

# Comparison of Gains Predicted by Several Selection Methods for Cold Tolerance Traits of Two Maize Populations<sup>1</sup>

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## ABSTRACT

Index selection was developed to help breeders practice simultaneous selection for several traits. Our objective was to compare selection differentials, expected gains, and relative index efficiencies of several indexes constructed to improve cold tolerance of two maize (*Zea mays* L.) populations. Cold tolerance traits were percentage emergence, emergence index (i.e., rate of emergence), and seedling dry weight.

Best predicted results for all traits were given by a rank summation index, a multiplicative, weight-free index, and a base index (index weights were reciprocals of phenotypic standard deviations). These indexes were not seriously affected by unequal variances among traits and combined 1) simplicity of use, 2) freedom from need to estimate genetic parameters, and 3) good selection differentials and predicted gains in each trait and in the aggregate genotype. Our results also showed that selection for dry weight/plot identified lines with excellent percentage emergence and seedling dry weight.

*Additional index words:* *Zea mays* L., Selection index, Selection advance.

THE goal of many plant breeding programs is simultaneous improvement of a crop for several traits. Consequently, plant breeders must consider a number of traits during the selection process. Smith (1936) developed index selection to cope with the complex task of improving breeding material by selecting simultaneously for several quantitative traits. Hazel (1943) later extended index selection procedures by outlining methodology to estimate genetic variances

and covariances and by defining the aggregate genotype (i.e., genetic worth of an individual) as a linear function of genetic values, each weighted by their relative economic weights. The Smith-Hazel approach is considered the optimum index when accurate estimates of variances and covariances are available (Williams, 1962). Plant breeders, however, often do not have reliable estimates of variances and covariances or the information that is needed to assign relative economic weights. Therefore, several researchers have suggested using indexes that are "weight-free" (i.e., do not use relative weighting factors) or are "parameter free" (i.e., do not use genetic variances and covariances).

Elston (1963) proposed a multiplicative index without economic weighting factors. Index values for each line are calculated by multiplying phenotypic deviations for each trait in the index (deviations from minimum or maximum values in the experiment also can be used). This index does not use estimates of phenotypic and genotypic variances and covariances. Mulamba and Mock (1978) developed a "parameter-free" index to improve density tolerance in maize (*Zea mays* L.). They constructed a rank summation index (RSI) by summing the ranks of the traits included in the index. Use of RSI also eliminates the need to assign relative economic weights, although weights can be used with RSI.

Pesek and Baker (1969) suggested that breeders usually would be better able to specify a desired gain than an economic weight for a trait. The index developed by Pesek and Baker (1969), therefore, uses desired gains to determine relative weights and maximizes expected response in proportion to the gain specified by the breeder.

Our objective was to compare selection differentials, expected gains, and relative index efficiencies of several indexes constructed to improve cold tolerance

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of two maize populations. Cold tolerance traits were percentage emergence at 30 days after planting, emergence index (a measure of rate of emergence for the 30-day period after planting), and seedling dry weight at 45 days after planting.

## MATERIALS AND METHODS

The data used to compare indexes were collected in a recurrent selection program designed to improve cold tolerance of two maize populations, BS13(SCT) and BSSS2(SCT) (Mock and Eberhart, 1972). Each cycle, 100 or 144  $S_1$ -lines from each population were grown in a simple lattice design with two replications at one location. Seeds of each  $S_1$ -line were planted in one row-plots, 1.52 m long, spaced 76.2 cm. Data were collected for percentage emergence at 30 days after planting, emergence index (a measure of rate of emergence for the 30-day period after planting), and seedling dry weight at 45 days after planting (Mock and Eberhart, 1972). A selection index was used to choose lines with highest percentage emergence and seedling dry weight and lowest emergence index values ( $k = 1.75$ ). Selected lines were recombined in a diallel to form a new population for the next cycle of selection (Mock and Bakri, 1976).

We calculated phenotypic and genotypic variances and covariances and heritabilities for cold-tolerance traits for C0 to C5 cycles of BS13(SCT) and for C0 to C4 cycles of BSSS2(SCT). These estimates are biased by genotype  $\times$  environment interactions, maternal effects, and by 1/4 of the dominance genetic variance. Genotype  $\times$  environment interactions likely are the most serious source of bias in our data. Maternal effects probably are more important for percentage emergence and emergence index than for seedling dry weight (Grogan, 1970). McConnell and Gardner (1979), however, studied reciprocal crosses of  $F_1$  hybrids and concluded that maternal effects were not important for percentage germination and seedling vigor. Grogan (1970) reviewed a number of studies suggesting that cold tolerance traits were controlled primarily by additive, multiple-gene systems. One recent study, however, used generation means analyses to show that most genetic variability for percentage germination and seedling vigor in 15 maize crosses was nonadditive (McConnell and Gardner, 1979).

Estimates of genetic parameters and  $S_1$ -line means were used to compare various selection indexes in terms of: 1) selection differentials, 2) predicted gain in each trait, and 3) predicted gain for the aggregate genotype. Selection differentials for each trait were computed by subtracting the cycle mean from the mean of the selections (10% selection intensity) and were expressed as a percentage of the appropriate single-trait differential.

The general procedures we used to compute index parameters were outlined by Lin (1978). The selection index ( $I$ ) and

aggregate genotype ( $H$ ) were defined as:  $I = \sum_{i=1}^n b_i X_i =$

$X' b$  and  $H = \sum_{i=1}^n a_i g_i = g' a$ , where  $X$  = vector of  $m$  phenotypic

values,  $b$  = vector of  $m$  index weights,  $g$  = vector of  $n$  genetic values,  $a$  = vector of relative economic weights (i.e., 1, -1, 1 for percentage emergence, emergence index, and seedling dry weight, respectively). Smith (1936) demonstrated that the correlation between  $I$  and  $H$  was highest when  $b = P^{-1}G a$ , where  $P$  and  $G$  were phenotypic and genotypic variance-covariance matrices, respectively. Gains predicted for each trait by the Smith-Hazel (SH) index were calculated as follows:  $\Delta = k G b / (b' P b)^{1/2}$ ,  $k = 1.75$ .

The desired gain index (DG) proposed by Pesek and Baker (1969) substitutes a vector of desired gains ( $h$ ) for  $\Delta$  in the predicted gain formula; hence,  $b = G^{-1} h$  for DG. We used four sets of desired gains because gains were difficult to specify for emergence index and seedling dry weight. Also, predicted gains were sensitive to the amount of gain specified. Gains for DG1 were determined as the difference between the cycle means for percentage emergence, emergence index, and seedling dry weight and 95%, 14 days, and 4 dg/plant, respectively. Likewise, goals for DG2 were set at 95%, 12 days, and 5 dg/plant. High cycle means for seedling dry weight in the C4 cycle made it necessary to set goals for DG1 of 6 and 7 dg/plant for BSSS2(SCT)C4 and BS13(SCT)C4, respectively. Similarly, DG2 goals were 7 dg/plant for BSSS2(SCT)C4 and 8 dg/plant for

BS13(SCT)C4. We also used desired gains of one genetic standard deviation for each trait (DG3) and equal to 10% of the cycle mean (DG4). Additionally, a base index (BASE) was computed by using equal index weights for each trait (Williams, 1962).

The Elston (1963) weight-free index (EWF) was calculated as  $I = (X_1 - l_1)(X_2 - l_2)(X_3 - l_3)$ .  $S_1$ -line means for each cold tolerance trait were used for  $X_1$ ,  $X_2$ , and  $X_3$ . Minimum values for each experiment were used for  $l$  values. It was not possible to calculate predicted gains for EWF because EWF is a curvilinear index. Baker (1974), however, showed that EWF (composed of two traits) could be closely approximated by the linear index,

$I = \sum_{i=1}^n X_i / \sigma_{p_i}$ , where  $\sigma_{p_i}$  = phenotypic standard deviation for the  $i^{\text{th}}$  trait. Thus, approximate predicted gains ( $\Delta$ ) for EWF can be obtained by using this linear index (BSD) with  $1/\sigma_{p_i}$  as

index weights (Baker, 1974).

All lines in each cycle were ranked from lowest to highest for each trait (emergence index values were premultiplied by -1.0), and rank summation index (RSI) (Mulamba and Mock, 1978) was calculated by summing the ranks of the three traits,

$I = \sum_{i=1}^n \text{Rank } X_i$ . Although it was not possible to obtain pre-

dicted gains for RSI, we found that RSI could be approximated by BSD because both indexes transform the data so that the variances for each trait are equal. (RSI also changes the shape of the distribution for each trait, but RSI approaches a normal distribution as  $n$  increases.) Additionally, we calculated rank correlation coefficients among several indexes because theoretical considerations suggested that correlations among RSI, BSD, and EWF should be high.

Several studies have shown that single-trait selection methods produce maximum gain for the primary trait. Therefore, single-trait indexes were computed for percentage emergence (PEX), emergence index (EIX), and seedling dry weight (SDWX). We used economic weights of 1 and 0 for primary and secondary traits, respectively. Selection differentials and predicted gains were derived for single-trait selection schemes by setting index weights equal to 1 for the primary trait and equal to 0 for other traits. Selection differentials also were obtained for dry weight/plot, which was calculated as the product of seedling dry weight, percentage emergence, and numbers of seeds planted/plot.

Predicted gains for all indexes were expressed in genetic standard deviation units, and relative index efficiencies were computed by expressing predicted gain for each trait as a percentage of the gain predicted by single-trait selection. Finally, the relative selection efficiency of each index to improve cold tolerance was evaluated by expressing gain predicted in the aggregate genotype (i.e., sum of genetic gains for three traits) by each index as a percentage of the gain predicted by the SH index.

## RESULTS

Estimates of genetic variance were largest for percentage emergence and smallest for seedling dry weight in both BS13(SCT) and BSSS2(SCT) (Table 1). However, the relative differences in genetic variance among the traits were not reflected in heritability ( $h^2$ ) values. Phenotypic and genotypic correlations among traits usually were higher in BS13(SCT) than in BSSS2(SCT) cycles, indicating that stronger genetic relationships existed among traits in BS13(SCT) than in BSSS2(SCT).

We observed large differences among selection indexes for mean and range of selection differentials (Table 2). RSI, EWF, BSD, and DG3 usually gave largest selection differentials for each trait across all cycles of BS13(SCT) and BSSS2(SCT). Ranges in Table 2 indicated that selection differentials for RSI, EWF, and BSD also were more uniform in size across all cycles than were those for other indexes. SH and

**Table 1. Estimates of genetic variance ( $\sigma_g^2$ ), heritabilities ( $h^2$ ), and phenotypic ( $r_{ph}$ ) and genotypic correlations ( $r_g$ ) for cold tolerance traits of BS13(SCT) and BSSS2(SCT) maize populations.**

Trait		BS13(SCT)†		BSSS2(SCT)‡	
		$\bar{X}$	Range	$\bar{X}$	Range
Percentage emergence	$\sigma_g^2$	127.90 ± 9.58	14.71 ± 6.11, 327.30 ± 46.55	118.13 ± 10.92	32.46 ± 14.85, 238.33 ± 37.01
	$h^2$	0.61	0.39, 0.85	0.65	0.36, 0.79
Emergence index	$\sigma_g^2$	3.52 ± 0.27	0.13 ± 0.05, 15.52 ± 2.25	1.77 ± 0.14	0.09 ± 0.08, 6.29 ± 0.94
	$h^2$	0.49	0.28, 0.84	0.47	0.21, 0.82
Seedling dry wt	$\sigma_g^2$	0.21 ± 0.02	0.03 ± 0.01, 0.66 ± 0.21	0.13 ± 0.02	0.04 ± 0.01, 0.24 ± 0.08
	$h^2$	0.61	0.41, 0.78	0.54	0.46, 0.80
Percentage emergence-emergence index	$r_{ph}$	-0.32**	-0.53**, -0.01	-0.24**	-0.59**, -0.01
	$r_g$	-0.57	-0.92, -0.19	-0.20	-0.73, 0.11
Percentage emergence-seedling dry wt	$r_{ph}$	0.41**	0.11, 0.74**	0.22**	-0.09, 0.42**
	$r_g$	0.54	0.21, 0.85	0.11	-0.42, 0.45
Emergence index-seedling dry wt	$r_{ph}$	-0.33**	-0.52**, 0.10	-0.10	-0.43**, 0.17
	$r_g$	-0.44	-0.69, -0.04	0.10	-0.36, 0.41

\*\* Significant at the 1% level of probability.

† Mean and range over six cycles of selection.

‡ Mean and range over five cycles of selection.

**Table 2. Selection differentials (10% selection intensity) for cold tolerance for various selection indexes expressed as a percentage of the single-trait selection differential.**

Index	BS13(SCT)			BSSS2(SCT)		
	Percentage emergence	Emergence index	Seedling dry wt	Percentage emergence	Emergence index	Seedling dry wt
RSI	75.7†	70.4	53.1	76.8	62.9	57.9
	53.3, 97.9	53.9, 88.5	43.8, 85.7	69.1, 84.7	44.4, 88.9	49.6, 72.3
EWF	64.9	73.2	75.3	61.8	63.6	76.5
	43.3, 97.9	53.9, 88.5	60.9, 92.8	51.8, 82.3	52.6, 81.5	58.5, 87.8
BSD	69.9	74.1	72.1	62.4	45.5	75.9
	55.4, 97.4	61.5, 89.5	52.2, 92.8	59.6, 68.1	-3.7, 68.4	61.0, 87.7
SH	93.3	57.7	39.1	91.6	14.4	17.5
	82.8, 100.4	36.4, 80.8	16.2, 59.5	87.1, 98.5	-50.0, 68.4	-22.0, 46.0
BASE	98.3	49.9	35.8	99.0	30.0	20.7
	93.9, 101.2	27.3, 80.8	4.4, 72.6	97.0, 100.0	5.3, 57.9	3.2, 52.3
DG1	-12.6	76.4	39.4	28.3	29.9	46.7
	-40.0, 61.7	54.6, 100.0	-1.0, 96.4	6.4, 44.0	-57.9, 90.0	-75.6, 100.9
DG2	-19.7	73.6	34.2	23.3	41.1	42.8
	-60.7, 56.5	53.9, 92.3	-23.8, 95.2	6.4, 45.4	-57.9, 90.0	-75.6, 90.4
DG3	59.1	63.3	76.5	53.3	40.8	52.7
	20.3, 97.4	22.2, 80.8	57.1, 91.7	26.0, 73.4	-57.9, 77.8	-61.0, 93.0
DG4	16.1	81.8	23.5	35.9	24.3	39.3
	-38.0, 58.0	73.1, 92.3	-29.1, 96.4	6.4, 59.6	-57.9, 88.9	-75.6, 86.2
PEX	94.9	57.8	35.2	92.1	11.2	4.8
	84.7, 100.4	36.4, 80.8	19.8, 59.5	87.1, 99.0	-50.0, 63.2	-46.0, 39.1
EIX	60.1	85.0	41.9	30.3	74.3	-22.8
	37.0, 87.3	75.6, 94.7	-2.2, 76.2	-36.2, 68.4	42.1, 94.7	-65.9, 41.9
SDWX	47.9	32.3	93.2	12.1	-11.9	97.4
	0.0, 87.3	0.0, 63.2	80.4, 100.0	-24.8, 39.9	-47.4, 40.0	86.3, 104.6
Percentage emergence	100.0	35.9	26.4	100.0	17.0	14.2
		9.1, 73.1	-15.2, 72.6		0.0, 37.0	-6.5, 43.1
Emergence index	26.0	100.0	27.4	23.5	100.0	13.0
	-13.3, 50.0		-3.2, 36.9	-23.0, 55.7		-4.0, 64.6
Seedling dry wt	36.7	28.2	100.0	24.3	11.3	100.0
	5.6, 72.5	0.0, 53.9		2.1, 41.9	-21.1, 50.0	
Dry wt/plot	70.2	34.0	86.1	66.6	20.8	89.6
	45.6, 97.4	11.1, 47.4	78.5, 97.3	53.9, 78.3	-10.5, 50.0	79.3, 96.9

† Mean (first line) and range (second line) over six cycles of selection of BS13(SCT) and five cycles of selection of BSSS2(SCT).

BASE gave larger selection differentials for percentage emergence than for emergence index and seedling dry weight because these indexes placed most emphasis on the trait with largest genetic variance (i.e., percentage emergence). SH occasionally gave negative selection differentials for emergence index and seedling dry weight in BSSS2(SCT). The DG indexes also produced negative selection differentials (Table 2). Across BS13(SCT) cycles, for example, average selection differentials for percentage emergence were

-12.6% for DG1 and -19.7% for DG2. Ranges showed that selection differentials for DG indexes were much less consistent across cycles of BS13(SCT) and BSSS2(SCT) than were those for RSI, EWF, BSD, and BASE.

In BS13(SCT) and BSSS2(SCT), selection differentials produced by PEX, EIX, and SDWX for their respective primary traits were smaller than were differentials for corresponding single-trait selection methods (Table 2). Single-trait indexes, however, usually pro-

**Table 3. Predicted gains (genetic standard deviations) for cold tolerance traits of BS13(SCT) and relative index efficiencies for several selection indexes (single-trait selection = 100%).**

Index	Predicted gains			Relative index efficiencies		
	Percentage emergence	Emergence index	Seedling dry wt	Percentage emergence	Emergence index	Seedling dry wt
BSD	1.17† 0.98, 1.38	-1.11 -1.29, -0.87	1.14 1.11, 1.29	87.0 76.0, 92.1	91.9 54.7, 119.4	82.6 65.4, 103.3
SH	1.39 1.16, 1.64	-0.98 -1.52, -0.62	0.84 0.54, 1.23	103.2 99.2, 105.5	81.2 38.5, 123.0	62.5 36.0, 101.7
BASE	1.38 1.13, 1.62	-0.88 -1.44, -0.52	0.80 0.38, 1.11	102.7 100.0, 103.1	72.8 32.3, 118.0	59.6 26.0, 100.0
DG1	0.19 0.05, 0.70	-0.64 -1.05, -0.14	0.57 0.03, 0.81	14.2 3.9, 43.2	53.0 11.5, 79.6	42.1 2.5, 92.3
DG2	0.14 0.04, 0.52	-0.61 -1.05, -0.10	0.59 0.04, 1.46	10.5 2.7, 32.1	50.8 8.2, 79.6	43.7 3.3, 94.2
DG3	1.02 0.66, 1.17	-1.02 -1.17, 0.66	1.02 0.66, 1.17	75.4 44.0, 91.4	84.0 54.1, 120.4	75.7 64.7, 92.6
DG4	0.33 0.02, 0.65	-0.87 -1.60, -0.29	0.23 0.04, 0.53	24.1 1.4, 50.8	71.7 23.8, 100.0	16.8 3.3, 62.3
PEX	1.40 1.16, 1.67	-0.89 -1.49, -0.32	0.79 0.37, 1.22	103.8 100.0, 105.5	73.5 19.9, 122.1	58.5 24.7, 100.8
EIX	0.93 0.33, 1.51	-1.34 -1.63, -1.11	0.75 0.03, 1.19	69.2 20.4, 100.7	110.8 101.2, 125.4	55.8 2.2, 94.2
SDWX	0.81 0.32, 1.31	-0.73 -1.11, -0.03	1.41 1.31, 1.59	60.3 24.8, 94.2	60.0 2.9, 107.5	105.1 100.7, 114.3
Percentage emergence	1.35 1.10, 1.62	-0.75 -1.37, -0.19	0.74 0.27, 1.18	100.0	61.9 11.8, 112.3	55.0 18.0, 97.5
Emergence index	0.64 0.19, 1.13	-1.21 -1.61, -0.93	0.50 0.05, 0.90	47.5 11.7, 75.3	100.0	37.4 3.2, 68.7
Seedling dry wt	0.69 0.32, 1.06	-0.57 -0.94, -0.05	1.34 1.12, 1.55	51.0 24.8, 74.1	47.3 3.1, 85.0	100.0

† Mean (first line) and range (second line) over six cycles of selection of BS13(SCT).

**Table 4. Predicted gains (genetic standard deviations) for cold tolerance traits of BSSS2(SCT) and relative index efficiencies for several indexes (single-trait selection = 100%).**

Index	Predicted gains			Relative index efficiencies		
	Percentage emergence	Emergence index	Seedling dry wt	Percentage emergence	Emergence index	Seedling dry wt
BSD	0.94† 0.24, 1.25	-0.51 -1.20, 0.10	0.59 0.11, 0.88	70.0 22.6, 86.2	43.5 -12.4, 85.7	42.8 9.2, 65.7
SH	1.40 1.14, 1.55	-0.55 -1.26, -0.01	0.12 -0.72, 0.65	104.3 98.7, 109.0	46.8 -1.2, 105.3	8.5 -60.0, 48.5
BASE	1.33 1.01, 1.53	-0.45 -1.15, 0.17	0.24 -0.39, 0.63	99.1 95.3, 102.1	38.3 -21.0, 82.1	17.4 -32.5, 44.4
DG1	0.16 0.02, 0.47	-0.33 -0.95, -0.02	0.55 0.09, 1.36	12.2 1.4, 32.4	27.7 2.5, 101.1	40.1 5.7, 103.8
DG2	0.08 0.02, 0.42	-0.38 -0.95, -0.09	0.48 0.07, 1.03	6.3 1.4, 12.4	32.2 11.1, 101.1	35.4 5.8, 78.6
DG3	0.53 0.07, 0.92	-0.53 -0.92, -0.07	0.53 0.07, 0.92	39.7 6.6, 66.4	45.2 8.6, 86.2	38.9 5.8, 70.2
DG4	0.46 0.03, 1.04	-0.49 -1.01, 0.29	0.25 0.01, 0.65	34.2 2.1, 85.3	41.7 -30.9, 72.1	18.6 0.8, 49.6
PEX	1.40 1.14, 1.57	-0.48 -1.23, 0.12	0.14 -0.76, 0.76	104.6 100.0, 109.0	40.5 -7.6, 96.5	10.4 -63.3, 44.8
EIX	0.42 -0.12, 1.26	-1.51 -2.24, -0.96	-0.71 -1.59, 0.41	31.2 -76., 86.9	128.4 101.9, 196.5	-51.6 -101.9, 30.6
SDWX	0.18 -0.60, 0.90	0.79 -0.29, 1.95	1.51 1.38, 1.83	13.4 -56.6, 51.0	-67.5 -135.8, 116.6	110.1 103.0, 119.2
Percentage emergence	1.34 1.06, 1.57	-0.37 -1.06, 0.17	0.24 -0.44, 0.73	100.0	31.1 -1.3, 75.7	17.7 -36.7, 51.4
Emergence index	0.33 -0.13, 1.02	-1.18 -1.59, -0.81	-0.39 -0.97, 0.34	24.3 -12.3, 70.3	100.0	28.4 -61.8, 25.4
Seedling dry wt	0.24 -0.50, 0.66	0.47 -0.48, 0.81	1.37 1.20, 1.57	17.8 -47.2, 42.0	-40.1 -117.5, 51.1	100.0

† Mean (first line) and range (second line) over five cycles of selection of BSSS2(SCT).

**Table 5. Means and ranges of rank correlation coefficients among various selection indexes in BSSS2(SCT) (above diagonal) and BS13(SCT) (below diagonal).\*,\*\***

Index	Index					
	RSI	EWF	BSD	SH	BASE	DG3
RSI		0.95†	0.92	0.64	0.76	0.67
		0.93, 0.99	0.69, 0.98	0.24, 0.89	0.64, 0.88	-0.46, 0.97
EWF	0.97		0.91	0.55	0.66	0.65
	0.95, 0.99		0.70, 0.97	0.10, 0.81	0.52, 0.87	-0.59, 0.97
BSD	0.99	0.98		0.58	0.70	0.63
	0.98, 0.99	0.97, 0.99		0.24, 0.87	0.64, 0.75	-0.47, 0.99
SH	0.86	0.82	0.85		0.94	0.43
	0.83, 0.89	0.72, 0.88	0.79, 0.89		0.87, 0.99	0.10, 0.71
BASE	0.81	0.75	0.80	0.98		0.53
	0.73, 0.92	0.59, 0.95	0.69, 0.94	0.97, 0.99		0.18, 0.71
DG3	0.92	0.93	0.94	0.75	0.69	
	0.75, 0.99	0.84, 0.98	0.79, 0.99	0.42, 0.92	0.35, 0.90	

\*,\*\*  $r > 0.16$  and  $0.21$  significant at 0.05 and 0.01 levels of probability, respectively. selection of BS13(SCT) and five cycles of selection of BSSS2(SCT).

† Mean (first line) and range (second line) over six cycles of

duced larger selection differentials for secondary traits in BS13(SCT) than did single-trait selection methods. In BSSS2(SCT), genetic correlations among traits were small (Table 1), and single-trait indexes did not always produce larger differentials for secondary traits. Additionally, dry weight/plot gave large selection differentials for percentage emergence and seedling dry weight; differentials for emergence index were small, but they were in the desired direction (Table 2).

Generally, larger genetic gains were predicted for BS13(SCT) (Table 3) than for BSSS2(SCT) (Table 4). Our data showed that BSD, SH, BASE, and DG3 gave large predicted gains in BS13(SCT), with moderate fluctuations in predicted gains across cycles (Table 3). Similar results were shown for BSD and DG3 in BSSS2(SCT), but SH and BASE predicted small gains for seedling dry weight in BSSS2(SCT) cycles (Table 4). Also, rank correlations between BSD and SH were higher for BS13(SCT) cycles than for BSSS2(SCT) cycles (Table 5).

In nearly all comparisons, DG3 predicted larger genetic gains in each trait than did other DG indexes (Tables 3 and 4). In BS13(SCT), for example, gains predicted by DG3 for percentage were at least three times larger than those predicted by DG1, DG2, and DG4 (Table 3). Single-trait indexes always produced larger predicted gains in primary traits than did their corresponding single-trait selection methods (Tables 3 and 4). Similar results usually were observed for secondary traits.

Rank correlations between BSD and RSI and between BSD and EWF in BS13(SCT) were 0.97\*\* or higher (Table 5), corroborating theoretical calculations that predicted gains for BSD should approximate predicted gains for RSI and EWF in BS13(SCT). In BSSS2(SCT), rank correlations between BSD and RSI and EWF were high, but the ranges of coefficients indicated that BSD would not be a reliable predictor for RSI and EWF in some BSSS2(SCT) cycles.

Relative index efficiencies (Tables 3 and 4) demonstrated that indexes differed in selection efficiency. Across all traits in BS13(SCT), for example, DG1, DG2, and DG4 were much less efficient than all other in-

**Table 6. Predicted gain in the aggregate genotype ( $\Delta H$ )† and predicted relative selection efficiencies for several methods of improving cold tolerance in BS13(SCT) and BSSS2(SCT).**

Index	BS13(SCT)‡		BSSS2(SCT)§	
	$\Delta H$	Relative selection efficiency	$\Delta H$	Relative selection efficiency
BSD	3.39	108.3	2.04	98.6
	2.74, 3.78	94.3, 125.3	0.25, 3.06	58.1, 117.8
SH	3.21	100.0	2.07	100.0
	2.65, 4.01		0.43, 2.89	
BASE	3.06	94.8	2.02	97.7
	2.18, 4.02	84.8, 104.8	0.45, 2.66	92.0, 104.7
DG1	1.40	45.8	1.04	50.3
	0.64, 3.06	11.2, 98.7	0.20, 1.96	10.6, 67.8
DG2	1.34	44.0	0.95	45.9
	0.35, 2.75	8.7, 88.7	0.19, 1.60	10.8, 55.4
DG3	3.05	98.0	1.60	77.3
	1.98, 3.51	49.4, 123.4	0.21, 2.76	21.1, 114.1
DG4	1.42	46.5	1.20	58.0
	0.59, 2.48	16.1, 80.0	0.21, 2.39	11.3, 87.7
PEX	3.07	95.3	2.02	97.6
	2.51, 4.02	89.8, 100.3	0.43, 2.85	95.7, 100.0
EIX	3.02	94.1	1.22	58.9
	1.95, 3.81	71.9, 120.4	0.09, 3.10	20.9, 134.2
SDWX	2.95	91.8	0.90	43.3
	1.92, 3.62	74.7, 107.2	-0.27, 2.25	5.5, 105.6
Percentage emergence	2.85	87.9	2.02	97.6
	2.01, 3.89	78.2, 97.0	0.45, 2.50	86.5, 104.7
Emergence index	2.35	73.8	1.11	53.6
	1.73, 2.98	59.0, 92.1	0.13, 2.33	23.1, 80.6
Seedling dry wt	2.60	82.4	1.17	56.5
	1.98, 3.03	60.6, 104.2	-0.11, 2.30	-25.6, 108.0

† Genetic standard deviation units. ‡ Mean (first line) and range (second line) for C0 through C5 cycles of selection.

§ Mean (first line) and range (second line) for C0 through C4 cycles of selection.

dexes (Table 3). In BSSS2(SCT) however, only BSD displayed good average index efficiencies for each trait. SH and BASE were uniformly efficient across BS13(SCT) cycles, but ranges in Table 4 indicated that their relative efficiencies were considerably different for each trait in BSSS2(SCT). Relative index efficien-

cies also showed that single-trait indexes and selection methods were much less efficient for secondary traits in BSSS2(SCT) than they were in BS13(SCT) (Tables 3 and 4).

All selection indexes predicted larger changes in the aggregate genotype ( $\Delta H$ ) for BS13(SCT) cycles than for BSSS2(SCT) cycles (Table 6). BSD, BASE, SH, PEX, and percentage emergence predicted greatest changes for  $\Delta H$  in both BS13(SCT) and BSSS2(SCT), and across all cycles of both populations, BSD, BASE, and PEX were nearly as efficient as SH. DG3 also predicted high  $\Delta H$  in BS13(SCT), but DG3 exhibited inconsistent results across BSSS2(SCT) cycles. DG1, DG2, and DG4 displayed lower relative selection efficiencies than all other indexes and single-trait selection methods. Additionally, single-trait indexes and single-trait selection methods displayed larger ranges for  $\Delta H$  in BSSS2(SCT) than in BS13(SCT) (Table 6).

### DISCUSSION

Mock and Eberhart (1972) proposed that selection for improved cold tolerance should involve simultaneous improvement in percentage emergence, emergence index (i.e., rate of emergence), and seedling dry weight. Later, Mock and Bakri (1976) concluded that SH placed too much emphasis on percentage emergence when economic weights were equal for all traits. These authors pointed out, however, that it was difficult to assign meaningful weights for cold-tolerance traits and suggested that the DG index procedure would be a logical alternative to SH. Our results, however, indicated that DG1, DG2, and DG4 would not be desirable indexes to use to improve cold-tolerance traits. DG3 usually gave good selection differentials and predicted gains in BS13(SCT), but, in BSSS2(SCT), DG often produced negative selection differentials and mediocre predicted gains for each trait and for the aggregate genotype. Our results also suggested that predicted gains were very sensitive to the relative amount of gain specified for each trait. The DG index performance was especially poor when relatively large gains were specified for one trait and small gains were desired for other traits. Furthermore, it was rather difficult to specify meaningful desired gains for emergence index and seedling dry weight.

Eagles and Frey (1974) recommended use of BASE to improve economic value of oats (*Avena sativa* L.) because: 1) BASE was relatively simple to use, 2) logical economic values were available for their traits, and 3) BASE gave predicted and actual gains that were equivalent to SH. We also found that BASE and SH predicted nearly identical genetic gains for each trait and for genetic worth, and that BASE and SH ranked lines similarly (Table 5). However, we encountered several problems with BASE and SH because variance for each trait were substantially different and because SH and BASE maximized gain for the aggregate genotype rather than for each trait in the index. Thus, with equal economic weights for each trait, SH and BASE placed most weight on the trait with largest genetic variance (i.e., percentage emergence), and less weight was given to emergence index and seedling dry weight. Also, SH and BASE occasionally predicted large

decreases in seedling dry weight; these decreases likely were caused by undesirable correlations in a few cycles. SH and BASE probably should not be used with equal economic weights in our selection programs because emergence index and seedling dry weight need more improvement than percentage emergence in BS13(SCT) and BSSS2(SCT) (Mock and Bakri, 1976). SH and BASE may have given better results if relatively larger economic weights had been given to emergence index and seedling dry weight. Accurate monetary values cannot be placed on cold-tolerance traits; therefore, the rationale for assigning economic weights for SH and BASE would parallel rationale used to specify desired gains (e.g., 5% emergence is equal to 1 dg of seedling dry weight compared to desired gains of 15% for percentage emergence and 3 dg for seedling dry weight).

The single-trait index, PEX, showed good average predicted gains and selection differentials for each trait in BS13(SCT), but predictions for PEX in BSSS2(SCT) were not acceptable. Use of PEX also would require estimation of genetic parameters. Selection based on percentage emergence would be less complicated than use of PEX, but single-trait selection for percentage emergence predicted small advances in other traits.

Our data suggested that breeders should consider the use of RSI, EWF, or BSD to improve composite traits, such as cold tolerance, involving individual traits without logical economic weights. These indexes also merit consideration when variances of index traits differ substantially in size. We found that RSI, EWF, and BSD combined 1) simplicity of use, 2) freedom from need to estimate genetic parameters, and 3) good selection differentials and predicted gains in each trait and in the aggregate genotype across cycles of both populations. Plant breeders often are interested in the dependability of a selection method across selection cycles, and these indexes usually gave small ranges in size of predicted gains across cycles.

Breeders also should consider using dry weight/plot to improve cold tolerance of maize populations. In our study, selection based on dry weight/plot identified lines with excellent percentage emergence and seedling dry weight. Selection differentials for seedling dry weight were larger than those for percentage emergence, even though variances for percentage emergence were much larger than those for seedling dry weight (Table 1). Selection for improved dry weight/plot probably would not result in large improvements in emergence index (Table 2). However, data used to calculate emergence index must be collected on an every-other-day basis, and selection usually is based on experiments grown only in one location. As a result, estimates of genetic parameters used to construct selection indexes are biased by genotype  $\times$  environment interactions. Several researchers have reported that errors in estimating genetic parameters can seriously affect the accuracy of an index (Brim et al., 1959; Heidhues, 1961; Williams, 1962; Harris, 1964). Also, Mock (1979) found that cold tolerance traits displayed significant genotype  $\times$  environment interactions. Selection for dry weight/plot would be a logical way to cope with genotype  $\times$  environment interactions because data can be easily collected at several locations.

Greater gains for cold tolerance in a recurrent selection program likely would be realized by basing selection on data for dry weight/plot collected at several locations rather than on an index constructed with data biased by genotype  $\times$  environment interactions.

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