

# INCORPORATION OF ELITE SUBTROPICAL AND TROPICAL MAIZE GERMPLASM INTO ELITE TEMPERATE GERMPLASM<sup>1</sup>

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**ABSTRACT** - Elite germplasm and adequate genetic variation are essential in successful plant breeding programs. Maize (*Zea mays* L.) breeding programs in the U.S. Corn Belt have realized significant genetic advance with a limited sample of the available maize germplasm. The objective of our study was the incorporation of elite subtropical and tropical germplasm into elite U.S. Corn Belt germplasm. Crosses, backcrosses, and testcrosses were evaluated to identify superior progenies that were intermated to form germplasm sources that include 75% temperate germplasm and either 25% subtropical or 25% tropical germplasm. Backcrosses (25%) and testcrosses (12.5%) with 25% exotic germplasm had maturities and agronomic traits similar to the elite temperate germplasm sources. The populations formed by intermating the superior backcross progenies, based on backcross and testcross data, will provide additional germplasm resources for future use in temperate maize breeding programs.

**KEY WORDS:** *Zea mays* L.; Corn; Germplasm resources; Introgression.

## INTRODUCTION

Genetic variability is necessary in maize (*Zea mays* L.) breeding populations to permit effective selection of future genetic gains. Consistent genetic

improvements in temperate maize breeding programs have been achieved with an estimated 2 to 5% of the available races of maize (GOODMAN and BROWN, 1988). Future genetic gains may require greater genetic diversity. 'Lancaster Sure Crop' and 'Reid Yellow Dent' germplasm are important components of U.S. Corn Belt breeding programs, which were derived from only one of the approximately 140 races of maize (GOODMAN and BROWN, 1988). Potential value of exotic germplasm sources in U.S. Corn Belt maize breeding programs was suggested by BROWN (1953, 1975) and WELLHAUSEN (1956, 1965), but their use has been limited (GOODMAN, 1985, 1999).

Exotic germplasm sources include either materials that are not adapted to their target environments (e.g., tropical) or that have not received significant breeding efforts within specific environments (e.g., adapted open-pollinated varieties, such as 'Leaming', 'Midland', 'Pride of Saline', etc.). Introduction and use of subtropical and tropical germplasm in temperate area breeding programs are limited because of photoperiod response and poor agronomic traits (e.g., root and stalk strength) necessary for temperate maize production areas. The primary limitation for direct use of other adapted sources is the lack of breeding efforts for productivity and agronomic traits compared with the emphasis given to Reid Yellow Dent and Lancaster Sure Crop. Another factor that can limit immediate use of exotic germplasm sources, both adapted and unadapted, is how they respond to the broad heterotic groups of Reid Yellow Dent and Lancaster Sure Crop. Use of exotic germplasm in current U.S. Corn Belt maize breeding programs would be enhanced if the exotic sources have had vigorous selection for productivity and important agronomic traits. The objectives of our study were: 1) to introgress elite subtropical and tropical germplasm into elite germplasm adapt-

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ed to the U.S. Corn Belt and 2) to maintain and introgress the broad heterotic groups of the subtropical and tropical areas with the heterotic groups widely used in the U.S. Corn Belt. The elite germplasm sources were developed by recurrent selection methods by the cooperative state-federal maize breeding program at Iowa State University for temperate sources and by the International Center for Maize and Wheat Improvement (CIMMYT) for tropical and subtropical sources.

## MATERIALS AND METHODS

Selected subtropical and tropical germplasm sources were crossed to six synthetic populations adapted to the U.S. Corn Belt (Table 1). The subtropical sources included five highly recommended subtropical inbreds available from CIMMYT. The tropical sources included 11 tropical populations or pools that have undergone 2 to 29 cycles of recurrent selection for grain production and other agronomic traits at CIMMYT. The six temperate synthetic populations have undergone 3 to 13 cycles of recurrent selection for grain production, maturity, and root and stalk strength, which were conducted in Iowa. All germplasm sources were considered elite materials in the maize breeding programs conducted at CIMMYT and in Iowa. Materials were selected that represented the important heterotic groups for the CIMMYT subtropical and tropical breeding programs (Tuxpeno and non-Tuxpeno) and for the U.S. Corn Belt [Reid Yellow Dent or Iowa Stiff Stalk Synthetic (BSSS) and Lancaster Sure Crop or non-BSSS] (Table 1). It was decided a priori to maintain the respective heterotic alignments by introgressing Tuxpeno sources to BSSS sources and non-Tuxpeno sources to non-BSSS sources. The goal was to introgress favorable alleles of the subtropical and tropical heterotic groups to the adapted temperate heterotic groups. Hereafter, the heterotic group BSSS-Tuxpeno will be designated as BSSS, and the non-BSSS, non-Tuxpeno heterotic group as non-BSSS.

All crosses were produced by CIMMYT personnel near El Batán, Mexico, during the summer of 1995 (Table 2). For crosses that involved heterozygous and heterogeneous populations, attempts were made to include a minimum sample of 100 plants for each population. Hand pollinations were done in all instances. Pollinated ears were harvested, dried, and equal number of kernels (5 in most instances) were taken from each ear to form a bulk of each cross. All crosses would include 50% U.S. Corn Belt germplasm and 50% either subtropical or tropical germplasm. For the subtropical group, crosses also were produced between the elite CIMMYT inbred lines and B73 and B97, which are representatives of the BSSS (B73) and non-BSSS (B97) heterotic groups.

Because of the possible photoperiod effects to evaluate crosses in temperate areas, reciprocal backcrosses were produced during the 1995-1996 winter season at Tlaltizapan (subtropical) and at Poza Rica (tropical), Mexico. Backcrosses to the respective parents were attempted for 100 plants in each population. Bulk pollen (across individual plants and flowering dates) from the recurrent adapted populations was used to produce the backcross (BC1) seed. Bulk pollen was used to reduce assortive mating of plants with similar flowering times. Backcrosses to the

TABLE 1 - *Germplasm sources used for introgression of elite subtropical and tropical maize germplasm with elite U.S. Corn Belt maize germplasm.*

Germplasm sources	Heterotic groups	References
— Temperate —		
BS10(FR)C11	BSSS <sup>†</sup>	HALLAUER <i>et al.</i> (1974) ECHANDI and HALLAUER (1996)
BS11(FR)C11	non-BSSS	HALLAUER <i>et al.</i> (1974) ECHANDI and HALLAUER (1996)
BSSS(R)C13	BSSS	HALLAUER <i>et al.</i> (1974) ECHANDI and HALLAUER (1996)
BSCB1(R)C13	non-BSSS	HALLAUER <i>et al.</i> (1974) ECHANDI and HALLAUER (1996)
BS13(S)C8	BSSS	HALLAUER and SMITH (1979) HOLTHAUS and LAMKEY (1995)
BS26(S)C3	non-BSSS	HALLAUER (1986)
B73	BSSS	RUSSELL (1972)
B97	non-BSSS	HALLAUER <i>et al.</i> (1994)
— Subtropical —		
CML323	B <sup>‡</sup>	CIMMYT (1998)
CML324	B	CIMMYT (1998)
CML327	A	CIMMYT (1998)
CML328	B	CIMMYT (1998)
G18C19 (HM100-4-1-1-1-2)	A	H.S. CORDOVA (per. com., 1999)
— Tropical —		
Pool 17 C29	B <sup>‡</sup>	VASAL <i>et al.</i> (1992a,b,c,d)
Pool 18 C25	A	VASAL <i>et al.</i> (1992a,b,c,d)
Population 21 (MRRS)C2	A	VASAL <i>et al.</i> (1992a,b,c,d)
Population 23 C3	B	VASAL <i>et al.</i> (1992a,b,c,d)
Population 24 C9	A	VASAL <i>et al.</i> (1992a,b,c,d)
Population 25 C3	B	VASAL <i>et al.</i> (1992a,b,c,d)
Population 27 C10	B	VASAL <i>et al.</i> (1992a,b,c,d)
Population 28 C10	A	VASAL <i>et al.</i> (1992a,b,c,d)
Population 32 (MRRS)C2	B	VASAL <i>et al.</i> (1992a,b,c,d)
Population 43 C10	A	VASAL <i>et al.</i> (1992a,b,c,d)
Population 49 C6	A	VASAL <i>et al.</i> (1992a,b,c,d)

<sup>†</sup> Broadly defined heterotic groups commonly used in U.S. Corn Belt maize breeding programs: Iowa Stiff Stalk Synthetic (BSSS) is primarily Reid Yellow Dent germplasm and non-BSSS is considered primarily Lancaster Sure Crop germplasm.

<sup>‡</sup> Broadly defined heterotic groups of the CIMMYT maize breeding programs: A is primarily Tuxpeno germplasm and B is designated as non-Tuxpeno germplasm because includes less Tuxpeno germplasm.

subtropical lines and tropical populations included 75% subtropical or tropical germplasm and 25% temperate germplasm and were retained for use in CIMMYT maize breeding programs. Backcrosses to the temperate lines and populations included 75% temperate germplasm and 25% subtropical or tropical germplasm and were evaluated at locations in the U.S. Corn Belt. The goal was to produce 100 backcross ears in all instances; the number ranged from 77 to 111 for the subtropical crosses and 52 to 127 for the 33 tropical crosses (Table 2).

TABLE 2 - Crosses produced between Iowa Stiff Stalk Synthetic (BSSS) and Tuxpeno inbred lines and maize populations and non-BSSS and non-Tuxpeno inbred lines and populations near El Batan, Mexico in 1995, number of backcrosses families (BC1) produced in 1995-1996 for backcrosses to U.S. Corn Belt germplasm, and number of BC1 backcrosses evaluated in testcrosses in 1998 (subtropical) and 1999 (tropical).

BC1 families evaluated	BSSS and Tuxpeno crosses	Non-BSS and non-Tuxpeno crosses	BC1 families evaluated
no.			no.
		— Subtropical —	
111† (15)‡	BS10(FR)C11 x CML327	BS11(FR)C11 x CML323	80† (26)‡
77† (23)	BSSS(R)C13 x CML327	BSCB1(R)C13 x CML323	82† (20)
104† (21)	BS13(S)C8 x CML327	BS26(S)C3 x CML323	107† (8)
43 (9)	B73 x CML327	B97 x CML323	7 (4)
55 (12)	B73 x G18(C19)	B97 x CML324	7 (1)
	—	B97 x CML328	11 (3)
Total 390 (80)			294 (62)
		—Tropical —	
27 (7)‡	BS10(FR)C11 x Pool 18 C25	BS11(FR)C11 x Pool 17 C29	27 (8)‡
27 (5)	“ x Population 21 (MRRS)C2	“ x Population 23 C3	27 (6)
27 (1)	“ x Population 24 C9	“ x Population 25 C3	27 (3)
27 (2)	“ x Population 28 C10	“ x Population 27 C10	27 (7)
27 (0)	“ x Population 43 C10	“ x Population 32 (MRRS)C2	27 (3)
27 (5)	“ x Population 49 C6	—	
Total 162 (20)			135 (27)
27 (8)	BSSS(R)C13 x Pool 18 C25	BSCB1(R)C13 x Pool 17 C29	27 (12)
27 (4)	“ x Population 21 (MRRS) C2	“ x Population 23 C3	27 (5)
27 (7)	“ x Population 24 C9	“ x Population 25 C3	27 (9)
27 (7)	“ x Population 28 C10	“ x Population 27 C10	27 (9)
27 (6)	“ x Population 43 C10	“ x Population 32 (MRRS) C2	27 (6)
27 (8)	“ x Population 49 C6		
Total 162 (40)			135 (41)
27 (10)	BS13(S)C8 x Pool 18 C25	BS26(S)C3 x Pool C29	27 (5)
27 (6)	“ x Population 21 (MRRS) C2	“ x Population 23 C3	27 (3)
27 (5)	“ x Population 24 C9	“ x Population 25 C3	27 (3)
27 (3)	“ x Population 28 C10	“ x Population 27 C10	27 (3)
27 (5)	“ x Population 43 C10	“ x Population 32 (MRRS) C2	27 (0)
27 (1)	“ x Population 49 C6	—	
Total 162 (40)			135 (13)
Total 486 (100)			405 (81)

† 100 BC1 families were planned for each population.

‡ Number of BC1 families selected for evaluation in testcrosses. Tester for the BC1 families of BSSS origin was LH185 (MBS, 2002), and tester for BC1 families of non-BSSS origin was LH198 (MBS, 2002).

### Subtropical

**Backcrosses:** The subtropical crosses and backcrosses were evaluated at the Agronomy and Agricultural Engineering Research Center near Ames, IA, in 1996. The initial trial included adapted parents, 11 crosses and 784 backcrosses progenies (Table 2) evaluated in a randomized complete block design with two replications. Plot size included one row, 3.81 m long, with 0.76 m between plots. Plant density after thinning was 62,000 plants ha<sup>-1</sup>. Minimum tillage, fertilization, and weed control practices recommended for optimum maize production were used for the experimental area. Data were collected on a plot basis for stand (% of number of plants plot<sup>-1</sup> relative to kernels planted), root lodging (% of plants leaning 30° or more from vertical), stalk lodging (% of plants broken at or below ear node), dropped ears (% of ears detached from plant), grain moisture (% at harvest), grain yield (t ha<sup>-1</sup> adjusted to 15.5% grain moisture), subjective seedling vigor rating (1 was good and 9 was poor) at the V5 stage (RICHIE *et al.*,

1989), and number of days from planting to time 50% of plants were shedding pollen. Entry means were used for statistical analyses. Replications and entries were considered as random effects. Sources of variation and degrees of freedom were orthogonally partitioned for each BC1 population (Table 2). The orthogonal partitions were made because of possible different error terms for the different BC1 populations. Analysis of homogeneity of error mean squares indicated pooling of error sum of squares was appropriate, and the pooled error was used in the final analyses.

High parent heterosis ( $H_{HP}$ ) was calculated for all traits within each BC1 population as  $(F_1 - P_1)F_1^{-1} \times 100$ , where  $F_1$  is observed mean of the initial crosses and  $P_1$  the observed mean of the adapted parent. Inbreeding depression (ID) was calculated for each trait for each BC1 population as  $(BC_1 - F_1)F_1^{-1} \times 100$ , where  $BC_1$  is the observed mean of the BC1 progeny. Averages of high parent heterosis and inbreeding depression for the BC1 populations for the two heterotic pools also were calculated.

*Testcrosses:* Based on a rank-summation index of the data for the backcross trials conducted in 1996, approximately 20% of the backcrosses were selected for further evaluation (MULAMBA and MOCK, 1978). Remnant seeds of the 80 selected BSSS BC1s and 62 selected non-BSSS BC1s were sown in 1997 topcross nurseries (Table 2). Two separate isolation fields were used to produce the testcrosses. For the BSSS group, the male pollinator was LH185 (MBS, 2002), a line representative of the non-BSSS heterotic group, and LH198 (MBS, 2002) was the male pollinator for the non-BSSS group of backcrosses.

The BC1 testcrosses were evaluated for yield and agronomic traits at five Iowa locations (Ames, Ankeny, Lewis, Grinnell, and Davenport) in 1998. Each trial included 169 entries evaluated in two-row plots 5.49 m long with 0.75 m between rows and two replications location<sup>-1</sup> in a 13 x 13 simple lattice design. In addition to the 142 BC1 testcrosses (Table 2), three entries of each subtropical line, B73 and B97 crossed to their respective testers, and the cross (LH198 x LH185) was included. All experiments were planted at greater than optimum stand densities and thinned at the V5 to V6 stage to final stands of 59,760 plants ha<sup>-1</sup>. Tillage, fertilization, and weed control practices considered optimum for maize production were used at each location. All plots were planted and harvested with equipment modified for small experimental plots.

Data were collected on all plots at all locations for stand (% of the number of plants plot<sup>-1</sup> relative to 59,760 plants ha<sup>-1</sup>), root and stalk lodging (%), dropped ears (%), grain yield (q ha<sup>-1</sup>), and grain moisture (%) at harvest. Flowering dates were recorded as number of days from date of planting to 50% of plants shedding pollen and to 50% of plants showing visible silks at Ames and Grinnell. Plant height (cm, measured from ground level to base of the flag leaf) and ear height (cm, measured from ground level to upper ear node) were recorded at Ames and Ankeny as the average of measurements on five competitive plants within each row of each plot. Test weight (kg/hl<sup>-1</sup> adjusted to 15.5% grain moisture) was recorded at Grinnell and Davenport. Plot data were used for statistical analyses for each location and for the combined analyses across locations. All sources of variation were considered as random effects in the individual location and combined analyses of variance. Phenotypic correlations between traits of the testcrosses were calculated from the combined analyses of variance and covariance (MODE and ROBINSON, 1959). Within the BSSS and non-BSSS groups, about 20% of the entries, based on testcross data, were selected for intermating to form BSSS (BS35) and non-BSSS (BS36) populations with 25% subtropical germplasm. A heritability index based on grain yield, grain moisture, and root and stalk lodging of the testcrosses was used to determine the backcross progenies to include for intermating (SMITH *et al.*, 1981). Remnant seed of the BC1 families used for intermating was from the same source used to evaluate BC1 families themselves (1996) and testcrosses of the selected backcrosses (1998). The bulk entry method was used for intermating the selected BC1 progenies. Equal quantities of seed from each bulk-entry cross were bulked. Two additional generations of intermating were conducted by open-pollination in fields isolated at least 200 m from other maize fields. A composite of 200 ears harvested from the center of the isolation fields formed BS35 and BS36.

### **Tropical**

*Backcrosses:* Approximately 2,800 BC1s were produced for the 33 crosses between the temperate and tropical populations (Table 2). Instead of including each individual backcross for the

33 crosses, 27 unselected BC1s, the tropical by temperate cross, and duplicate entries of the adapted population were evaluated for each of the 33 original crosses. The 990 entries were evaluated in a split-plot experimental design with two replications at the Agronomy and Agricultural Engineering Research Center in 1997. The 33 population crosses were randomly assigned to the whole plots. Within each whole-plot the 27 BC1 families, the F<sub>1</sub>, and two duplicate entries of the adapted recurrent parent were randomly assigned to the subplots. Each BC1 family, or subplot, is a unique collection of genotypes and represents a nested rather than a cross-classified arrangement. The design permits greater precision for detection of differences among BC1 families nested within population crosses than among population crosses. This was desirable because selection among BC1 families within population crosses was to be emphasized. Grouping of BC1 families by population also was considered desirable to reduce possible interaction effects (e.g., plant height) among these relatively diverse materials.

Entries were planted in single-row plots 3.81 m long with 0.76 m between plots. Plots were overplanted and thinned at the V5 to V6 stage to 55,110 plants ha<sup>-1</sup>. Data for mid-pollen shed were recorded as number of days after planting when 50% of the plants were shedding pollen. Before harvest, data for number of plants plot<sup>-1</sup>, plants broken at or below primary ear node (stalk lodging), plant leaning 30° or more from the vertical (root lodging), and number of ears detached from the plants (dropped ears) were recorded. Root and stalk lodging and dropped ears were expressed as percentages of final stand counts for each plot. Plots were machine harvested for data on grain weight per plot (adjusted to 15.5% grain moisture) and grain moisture at harvest (%). The experiment was analyzed as a split-plot design with BC1 families nested within whole plots. All effects were considered random except population crosses, which were considered fixed effects. High-parent heterosis, inbreeding depression, and phenotypic correlations were calculated between the six agronomic traits using the entry means.

*Testcrosses:* A selection index that included grain yield, grain moisture, and root and stalk lodging was used to select 100 BC1 families of BSSS origin and 81 BC1 families of non-BSSS origin (SMITH *et al.*, 1981). Remnant seed of the BC1 families selected for evaluation in testcross trials was planted in two isolation fields in 1998 (Table 2). Pollinator for the selected 100 BC1 families of BSSS origin was the inbred LH185, whereas pollinator for the selected BC1 families of non-BSSS origin was the inbred LH198 (Table 2). The methods for producing the testcross seed of the BC1 families were similar to those described for the subtropical materials except that a bulk of kernels from the 27 BC1 families of each of the 33 population crosses also was included in the topcross nurseries. Bults were formed by taking two kernels from each of the 27 BC1 families. The 54 kernels were distributed in two, 27-kernel rows in the appropriate isolation. Equal quantities of seed from each plant within the two rows were used as the seed source for evaluation in the testcross trials. The bulk of the BC1 families used to produce the topcross entries were included to gauge the indirect effects of selection based on BC1 families on testcrosses and to evaluate the association between traits measured on testcrosses of BC1 bulks with trait averages calculated on the corresponding BC1 testcrosses.

The testcross trials included 225 entries: 100 BSSS BC1s crossed to LH185 (Table 2), 81 non-BSSS BC1s crossed to LH198 (Table 2), 33 bulk entry testcrosses, three BSSS populations crossed to LH185, three non-BSSS populations crossed to LH198,



three single crosses (LH198 x B97, B104 x LH185, and LH198 x LH185), and two commercial hybrids (Cargill 7770 and Cargill 8011). BC1 testcrosses were to be compared with the adapted population testcrosses to determine effects of introgression of tropical germplasm into adapted temperate germplasm. The 225 entries were evaluated in a 15 x 15 simple lattice design at seven locations (Davenport, Columbus Junction, Hedrick, Grinnell, Ames, and Greenfield, IA and Fairberry, NE) in 1999. Plots included two rows 5.33 m long that were 1.52 m wide with 0.76 m between rows at all Iowa locations. At Fairberry, NE, the two-row plots were 7.16 m long with 0.76 between rows. Plots were overplanted and thinned to a uniform plant density that varied among locations, depending on field emergence. Final stands ranged from 54,963 plants ha<sup>-1</sup> at Fairberry, NE to 68,888 plants ha<sup>-1</sup> at Ames and Greenfield. Stand counts, root and stalk lodged plants, and dropped ear data were taken pre-harvest at all locations and expressed as percentages. Mid-pollen shed and mid-silk data were recorded at Grinnell, Hedrick, and Ames as number of days after planting that 50% of plants in a plot exhibited pollen shed or visible silks. Plant and ear heights (cm) were measured at Hedrick and Ames from the ground to base of tassel (plant height) and to top-ear node attachment (ear height). Plots were harvested by combines adapted for experimental maize plots to determine grain yield (q ha<sup>-1</sup> at 15.5%) and grain moisture (%) at harvest. Grain test weight was taken (kg hL<sup>-1</sup>) at all locations except Ames and Greenfield. Tillage, fertilizer, and pest control practices were those recommended for optimum maize production at each location.

Initially, single and multiple location analyses for a 15 x 15 simple lattice design were used, but there were either low (<6%) or no gains in relative efficiency with use of lattice analysis. Hence, analyses for a randomized complete block design were used for all traits of the testcrosses at each location and combined across locations. Simple product-moment correlations were calculated on the means across either entries or populations (OSTLE, 1954). Within the BSSS and non-BSSS groups about 20% of the entries, based on the testcross data, were selected for intermating to form BSSS (BS37) and non-BSSS (BS38) populations with 25% tropical germplasm. Heritability index was based on grain yield, grain moisture, and root and stalk lodging of the testcrosses and was used to select backcross progenies for intermating (SMITH *et al.*, 1981). Remnant seed of the BC1 families used in intermating was from the same source used to evaluate BC1 families themselves (1997) and testcrosses of the selected backcrosses (1999). Similar methods of intermating described for the subtropical BC1 selection were used to form BS37 and BS38.

## RESULTS AND DISCUSSION

The primary function of backcross evaluations was to serve as the first stage of a multitrait temperate evaluation that emphasized the adaptation and performance of the backcross progenies relative to the temperate recurrent parents. Evaluation of the backcross progenies served as a cost effective mechanism to screen 684 subtropical and 891 tropical backcrosses before the more resource intensive stage of testcross production and evaluation in multiple environments. Backcross progenies screened

for adaptive traits should provide a better level of adaptation and performance in testcrosses. Population crosses also were included to determine their performance relative to the backcrosses, testcrosses, and the temperate parents.

### Subtropical

*Backcrosses:* Significant differences ( $P \leq 0.05$ ) were detected among the backcross progenies for all traits except percentage of dropped ears (analyses not shown). Average root (27.3%) and stalk lodging (27.3%) were greater because of heavy rains and strong winds hit the plots soon after flowering, causing extensive lodging throughout the experimental area. Average yield was 55.3 q ha<sup>-1</sup> with average grain moisture of 27.0%.

Average for six traits for each set of backcrosses, their recurrent temperate parents, and crosses indicate similar flowering dates except for the CML327 donor parent, which averaged 1.3 to 3.3 days later than the adapted parent (Table 3). Days-to-pollen shed for the non-BSSS crosses were similar (2.1 days earlier to 0.9 days later) to the recurrent parents, and earlier than the BSSS crosses. Days-to-pollen shed suggest that major genes for nonadaptation to temperate environments were not prevalent within the exotic source materials included in crosses. Days-to-pollen shed generally increased linearly with increasing percentage of subtropical germplasm, but in most instances the differences were not significant (Table 3). Grain moisture levels of the crosses (27.1 to 31.9%) was greater than the temperate populations (21.9 to 26.9%) and the backcross (24.0 to 29.5%). The BSSS backcross had greater grain moisture differences (2.1 to 4.6%) relative to the recurrent parents than the non-BSSS backcrosses (-0.2 to 1.2%). The differences in grain moisture between the BSSS and non-BSSS crosses and backcrosses were due to the different donor parents (CML327 for BSSS and CML323 for non-BSSS); average grain moistures of the BSSS (24.5%) and non-BSSS (24.8%) recurrent parents were very similar (Table 3).

Average differences in grain yield of crosses and recurrent parents ranged from -11.1 to 17.5 q ha<sup>-1</sup> for the population crosses. BS10(FR)C13 was the only population that had cross (9.1 q ha<sup>-1</sup>) and backcross (11.1 q ha<sup>-1</sup>) grain yields less than the population recurrent parent. The average yield of the population crosses (63.4 q ha<sup>-1</sup>) was 9.6 q ha<sup>-1</sup> greater than the population mean (53.8 q ha<sup>-1</sup>) and 8.1 q ha<sup>-1</sup> greater than the average yield of the backcrosses (55.3 q ha<sup>-1</sup>) (Table 3). The exotic

TABLE 3 - Means of populations, inbreds, population crosses, inbred crosses, and backcrosses for grain yield and five agronomic traits for temperate and subtropical maize germplasm evaluated at Ames, IA, 1996.

Entries	Grain		Days to pollen shed	Lodging		Dropped ears
	Yield	Moisture		Root	Stalk	
	q ha <sup>-1</sup>	%	no.	%	%	%
BSSS* –						
(BS10(FR)C11 x CML327)BS10(FR)C11	52.8	27.6	81.0	45.2	38.5	0.4
BS10(FR)C11 x CML327	54.8	29.6	82.7	48.0	39.0	1.1
BS10(FR)C11	63.9	22.5	77.7	4.3	29.7	1.8
(BS13(S)C8 x CML327)BS13(S)C8	60.1	29.5	80.1	5.7	22.3	0.8
BS13(S)C8 x CML327	65.5	31.9	82.3	40.9	32.0	0.0
BS13(S)C8	57.1	26.9	78.1	2.6	18.1	0.8
(BSSS(R)C13 x CML327)BSSS(R)C13	54.8	28.1	80.0	4.7	20.5	1.1
BSSS(R)C13 x CML327	64.6	30.2	83.5	27.5	36.3	1.0
BSSS(R)C13	48.6	24.0	77.4	0.6	16.0	2.8
Backcross mean	55.9	28.4	80.4	18.5	27.1	0.8
Cross mean	61.6	30.6	82.8	38.8	35.8	0.7
Population mean	56.5	24.5	77.7	2.5	21.3	1.8
Non-BSSS* –						
(BS11(FR)C11 x CML323)BS11(FR)C11	60.4	24.0	76.8	34.4	29.0	0.2
BS11(FR)C11 x CML323	69.2	27.1	78.5	52.9	31.3	0.0
BS11(FR)C11	57.9	21.9	77.6	11.8	19.2	0.0
(BS26(S)C3 x CML323)BS26(S)C3	45.6	26.3	78.2	23.9	51.3	1.8
BS26(S)C3 x CML323	59.5	28.0	79.0	77.3	45.9	1.1
BS26(S)C3	42.0	26.0	77.3	4.1	33.6	1.3
(BSCB1(R)C13 x CML323)BSCB1(R)C13	57.9	26.4	78.3	61.7	17.3	0.2
BSCB1(R)C13 x CML323	66.7	27.2	78.0	74.4	25.5	0.0
BSCB1(R)C13	53.5	26.5	78.5	29.5	8.7	0.0
Backcross mean	54.6	25.6	77.8	40.0	32.5	0.7
Cross mean	65.1	27.4	78.5	68.2	32.5	0.4
Population mean	51.1	24.8	77.8	15.1	20.5	0.4
All backcross mean	55.3	27.0	79.1	29.3	37.8	0.8
All cross mean	63.4	29.0	80.7	53.5	35.0	0.5
All population mean	53.8	24.6	77.8	8.8	20.8	1.1
(B73 x CML327)B73	51.7	28.8	82.5	10.7	26.5	4.0
B73 x CML327	58.3	30.8	82.8	56.3	28.3	3.9
[B73 x G18(C19)]B73	51.5	25.9	80.0	6.8	29.6	3.0
B73 x G18(C19)	58.4	27.7	78.0	47.1	28.5	3.2
B73	33.4	22.4	81.2	0.3	29.0	0.0
(B97 x CML323)B97	56.0	25.6	78.1	58.0	17.6	0.0
B97 x CML323	68.9	28.4	79.5	93.1	36.9	0.0
(B97 x CML324)B97	38.3	26.0	79.9	58.9	11.1	0.0
B97 x CML324	47.8	30.4	81.3	19.7	9.9	9.3
(B97 x CML328)B97	48.0	27.0	79.9	48.2	20.5	0.0
B97 x CML328	62.1	30.3	82.0	38.6	21.0	6.3
B97	32.3	25.8	80.3	38.4	15.1	0.0
Backcross mean	49.1	26.7	80.1	36.5	21.1	1.4
Cross mean	59.1	29.5	80.7	51.0	24.9	4.5
Inbred mean	32.8	24.1	80.8	19.4	22.0	0.0

\* BSSS group includes Iowa Stiff Stalk Synthetic (BSSS) and Tuxpeno germplasm in crosses and backcrosses to BSSS. Non-BSSS group includes non-BSSS and non-Tuxpeno germplasm in crosses and backcrosses to non-BSSS.

sources contributed alleles for greater yield with average high-parent heterosis of 36.7% for the five BSSS population crosses and 56.6% for the six non-BSSS population crosses. Inbreeding depression ranged from -3.6% for BS10(FR)C11 to 15.2% for BSSS(R)C13 with an average inbreeding depression of 10.1% for the BSSS crosses. Average inbreeding depression for the six non-BSSS crosses was similar for each population and averaged 18.4%. Yield of the B73 and B97 crosses and backcrosses were similar to those for the populations except for B97 x CML324. It seems B97 and CML324 were perhaps less diverse than the other line crosses because B97 x CML324 was 14.1 q ha<sup>-1</sup> less than average of other four crosses (61.9 q ha<sup>-1</sup>) and B97 x CML324)B97 was 13.5 q ha<sup>-1</sup> less than the average of the other four testcrosses (51.8 q ha<sup>-1</sup>).

In most instances, the exotic germplasm sources contributed alleles that enhanced yield of crosses with maturity levels (grain moisture and days-to-pollen shed) that permitted valid evaluation of the crosses and backcrosses with the temperate recurrent parents. Multiple trait selection, based on an index that included greater grain yield, less grain moisture and increased resistance to root and stalk lodging was conducted within each set of backcrosses and across sets of backcrosses within heterotic groups to determine which ones would be evaluated further in testcrosses; 80 were selected from the BSSS group and 62 were selected from the non-BSSS group. The 80 selected BSSS backcross selections averaged 5.8 q ha<sup>-1</sup> greater yield, 0.4% less moisture, 4.7% less root lodging, and 6.1% less stalk lodging than the average of the 390 BSSS backcrosses. The 62 selected non-BSSS backcross selections averaged 5.1 q ha<sup>-1</sup> greater grain yield, 0.1% more grain moisture, 10.7% less root lodging, and 6.3% less stalk lodging. The different sets of backcrosses within the two heterotic groups were not equally represented by the selections included for further testing (Table 2). Selection intensities of 13.5 and 7.4% were used for the BS10 and BS26 backcrosses, respectively, because of their poorer performance within their heterotic groups (Table 3).

*Testcrosses:* The 1998 maize growing season at the five Iowa environments was typical, with timely planting and harvest times. Excess rainfall after planting delayed emergence and growth at Ames and Ankeny, a hailstorm at Lewis slightly reduced stands, and a severe windstorm at flowering caused minor green snapping of later genotypes at Ames. No adjustments were made for stands at Ames, in-

stead broken plants from green snap were included in the stalk lodging counts. Relative efficiency of the lattice analysis showed no advantage over a randomized complete block analysis for all traits at Lewis, Grinnell, and Davenport locations. But the relative efficiency of the lattice analysis was 10 to 28% greater than the randomized complete block design at the Ames and Ankeny locations for grain yield and moisture. Lattice adjusted means for all traits, therefore, were used in the final analyses. Data were collected for 10 traits; differences among the 169 entries were significant for all traits (analyses not shown), and the precision the trials was good for all traits (Table 4). Average grain yield (95.7 q ha<sup>-1</sup>), grain moisture (22.0%), root lodging (1.6%), and stalk lodging (5.1%) were obtained across the five environments. The means for the BSSS and non-BSSS testcrosses were similar (Table 4). The B73 and B97 backcrosses had the greatest average yields for their respective heterotic groups.

A selection index that included grain yield, grain moisture, and root and stalk was used to select 19 BSSS entries and 13 non-BSSS entries to include for intermating. Average yield of the 19 selected BSSS entries was 104.2 q ha<sup>-1</sup> compared with the average yield of 97.3 q ha<sup>-1</sup> for the four recurrent parents and 106.6 q ha<sup>-1</sup> for check hybrid LH198 x LH185. For the two maturity traits, the 19 BSSS selections had 0.7% more grain moisture and pollen shed was 0.9 day later than the average of the four recurrent parents and 2.4% more grain moisture and pollen shed was 1.2 days later than the check hybrid, LH198 x LH195. Similar to grain moisture and days to pollen shed, the differences between the selected testcrosses and the recurrent parents and check hybrids, the differences for root and stalk quality, test weight, and plant height were not significant. The range among testcrosses was greatest for grain yield (12.0 q ha<sup>-1</sup>) but relatively small for the other traits. The selected testcrosses did not include any from BS10 recurrent parent because of the poorer performance of the 111 backcrosses (Table 3) and the 15 backcrosses included in the testcrosses (Table 4). The 19 selected testcrosses included 10, 5, and 4 from the B73, BS13, and BSSS(R) recurrent parents. Remnant seed of the backcross progenies (25% exotic germplasm) were intermated with use of a partial diallel mating scheme to form BS35.

Only 13 entries were selected from the non-BSSS testcrosses (data not included). Average yields of the recurrent parents were very similar for the BSSS (97.3 q ha<sup>-1</sup>) and non-BSSS (97.4 q ha<sup>-1</sup>), but the

TABLE 4 - Means of testcrosses of selected backcrosses for yield and six agronomic traits evaluated at five Iowa locations during 1998 for temperate by subtropical maize crosses.

Pedigree	Grain		Days to pollen pollen shed	Lodging		Test weight	Plant height
	Yield	Moisture		Root	Stalk		
	q ha <sup>-1</sup>	%	no.	%	%	g kg <sup>-1</sup>	cm
BSSS*† –							
BS10(FR)C11 x CML327	91.2	22.5	71.4	1.8	5.2	220	226
BS13(S)C8 x CML327	97.1	22.7	71.4	2.2	3.9	219	224
BSSS(R)C13 x CML327	96.7	22.4	71.2	1.6	4.3	218	231
BS10(FR)C11	91.5	21.4	70.7	0.6	3.8	216	224
BS13(S)C8	98.3	21.3	69.8	0.8	3.0	219	229
BSSS(R)C13	90.7	21.8	69.6	1.9	5.0	214	228
B73 x G18(C19)	103.5	22.0	70.5	1.5	3.7	218	228
B73 x CML327	106.5	22.2	71.4	2.6	4.6	218	233
B73	109.0	21.0	70.2	0.6	8.6	223	243
LH185 testcross mean	98.3	21.9	70.6	1.5	4.7	218	230
Non-BSSS*‡ –							
BS11(FR)C11 x CML323	88.1	21.4	72.3	1.3	7.3	222	234
BS26(S)C3 x CML323	92.2	23.0	73.3	1.7	10.0	223	238
BSCB1(R)C13 x CML323	93.7	21.8	71.5	1.6	4.1	232	224
BS11(FR)C11	86.5	20.8	72.5	0.9	8.2	220	239
BS26(S)C3	92.9	22.8	72.3	0.6	8.6	223	243
BSCB1(R)C13	100.7	21.8	71.9	0.1	2.7	224	229
B97 x CML328	93.9	22.3	72.8	1.4	4.6	224	251
B97 x CML324	95.4	21.6	74.2	1.1	5.4	222	235
B97 x CML323	99.5	21.2	72.3	3.2	4.3	221	240
B97	110.1	20.8	71.9	1.4	2.3	220	250
LH198 testcross mean	95.3	21.8	72.5	1.3	4.5	223	238
LH198 x LH185	106.6	19.9	69.9	0.5	4.1	216	218
Grand mean	95.7	22.0	71.5	1.6	5.1	220	231
C.V. (%)	8.2	4.9	1.3	2.5	4.3	2.1	3.8
Repeatability	0.80	0.73	0.73	0.34	0.54	0.50	0.64
LSD (0.05)§	8.7	1.2	1.5	2.2	4.6	6.9	14.2

\* BSSS group includes Iowa Stiff Synthetic (BSSS) and Tuxpeno germplasm in crosses and backcrosses. Non-BSSS group includes non-BSSS and non-Tuxpeno germplasm in crosses and backcrosses.

† Tester for selected BSSS backcrosses was LH185.

‡ Tester for selected non-BSSS backcross was LH198.

§ Approximate LSD for individual testcrosses.

non-BSSS testcross mean (91.5 q ha<sup>-1</sup>) was 6.8 q ha<sup>-1</sup> less than the BSSS testcross mean (98.3 q ha<sup>-1</sup>), which follows the same trend as the yield of the backcrosses themselves (49.1 q ha<sup>-1</sup> non-BSSS vs. 55.9 q ha<sup>-1</sup> BSSS, Table 3). For the two maturity parameters, both were very similar for the testcross means and the averages of the selections. The selected 13 entries averaged 5.7 q ha<sup>-1</sup> more grain yield than average of 62 testcrosses, but 0.1 q ha<sup>-1</sup> less than the average of the recurrent parents. There were no significant differences between the means of the selected entries and the 62 testcrosses for the two maturity parameters and other agronomic traits. No entries were selected that included BS26 as the

recurrent parent. BS26 backcrosses had poorer performance than the other recurrent parents (Table 3) and only eight BS26 backcrosses were included in the testcross trials. Of the 13 selections, six were from BSCB1, four from B97, and three from BS11. A partial diallel mating scheme was used to intermate the 13 selections to form a non-BSSS population (BS36) that includes 25% subtropical germplasm.

### Tropical

*Backcrosses:* The backcross trial conducted at Ames in 1997 included 486 backcross progenies from the BSSS heterotic group and 405 backcross progenies from the non-BSSS group. Data were col-



TABLE 5 - Means of populations, population crosses, and backcrosses for grain yield and five agronomic traits for temperate and tropical germplasm evaluated at Ames, IA, 1997.

Entries	Grain		Days to pollen shed	Lodging		Dropped ears
	Yield	Moisture		Root	Stalk	
	q ha <sup>-1</sup>	%	no.	%	%	%
BSSS* –						
BS10(FR)C11 x Pool 18)BS10(FR)C11	46.7	22.6	79.4	0.9	13.7	4.0
BS10(FR)C11 x Pop. 21)BS10(FR)C11	51.1	25.1	84.4	0.4	21.4	2.6
BS10(FR)C11 x Pop. 24)BS10(FR)C11	48.2	23.7	82.3	0.4	23.8	3.2
BS10(FR)C11 x Pop. 28)BS10(FR)C11	49.6	25.3	83.2	0.5	21.0	4.5
BS10(FR)C11 x Pop. 43)BS10(FR)C11	46.6	27.1	83.7	0.4	23.0	2.1
BS10(FR)C11 x Pop. 49)BS10(FR)C11	52.2	24.8	83.0	0.1	18.5	3.9
Backcross mean	49.1	24.8	82.7	0.4	20.2	3.4
Cross mean	34.7	29.8	87.0	1.6	13.3	4.2
BS10(R)C11 mean	46.1	21.0	79.4	0.3	22.2	2.4
BS13(S)C8 x Pool 18)BS13(S)C8	53.1	21.8	78.6	0.4	12.7	1.1
BS13(S)C8 x Pop. 21)BS13(S)C8	54.5	25.3	83.0	0.0	12.2	1.4
BS13(S)C8 x Pop. 24)BS13(S)C8	48.7	25.2	82.4	0.2	14.1	2.6
BS13(S)C8 x Pop. 28)BS13(S)C8	53.8	25.2	82.4	0.5	18.8	1.0
BS13(S)C8 x Pop. 43)BS13(S)C8	53.6	26.3	83.2	0.2	15.3	1.3
BS13(S)C8 x Pop. 49)BS13(S)C8	52.7	24.2	82.2	0.0	15.2	1.2
Backcross mean	52.7	24.7	82.0	0.2	14.7	1.4
Cross mean	53.5	31.5	88.2	0.5	5.4	1.1
BS13(S)C8 mean	35.7	20.7	79.3	0.0	21.4	1.4
BSSS(R)C13 x Pool 18)BSSS(R)C13	49.1	20.9	79.5	0.5	11.9	5.6
BSSS(R)C13 x Pop. 21)BSSS(R)C13	44.6	25.7	82.1	0.5	11.5	1.9
BSSS(R)C13 x Pop. 24)BSSS(R)C13	41.5	22.4	81.8	0.8	12.3	4.7
BSSS(R)C13 x Pop. 28)BSSS(R)C13	46.7	24.5	81.1	0.6	6.9	3.3
BSSS(R)C13 x Pop. 43)BSSS(R)C13	47.1	25.4	82.4	0.1	12.9	3.2
BSSS(R)C13 x Pop. 49)BSSS(R)C13	48.3	23.5	81.9	0.2	10.2	4.1
Backcross mean	46.2	23.7	81.5	0.4	11.0	3.8
Cross mean	54.5	31.5	86.5	0.5	5.4	0.8
BSSS(R)C13	35.7	20.6	79.3	0.0	21.4	1.4
Backcross mean ( $\bar{X}$ )	49.4	24.4	82.0	0.4	15.3	2.9
Backcross-selected ( $\bar{S}$ )	56.3	23.1	81.2	0.3	9.6	1.8
Gain ( $\bar{X} - \bar{S}$ )	6.9	-1.3	-0.8	-0.1	-5.7	-1.1
Cross mean	44.1	30.0	86.4	0.9	9.6	2.5
Population mean	39.1	20.1	79.0	0.1	18.0	2.2
Non-BSSS* –						
BS11(FR)C11 x Pool 17)BS11(FR)C11	49.3	22.0	80.0	0.4	18.2	4.3
BS11(FR)C11 x Pop. 23)BS11(FR)C11	46.8	24.3	81.9	0.9	21.2	5.2
BS11(FR)C11 x Pop. 25)BS11(FR)C11	45.3	25.1	82.8	4.4	26.3	2.0
BS11(FR)C11 x Pop. 27)BS11(FR)C11	46.0	25.4	84.1	1.0	20.2	3.3
BS11(FR)C11 x Pop. 32)BS11(FR)C11	49.2	25.0	83.6	0.8	20.0	1.3
Backcross mean	47.3	24.4	82.5	1.5	21.2	3.2
Cross mean	38.9	28.4	85.5	2.0	17.6	2.6
BS11(FR)C11 mean	44.9	19.9	79.5	0.6	21.3	3.2
BS26(S)C3 x Pool 17)BS26(S)C3	34.4	23.3	79.2	0.7	20.4	2.4
BS26(S)C3 x Pop. 23)BS26(S)C3	34.1	24.7	82.3	0.9	23.4	6.1
BS26(S)C3 x Pop. 25)BS26(S)C3	32.3	25.5	82.5	0.5	24.1	5.5
BS26(S)C3 x Pop. 27)BS26(S)C3	38.6	24.6	83.6	0.7	18.1	5.3
BS26(S)C3 x Pop. 32)BS26(S)C3	35.9	26.5	82.1	0.7	22.3	5.6
Backcross mean	35.1	24.9	81.9	0.7	21.7	5.0
Cross mean	33.1	28.5	85.5	1.4	11.5	3.9
BS26(S)C3 mean	34.2	22.2	77.9	0.3	25.2	3.3
BSCB1(R)C13 x Pool 17)BSCB1(R)C13	46.9	22.0	78.7	0.6	9.0	1.5
BSCB1(R)C13 x Pop. 23)BSCB1(R)C13	42.3	23.0	81.2	0.7	9.8	1.5

TABLE 5 - *Continued.*

Entries	Grain		Days to pollen shed	Lodging		Dropped ears
	Yield	Moisture		Root	Stalk	
	q ha <sup>-1</sup>	%	no.	%	%	%
BSCB1(R)C13 x Pop. 25)BSCB1(R)C13	42.0	24.1	82.0	1.2	11.5	0.7
BSCB1(R)C13 x Pop. 27)BSCB1(R)C13	42.9	23.7	82.6	0.2	9.0	1.7
BSCB1(R)C13 x Pop. 32)BSCB1(R)C13	44.6	23.4	81.4	1.9	9.0	1.4
Backcross mean	43.7	23.2	81.2	0.9	9.7	1.4
Cross mean	41.5	28.3	84.4	1.9	8.3	0.6
BSCB1(R)C13 mean	32.9	17.8	78.0	0.6	14.4	1.3
All backcross mean ( $\bar{X}$ )	42.2	24.2	81.9	1.0	17.5	3.2
Backcross-selected ( $\bar{S}$ )	51.2	23.2	80.8	0.6	10.8	1.7
Gain ( $\bar{X} - \bar{S}$ )	9.0	-1.0	-1.1	-0.4	-6.7	-1.5
All cross mean	37.8	28.4	85.1	1.8	12.5	2.4
Population mean	37.3	20.0	78.5	0.5	20.3	2.6

\* BSSS group includes Iowa Stiff Stalk Synthetic (BSSS) and Tuxpeno germplasm in crosses and backcrosses to BSSS. Non-BSSS group includes non-BSSS and non-Tuxpeno germplasm in crosses and backcrosses to non-BSSS.

lected for seven traits and differences among 33 populations and among 27 backcross progenies within populations were significant ( $P \leq 0.05$ ) for all traits except percentage of dropped ears for progenies within populations (analyses not shown). Average grain yield of the backcrosses was 45.5 q ha<sup>-1</sup> with the BSSS and non-BSSS backcrosses averaging 49.4 and 42.0 q ha<sup>-1</sup>, respectively (Table 5). Average backcross means for the two maturity parameters and root and stalk lodging were similar for both sets of backcrosses. Root lodging (1.0%) was relatively low while stalk lodging averaged 17.5%. Among the non-BSSS backcrosses, those with BS26(S)C3 as the recurrent parent yielded significantly less than those with either BS11(FR)C11 or BSCB1(R)C13 as the recurrent parent. The donor parent Pool 17 had the greatest average yield, had lower grain moisture, and flowered earlier than the other donor parents for the non-BSSS backcrosses. Within the BSSS group, BS13(S)C8 had the greatest average grain yield (52.8 q ha<sup>-1</sup>), which was 17.0 q ha<sup>-1</sup> more than BS13(S)C8 per se. Donor parents had similar average backcross grain yields, but donor parent Pool 18 had significantly lower grain moisture and flowered earlier than the other five donor parents (Table 5). Estimates of high-parent heterosis and inbreeding depression for grain yield were not as consistent as for the subtropical materials. Average high-parent heterosis was 16.7% for the six BSSS crosses and 3.2% for the five non-BSSS crosses. But high-parent heterosis ranged from -24.7% for the six BS10(FR)C11 crosses to 50.1% for

the six BS13(S)C8 crosses. For the non-BSSS group, high-parent heterosis ranged from -14.1% for BS11(FR)C11 to 26.5% for BSCB1(R)C13. Average inbreeding depression estimates for yield were more consistent than estimates of heterosis for the BSSS (-18.4%) and non-BSSS (-14.7%) groups. BS10(FR)C11 (-42.6%) and BS11(FR)C11 (-27.1%) had the greatest estimates of inbreeding depression, whereas BSSS(R)C13 (-6.6%) and BSCB1(R)C13 (-6.7%) had similar estimates of inbreeding depression.

The presence of genetic variation and acceptable expression of agronomic traits among the backcross progenies permitted multiple trait selection among the backcross progenies. A selection index that included greater grain yield, less grain moisture, less root and stalk lodging, and fewer days to pollen shed was used to identify backcross progenies for further evaluations in testcrosses (Table 2). Testcrosses were produced in 1998 for 100 of 486 BSSS backcrosses (20.5%) and 81 of 405 non-BSSS backcrosses (20.0%).

*Testcrosses:* Data were collected on 11 traits for the testcross trials. Analyses of variance combined across the seven locations indicated significant ( $P \leq 0.01$ ) differences among testcrosses for all traits (analyses not shown). Average grain yield across locations was 74.1 q ha<sup>-1</sup>, ranging from 53.2 q ha<sup>-1</sup> at Greenfield, IA to 90.9 q ha<sup>-1</sup> at Ames, IA. Harvest grain moisture averaged 25.0%, ranging from 18.1% at Fairberry, NE to 32.2% for an early harvest at Hedrick, IA. There was a greater incidence of average root lodging (7.8%) than average stalk lodging

TABLE 6 - Means of testcrosses of selected backcrosses for yield and six agronomic traits evaluated at seven locations during 1999 for temperate by tropical maize crosses.

Pedigree	Grain		Days to pollen shed	Lodging		Dropped ears	Test weight	Plant height
	Yield	Moisture		Root	Stalk			
	q ha <sup>-1</sup>	%	no.	%	%	%	hg ha <sup>-1</sup>	cm
BSSS*†								
BS10(FR)C11 x Pool 18)BS10(FR)C11	75.2	23.9	69.7	8.8	2.7	0.1	74.2	238
BS10(FR)C11 x Pop. 21)BS10(FR)C11	67.3	25.8	71.2	9.8	3.9	0.2	74.5	252
BS10(FR)C11 x Pop. 24)BS10(FR)C11	69.8	27.7	74.1	8.3	4.4	0.0	74.1	246
BS10(FR)C11 x Pop. 28)BS10(FR)C11	69.6	26.9	75.4	9.6	3.6	0.2	75.4	244
BS10(FR)C11 x Pop. 43)BS10(FR)C11	—	—	—	—	—	—	—	—
BS10(FR)C11 x Pop. 49)BS10(FR)C11	64.8	26.4	73.1	10.0	4.5	0.3	73.7	247
Testcross mean	69.3	26.1	72.7	9.3	3.8	0.2	74.4	245
BS10(FR)C11	76.1	22.3	69.5	4.2	3.2	0.3	73.6	222
BS13(S)C8 x Pool 18)BS13(S)C8								
BS13(S)C8 x Pop. 21)BS13(S)C8	65.0	26.5	71.7	7.7	2.8	0.2	74.1	242
BS13(S)C8 x Pop. 24)BS13(S)C8	68.3	25.9	70.9	11.3	2.2	0.1	75.3	236
BS13(S)C8 x Pop. 28)BS13(S)C8	68.5	25.6	70.9	7.1	1.9	0.0	75.0	237
BS13(S)C8 x Pop. 43)BS13(S)C8	66.3	26.9	72.0	6.8	2.4	0.3	75.2	239
BS13(S)C8 x Pop. 49)BS13(S)C8	71.6	25.7	71.4	7.8	2.4	0.0	74.4	234
Testcross mean	69.4	25.8	71.0	8.0	2.2	0.1	74.8	237
BS13(S)C8	79.0	22.6	69.2	5.0	1.8	0.2	72.9	234
BSSS(R)C13 x Pool 18)BSSS(R)C13								
BSSS(R)C13 x Pop. 21)BSSS(R)C13	70.4	25.3	71.1	6.7	2.5	0.2	73.4	248
BSSS(R)C13 x Pop. 24)BSSS(R)C13	80.2	24.3	70.3	5.7	2.9	0.3	73.6	247
BSSS(R)C13 x Pop. 28)BSSS(R)C13	75.1	24.5	70.9	5.4	3.5	0.2	73.3	250
BSSS(R)C13 x Pop. 43)BSSS(R)C13	67.4	22.4	71.7	6.2	2.9	0.3	73.3	254
BSSS(R)C13 x Pop. 49)BSSS(R)C13	72.3	25.1	71.0	5.8	2.9	0.2	74.2	243
Testcross mean	73.7	24.2	70.8	5.9	2.8	0.2	73.5	248
BSSS(R)C13	77.2	21.7	69.0	2.8	2.6	0.2	71.8	239
All BSSS testcrosses	71.8	25.3	70.9	7.4	2.8	0.2	74.1	239
Non-BSSS*‡ –								
BS11(FR)C11 x Pool 17)BS11(FR)C11								
BS11(FR)C11 x Pop. 23)BS11(FR)C11	76.9	23.6	71.9	8.5	4.1	0.2	76.5	256
BS11(FR)C11 x Pop. 25)BS11(FR)C11	74.3	25.2	72.5	8.6	2.9	0.2	76.3	262
BS11(FR)C11 x Pop. 27)BS11(FR)C11	72.8	24.6	72.4	7.6	3.0	0.1	76.5	264
BS11(FR)C11 x Pop. 32)BS11(FR)C11	75.7	24.7	72.1	9.7	2.9	0.1	75.3	253
Testcross mean	74.4	24.3	72.0	8.3	3.3	0.1	76.1	258
BS11(FR)C11	73.4	21.6	70.7	4.6	4.1	0.1	75.5	251
BS26(S)C3 x Pool 17)BS26(S)C3								
BS26(S)C3 x Pop. 23)BS26(S)C3	74.3	25.8	72.5	9.1	5.2	0.1	76.2	267
BS26(S)C3 x Pop. 25)BS26(S)C3	74.2	25.6	71.8	7.4	3.3	0.2	75.9	252
BS26(S)C3 x Pop. 27)BS26(S)C3	80.1	24.8	71.9	6.9	5.1	0.1	76.3	258
Testcross mean	76.2	25.1	71.6	7.8	4.2	0.2	76.2	258
BS26(S)C3	80.5	22.9	71.0	5.6	4.0	0.1	74.9	263
BSCB1(R)C13 x Pool 17)BSCB1(R)C13								
BSCB1(R)C13 x Pop. 23)BSCB1(R)C13	82.0	25.1	71.0	9.5	2.9	0.1	76.6	256
BSCB1(R)C13 x Pop. 25)BSCB1(R)C13	80.5	24.7	71.1	7.7	2.5	0.0	76.7	257
BSCB1(R)C13 x Pop. 27)BSCB1(R)C13	81.6	25.6	71.7	9.0	2.2	0.1	76.8	261
BSCB1(R)C13 x Pop. 32)BSCB1(R)C13	76.4	26.0	71.4	10.0	2.0	0.1	76.1	259
Testcross mean	79.0	25.1	71.1	8.9	2.4	0.1	76.6	257
BSCB1(R)C13	82.4	23.0	70.2	7.4	2.8	0.0	76.3	247
All Non-BSSS testcrosses	76.8	24.7	71.3	8.3	3.0	0.1	76.4	257
B97 x LH198	90.8	22.5	70.7	8.7	1.8	0.2	76.0	259
B104 x LH185	82.6	24.3	69.8	5.5	0.6	0.0	75.2	245
LH198 x LH185	89.7	20.6	69.7	3.1	2.0	0.0	74.0	245

\* BSSS group includes Iowa Stiff Stalk Synthetic (BSSS) and Tuxpeno germplasm in crosses and backcrosses to BSSS. Non-BSSS group includes non-BSSS and non-Tuxpeno germplasm in crosses and backcrosses to non-BSSS.

† Tester for selected BSSS backcrosses was LH185.

‡ Tester for selected non-BSSS backcrosses was LH198.

(2.9%), which is opposite to the data for the backcrosses themselves (Table 5). Compared with mean of the six recurrent parent testcrosses, the testcrosses averaged 2.6% more grain moisture, shed pollen 1.2 days later, and were 5 cm taller indicating that one backcross developed materials adapted to the temperate environments (Table 6).

Non-BSSS testcrosses averaged 5.0 q ha<sup>-1</sup> higher grain yield than the BSSS testcrosses (Table 6). The differences between the two sets of testcrosses for the other traits were not significant; the largest difference (15.3 cm) was shorter average plant height of BSSS testcrosses, which was probably because of the LH185 tester. Among the recurrent parents, BSSS(R)C13 had the greatest average testcross yield (73.9 q ha<sup>-1</sup>) for the BSSS group and BSCB1(R)C13 (79.0 q ha<sup>-1</sup>) for the non-BSSS group. Among the donor parents, Pool 18 had the greatest average testcross yield (76.3 q ha<sup>-1</sup>) with BS10(FR)C11, BS13(S)C8, and BSSS(R)C13 recurrent parent backcrosses and had the lowest average harvest grain moisture (23.9%); results are similar to the backcross per se trial (Table 5). The lower average yield of the BSSS testcrosses was because of the lower testcross yields of the donor parents, Populations 21 (67.6 q ha<sup>-1</sup>), 43 (66.8 q ha<sup>-1</sup>), and 49 (67.7 q ha<sup>-1</sup>), whereas all of the non-BSSS testcrosses donor parents averaged 74.5 q ha<sup>-1</sup> or greater yields. Differences between the BSSS and non-BSSS testcross means were relatively small with the non-BSSS testcrosses having a trend for greater test weight and plant height.

Phenotypic correlations were computed between 10 traits within heterotic groups for the testcrosses (correlations not shown). Except for plant and ear height and days-to-pollen shed and silk emergence, there were no consistent trends of the correlations between the BSSS and non-BSSS groups. Grain yield and grain moisture is an example:  $r = 0.06$  for BSSS testcrosses and  $r = -0.75^{**}$  for the non-BSSS testcrosses. Correlations between the bulks of the testcrosses and averages of the testcrosses for the 31 backcrosses suggest the bulks can have predictive value of the backcrosses of different populations (data not shown). For more highly heritable traits, the average correlations were 0.72 (days to mid silk), 0.73 (days-to-mid pollen shed), 0.77 (ear height), 0.82 (plant height), and 0.86 (test weight). The correlations were lower for grain yield (0.50), grain moisture (0.62), and root (0.38) and stalk (0.53) lodging. Except for root lodging, all correlations were significant at  $P \leq 0.05$ .

Testcross data were used to determine the backcross progenies intermated to form the elite temperate-tropical germplasm pools based on an index that emphasized greater grain yield, less grain moisture, and less root and stalk lodging. Yields of the selected testcrosses were similar to the testcrosses of the recurrent parents (data not included). Average yield of 20 BSSS testcross progenies was 78.0 q ha<sup>-1</sup>, which was similar to the average testcross yield of the three recurrent parents (77.4 q ha<sup>-1</sup>). Average differences between the selected testcrosses and recurrent parent testcrosses were positive for all traits except stalk lodging, but the differences were not significant in most instances. For the non-BSSS group testcrosses, the same trends were present between the selected testcrosses and testcrosses of the recurrent parents.

Among the 20 BSSS selected testcrosses, two BS10(FR)C11 backcrosses were included, both with Pool 18 as the donor parent. Few BS10(FR)C11 backcross progenies were selected because yields of BS10(FR)C11 progenies that included Populations 21, 24, 28, and 43 were less than BS10(FR)C11 x LH185. Six selections included BS13(S)C8 backcross progenies with 3, 2, and 1 selections from Pool 18 and Populations 49 and 43, respectively, the donor parents. Other high yielding BS13(S)C8 backcross progenies were not included because of poor root strength (data not shown). The three selections that included Pool 18 germplasm had the least grain moisture of the six BS13(S)C8 selections. BSSS(R)C13 related backcross progenies had either comparable or better yields compared with recurrent parent testcrosses, resulting in 12 BSSS(R)C13 selections. The best yielding testcross of the 20 BSSS selections was the BSSS(R)C13 x Pop. 24)BSSS(R)C13-8 progeny (82.5 q ha<sup>-1</sup>). The 12 BSSS selections averaged significantly greater test weights than BSSS x LH185, suggesting desirable alleles for improved grain hardness were transferred during backcrossing. Genetic contributions of the donor parents were not equally represented in the 20 BSSS selections. Eight selections that included Pool 18 germplasm were chosen from each recurrent parent, but Population 21 germplasm was not represented in any of the selections. One selection from Population 43 was included but grain moisture and days to mid-pollen shed were greater than average of the testcrosses. The 20 selections were intermated to form BS37, a germplasm pool of elite BSSS-Tuxpeno germplasm.

Sixteen backcross progenies were selected from

the 81 non-BSSS testcrosses. Of the 16 selections, 10 had grain yields greater than the average of the recurrent parent testcrosses, although not significant in all instances. Differences between the means of the 16 selections and the 81 testcrosses were significant for grain yield and moisture, root lodging, and days to pollen shed. Germplasm of the recurrent and donor parents was not equally represented among the 16 non-BSSS selections. There were eight selections that included BSCB1 as the recurrent parent and six that included Pool 17 as the donor parent. Each of the recurrent and donor parents was included in at least one selection. The greatest yielding testcross ( $87.6 \text{ q ha}^{-1}$ ) was BSCB1 x Pop. 23)BSCB1-19, which was above average for grain moisture (25.0%) and plant height (263 cm). Testcrosses that included donor parent Pool 17 averaged 23.7% grain moisture, which was 1.5% greater than the average of the three recurrent parents. BSCB1 had the best GCA with the tropical donor parents. Remnant seed of the 16 backcross progenies with the best testcross performance were intermated to form the BS38 population of elite non-BSSS non-Tuxpeno germplasm.

### CONCLUSION

One of the main concerns with the introduction and evaluation of tropical germplasm in temperate areas is the photoperiod effects for later maturity and greater plant stature (OYERVIDES *et al.*, 1985). Evaluation of backcrosses to temperate recurrent parents (25% tropical) and testcrosses of backcrosses with use of temperate testers (12.5% tropical) had flowering dates and harvest moisture levels that were, in most instances, not greater than the recurrent parents and checks. The other agronomic traits also were within the ranges of expressed by the recurrent parents. Pools 17 and 18 were the more important contributors to the germplasm pools probably because of previous selection for earlier maturity in their original environments. The original objective of study was to incorporate elite subtropical and tropical germplasm into elite temperate germplasm to combine favorable alleles for grain yield and other agronomic traits into germplasm pools adapted to temperate environments. The genetic materials included in the crosses were based on the heterotic alignment commonly used in the temperate (BSSS and non-BSSS) and tropical (Tuxpeno and non-Tuxpeno) areas. Materials classified

as primarily Tuxpeno were crossed with materials included in the BSSS (i.e., Reid Yellow Dent) group. Similarly, materials with either less or no Tuxpeno germplasm were crossed with materials classified as non-BSSS (i.e., Lancaster Sure Crop). Two-stage testing for multiple-trait selection was used to identify the superior backcross progenies used for intermating the four sets of selections. The four populations (BS35, BS36, BS37, and BS38) formed by intermating include 75% temperate and 25% exotic germplasm and are adapted for use in temperate area breeding programs. Our results suggest 25% elite exotic germplasm can be incorporated in the important U.S. heterotic groups without disrupting the highly productive combining ability for grain yield expressed in BSSS and non-BSSS hybrid combinations. Elite semi-exotic germplasm also produced hybrids (12.5% exotic) with acceptable harvest grain moisture levels, resistance to root and stalk lodging, shorter ear and plant heights, critical attributes for acceptance in the U.S. Corn Belt.

### REFERENCES

- BROWN W.L., 1953 Sources of germplasm for hybrid corn. pp. 11-16. *In*: D. Wilkmsn (Ed.), Proc. 8th Annu. Hybrid Corn Industry Res. Conf., Chicago, IL, 8-11 December. American Seed Trade Assoc., Washington, D.C.
- BROWN W.L., 1975 A broader germplasm base in corn and sorghum. pp. 81-89. *In*: H.L. Lopez, D. Wilkmsn (Eds.), Proc. 30th Annu. Hybrid Corn Industry Res. Conf., Chicago, IL, 9-11 December. American Seed Trade Assoc., Washington, D.C.
- CIMMYT, 1998 A complete listing of improved maize germplasm from CIMMYT. Maize Program Special Report. CIMMYT, Mexico, D.F.
- ECHANDI C.R., A.R. HALLAUER, 1996 Evaluation of U.S. Corn Belt and tropical maize varieties and their diallel crosses. *Maydica* **41**: 317-324.
- GOODMAN M.M., 1985 Exotic maize germplasm: status, prospects, and remedies. *Iowa State J. Res.* **59**: 497-527.
- GOODMAN M.M., 1999 Developing temperate inbreds from tropical germplasm: Rational, results, and conclusion. *Illinois Corn Breed. School* **35**: 1-19.
- GOODMAN M.M., W.L. BROWN, 1988 Races of corn. pp. 33-79. *In*: G.F. Sprague, J.W. Dudley (Eds.), *Corn and Corn Improvement*. 3rd ed., ASA, Madison, WI.
- HALLAUER A.R., 1986 Registration of BS26 maize germplasm. *Crop Sci.* **26**: 838-839.
- HALLAUER A.R., O.S. SMITH, 1979 Registration of BS13(S2)C1 and BS16 maize germplasm. *Crop Sci.* **19**: 755.



- HALLAUER A.R., S.A. EBERHART, W.A. RUSSELL, 1974 Registration of maize germplasm. *Crop Sci.* **14**: 341-342.
- HALLAUER A.R., K.R. LAMKEY, W.A. RUSSELL, P.R. WHITE, 1994 Registration of B97 and B98, two parental inbred lines of maize. *Crop. Sci.* **34**: 318-319.
- HOLTHAUS J.F., K.R. LAMKEY, 1995 Response to selection and changes in genetic parameters for 13 plant and ear traits in two maize recurrent selection programs. *Maydica* **40**: 357-370.
- MBS, 2002 Genetic Handbook. 29 (ed.). MBS Genetics, L.L.C., Story City, IA.
- MODE C.F., H.F. ROBINSON, 1959 Pleiotropism and the genetic variance and covariance. *Biometrics* **15**: 518-537.
- MULAMBA N.N., J.J. MOCK, 1978 Improvement of yield potential of the Eto Blanco maize (*Zea mays* L.) population by breeding for plant traits. *Egyptian J. Genet. Cytol.* **7**: 40-51.
- OSTLE B., 1954 Statistics in Research. Iowa State Univ. Press, Ames, IA 50011.
- OYERVIDES-GARCIA M., A.R. HALLAUER, H. CORTEZ-MENDOZA, 1985 Evaluation of improved maize populations in Mexico and the U.S. Corn Belt. *Crop Sci.* **25**: 115-120.
- RITCHIE S.W., J.J. HANWAY, G.O. BENSON, 1989 How a corn plant develops. Spec. Rept. No. 48. Iowa State Univ. Press. Ames, IA.
- RUSSELL W.A., 1972 Registration of B70 and B73 parental lines of maize. *Crop Sci.* **12**: 721.
- SMITH O.S., A.R. HALLAUER, W.A. RUSSELL, 1981 Use of index selection in recurrent selection programs in maize (*Zea mays* L.). *Euphytica* **30**: 611-618.
- VASAL S.K., G. SRINIVASAN, J. CROSSA, D.L. BECK, 1992a Heterosis and combining ability of CIMMYT's subtropical and temperate early-maturity maize germplasm. *Crop Sci.* **32**: 884-890.
- VASAL S.K., G. SRINIVASAN, F. GONZALEZ C., G.C. HAN, S. PANDEY, D.L. BECK, J. CROSSA, 1992b Heterosis and combining ability of CIMMYT's tropical x subtropical maize germplasm. *Crop Sci.* **32**: 1483-1489.
- VASAL S.K., G. SRINIVASAN, G. C. HAN, F. GONZALEZ C., 1992c Heterotic patterns of eighty-eight white subtropical CIMMYT lines. *Maydica* **37**: 319-327.
- VASAL S.K., G. SRINIVASAN, S. PANDEY, H.S. CORDOVA, G.C. HAN, F. GONZALEZ C., 1992d Heterotic patterns of ninety-two white tropical CIMMYT maize lines. *Maydica* **37**: 259-270.
- WELLHAUSEN E.J., 1956 Improving American corn with exotic germplasm. pp. 85-96. *In*: I. Sutherland (Ed.), Proc. 11th Annu. Hybrid Corn Industry Res. Conf., Chicago, IL, 8-10 December. American Seed Trade Assoc., Washington, D.C.
- WELLHAUSEN E.J., 1965 Exotic germplasm for improvement of Corn Belt maize. pp. 31-45. *In*: J.I. Sutherland (Ed.), Proc. 20th Annu. Hybrid Corn Industry Res. Conf., Chicago, IL, 8-9 December. American Seed Trade Assoc., Washington, D.C.