Selection Among and Within S1 Lines of Maize on S2 Line and Testcross Performance

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Selection Among and Within $S_1$ Lines of Maize on $S_2$ Line and Testcross Performance

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Most maize (Zea mays L.) breeders practice visual selection among lines during inbreeding, but may not be certain of the effectiveness of such selection. Visual selection among and within 1,636 $S_1$ lines of maize derived from 'Lancaster Composite' was used to select 200 $S_2$ lines, and a random set of 200 $S_1$ lines also was developed. Yield trials of the 400 $S_2$ lines in three environments and their testcrosses to (B73 × B84) in four environments were conducted to determine whether visual selection was effective in choosing high-yielding and agronomically desirable lines with superior combining ability.

Yield of the visually selected $S_1$ lines (3.11 Mg ha$^{-1}$) was significantly (P<0.05) greater than that of the unselected lines (2.94 Mg ha$^{-1}$), but there was no difference in testcross means. Visually selected $S_1$ lines had slightly greater mean grain moisture and slightly less mean stalk lodging than unselected lines in individual environments. Testcrosses of visually selected lines had greater grain moisture and less stalk lodging than testcrosses of unselected lines in individual environments. Estimates of genetic variance, heritability, and gain from selection were not consistently affected by visual selection. Many superior $S_2$ lines and testcrosses were unselected lines, showing that visual selection failed to identify many desirable genotypes. Our results suggest that visual selection should not be used to attempt to select the most superior genotypes, but should emphasize discarding of undesirable genotypes before yield testing.

INDEX DESCRIPTORS: Zea mays L., Corn, Corn Breeding, Breeding methods, Recurrent selection.

**MATERIALS AND METHODS**

The maize population used in this study was 'Lancaster Composite', a genetically broad-base population synthesized between 1977 and 1980 at Iowa State University from inbred lines and populations of 'Lancaster Surecrop' origin. No previous selection had been conducted in Lancaster Composite at the time this study was initiated. $S_1$ progenies were obtained by self-pollination of unselected $S_0$ plants in Florida during winter 1979-1980, and the 1,636 $S_1$ progenies produced were evaluated in summer 1980 in a breeding nursery and a corn borer screening nursery, both near Ames, Iowa. One-row plots with one replication were used at each location. Plots contained 25 and 13 plants in the breeding and corn borer screening nurseries, respectively. At the corn borer nursery, the $S_1$ progenies were infested with two European corn borer egg masses (Ostrinia nubilalis Hübner) four times the last 10 days of June. Ratings on a 1 to 9 scale (1 = resistant and 9 = susceptible) were made about 3 weeks after infestation. Progenies susceptible (ratings 7 to 9) to first-generation corn borer leaf feeding were discarded before flowering in the breeding nursery and plants within remaining $S_1$ progenies were self-pollinated to produce $S_2$ progenies. Progenies in the corn borer nursery were inoculated with Helminthosporium turcicum Pass. on 11 August and rated for relative lesion number and size on 16 September. Pollinated plants were inoculated in mid-August in the second elongated internode with a stalk rot spore suspension containing Diplodia maydis, Gibberella zeae, Fusarium moniliforme, and Colletotrichum graminicola (Ces.) Wils. Based on the disease ratings, susceptible progenies were discarded at harvest.

Two sets of $S_2$ progenies were chosen at harvest in 1980. For one set, selection was based on maturity (date of pollination), seed set, ear size, resistance to stalk rot and leaf blight organisms on a scale of 0.5 to 5.
Machine-planted, two-row plots 5.5 m long spaced 76 cm were used for each entry in the yield trials. Each entry in the root-pulling experiments was planted in a single-row plot 3.05 m long with 76 cm between plots. Root-pulling plots were hand-planted in 1981 and 1982 and machine-planted in 1983. Plants in the hand-planted plots were spaced 25.4 cm within the row. All yield trial plots were machine-planted in 1983.

In 1981, seed of the 400 S2 progenies were planted in isolation for testcrossing to B84 x B73, a tester of 'Iowa Stiff Stalk Synthetic' origin. The S2 lines were detasseled, and, at harvest, seed from approximately 13 plants of each line was bulked within lines to provide testcross seed. Because seed from each S2 line was bulked, the crosses were genetically equivalent to S1 plant x tester crosses.

The 400 S2 lines were evaluated in yield trials at three Iowa locations (Ames, Ankeny, and Martinsburg) in 1981. An additional experiment was grown at the Ames corn borer screening nursery for collection of vertical root-pulling data. The 400 testcrosses were evaluated at these three locations in 1982 and 1983, but the Ankeny and Martinsburg locations were destroyed by windstorm and drought, respectively, in 1983. The experimental design at each location in all years was a split plot, with whole plots arranged in an incomplete block design with two replications. The 400 entries (S2 lines in 1981 and testcrosses in 1982 and 1983) were divided into 10 sets of 40 entries each. Within each set, 20 visual and 20 unselected entries were included. Main plots in the split-plot design were selection types (visual or unselected) because the 20 entries of a selection type within a set were planted as a block. Subplots were individual entries nested within selection types. Selection types were randomized within each replication within each set, and entries were randomized within selection types.

Machine-planted, two-row plots 5.5 m long spaced 76 cm were used for each entry in the yield trials. Each entry in the root-pulling experiments was planted in a single-row plot 3.05 m long with 76 cm between plots. Root-pulling plots were hand-planted in 1981 and 1982 and machine-planted in 1983. Plants in the hand-planted plots were spaced 25.4 cm within the row. All yield trial plots were machine-harvested, with no gleaning for dropped ears.

Data collected on all plots in each experiment included: 1) plants per plot (stand, thousands ha^-1), 2) plants per plot leaning 30° or more from the vertical (root lodging), 3) plants per plot broken below the ear (stalk lodging), 4) dropped ears per plot, 5) percentage grain moisture at harvest, and 6) shelled grain yield (Mg ha^-1) converted to 15.5% grain moisture. Dropped-ear data were not taken at Ames in 1983. Root and stalk lodging and dropped ears were expressed as percentages of counted stands. Vertical root-pull resistance was measured each year in all plots in the corn borer screening nursery approximately 3 weeks after the beginning of anthesis, in the same manner as that reported by Kevern and Hallauer (1985).

An analysis of variance was computed for each trait for each set, pooled over sets for each environment, and combined across environments. Data were available from three environments for all S2 traits except root-pull resistance, for which data were gathered in only one environment. Data from four environments were available for all testcross traits except dropped ears (three environments) and vertical root-pull resistance (two environments). Analyses of variance were performed using plot means for grain moisture and root pull and plot totals for the other traits. In all analyses in which they appeared, environments, sets, replications, and entries within selection types were considered random effects, and selection types were considered fixed effects. Entry sums of squares (380 df) and environment X entry sums of squares (760 and 1140 df for S2 and testcross experiments, respectively) were partitioned into sums of squares for visually selected and unselected entries (190 df each) and their interactions with environments. Genotype (G) and genotypexenvironment (GxE) variance component estimates for each group were calculated by equating observed mean squares with their expected values. Variance component estimates from the visually selected and unselected entries were considered significantly different if the range of estimates, plus or minus twice their standard errors, did not overlap.

Heritability estimates on an entry mean basis were calculated as \( h^2 = \frac{\sigma^2_f}{\sigma^2_e + \sigma^2_G} \), where \( \sigma^2_f \) is an estimate of experimental error and \( h^2 \) and \( e \) are number of replications and environments, respectively. Estimates of genetic gain per year for direct selection for a trait, and correlated responses in other traits, were calculated for both the visually selected and unselected groups of S2 progenies and testcrosses as \( \Delta G = k b G / (b^2 P b) \), respectively. Predicted gains (or selection among S2 lines) were based on a 3-year selection cycle, progeny evaluation using two replications in each of three environments, 12.5% selection intensity (k = 1.65), and recombination of S2 seed. Gains from selection among testcrosses were predicted by assuming progeny evaluation using two replications in each of four environments, recombination of S1 seed, and other variables the same as for the S2 lines.

The 50 best S2 lines of the 400 total entries were selected for single-trait superiority for grain yield, grain moisture, stalk lodging, and vertical root-pull resistance by using entry means calculated across all environments. A Smith-Hazel (Hazel and Lush, 1942) index using entry means for five traits (grain yield, grain moisture, stalk lodging, root lodging, and root-pull resistance) also was used to make selection for S2 lines. Estimated gains for each trait from each Smith-Hazel index were calculated as: \( \Delta G = k b G / (b^2 P b) \), where \( b \) is the vector of index weights, \( G \) is the genetic variance-covariance matrix, and \( P \) is the phenotypic variance-covariance matrix. The economic weights (\( a \) values) chosen for grain yield, grain moisture, root and stalk lodging, and root pull were 1.0, 0.5, -0.5, -0.5, and 0.25, respectively.

RESULTS

S2 Line Selection Type Means

Significant differences (P<0.05) between means of the visually selected and unselected groups of S2 lines from the combined analysis were detected only for grain yield and stand (Table 1). Visual selection successfully chose a group of lines with mean grain yield (0.17 Mg ha^-1) and stand (2.6%) greater than that of the unselected lines. Environment X selection type interaction mean squares were not significant for all traits (data not shown), showing that selection type means changed little relative to one another across environments.

Examination of selection type means in individual environments revealed a significant difference for grain yield only at Martinsburg. Although differences between selection type means at Ames and Ankeny were not significant, the visually selected group had greater grain yield than the unselected group in all environments, indicating a consistent trend for the slight improvement of grain yield via visual selection (Table 1). No significant differences existed between selection type means for grain moisture in any environment, but the visually selected group tended to have slightly greater moisture in each environment. A trend toward improved stalk lodging resistance for the visually selected group was established in each environment, ranging from 0.7% less at Ames to 5.1% less at Martinsburg, but differences were not significant. No significant differences between selection type means were observed for root lodging, dropped ears, or root pulling resistance. Stand percentage of the visually selected group was significantly greater than that of the unselected group in two of

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Table 1. Means of S₂ line and S₁ line testcross selection types combined over all environments.

<table>
<thead>
<tr>
<th>Progeny evaluation</th>
<th>Selection type</th>
<th>Yield (Mg ha⁻¹)</th>
<th>Grain moisture (%)</th>
<th>Stalk lodging (%)</th>
<th>Root lodging (%)</th>
<th>Dropped ears (%)</th>
<th>Stand (%)</th>
<th>Root pull (kg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>S₂ lines</td>
<td>VS</td>
<td>3.11 ± 0.03</td>
<td>25.0 ± 0.09</td>
<td>15.5 ± 0.49</td>
<td>2.3 ± 0.15</td>
<td>0.6 ± 0.05</td>
<td>81.0 ± 0.28*</td>
<td>119 ± 0.7b</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>2.94 ± 0.02</td>
<td>24.3 ± 0.08</td>
<td>17.9 ± 0.18</td>
<td>2.4 ± 0.18</td>
<td>0.6 ± 0.05</td>
<td>78.4 ± 0.27</td>
<td>118 ± 0.6b</td>
</tr>
<tr>
<td>S₁ testcross</td>
<td>VS</td>
<td>8.10 ± 0.03</td>
<td>23.2 ± 0.05</td>
<td>18.8 ± 0.33</td>
<td>6.3 ± 0.22</td>
<td>0.5 ± 0.04</td>
<td>84.9 ± 0.22</td>
<td>158 ± 0.8e</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>8.10 ± 0.03</td>
<td>22.9 ± 0.05</td>
<td>20.7 ± 0.35</td>
<td>6.5 ± 0.22</td>
<td>0.5 ± 0.04</td>
<td>86.9 ± 0.18</td>
<td>159 ± 0.8e</td>
</tr>
</tbody>
</table>

*Selection type means differed at 0.05 probability level.

Table 2. Estimates of components of variance and heritabilities for S₂ lines and S₁ line testcross selection types combined from analysis of variance.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Selection type</th>
<th>S₂ estimates</th>
<th>Testcross estimates</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>βG²</td>
<td>βGE</td>
</tr>
<tr>
<td>Yield (Mg ha⁻¹)*</td>
<td>VS</td>
<td>84.0 ± 9.9</td>
<td>17.0 ± 3.0</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>83.7 ± 9.9</td>
<td>16.2 ± 2.9</td>
</tr>
<tr>
<td>Grain moisture (%)</td>
<td>VS</td>
<td>4.3 ± 0.6</td>
<td>2.3 ± 0.3</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>4.0 ± 0.6</td>
<td>1.9 ± 0.3</td>
</tr>
<tr>
<td>Stalk lodging (%)</td>
<td>VS</td>
<td>115.0 ± 17.0</td>
<td>97.0 ± 10.5</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>138.4 ± 20.3</td>
<td>122.3 ± 12.3</td>
</tr>
<tr>
<td>Root Lodging (%)</td>
<td>VS</td>
<td>23.2 ± 2.9</td>
<td>5.9 ± 1.1</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>12.2 ± 2.0</td>
<td>11.5 ± 1.5</td>
</tr>
<tr>
<td>Dropped ears (%)⁴</td>
<td>VS</td>
<td>41.8 ± 9.5</td>
<td>26.5 ± 10.9</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>15.1 ± 7.8</td>
<td>45.4 ± 12.1</td>
</tr>
<tr>
<td>Stand (%)</td>
<td>VS</td>
<td>45.5 ± 6.3</td>
<td>13.9 ± 3.6</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>111.3 ± 12.9</td>
<td>12.5 ± 3.5</td>
</tr>
<tr>
<td>Root pull (kg)</td>
<td>VS</td>
<td>255.4 ± 50.2</td>
<td>——⁵</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>349.4 ± 53.7</td>
<td>——⁵</td>
</tr>
</tbody>
</table>

*S refers to visually selected and RS to unselected entries.

⁵h² is the heritability calculated on entry means as (βG² / (β² + βGE² / e + βG² )).
⁴Mg ha⁻¹ × 10² for yield components of variance.
⁵% × 10² for dropped ears components of variance.
*Genetic variance was not considered significant; therefore, h² was not calculated.
⁶S₂ root-pull data taken in one environment only.

three environments.

S₂ Line Testcross Selection Type Means

Testcross selection type means did not differ significantly for any trait in the combined analyses (Table 1). The environment × selection type interaction in the combined analyses was not significant for any trait (data not shown). Mean grain yield of the two groups of testcrosses, averaged over all environments, was identical. No consistent trend for yield of selection types was indicated by data from individual environments. For several other traits, trends noted in S₁ testcrosses of unselected lines at Ames in 1982. Selection type means did not differ significantly in any environment for either percentage of dropped ears or root-pulling resistance, and no trend was evident for either trait. Testcrosses of visually selected lines had a smaller mean stand percentage than testcrosses of unselected lines in all environments, and in two environments (Ames 1982 and Martinsburg 1982), the differences were significant. These results are the reverse of those observed in the S₂ data.

Estimates of Genetic Variance and Gain From Selection

Genetic variance and heritability estimates calculated from the combined analyses of variance for both S₂ lines and testcrosses are presented in Table 2. Significant genetic variability was present for all the traits in the S₂ lines except for dropped ears in the unselected group. All genotype × environment interaction components for the S₂ lines also were significant but generally were smaller than their corresponding genetic variance components. The genotype × environment interaction was largest for stalk lodging and dropped ears and of least relative importance for grain yield. Genetic and genotype × environment variance component estimates for the visually...
selected S₂ lines were not significantly different from their corresponding estimates from the unselected lines for grain yield, grain moisture, and stalk lodging. Genetic variance component estimates from the two selection types also were not significantly different for S₂ line root-pulling resistance. Estimates of genetic and genotype × environment variance components for root lodging among visually selected S₂ lines were significantly greater and smaller, respectively, than the estimates among the unselected lines. The genetic variance component estimate for stand percentage from the unselected lines was more than twice as large as that from the visually selected lines. As would be expected, given the similarity of variance component estimates from the two selection types, heritability estimates for the visually and unselected S₂ lines were similar for all traits.

Genetic variance component estimates from the testcrosses were usually smaller than those from the S₂ lines because the variation due to additive effects among S₂ lines was expected to be greater than among S₁ testcrosses. Differences in estimates from the two progeny types are confounded with a year effect, however, because lines and testcrosses were grown in different years. Significant genetic variability existed for all testcross traits with the exception of dropped ears in the unselected group. All estimates of genotype × environment interaction variance were significant, with the exception of the estimates for dropped ears in both selection types and the estimate root-pulling resistance in the visually selected group. Genotype × environment interaction variance components for both grain yield and stalk lodging were large and exceeded their respective estimates of genetic variances for both traits and both selection types. For all traits except percentage of stand and dropped ears, estimates of variance from the two selection types were similar and not significantly different. Heritability values were smaller than those estimated from the S₂ lines for most traits and ranged from 0.48 for vertical root-pulling resistance in the unselected group to 0.78 for grain moisture in the visually selected group. Estimated heritabilities for each trait were similar for each selection type, with neither selection type consistently showing greater heritabilities.

Predicted genetic gains and correlated responses from single-trait selection, and predicted gain from Smith-Hazel index selection, are shown in Table 3. For each trait, gains predicted for selection among visually selected or unselected S₂ lines were similar, with neither group of entries consistently showing greater predicted gains. Similar results were obtained for selection among testcrosses of either selection type. Predicted correlated responses were variable between the selection types. Of the 20 correlated responses predicted for S₂ selection, 11 were more advantageous to the breeder in the visually selected group, seven were better in the unselected group, and two were equivalent. Of 20 correlated responses predicted for testcross selection, nine and eight were more favorable in the visually selected and unselected groups, respectively, and three were identical in both groups. Predicted gains from Smith-Hazel index selection did not show a consistent advantage for either selection type, whether consid-

### Table 3. Predicted direct gains and correlated responses for single-trait and Smith-Hazel (SH) (Hazel and Lush, 1942) index selection among S₂ lines and S₁ line testcrosses.

<table>
<thead>
<tr>
<th>Selected trait</th>
<th>Selection type</th>
<th>Yield</th>
<th>Grain moisture</th>
<th>Stalk lodging</th>
<th>Root lodging</th>
<th>Root pull</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>S₂ progeny</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yield</td>
<td>VS</td>
<td>0.47</td>
<td>0.2</td>
<td>0.1</td>
<td>0.4</td>
<td>3.1</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>0.47</td>
<td>0.3</td>
<td>-0.4</td>
<td>0.0</td>
<td>3.2</td>
</tr>
<tr>
<td>Grain moisture</td>
<td>VS</td>
<td>-0.08</td>
<td>-1.0</td>
<td>2.0</td>
<td>-0.6</td>
<td>-3.8</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>-0.13</td>
<td>-1.0</td>
<td>2.5</td>
<td>-0.3</td>
<td>-6.5</td>
</tr>
<tr>
<td>Stalk lodging</td>
<td>VS</td>
<td>0.00</td>
<td>0.4</td>
<td>-5.0</td>
<td>0.1</td>
<td>1.6</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>0.03</td>
<td>0.4</td>
<td>-5.5</td>
<td>0.1</td>
<td>1.5</td>
</tr>
<tr>
<td>Root lodging</td>
<td>VS</td>
<td>-0.08</td>
<td>-0.3</td>
<td>0.3</td>
<td>-2.4</td>
<td>5.0</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>0.00</td>
<td>-0.2</td>
<td>0.5</td>
<td>-1.5</td>
<td>5.1</td>
</tr>
<tr>
<td>Root pull</td>
<td>VS</td>
<td>0.17</td>
<td>0.5</td>
<td>-1.2</td>
<td>-1.5</td>
<td>7.9</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>0.16</td>
<td>0.8</td>
<td>-1.0</td>
<td>-1.1</td>
<td>9.5</td>
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<tr>
<td>All traits in</td>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SH index</td>
<td>VS</td>
<td>0.40</td>
<td>0.3</td>
<td>-2.1</td>
<td>-0.6</td>
<td>6.3</td>
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<tr>
<td></td>
<td>RS</td>
<td>0.41</td>
<td>0.6</td>
<td>-2.7</td>
<td>-0.5</td>
<td>6.3</td>
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<tr>
<td><strong>Testcross progeny</strong></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Yield</td>
<td>VS</td>
<td>0.48</td>
<td>0.3</td>
<td>-1.6</td>
<td>0.2</td>
<td>1.2</td>
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<tr>
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<td>RS</td>
<td>0.41</td>
<td>0.7</td>
<td>-1.8</td>
<td>0.4</td>
<td>2.6</td>
</tr>
<tr>
<td>Grain moisture</td>
<td>VS</td>
<td>-0.16</td>
<td>-1.1</td>
<td>1.9</td>
<td>-1.2</td>
<td>-0.7</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>-0.32</td>
<td>-1.2</td>
<td>1.5</td>
<td>-1.2</td>
<td>-1.3</td>
</tr>
<tr>
<td>Stalk lodging</td>
<td>VS</td>
<td>0.17</td>
<td>0.4</td>
<td>-4.1</td>
<td>-0.1</td>
<td>-1.5</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>0.16</td>
<td>0.3</td>
<td>-4.8</td>
<td>-0.4</td>
<td>0.5</td>
</tr>
<tr>
<td>Root lodging</td>
<td>VS</td>
<td>-0.03</td>
<td>-0.3</td>
<td>-0.1</td>
<td>-3.7</td>
<td>5.8</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>-0.05</td>
<td>-0.3</td>
<td>-0.7</td>
<td>-3.4</td>
<td>5.7</td>
</tr>
<tr>
<td>Root pull</td>
<td>VS</td>
<td>0.06</td>
<td>0.1</td>
<td>0.7</td>
<td>-2.1</td>
<td>10.7</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>0.12</td>
<td>0.1</td>
<td>-0.3</td>
<td>-2.1</td>
<td>9.8</td>
</tr>
<tr>
<td>All in SH index</td>
<td>VS</td>
<td>0.41</td>
<td>0.2</td>
<td>-2.4</td>
<td>-1.6</td>
<td>3.8</td>
</tr>
<tr>
<td></td>
<td>RS</td>
<td>0.33</td>
<td>0.6</td>
<td>-3.6</td>
<td>-1.5</td>
<td>5.8</td>
</tr>
</tbody>
</table>

*VS refers to visually selected and RS to randomly selected entries.
eration was for the $S_2$ lines or testcrosses for all traits.

Only slightly more than half of the 50 entries selected for superior-
ty for $S_2$ grain yield, stalk lodging, root pull, and in the $S_2$ Smith-
Hazel selection index were visual selections (Table 4). Unselected lines
outnumbered visually selected lines 33 to 17, or nearly two to one, in
the 50 $S_2$ lines with lowest grain moisture. Testcrosses of unselected
lines slightly outnumbered testcrosses of visually selected lines in the
50 testcrosses superior for all traits except grain yield (Table 4).

**DISCUSSION**

The primary purpose of visual selection in recurrent selection or
early testing schemes is to avoid using expensive yield trial resources
to test undesirable genotypes. Presumably, genotypes selected for
yield testing are superior for some trait or traits to a random sample of
genotypes from the population. In this study, the trend for average
superiority for grain yield of the visually selected $S_1$ lines over the
unselected lines was surprising. Visual evaluation of yield potential
usually has been unsuccessful for improvement of line yield, and some
selection for ear size and seed set was done when choosing the
unselected lines because of the need for adequate seed for yield trials.
Improving grain yield of inbred lines per se is not usually considered
an objective of visual selection, but if small gains can be accomplished
while selecting against undesirable agronomic types, this is obviously
desirable.

The trend (nonsignificant in this study) for visual selection to
choose lines and plants with slightly later maturity, indicated by the
slightly greater mean grain moisture of the visually selected group of
$S_1$ lines, agrees with findings of other investigators that visual
selection may result in selection of later-maturing genotypes (McKen-
The relationship between visual selection and later maturity in maize
may be related to the later-maturing genotypes staying green and
healthier-appearing in comparison with earlier genotypes and, thus,
being phenotypically more attractive to selection. Maize breeders,
however, should try to avoid selection of later-maturing plants and
lines.

Although the trend of $S_1$ selection type means indicated some
success in visual selection against stalk-lodging susceptibility, the lack
of a greater difference between the two groups of lines was disappoint-
ing. One of the objectives of many breeders using visual selection
among and within $S_1$ lines is to eliminate genotypes susceptible to
stalk lodging. Because the set of unselected lines was developed
without selection of stalk quality, selection pressure for improved
stalk-rot resistance and, consequently, stalk lodging resistance would
be expected to be greater for the visually selected lines. Stalk-rot and
stalk-lodging variability were present to allow selection opportuni-
ties, and an adequate number of lines and plants were screened to
allow selection intensities stringent enough to provide for progress
had desirable genotypes been correctly identified. Either some of the
plants selected as disease-free were escapes, or the spread of infection
resulting from the artificial inoculation technique was not well
 correlated with field resistance to stalk rot and stalk lodging.
Although visual evaluation of stalk-rot resistance by this technique
did have a desirable impact on $S_2$ line stalk-lodging resistance,
addition of other techniques to accentuate stalk-quality differences
among genotypes may be desirable. These techniques could include
planting $S_1$ lines more densely and harvesting them later in the season
to allow more natural stalk lodging before selection. In this study, $S_1$
lines were planted at a moderate density (54.9 M ha$^{-1}$) in the
breeding nursery and harvested in late September.

Lack of success of visual selection for reducing root lodging of $S_2$
lines was less surprising than for stalk lodging. Selection for root-
lodging resistance was based on natural root lodging. Expression of
root lodging in a breeding nursery is often sporadic and may reflect
environmental differences rather than genotypic differences. This,
along with poor expression of root lodging in the breeding nursery
when selections were made, probably accounts for the lack of success
of visual selection for improvement of root-lodging resistance. Addition-
ally, occurrence of root lodging in the $S_2$ yield trials was never
large enough to allow evaluation of differences between selection
types. The most plausible explanation for improvement of mean stand
percentage of the visually selected $S_2$ lines is that visual selection for
large, well-filled ears and desirable plants resulted in selection
pressure for disease-free seed from healthy maternal genotypes.

Selection among and within $S_1$ lines had little effect on line testcross
performance for most traits. The single-cross tester used may have
masked small grain yield differences between testcross selection types
that were more evident in the lines themselves. Testcross selection
type means for grain moisture and stalk lodging revealed trends for
those traits similar to those observed in the $S_2$ lines. Reduced mean
stalk lodging of the testcrosses of visually selected lines in all
environments shows that the slight improvement made in average
line stalk quality was also imparted to their testcrosses.

Selection had few consistent effects on line or testcross estimates of
genetic variances and genotype X environment variance components,
heritabilities, correlations among traits, or predicted gains. Differ-
ences between selection types were observed occasionally for the
estimates of some parameters, but they did not favor either selection
type consistently. Selection practiced evidently did not alter gene
frequency enough to change estimates of population genetic param-
teters relative to those that would be obtained from an unselected
sample.

Although selection resulted in slight improvement of $S_2$ line grain-
yield and $S_2$ and testcross stalk-lodging means, many of the individual
$S_2$ and testcross entries superior for important traits were unselected
entries. Obviously, many desirable and productive genotypes were not
chosen by visual selection. These results are in agreement with studies
conducted in self-pollinating species, which have suggested that
visual selection is better suited for discarding undesirable genotypes
rather than for selecting desirable ones (Frey, 1962; Hanson et al.,
1962; Atkins, 1964). Visual selection is known to be an effective
means of discarding these undesirable genotypes before yield-testing.
Our results indicate that it is also worthwhile for the breeder to use
visual selection techniques for stalk quality and grain yield. Rather
than attempt to select for disease-free stalks and large, well-filled ears,
as was done in this study, better results might be obtained for these
traits by planting $S_1$ lines more densely to impose greater stress,
leaving lines in the field as long as possible, and then discarding lines
with unacceptable stalk breakage and barrenness. Other studies
(Russell and Teich, 1967; El-Lakany and Russell, 1971; Russell and
Machado, 1978) have indicated positive results from visual selection
using dense plantings. Beyond discarding undesirable genotypes, the

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**Table 4. Number of visually selected entries present out of a total of 50 superior entries selected for the indicated trait.**

<table>
<thead>
<tr>
<th>Progeny type</th>
<th>Yield</th>
<th>Grain moisture</th>
<th>Stalk lodging</th>
<th>Root pull</th>
<th>Smith-Hazel index</th>
</tr>
</thead>
<tbody>
<tr>
<td>$S_2$</td>
<td>28</td>
<td>17</td>
<td>26</td>
<td>28</td>
<td>29</td>
</tr>
<tr>
<td>Testcross</td>
<td>28</td>
<td>20</td>
<td>24</td>
<td>23</td>
<td>23</td>
</tr>
</tbody>
</table>
breeder's best option seems to be to test in replicated yield trials as many remaining progenies as resources will allow. Reliance on visual selection alone can be expected to result in the loss of superior inbreds and hybrids.

REFERENCES


