9.17	238
54	40 x 37	P502c1#-488-2-2-1-B-2-B x P502c1#-480-3-4-1-1-4-2-B	1	4.32	4.31	9.68	124
55	28 x 34	P501c1#-401-3-1-2-B-3-B x P501c1#-886-3-1-1-B-1-1-B	1	2.74	4.09	10.67	160
Máximo ¶						<b>10.62</b>	<b>238</b>
Mean						<b>6.12</b>	<b>32</b>
Mínimo						<b>3.39</b>	<b>-6</b>

† Entry numbers correspond to the SSCW9810 related crosses trial. ‡ GS = Generation of separation of the two lines involved according to the number of selfs. § Entries 53, 54 and 55, are single crosses between non-related lines from Populations 501, 502, and 501, respectively. ¶ The values maximum, mean, and minimum are calculated for the 55 entries.

TABLE 10 - ANOVA for grain yield ( $t\ ha^{-1}$ ) from the conventional and modified single cross trial (SSCW9921) grown at six locations, Mexico, 1999.

Source of variation	DF†	SS‡	MS§
Locations(Locs.)	5	3330.61	666.12**
Replications (Locations)	6	78.82	13.14
Block (Replications x Locations)	108	95.02	0.88
Entries (adjusted)	59	127.71	2.16**
Conventional Single Crosses (CSC)	12	18.91	1.58ns
Modified Single Crosses (MSC)	41	76.09	1.86**
Checks	4	16.60	4.15**
CSC vr. MSC	1	0.40	0.40ns
MSC vr. Checks	1	4.46	4.46ns
<i>Genotype x environment</i>	295	294.28	1.00**
CSC*Locs.	60	38.89	0.65ns
MSC*Locs.	205	167.11	0.82*
Checks*Locs.	20	44.69	2.23**
CSC vr. MSC*Locs.	5	0.43	0.09ns
MSC vr. Checks*Locs.	5	8.94	1.79ns
<i>Error</i>			
Residual	246	173.99	0.71
Effective	246	158.00	0.64
<i>Total</i>	719		
Coefficient of variation (%)	7.57		
LSD ( $\alpha = 0.05$ ) $t/ha^{-1}$	0.83		
R.E.	142.46		
Standard Error (Diff.)	0.343		
Mean ( $t\ ha^{-1}$ )			
Conventional single crosses	9.62		
Modified single crosses	9.56		
Checks (Include local checks and CIMMYT reference)	9.93		
General	9.60		

† DF = Degree of freedom. ‡ SS = Sum of squares. § MS = Mean square. †† R.E.= Lattice efficiency compared to a randomized complete block.

\*\* , \* and ns = significance at an  $\alpha$  of 0.01, 0.05 and non-significance.

rated at  $S_6$  (16.3%), and 6 crosses from lines separated at  $S_7$  (13.5%). Regression estimates for the related crosses, excluding those separated at  $S_1$ , showed a polynomial tendency of second order for heterosis. The results obtained from these two trials indicated that, in many crosses between sister lines, we were still able to exploit a set of genes that expressed strong heterosis, a result that would be of value in improving the performance of the female parent for seed production of modified single-cross hybrids.

In breeding programs that must produce inexpensive hybrid seed, a broad line can be formed us-

ing two to four sister lines derived from a project similar to the one proposed here. Such broad lines can be effectively used as seed parents, reducing the cost of hybrid seed relative to conventional hybrids (STRINGFIELD, 1972).

### **Phase III: conventional and modified single crosses (SSCW9921 trial) test**

In Phase III we compared the original conventional single crosses (CSC) identified in Phase I and the modified single-cross (MSC) versions developed based on Phase II results. In this trial, each conven-

TABLE 11 - Yields ( $t\ ha^{-1}$ ) of the best modified single-cross hybrids vs those for conventional single-cross hybrids for each group from the sub-tropical white maize trial SSCW9921 sown at six locations, Mexico, 1999.

Entry Trial SSCW9921	Ent. 98†	GS‡	Pedigree	Yield	Rank trial	Heterosis female parent (%)
1			<b>P501c1#-401-3-1-2-B-B-B x P502c1#-771-2-2-1-1-B-B</b>	<b>9.99</b>	12	
3	22	4	(P501c1#-401-3-1-3-B x P501c1#-401-3-1-2-B-3-B) x P502c1#-771-2-2-1-1-2-B-B	10.16	7	77
4	22	4	(P501c1#-401-3-1-3-B x P501c1#-401-3-1-2-B-3-B) x P502c1#-771-2-2-1-3-1-6-B-B	10.16	5	77
5			<b>P501c1#-886-3-1-1-B-B-B x P502c1#-771-2-2-1-3-B-B</b>	<b>10.16</b>	6	
6	43	4	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-886-3-1-1-B-1-1-B-B	10.08	10	31
9	26	6	(P501c1#-886-3-1-1-B-B x P501c1#-886-3-1-1-B-1-1-B) x P502c1#-771-2-2-1-1-2-B-B	9.79	20	19
10			<b>P501c1#-140-3-1-1-B-B-B x P502c1#-488-2-2-1-B-B-B</b>	<b>9.07</b>	54	
12	31	3	(P502c1#-488-2-4-1-2 x P502c1#-488-2-2-1-B-2-B) x P501c1#-140-3-1-1-B-1-B-B	9.40	43	76
13	32	6	(P502c1#-488-2-2-1-B-3-B x P502c1#-488-2-2-1-B-2-B) x P501c1#-140-3-1-1-B-1-B-B	9.61	30	22
14			<b>P501c1#-303-1-1-2-2-B-B x P502c1#-771-2-2-1-3-B-B</b>	<b>10.40</b>	2	
15			<b>P501c1#-303-1-1-1-2-B-B x P502c1#-771-2-2-1-3-B-B</b>	<b>9.54</b>	36	
16	43	4	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-303-1-1-1-2-1-1-B-B	9.98	13	31
25	12	6	(P501c1#-303-1-1-1-2-B x P501c1#-303-1-1-1-2-1-1-B) x P502c1#-771-2-2-1-1-2-B-B	9.97	14	28
26			<b>P501c1#-401-3-1-2-B-B-B x P502c1#-771-1-1-1-B-B-B</b>	<b>9.14</b>	52	
27	34	4	(P502c1#-771-1-1-3-B x P502c1#-771-1-1-1-B-1-1-B) x P501c1#-401-3-1-2-B-3-B-B	9.18	50	67
28	22	4	(P501c1#-401-3-1-3-B x P501c1#-401-3-1-2-B-3-B) x P502c1#-771-1-1-1-B-1-1-B-B	9.45	40	77
29			<b>P501c1#-284-1-1-3-B-B-B x P502c1#-771-2-2-1-3-B-B</b>	<b>9.60</b>	31	
30	41	5	(P502c1#-771-2-2-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-284-1-1-3-B-1-2-B-B	8.90	58	20
31	43	4	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-284-1-1-3-B-1-2-B-B	9.72	24	31
32			<b>P501c1#-303-1-1-2-2-B-B x P502c1#-480-3-4-1-1-B-B</b>	<b>9.59</b>	32	
36	14	4	(P501c1#-303-1-1-2-2-1-4-B x P501c1#-303-1-1-1-2-1-1-B) x P502c1#-480-3-4-1-1-4-2-B-B	9.65	27	56
37	17	4	(P501c1#-303-1-1-1-1-B x P501c1#-303-1-1-2-2-1-3-B) x P502c1#-480-3-4-1-1-4-2-B-B	9.57	34	29
39			<b>P501c1#-140-1-1-3-3-B x P502c1#-771-2-2-1-1-B-B</b>	<b>9.03</b>	55	
40	37	4	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-1-2-B) x P501c1#-140-1-1-3-3-1-2-B-B	8.52	59	18
41			<b>P501c1#-140-3-1-1-B-B-B x P502c1#-771-2-2-1-3-B-B</b>	<b>10.12</b>	8	
42	41	5	(P502c1#-771-2-2-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-140-3-1-1-B-1-B-B	10.08	9	20
43			<b>P501c1#-303-1-1-1-2-B-B x P502c1#-488-2-2-1-B-B-B</b>	<b>9.43</b>	42	
44	31	3	(P502c1#-488-2-4-1-2 x P502c1#-488-2-2-1-B-2-B) x P501c1#-303-1-1-1-2-1-1-B-B	9.64	28	76
45	32	6	(P502c1#-488-2-2-1-B-3-B x P502c1#-488-2-2-1-B-2-B) x P501c1#-303-1-1-1-2-1-1-B-B	9.44	41	22
48			<b>P501c1#-284-1-1-3-B-B-B x P502c1#-771-1-1-1-B-B-B</b>	<b>9.50</b>	38	
49	34	4	(P502c1#-771-1-1-3-B x P502c1#-771-1-1-1-B-1-1-B) x P501c1#-284-1-1-3-B-1-2-B-B	9.19	49	67
50			<b>P501c1#-441-1-1-1-B-B x P502c1#-771-2-2-1-3-B-B</b>	<b>9.46</b>	39	
52	43	4	(P502c1#-771-2-2-3-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B) x P501c1#-441-1-1-1-B-1-1-B-B	9.92	17	31
53	25	7	(P501c1#-441-1-1-1-B-1-2-B x P501c1#-441-1-1-1-B-1-1-B) x P502c1#-771-2-2-1-3-1-6-B-B	9.21	48	17
54*	54	1	(P502c1#-488-2-2-1-B-2-B x P502c1#-480-3-4-1-1-4-2-B) P501c1#-140-1-1-3-3-1-2-B-B	9.16	51	124
55*	55	1	(P501c1#-401-3-1-2-B-3-B x P501c1#-886-3-1-1-B-1-1-B) P502c1#-771-2-2-1-3-1-6-B-B	10.17	4	160
56		2	(P502c1#-771-1-1-1-B-1-1-B x P502c1#-771-2-2-1-1-2-B) P501c1#-401-3-1-2-B-3-B-B	9.87	19	
57		2	(P502c1#-771-1-1-1-B-1-1-B x P502c1#-771-2-2-1-3-1-6-B) P501c1#-303-1-1-2-2-1-3-B-B	9.79	21	

TABLE 11 - *Continued*

Entry Trial	Ent. 98†	GS‡	Pedigree	Yield	Rank trial	Heterosis female parent (%)
58*			CML 78 x CML 321 (CIMMYT)	9.53	37	
59*			CML 78 x CML 373 (CIMMYT)	10.17	3	
60*			Local check (different in each location)	10.62	1	
			Maximum	10.40		
			Mean	9.60		
			Minimum	8.37		
			Coefficient of variation (%)	7.57		
			LSD ( $\alpha = 0.05$ ) t/ha <sup>-1</sup>	0.83		

† Ent. 98 = entry of the single crosses selected from the related single cross trial (SSCW9810) tested in 1998 and included as female in the modified single crosses. ‡ GS = generation of separation of the two lines involved in the related cross, according to the numbers of selfs.

\* Entries 54, 55, 58, 59, 60 were considered checks.

tional single cross had at least one (but in most cases more) modified single-cross version for comparison. The trial thus comprised 12 distinct groups, each containing a conventional single cross plus the corresponding modified versions. The ANOVA across 6 locations for the SSCW9921 trial, showed that there were highly significant differences among locations, entries, and G x E (Table 10). From the breakdown of the variance among entries, there was no significant variation among (CSC) in contrast to the highly significant differences among (MSC). Differences between MSC and CSC hybrids were nonsignificant, as expected and in agreement with the results of CHEN *et al.* (1994) and CORDOVA *et al.* (2000) meaning that yield performance for each pair of hybrids could be determined by similar set genes for both groups, CSC and MSC. Similar results were observed for the breakdown of G x E. The mean yield of the 13 CSC was 9.6 t ha<sup>-1</sup>, compared with 9.6 t ha<sup>-1</sup> for the 42 MSC.

Table 11 shows each CSC and the best two MSC's versions for grain yield. Hybrids 3, 4, 12, 27, 28, 36, and 44 were modified single crosses whose female parent was a related single cross that showed very good high parent heterosis (56 to 77%). All outyielded their corresponding conventional single crosses. For all 12 conventional hybrids, there was at least one modified single-cross version that yielded as well or better, implying, as stated above, that similar set of genes are associated with yield in both types of hybrids (CSC and MSC).

Entry 55 (Table 11) is a three way cross that

ranked fourth in the trials compared with modified single crosses. The parental lines of entry 55 were extracted from the same heterotic groups as those used in forming the modified single crosses, but two of the parental lines diverged at an early stage during the process of inbreeding, and entry 55 could therefore be considered a "modified single in the broad sense". The female and male parents are from opposite heterotic groups, and the cross of two sister lines forms the seed parent; however, such "modified single in the broad sense" hybrids will be more variable than modified single cross hybrids.

## CONCLUSIONS

This study confirms the potential value of modified single-cross maize hybrids for developing country production settings, where many farmers earn little cash and are reluctant to purchase relatively expensive hybrid maize seed. Modified single crosses can offer farmers yields comparable to those of conventional single-cross hybrids, but at a much lower cost. So, in addition to developing three-way crosses, maize breeders targeting tropical settings should form and test modified single-cross versions of the elite, conventional single crosses they identify during routine hybrid development. In this way, with a small additional investment, breeders can greatly increase the value of their work on single-crosses. As a final note, we raise the following points:

- The related crosses selected from Phase II expressed a level of high parent heterosis that makes them attractive as female parents for modified single crosses.
- From the results of this study, the  $S_4$  generation of inbreeding could be considered the best generation for separating lines for subsequent use in related crosses, a conclusion that agrees with the report of CHEN *et al.* (1994) and CORDOVA *et al.* (2000).
- The results described herein also suggest an alternative for using selected related crosses as testers to screen lines at both early and advanced stages of breeding.

ACKNOWLEDGEMENTS - We thank the scientists and field staff from CIMMYT, INIFAP, and the private seed companies AS-GROW, ASPROS, Cargill, CERES, Dekalb, GENOTEC, and Pioneer, who directly or indirectly participated in conducting trials for this research. We also thank colleagues from CIMMYT who helped review this paper.

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