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Disciplines

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Performance of High \times High, High \times Low, and Low \times Low Crosses of Lines from the BSSS Maize Synthetic¹

Kendall R. Lamkey and Arnel R. Hallauer²

ABSTRACT

Twenty-four high- and 24 low-yielding lines per se selected from 247 random inbred lines of the 'Iowa Stiff Stalk Synthetic' (BSSS) maize (*Zea mays* L.) population were used to produce 48 high \times high (HH), 96 high \times low (HL), and 48 low \times low (LL) single-cross hybrids. The objectives of the study were to determine how crosses of lines selected for yield per se perform, and to examine the relationship of per se and hybrid performance. The 192 hybrids were evaluated in two replications at each of six Iowa environments. There were significant differences among HH, HL, and LL hybrid group means for grain yield and they were ranked (HH > HL > LL) as expected under a model assuming partial to complete dominance. The data suggests that on the average overdominance was not important for yield in BSSS. Correlations of inbred line traits with the same traits of the hybrids were larger than correlations of inbred line traits with hybrid yield. The correlations of inbred traits with hybrid yield were too small to be of predictive value. The data suggested that selection among lines per se for yield could be used to separate a population into a group of high and low combining lines based on their per se performance. However, per se performance within groups was not related to either specific or general combining ability. After selection for per se performance the smaller group of selected lines could be crossed to a series of testers to identify lines with the greatest hybrid potential.

Additional index words: *Zea mays* L., Gene action, Correlations, Quantitative genetics, Corn.

QUANTITATIVE genetic theory has been used extensively to estimate genetic parameters in random mating populations (Hallauer and Miranda, 1981). Breeders of crop species have been interested in the performance of crosses of high- and low-yielding lines. The interest has ranged from the estimation of gene action to determining the type of cross (high \times high, high \times low, low \times low) to use for the extraction of elite inbred material. Selection of the high- and low-yielding lines from a random group of lines representative of a common gene pool allows the performance of high \times high, high \times low, and low \times low groups to be written as functions of quantitative genetic parameters in the original base population. These parameters could then be used to make inferences about the original base population.

Lonnquist (1953) evaluated high \times high (HH), high \times low (HL), and low \times low (LL) crosses of inbred lines from the maize cultivar 'Krug', which were selected for divergent yielding ability in testcrosses with WF9 \times M14. The hybrid group means ranked HH > HL > LL, and Lonnquist concluded that his results supported the hypothesis of the action of partially dominant favorable alleles in determining hybrid vigor. Lonnquist and Lindsey (1964) evaluated HH, HL, and

LL crosses of lines selected for performance per se and in crosses with an unrelated tester. They concluded that the yield trend from intercrosses of lines per se gave results expected when additive gene action predominates, and the results from the unrelated testcrosses were evidence of overdominant gene action. Furthermore, they indicated that selection among lines per se would be expected to emphasize additive effects rather than heterotic loci. Similar results were reported by Lonnquist (1968). Results of crossing high- and low-yielding lines of wheat (*Triticum aestivum* L. em Thell.), barley (*Hordeum vulgare* L. emend. Lam.), and cotton (*Gossypium hirsutum* L.) were similar to those of maize, although the selected lines were not representative of a common gene pool (Ramey, 1963; Upadhyaya and Rasmusson, 1967; Busch et al., 1974; Bitzer et al., 1982).

In this study, we selected 24 high- and 24 low-yielding lines per se from 247 random inbred lines of 'Iowa Stiff Stalk Synthetic' (BSSS) to produce two groups of selected lines. Single-cross hybrids were produced within and between the two groups. Our objectives were to determine how crosses of lines selected for yield per se perform and to examine the relationship of per se and hybrid performance.

MATERIALS AND METHODS

Genetic Materials

In 1962, selfing was initiated in the Iowa Stiff Stalk Synthetic (BSSS) maize population to generate a set of random inbred lines (Hallauer and Sears, 1973). Initially, 250 random S₀ plants were selfed and planted ear-to-row in 10-plant rows. Excluding end plants, three consecutive plants were self-pollinated to minimize selection within the row. At harvest, the middle ear of the three self-pollinated ears was saved to propagate the line to the next generation. This procedure was repeated until the S₆ generation, when the lines were increased for evaluation by bulk selfing. Three lines were lost during the inbreeding process, and 247 lines were available for evaluation. The lines undergoing evaluation were highly homozygous and for purposes of this study will be assumed to have an inbreeding coefficient (*F*) of one.

Obilana and Hallauer (1974) evaluated the 247 random lines to estimate additive genetic variance in BSSS. On the basis of their results, 24 high- and 24-low yielding lines per se were selected for use in this study. After selection of the lines, four groups of hybrids were produced: high \times high (HH), high \times low (HL1), low \times high (HL2), and low \times low (LL). A 4 \times 4 Design II mating scheme (Comstock and Robinson, 1948) was used to produce the hybrids in each group. To demonstrate the crossing procedure, consider eight randomly chosen lines from the high series and arbitrarily designate four as males (MH) and four as females (FH). Also, consider eight randomly chosen lines from the low series and arbitrarily designate four as males (ML) and four as females (FL). The HH, HL1, HL2, and LL groups were produced by crossing FH \times MH, FH \times ML, FL \times MH, and FL \times ML, respectively. The procedure was repeated for the

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remaining 16 high and 16 low lines, resulting in 48 hybrids in each of the four groups, for a total of 192 hybrids.

Experimental Procedures and Data Collection

The 192 hybrids were evaluated in three sets of a replication-in-sets design. Each set was a modified split plot, with four main plots arranged in a randomized complete block design with two replications. Main plots were the HH, HL1, HL2, and LL groups corresponding to a given group of eight high- and eight low-yielding lines. Each main plot contained 16 subplots, for a total of 64 entries per set. The experiment was grown in six Iowa environments (year-location combinations) over a 4-yr period. The experiment was grown at the Agronomy and Agricultural Engineering Research Center near Ames for 4 yr (1981 to 1984) and at the Iowa State University Research Center in Ankeny for 2 yr (1983 and 1984). Fertilizer applications were 80 kg ha⁻¹ for P₂O₅ and K₂O applied the previous fall, and 180 kg ha⁻¹ N applied before planting in the spring as urea.

In 1981 and 1982, subplots consisted of one row 5.08 m long, with 0.76 m between subplots. Subplots were overplanted by hand and thinned to 18 plants per plot (46 622 plants ha⁻¹). Subplots consisted of one row 5.40 m long, with 0.76 m between subplots in 1983 and 1984. Subplots were overplanted with a machine and thinned to 19 plants per plot (46 292 plants ha⁻¹).

Data were collected for yield (Mg ha⁻¹) of shelled grain, kernel-row number, ear length (cm), ear diameter (cm), cob diameter (cm), kernel depth (cm), stand (1000 plants ha⁻¹), number of days from planting to silking, and plant and ear height (cm). All plants in a plot were hand-harvested and dried to a uniform moisture before shelling to determine yield. Kernel-row number, ear length, ear diameter, and cob diameter were calculated as the average of measurements on five randomly chosen ears per plot. Kernel depth was calculated as half the difference between ear and cob diameter. Stand was recorded after thinning as the number of plants per plot and then converted to 1000 plants ha⁻¹. Days to silk were recorded as the number of days after planting to 50% silk emergence. Plant and ear heights were calculated as the average of measurements on five competitive plants per plot and measured as the height from the ground to the node of the flag leaf (plant height) and the highest ear-bearing node (ear height).

Yield and stand data were collected in six environments; plant and ear height data were collected in five environments; days to silk was recorded in four environments; and kernel-row number, ear length, ear diameter, cob diameter, and kernel depth were measured in three environments.

Statistical Analysis

The analysis of variance for an individual set in a given environment was partitioned according to the analysis for a split-plot experiment except that hybrids (subplot treatments) are nested within main plots. This analysis was pooled over sets and environments to give the combined analysis of variance. All effects in the model were considered random except main plots. The environment × main plot and environment × main plot × set interactions were pooled to give the environment × main plots within sets source of variation. The *F* tests and degrees of freedom for main plots × sets and environments × main plots within sets were synthesized according to the approximation given by Satterthwaite (1946). Main plots were tested by using the main plot × set interaction and all standard errors for main plot means were calculated by using the main plot × set inter-

action. The sums of squares and degrees of freedom for main plots were partitioned into three single degree of freedom contrasts: HH vs. LL, HL vs. 1/2(HH + LL), and HL1 vs. HL2. These contrasts have genetic interpretations described in the Theory section.

The data used to select the high- and low-yielding inbred lines were also used to calculate correlations between inbred and hybrid means. The inbred line data were means over two replications evaluated at each of three locations. Details of the study were reported by Obilana and Hallauer (1974). Rank correlations between inbreds and hybrids were calculated within each hybrid group, between the midparent and their respective hybrids for the same plant and ear traits of the inbred lines and hybrids; and for plant and ear traits of the inbred lines with yield of the hybrids.

Theory

Means and Heterotic Deviations

Let the frequency of the favorable allele in BSSS be *P*. Assume that selection in the high and low direction resulted in a change in gene frequency and let the frequency of the favorable allele be *P*^H and *P*^L for the high- and low-yielding lines, respectively, where *P*^H > *P*^L. Frequencies *P*^H and *P*^L can be expressed relative to the allele frequency in BSSS as:

$$P^H = P + \Delta P^H; \text{ and}$$

$$P^L = P - \Delta P^L$$

where

ΔP^H is the change in allele frequency in the high direction, and

ΔP^L is the change in allele frequency in the low direction.

Assume that the hybrids in the high × high (HH) and low × low (LL) groups represent a random sample of hybrids from populations with allele frequencies of *P*^H and *P*^L, respectively, and that the hybrids in the high × low (HL) group represent a random sample of hybrids from the cross of two populations with allele frequencies of *P*^H and *P*^L. Then, by assuming no epistasis and reducing the model developed by Smith (1983) to two alleles per locus, the genetic expectations of the means of the three groups of hybrids can be expressed as:

HH = genetic expectation of the mean of the high × high hybrids

$$= AO + 2DO + 2[Al(H) + Dl(H)] - 2DQ(H);$$

HL = genetic expectation of the mean of the high × low hybrids

$$= AO + 2DO + [Al(H) + Dl(H)] - [Al(L) + Dl(L)] + 2HQ; \text{ and}$$

LL = genetic expectation of the mean of the low × low hybrids

$$= AO + 2DO - 2[Al(L) + Dl(L)] - 2DQ(L),$$

where

$$AO = (2P-1)a;$$

$$DO = 2P(1-P)d;$$

$$Al(H) = \Delta P^H a;$$

$$Al(L) = \Delta P^L a;$$

$$Dl(H) = \Delta P^H(1-2P)d;$$

$$Dl(L) = \Delta P^L(1-2P)d;$$

$$DQ(H) = (\Delta P^H)^2 d;$$

$$DQ(L) = (\Delta P^L)^2 d; \text{ and}$$

$$HQ = \Delta P^H \Delta P^L d.$$

The *P* is the frequency of the favorable allele in a two-allele system; *a*, *d*, and $-a$ are the genotypic values of *AA*, *Aa*, and *aa*, where *A* is the favorable allele, and ΔP is the change in frequency of the favorable allele.

The complexity of the expressions for the means can be reduced by assuming that the change in allele frequency is equal in the high and low directions; i.e., $\Delta P^H = \Delta P^L = \Delta P$. Then, the group means can be written as:

$$HH = \mu_R + 2[Al + Dl] - 2DQ;$$

$$HL = \mu_R + 2DQ; \text{ and}$$

$$LL = \mu_R - 2[Al + Dl] - 2DQ,$$

where

$$\mu_R = AO + 2DO = (2P-1)a + 2P(1-P)d;$$

$$2[Al + Dl] = 2\Delta P[a + (1-2P)d]; \text{ and}$$

$$2DQ = 2(\Delta P)^2 d = (P^H - P^L)^2 d / 2.$$

The equations for the group means can be used to obtain least-squares estimates of μ_R , $2[Al + Dl]$, and $2DQ$. The estimating equations are:

$$\mu_R = (HH + 2HL + LL)/4;$$

$$2[Al + Dl] = (HH - LL)/2; \text{ and}$$

$$2DQ = [2HL - HH - LL]/4.$$

Two of these terms, $2[Al + Dl]$ and $2DQ$ are of interest. $2Al = 2\Delta Pa$ is always positive, unless $\Delta P < 0$. Assuming that $\Delta P > 0$, $2Dl = 2\Delta P(1-2P)d$ can be positive or negative, depending on whether $P > 0.5$ or $P < 0.5$ in the reference population. The sum $2Al + 2Dl$ can be negative only if $d > a$ and $P > (a + d)/2d$, where $P = (a + d)/2d$ is the allele frequency where selection is ineffective; i.e., when $\alpha = a + (1-2p)d = 0$ (Comstock et al., 1949). Therefore, overdominance can be detected with this model only if the allele frequency is greater than $(a + d)/2d$. The equation $2DQ = 2(\Delta P)^2 d$ measures the heterosis due to the difference in allele frequency between high and low populations.

The assumption that $\Delta P^H = \Delta P^L$ can be relaxed with little consequence unless selection is extremely asymmetrical. Under minor asymmetry [i.e., $\Delta P^H - \Delta P^L < \max(\Delta P^H, \Delta P^L)$], the primary effect of asymmetry is to cause HL to fluctuate around the midpoint of HH and LL. The direction of the fluctuation of HL provides an indication of whether $\Delta P^H > \Delta P^L$ or $\Delta P^L > \Delta P^H$. When the assumption that $\Delta P^H = \Delta P^L$ is relaxed, the expectation of the parameter estimates are:

$$E(AO + 2DO) = \mu_R + (\Delta P^H - \Delta P^L)\alpha - (\Delta P^H - \Delta P^L)^2 d / 2;$$

$$E(2Al + 2Dl) = (\Delta P^H + \Delta P^L)\alpha - [(\Delta P^H)^2 - (\Delta P^L)^2]d;$$

$$\text{and}$$

$$E(2DQ) = 1/2(\Delta P^H + \Delta P^L)^2 d.$$

RESULTS AND DISCUSSION

Environmental conditions were excellent for maize production in 1981, 1982, and 1984, and average in 1983. Mean grain yields were 6.82, 5.77, 3.93, and 6.04 Mg ha⁻¹ in 1981, 1982, 1983, and 1984, respectively. Yields at Ames in 1983 were excellent for the year, but at Ankeny dry conditions during pollination and grain filling resulted in low yields (2.80 Mg ha⁻¹). The

mean grain yield and coefficient of variation, averaged over environments, were 5.42 Mg ha⁻¹ and 13.7%, respectively.

There were significant differences ($P \leq 0.05$) among main plots for yield and days to silk (data not shown). The set \times main plot interaction was significant for kernel-row number, ear length, days to silk, and plant height. There were significant differences among groups (HH, HL, and LL) for yield, days to silk, and stand. Variation among groups accounted for more than 99% of the variation among main plots for yield and days to silk. The contrast of HL1 vs. HL2 was significant for ear height and stand. The environment \times main plots within sets interaction was significant for yield, kernel-row number, ear length and diameter, plant height, and stand. There were significant differences among hybrids within groups for all traits.

The selection differentials in the high and low direction for yield were 1.31 and -1.25 Mg ha⁻¹, respectively (Table 1). Selection for high and low yield caused days to silk to deviate -3.92 and 3.55 days from the population mean, respectively. The large divergence of parent means for days to silk suggests that line per se yields may be partially confounded with silking date. Obilana and Hallauer (1974) reported a genetic correlation of -0.49 between yield and days to silk for the group of 247 lines derived from BSSS. They attributed the correlation to either a lack of pollen for the late-maturing inbred lines or a lack of vigor because of the late maturity within the inbred lines. The deviations from the population mean for the other traits were generally small.

The group means for yield were ranked as expected under a model with partial to complete dominance (Table 2). The HH group was 0.43 and 1.05 Mg ha⁻¹ higher yielding than the HL and LL groups, respectively. The estimate of $2(Al + Dl)$ for yield was 0.53 ± 0.12 Mg ha⁻¹ and measures the average response to selection in the high and low directions. The significant estimate of $2(Al + Dl)$ indicates that selection for high- and low-yielding inbred lines per se was effective at changing the average frequency of the favorable allele in the high and low directions. The positive value of $2(Al + Dl)$ suggests that on the average overdominance was not important for yield in BSSS. However, the model can detect overdominance only at loci where the frequency of favorable alleles was greater than $(a + d)/2d$ for $d > a$.

The LL group was 3.6 and 1.6 days later silking than the HH and HL groups, respectively. These differences

Table 1. Means and ranges for yield, and plant and ear traits of the 24 high- and 24 low-yielding lines and the 247 random lines of BSSS from which the high and low lines were selected. Data were summarized from Obilana (1972).

Traits	Selected lines					SE (\bar{X})	Population	
	Mean		Range		Mean		Range	
	High	Low	High	Low				
Yield (Mg ha ⁻¹)	3.21	0.65	2.91 - 3.86	0.31 - 0.94	0.59	1.90	0.01 - 3.85	
Kernel rows (no.)	16.6	13.3	12.8 - 20.0	10.4 - 15.8	0.14	15.1	10.4 - 20.3	
Ear length (cm)	13.3	10.5	11.1 - 16.9	7.7 - 13.5	0.18	12.0	4.7 - 16.9	
Ear diameter (cm)	3.6	3.1	3.2 - 4.2	2.4 - 3.8	0.04	3.3	2.4 - 4.2	
Cob diameter (cm)	2.3	2.3	2.1 - 2.8	1.6 - 2.6	0.03	2.3	1.6 - 2.8	
Kernel depth (cm)	1.3	0.8	1.0 - 1.4	0.4 - 1.5	0.03	1.0	0.4 - 1.5	
Days to silk (no.)	78.8	86.3	73.5 - 84.5	77.7 - 92.5	0.21	82.8	72.0 - 93.3	
Plant height (cm)	158.3	153.3	123.1 - 185.4	105.2 - 194.4	0.91	154.9	105.2 - 204.5	
Ear height (cm)	67.8	66.5	46.2 - 84.7	33.5 - 96.0	0.58	66.8	33.5 - 107.3	
Stand (1000 plants ha ⁻¹)	37.5	38.5	28.7 - 41.7	29.9 - 41.7	0.49	38.0	11.8 - 41.7	

were small relative to the difference between the high- and low-yielding lines per se. The correlations within groups, between yield and days to silk were -0.23 (HH), -0.34^{**} , significant at the 0.01 probability level (HL), and -0.39^{**} (LL), suggesting that yield of the hybrids was confounded with silking date. Lack of pollen or vigor was not a problem for late-maturing hybrids, and the relationship between days to silk and yield possibly was due to pleiotropy or linkage. For days to silk, $2(AI + DI) = -1.82 \pm 0.45$ and measures the average correlated response to selection in the high and low directions when selection was for yield. The significant estimate of $2(AI + DI)$ suggests that selection for yield changed the allele frequencies for days to silk.

The estimates of $2DQ$ for yield and days to silk were 0.05 ± 0.06 and 0.10 ± 0.20 , respectively. The $2DQ$ estimates heterosis due to the square of the difference in allele frequency between the high and low populations. The nonsignificance of $2DQ$ for yield and days to silk indicates that the mean of the HL group was an estimate of the mean of noninbred BSSS and that the heterosis observed was due to the inbreeding of the lines. Therefore, one cycle of selection was not enough to observe heterosis due to a difference in allele frequencies between the high and low populations.

Differences among groups for kernel-row number, ear length, ear diameter, cob diameter, kernel depth, plant height, and ear height were not significant (Table 2). The lack of significant differences among the ear traits was unexpected given the magnitude of the heritabilities for yield and the ear traits, and the genetic correlations between yield and the ear traits reported by Obilana and Hallauer (1974) for the group of 247 lines derived from BSSS. This suggests that the yield differences observed among groups were due to changes in yield component traits that were not measured. The genetic correlations between yield, and plant and ear height were 0.07 and 0.02, respectively (Obilana and Hallauer, 1974), which explains the lack of significant differences among hybrid groups for these traits.

Our results do not support certain conclusions reached by Lonnquist (1968) and Lonnquist and Lindsey (1964). The higher level of performance of the HL group in their studies does not necessarily indicate the presence of overdominant gene action, but it may suggest the presence of unequal changes in gene frequency in the high and low directions. The probability of unequal changes in gene frequency was high in both stud-

ies because only three high and low lines were selected. Therefore, their results do not allow the separation of the effects of unequal changes in gene frequency from overdominant gene action.

Rank correlations of inbred line (midparent) traits with the same traits of the hybrids were larger than the correlations of inbred line traits with hybrid yield (Table 3). The magnitude of the trait vs. trait correlations for days to silk, plant height, ear height, and cob diameter were consistent across hybrid groups. The trait vs. trait correlations of the ear traits were not as consistent across hybrid groups and were generally larger in the HH group. The general trend of the trait vs. trait correlations was to be large in the HH group, intermediate in the HL group, and small in the LL group.

Of the 27 possible correlations between inbred line traits and hybrid yield, only six were significant ($P \leq 0.01$ and 0.05). The correlations of days to silk with yield were negative and significant in the HL and LL groups, suggesting that silking date was important in determining yield among low yielding hybrids. Most of variation among HL and LL hybrids for silking date was due to a high frequency of late flowering genotypes. Correlations between yield of inbred lines and yield of hybrids were nonsignificant and small, although the correlations did show an increasing trend from the HH to LL hybrid groups.

The inbred lines used in this study were a selected sample of those used by Gama and Hallauer (1977).

Table 3. Rank correlation coefficients of the means of two inbreds with their specific hybrid within the high \times high, high \times low, and low \times low hybrid groups.

Trait	High \times high		High \times low		Low \times low	
	Trait vs. Trait	Trait vs. Yield	Trait vs. Trait	Trait vs. Yield	Trait vs. Trait	Trait vs. Yield
Yield	-0.14	--	0.07	--	0.22	--
Kernel-row no.	0.82**	-0.06	0.64**	0.16	0.55**	0.45**
Ear length	0.44**	0.09	0.34**	0.03	0.31*	-0.01
Ear diameter	0.58**	0.00	0.45**	0.05	0.35*	0.18
Cob diameter	0.67**	-0.11	0.68**	0.09	0.59**	0.16
Kernel depth	0.30*	0.10	0.18	0.01	0.08	0.06
Days to silk	0.71**	0.22	0.64**	-0.22*	0.59**	-0.31*
Plant height	0.79**	0.29*	0.58**	0.08	0.61**	0.05
Ear height	0.79**	0.49**	0.74**	0.21*	0.68**	0.15
n †	48		96		48	

*,** Significant at the 0.05 and 0.01 probability levels, respectively.
† Number of observations.

Table 2. Means and range for yield, and plant and ear traits of the high \times high (HH), high \times low (HL), and low \times low (LL) hybrid groups from BSSS averaged over environments.

Traits	Groups						LSD (0.05)†	LSD (0.05)‡
	High \times high		High \times low		Low \times low			
	Mean	Range	Mean	Range	Mean	Range		
Yield (Mg ha ⁻¹)	5.90	3.65-7.08	5.47	2.83-7.66	4.85	2.22-7.24	0.46	0.40
Kernel rows (no.)	18.1	14.4-21.9	18.2	14.3-22.8	18.2	14.1-22.3	NS	NS
Ear length (cm)	16.9	14.6-21.0	16.8	14.0-20.3	16.5	10.7-19.1	NS	NS
Ear diameter (cm)	4.8	4.4-5.2	4.7	4.2-5.3	4.7	4.2-5.5	NS	NS
Cob diameter (cm)	2.8	2.5-3.1	2.8	2.5-3.2	2.8	2.5-3.1	NS	NS
Kernel depth (cm)	0.96	0.7-1.1	0.95	0.7-1.2	0.94	0.8-1.3	NS	NS
Days to sil (no.)	87.2	85.2-91.7	89.2	84.5-94.7	90.8	85.7-97.2	1.7	1.5
Plant height (cm)	221	184-254	226	189-270	225	187-262	NS	NS
Ear height (cm)	108	79-130	112	70-143	113	83-145	NS	NS

† For comparing the high \times high mean with the low \times low mean.

‡ For comparing the high \times low mean with either the high \times high or low \times low mean.

Selection apparently has some effect on the magnitude of trait vs. trait and trait vs. yield correlations, although whether the observed changes among hybrid groups were due to sampling or genetic causes was not evident. The correlations of plant and ear traits of the inbreds and the same traits of the hybrids reported here were larger than those reported by Gama and Hallauer (1977), whereas the correlation of inbred traits with hybrid yield were similar. Russell and Machado (1978) reported correlations between inbreds and hybrids, where the inbreds were a selected group based on five different selection criteria. Their correlations between plant and ear traits of inbreds and hybrid yield were larger than those reported here and in the study by Gama and Hallauer (1977). In particular, the correlations between ear length and yield of the inbred and hybrid yield were greater than 0.30 and significant. Although these correlations were not large enough to be of predictive value, they do indicate the importance of the genetic structure of the population on the magnitude of inbred-hybrid correlations. Russell and Machado (1978) derived their lines from BS1, a broad genetic base population (Russell, 1979).

Selection among lines per se for high and low yield was effective at dividing the lines into groups with high and low average performance for yield in hybrids. The number of hybrids above the estimated mean of non-inbred BSSS ($\mu_R = 5.42 \text{ Mg ha}^{-1}$), expressed as a percentage of the number of hybrids in the group was 62.5% (HH), 49.0% (HL), and 27.0% (LL). The HL group produced the highest yielding hybrid in the study; however, 96 HL hybrids were evaluated compared with 48 HH and 48 LL hybrids, thus increasing the probability of finding high-yielding hybrids in the HL group. However, selecting the highest-yielding inbred line within groups does not identify the line with the highest average performance in hybrids. Because of the Design II scheme used to produce the hybrids, each line was crossed to four high- and four low-yielding lines (testers). The rank correlations between the high parent means and the mean of the high parent when crossed to high and low testers were -0.17 and 0.02 , respectively. The rank correlations between the low parent means and the mean of the low parent when crossed to high and low testers were 0.11 and 0.31 , respectively. These data suggest that line performance within groups is not indicative of hybrid performance within groups regardless of the type of tester used.

Both high- and low-yielding testers were equally effective at discriminating among lines for combining ability of yield. The rank correlations between testcross means for the high and low testers were 0.61^{**} and 0.74^{**} for the high and low parents, respectively. The genetic variance among testcross family means for the high-yielding parents were similar in magnitude when a high-yielding tester ($\hat{\sigma}_{TC}^2 = 0.15 \pm 0.07$) was used as when a low-yielding tester ($\hat{\sigma}_{TC}^2 = 0.13 \pm 0.07$) was used; however, the genetic variance among testcross family means for the low-yielding parents was 2.7 times larger when a low-yielding tester ($\hat{\sigma}_{TC}^2 = 0.48 \pm 0.19$) was used as when a high-yielding tester ($\hat{\sigma}_{TC}^2$

$= 0.18 \pm 0.08$) was used. Hallauer and Lopez-Perez (1979) reported an increase in the genetic variance among testcrosses when a low-yielding tester was used with a random group of lines. Our results suggest that the increase in genetic variance obtained by using a low-yielding tester was due primarily to lines with low performance per se.

These data suggest that selection among lines per se for yield can be used to separate a population into a group of high and low combining lines based on their per se performance. However, per se performance within groups is not related to either specific combining ability or general combining ability. After selection for per se performance the smaller group of selected lines can be crossed to a series of testers to identify the lines with the greatest hybrid potential.

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