not prevent occurrence of lettuce infectious yellows, but could ameliorate its effect on lettuce production.

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Comparison of Six Methods of Multiple-trait Selection for Fruit Yield and Quality Traits in Three Fresh-market Cucumber Populations

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Abstract. **Six selection indices (Smith–Hazel, desired gain, simple-weighted, rank summation, Elston's weight-free, and Baker's standard deviation) were compared to determine the effectiveness of each in identifying superior families for improving 8 fruit yield and quality traits in 3 fresh-market cucumber populations differing in genetic diversity (elite, medium-base, and wide-base). The rank summation, Elston's weight-free, and Baker's standard deviation indices were constructed with 5 traits as well as with the full 8 traits to determine whether measurement of fewer traits would suffice. The Smith–Hazel and desired gain indices were constructed using 5 traits only, since the 8-trait indices had problems with trait colinearity. The effectiveness of the indices was measured by calculating selection differentials for each index. In the elite population, the Smith–Hazel index produced negative selection differentials for all 8 traits studied. In the medium-base and wide-base populations, the Smith–Hazel index had positive differentials, but the desired gain index had negative differentials for the 8 traits studied. The simple-weighted, rank-summation, Elston's weight-free, and Baker's standard deviation indices all had positive selection differentials for the traits of interest in all 3 populations. The best index was the rank summation for 5 traits, since it had the highest overall selection differential of those measured and was easiest to calculate.**

The effectiveness of a plant breeding program depends on the ability of a breeder to select superior individuals or families for the many traits of interest. One method of identifying superior individuals and families for multiple traits is the use of selection indices. There are many such indices available to the breeder to aid in the selection process.

Elston (6) proposed a multiplicative index constructed without economic weighting of the traits, here referred to as Elston's weight-free (EWF) index. Index values are calculated by multiplication of phenotypic deviations for each trait in the index. Use of the EWF index does not require estimates of genetic

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variances and covariances. Mulamba and Mock (10) described a rank summation (RS) index, which they called a "parameter-free" index, to improve density tolerance in maize (*Zea mays* L.). Index values were calculated by summing the ranks of the traits included in the index. Like the EWF index, the RS index eliminates the need to assign relative economic weights to traits.

Pesek and Baker (11) proposed the desired gain (DG) index, in which the breeder specifies a desired gain value rather than an economic weight for each trait. This index uses desired gains to determine the relative weights of traits and maximizes expected response in proportion to the gain specified by the breeder. Baker's standard deviation (BSD) index is a linear index based on summation of the mean of each trait divided by its standard deviation (1). Wehner (15) constructed the simple-weighted index (SW), in which each trait was corrected so that its value increased as the trait improved. Next, the traits were transformed so that all traits were measured on a similar scale (e.g., 1 to 10). Each trait then was multiplied by the fraction of 1.00 that the breeder wished to assign it to indicate its importance in the aggregate genotype. The sum of the resulting values is used to calculate the genetic worth of the individual (aggregate genotype).

The Smith–Hazel (SH) index is considered the optimum index when accurate estimates of variances and covariances are available (7, 13). However, this index requires a quantitative genetic study to estimate genetic variances and covariances and the assignment of relative economic weights to each trait.

This study was undertaken to determine whether any of the less-complicated indices can be used instead of the Smith–Hazel index for improving multiple traits in cucumber, and to compare the effectiveness of the selection indices in measuring the actual value of the genotype of an individual. Indices also were evaluated using economic gain in the genetic value realized by using the different indices for selection of superior individuals.

Materials and Methods

Populations tested. Three North Carolina fresh-market (slicer) cucumber populations were used for this experiment: N.C. Wide Base Slicer (NCWBS), N.C. Medium Base Slicer (NCMBS), and N.C Elite Slicer 1(NCES1).

The NCWBS population was developed by intercrossing 1063 lines in the field in 1981 (including 720 plant introduction lines from the USDA Plant Introduction Station at Ames, Iowa, and 343 cultivars and breeding lines from seed companies and breeding programs around the world). Seeds from the long fruits (>150 mm in length) then were planted as half-sib families in 1982, with family rows alternating with rows of composite pollinator (seed of all families mixed together) for a 2nd intercross. Pollen rows were sprayed with silver nitrate, and family rows were sprayed with (2-chloroethyl) phosphonic acid (ethrel) to maximize intercrossing and minimize self- and sib-pollination (17).

The NCMBS population was developed by intercrossing 152 lines in the field in 1981 (96 cultivars from the United States, 31 cultivars from the Netherlands, 18 breeding lines from the United States and the Netherlands, and 7 plant introduction lines from The People's Republic of China). The fruit were harvested and seed from each were planted in 1982 for intercrossing of the half-sib families as described for the NCWBS population above.

The NCES1 population was developed by intercrossing the following cultivars or lines in 1981: WI 1321 and WI 1394 (C.E. Peterson, USDA, Madison, Wis.), Expt. 7 and Expt. 22 (T. Sakata & Co., Japan), Sprint 440 (Asgrow Seed), Tablegreen 72F and Poinsett 76 (H.M. Munger, Cornell Univ., Ithaca, N.Y.), and Dasher (PetoSeed Co.). The F_1 progeny of paired crosses were intercrossed in all possible combinations in the greenhouse in Spring 1982, and the F_2 progeny were intercrossed in the field in Summer 1982.

Table 1. Scoring system for evaluation of fruit quality traits in the 1984 test of families developed from 3 fresh-market cucumber populations using a North Carolina Design I analysis.

	Trait			
Score	Shape	Color	Seedcell size	Overall performance
1	Pointed, crooked	White	Extra-large	Poor
2		Yellow-white	Very large	Fair
3		Yellow-green	Large	Average
4		Light green	Medium-large	Good$^-$
5	Tapered, curved	Med.-light green	Medium	Good
6		Medium green	Medium-small	Good$^+$
7		Med.-dark green	Small	Excellent$^-$
8		Dark green	Very small	Excellent
9	Blocky, straight	Very dark green	Extra-small	Excellent$^+$

The mating design to estimate the variance components in the reference populations was a North Carolina Design I (2, 3). In this study, 72 S_0 plants were chosen at random from each population and designated as males. Each male was mated with 3 S_0 plants chosen at random and designated as females. Pollinations were made in the field and in the greenhouse with one cross for each pair of plants to produce about 100 seeds per full-sib family. Crosses were made at random, determining which plants were to be crossed before planting to avoid crossing related plants.

Field evaluation. Seeds of the 216 full-sib families produced by the mating design were planted at the Horticultural Crops Research Station near Clinton, N.C. using a nested design with full-sib families (females) nested in the half-sib families (males). The experiment was planted in 2 replications in each of 2 seasons on 11 May 1984 (spring season) and 7 Aug. 1984 (summer season).

Plots were thinned to 15 plants and maintained with standard cultural practices. The soil had been treated the previous October with the nematicide dichloropropene at 93.4 liter·ha^{-1}. Prior to bed formation in the spring, fertilizer (90N–20P–72K, kg·ha^{-1}). After bed formation and seeding, ethalfluralin was applied to the soil surface at the rate of 1.5 kg·ha^{-1}. Postplant fertilizer consisted of a sidedress application of 34 kg·ha^{-1} N just before vine tipover. Irrigation was applied as needed to supplement natural rainfall and to provide about 25 to 35 mm of water each week.

Fruit yield and quality traits were measured using once-over harvest of small plots. That method was more efficient in evaluating families for yield than single-plant or multiple-harvest systems (18). Rows were 1.5 m apart and plots were 1.5 m long—the optimum plot size for measurement of yield of fresh-market cucumbers in a once-over harvest system (20). Plots were separated at each end by alleys 1.5 m wide. Plot end borders were not used, since no significant interaction of borders with genotypes has been measured in these types of trials (16).

Plots were evaluated in the spring, 62 and 66 days after planting, and in the summer 56 and 71 days after planting for sets

Table 2. Coefficients used to construct the Smith–Hazel (SH5), simple weighted (SW8), and desired gain (DG5) indices in elite, medium-base, and wide-base fresh-market cucumber populations.[z]

	Coefficients							
					Fruit quality			
	Fruit yield							
Index	Total	Marketable[y]	Early[y]	Culls (%)	Shape[y]	Color	Seed-cell size[y]	Overall performance[y]
				Elite population				
SH5	---	0.35	1.04	---	−0.45	---	0.14	−0.96
DG5	---	0.001	0.12	---	0.16	---	0.30	−0.09
SW8	0.10	0.20	0.15	0.10	0.20	0.07	0.07	0.11
				Medium-base population				
SH5	---	−0.06	1.14	---	1.03	---	2.63	2.80
DG5	---	−0.18	−1.33	---	−0.72	---	0.77	2.93
SW8	0.10	0.20	0.15	0.10	0.20	007	0.07	0.11
				Wide-base population				
SH5	---	0.17	0.36	---	2.26	---	0.30	1.06
DG5	---	0.01	0.90	---	−8.47	---	−5.75	0.51
SW8	0.10	0.20	0.15	0.10	0.20	0.07	0.07	0.11

[z]The remaining 6 indices not listed in this table (RS5, RS8, EWF5, EWF8, BSD5, BSD8) were calculated without coefficients for each trait (as described in Materials and Methods).
[y]Indicates the traits used in calculation of the 5-trait indices (SH5, DG5, RS5, EWF5, and BSD5).

Table 3. Pearson product-moment correlations among 9 selection indices calculated for 5 or 8 fruit yield and quality traits for the NCES1, NCMBS, and NCWBS cucumber populations.[z]

	Index								
Index[y]	SH5	DG5	SW8	RS5	RS8	EWF5	EWF8	BSD5	BSD8
SH5	---	−0.81	−0.96	−0.74	−0.79	−0.37	−0.36	−0.92	−0.90
	---	−0.42	0.89	0.85	0.90	0.80	0.77	0.95	0.90
	---	−0.98	0.99	0.67	0.82	0.56	0.63	0.96	0.95
DG5	---	---	0.93	0.85	0.90	0.77	0.63	0.97	0.95
	---	---	−0.76	−0.08[NS]	−0.31	−0.05[NS]	−0.21	−0.66	−0.74
	---	---	−0.98	−0.72	−0.85	−0.69	−0.73	−0.99	−0.96
SW8	---	---	---	0.78	0.86	0.53	0.52	0.98	0.98
	---	---	---	0.65	0.79	0.52	0.59	0.99	0.99
	---	---	---	0.65	0.83	0.57	0.67	0.96	0.98
RS5	---	---	---	---	0.95	0.78	0.52	0.86	0.78
	---	---	---	---	0.94	0.74	0.64	0.73	0.65
	---	---	---	---	0.93	0.83	0.67	0.80	0.61
RS8	---	---	---	---	---	0.74	0.64	0.90	0.90
	---	---	---	---	---	0.75	0.73	0.83	0.82
	---	---	---	---	---	0.77	0.76	0.89	0.82
EWF5	---	---	---	---	---	---	0.68	0.66	0.60
	---	---	---	---	---	---	0.93	0.63	0.59
	---	---	---	---	---	---	0.86	0.76	0.58
EWF8	---	---	---	---	---	---	---	0.55	0.62
	---	---	---	---	---	---	---	0.65	0.66
	---	---	---	---	---	---	---	0.76	0.72
BSD5	---	---	---	---	---	---	---	---	0.97
	---	---	---	---	---	---	---	---	0.98
	---	---	---	---	---	---	---	---	0.93

[z]NCES1 on the top, NCMBS in the middle, and NCWBS on the bottom in each group of 3 correlations. All correlations significant at the 5% level unless labeled not significant (NS).
[y]Indices are abbreviated as follows (where the number indicates the number of traits used to calculate the index): SH5 is Smith–Hazel, DG5 is desired-gain, SW8 is simple-weighted, RS5 and RS8 are rank-summation, EWF5 and EWF8 are Elston's weight-free, and BSD5 and BSD8 are Baker's standard deviation.

1 and 2, respectively. Fruit were harvested at the green stage (about 15% of the fruit >60 mm in diameter). The stage where 9% to 20% of the fruit are oversized was recommended by Miller and Hughes (9) for optimum yield in pickling cucumbers harvested once-over, so we used a similar standard for fresh-market cucumbers.

Plots were defoliated using paraquat to make data collection at harvest stage more efficient (19). Once-over harvest yield

Table 4. Selection differentials (10% selection intensity) for 3 yield and 5 quality traits in the North Carolina Elite Slicer 1 cucumber population for various selection indices expressed as a percentage of single trait population mean.

	Selection differential							
	Fruit yield				Fruit quality			
Index[z]	Total	Market-able	Early[y]	Culls[x] (%)	Shape[w]	Color[w]	Seed-cell size[w]	Overall performance[w]
SH5	−45.8	−94.0	−53.6	−13.6	−11.3	−3.9	7.0	−11.5
DG5	25.6	25.8	114.3	−6.6	1.6	1.3	−7.0	−3.3
SW8	34.0	33.0	32.1	−4.4	4.8	2.6	−7.0	0.0
RS5	22.7	27.8	85.7	22.4	11.3	3.9	−1.8	9.8
RS8	25.6	26.3	85.7	3.1	8.1	3.9	−1.8	6.6
EWF5	18.9	20.6	135.7	5.7	6.5	1.3	−3.5	1.6
EWF8	16.0	16.0	96.4	−19.7	1.6	1.3	−3.5	−3.3
BSD5	30.3	31.4	82.1	3.5	8.1	1.3	−3.5	3.3
BSD8	31.3	27.3	64.3	−14.5	3.2	3.9	−7.0	−3.3

[z]Indices are abbreviated as follows (where the number indicates the number of traits used to calculate the index): SH5 is Smith–Hazel, DG5 is desired-gain, SW8 is simple-weighted, RS5 and RS8 are rank-summation, EWF5 and EWF8 are Elston's weight-free, and BSD5 and BSD8 are Baker's standard deviation.
[y]Early yield is the number of oversized fruits (>60 mm in diameter) per plot at harvest.
[x]Negative values represent an increase in the percentage of culls, considered undesirable.
[w]Scored 1 to 9 (1 = poor, 5 = good, 9 = excellent+; except for color, which was scored 1 = white, 5 = medium-light green, 9 = very dark green).

Table 5. Selection differentials (10% selection intensity) for 3 yield and 5 quality traits in the North Carolina Medium Base Slicer cucumber population for various selection indices expressed as a percentage of single trait population mean.

	Selection differential							
	Fruit yield				Fruit quality			
Index[z]	Total	Market-able	Early[y]	Culls[x] (%)	Shape[w]	Color[w]	Seed-cell size[w]	Overall performance[w]
SH5	30.6	32.8	116.0	9.0	8.5	0.0	0.0	8.9
DG5	−41.1	−39.7	0.0	−53.9	6.8	−5.5	−6.9	−3.6
SW8	40.6	38.5	58.7	−1.6	3.4	1.4	1.7	3.6
RS5	25.1	29.3	86.5	15.9	11.9	2.8	−5.2	12.5
RS8	28.3	29.3	94.4	4.1	8.5	1.4	−5.2	5.4
EWF5	23.7	24.7	122.2	1.2	5.1	−2.8	−6.9	1.8
EWF8	24.7	19.5	114.3	−11.8	0.0	−1.4	−1.7	0.0
BSD5	40.2	38.5	70.6	−0.8	3.4	1.4	1.7	5.4
BSD8	38.4	32.2	70.6	−11.4	0.0	1.4	3.4	1.8

[z]Indices are abbreviated as follows (where the number indicates the number of traits used to calculate the index): SH5 is Smith–Hazel, DG5 is desired-gain, SW8 is simple-weighted, RS5 and RS8 are rank-summation, EWF5 and EWF8 are Elston's weight-free, and BSD5 and BSD8 are Baker's standard deviation.
[y]Early yield is the number of oversized fruits (>60 mm in diameter) per plot at harvest.
[x]Negative values represent an increase in the percentage of culls, considered undesirable.
[w]Scored 1 to 9 (1 = poor, 5 = good, 9 = excellent+; except for color, which was scored 1 = white, 5 = medium-light green, 9 = very dark green).

was measured using fruit number rather than fruit weight or value due to its greater reliability in pickling cucumbers (5). Total fruit number and marketable fruit number (total fruit number − number of culls) were measured for each plot, and early yield was measured by counting the number of oversized fruit (>60 mm in diameter) per plot. Fruit shape, color, seedcell size, and overall performance were rated on a scale of 1 to 9 (Table 1).

Selection indices. Nine selection indices were used in this study, 4 calculated using 8 traits, and 5 calculated using 5 traits (Table 2). The Smith–Hazel Index (SH5) was calculated using 5 traits because of problems with colinearity that occurred in the 8-trait index. Thus, only the 5-trait index will be discussed in this study. SH5 was calculated as follows:

$$SH5 = \Sigma b_i x_i = x'b, \text{ and}$$

$$\text{total genetic worth } (H) = \Sigma a_i g_i = g'a, \text{ where}$$

x = vector of m phenotypic values,
b = vector of m index weights,
g = vector of n genetic values, and
a = vector of relative economic weights for each trait (12).

The correlation between SH5 and H is highest when $b = P^{-1}Ga$, where P and G are the phenotypic and genotypic variance–covariance matrices, respectively.

The desired gain index (DG5) substitutes a vector of desired gains (h) for gain from selection (Gs) into the equation for

Table 6. Selection differentials (10% selection intensity) for 3 yield and 5 quality traits in the North Carolina Wide Base Slicer cucumber population for various selection indices expressed as a percentage of single trait population mean.

	Selection differential							
	Fruit yield				Fruit quality			
Index[z]	Total	Market-able	Early[y]	Culls[x] (%)	Shape[w]	Color[w]	Seed-cell size[w]	Overall performance[w]
SH5	37.1	37.6	68.9	6.2	4.1	51.4	0.0	0.0
DG5	−45.4	−46.8	−62.2	−4.1	−8.2	51.4	4.3	−14.3
SW8	37.1	29.1	66.7	−4.9	−2.0	48.6	−2.3	−7.1
RS5	19.5	34.0	71.1	27.6	20.4	65.7	−4.5	19.0
RS8	25.8	29.8	80.0	8.7	12.2	60.0	−6.8	11.9
EWF5	21.0	31.2	115.6	19.8	12.2	51.4	−4.5	7.1
EWF8	27.3	22.7	102.2	−3.8	6.1	54.3	−4.5	2.4
BSD5	34.1	40.4	86.7	14.6	8.2	54.3	0.0	7.1
BSD8	35.1	17.7	55.6	−20.1	−4.1	51.4	2.3	−9.5

[z]Indices are abbreviated as follows (where the number indicates the number of traits used to calculate the index): SH5 is Smith–Hazel, DG5 is desired-gain, SW8 is simple-weighted, RS5 and RS8 are rank-summation, EWF5 and EWF8 are Elston's weight-free, and BSD5 and BSD8 are Baker's standard deviation.
[y]Early yield is the number of oversized fruits (>60 mm in diameter) per plot at harvest.
[x]Negative values represent an increase in the percentage of culls, considered undesirable.
[w]Scored 1 to 9 (1 = poor, 5 = good, 9 = excellent+; except for color, which was scored 1 = white, 5 = medium-light green, 9 = very dark green).

predicted gains ($Gs = bG^{-1}$); therefore, $b = G^{-1}h$. Thus, vector b will result in a selection index, $DG5 = b'P$, which will maximize the expected response to selection in proportion to the desired response (11). The desired gain index was calculated using 5 traits for the same reason as the SH5 index.

Elston's (6) weight-free index (EWF) was calculated as follows:

$$EWF = (\bar{x}_1 - d_1)(\bar{x}_2 - d_2)\ldots(\bar{x}_i - d_i), \text{ where}$$

$\bar{x}_i$ = mean of the ith trait, and
d_i = minimum value for the ith trait.

The EWF index for an individual or family where one or more of its traits are the lowest in the test ($d_i = 0$) will be zero. EWF is curvilinear, so it is not possible to calculate predicted gains. EWF was calculated using both 5 and 8 traits to determine which provided the best population improvement.

Baker's standard deviation index (BSD) was calculated using both 5 and 8 traits as follows:

$$BSD = \Sigma\, \bar{x}_i/\sigma_{Pi}, \text{ where}$$

$\bar{x}_i$ = mean of the ith trait, and σ_{Pi} = phenotypic standard deviation of the ith mean.

The rank summation index (RS) was the easiest index to calculate, since it involved no weightings but only summing the ranks of each family for the traits of interest. RS was developed with 5 and 8 traits, and was calculated as follows:

$$RS = \Sigma\, \text{Rank}\ \bar{x}_i$$

where Rank $\bar{x}_i$ is the rank of the ith mean (9).

The simple-weighted index (SW) was calculated using both 5 and 8 traits, and with 2 different weightings that favored the yield traits or the quality traits, respectively. Since there were no important differences among the 4 different ways of calculating the index, it was decided to use the 8-trait index that favored the quality traits slightly over the yield traits (SW8). SW8 was most interesting to us, since SW8 is the standard index used in the North Carolina State Univ. cucumber breeding program at present. The index was calculated as follows:

$SW8 = \Sigma\, a_i\bar{x}_i$, where
a_i = fraction of 1.00 indicating the importance of the ith trait in the aggregate genotype, and
$\bar{x}_i$ = scaled mean of the ith trait, where the means are scaled so all are on a 1 to 10 basis.

Indices based on the most important 5 out of the 8 traits (marketable and early fruit yield, fruit shape, seedcell size, and overall performance) were calculated for the RS, EWF, and BSD indices in addition to using all 8 of the traits measured in this study to determine whether the 5-trait indices could be substituted to save work in data collection. The SH and DG indices were constructed using 5 traits as mentioned before because, in the elite and medium-base populations, colinearity existed among several traits and may have adversely affected the indices (14). The coefficients used to construct the SH5, DG5, and SW8 indices are listed in Table 2.

The degree to which an index approximated the Smith–Hazel index was measured using Pearson product-moment and Spearman rank correlations for 216 families in each of the 3 populations, and by comparing selection differentials for each index in each population. Selection differentials were calculated for each trait by subtracting the mean of the top 22 families (10% selection intensity) selected by each index minus the overall mean for the population (4). This value then was converted to percentage gain over the population mean for each of the 8 traits measured. The selection differentials for the percentage of culls were multiplied by −1 so that a decrease in the mean percentage of culls would be shown as a positive value to represent the desired effect of selection.

Results and Discussion

In the elite population, the SH5 index was negatively correlated ($r = -0.36$ to -0.96) with all other indices. The other indices (DG5, SW8, RS5, RS8, EWF5, EWF8, BSD5, and

BSD8) were all positively correlated ($r > 0.52$) with each other (Table 3).

In the medium-base and wide-base populations, the SH5 index was highly correlated with all indices except the DG5 index. All indices were strongly correlated with each other, except for the DG5 index, which was negatively correlated with all indices used in this study (Table 3). The SW8, BSD5, and BSD8 indices were correlated at least 0.89 with the SH5 index in identifying superior individuals in those 2 populations. Furthermore, the remaining indices appear to approximate adequately the performance of the SH5 index in the 2 populations.

In all 3 populations, the RS5, RS8, EWF5, EWF8, SW8, BSD5, and BSD8 indices were significantly correlated with each other, indicating that any of those 7 indices can be substituted for the others with modest effect. However, there were a few exceptions (i.e., EWF5 and SW8 in all 3 populations had correlations <0.60) for some of the above indices, depending on the population and index.

Selection differentials were used to measure the effectiveness of the indices in identifying superior individuals for the traits of interest in the 3 populations studied. In the elite population, the SH5 index had negative selection differentials for all traits except seedcell size, indicating the SH5 index was not effective in selecting for improving the traits of interest in the elite population (Table 4). The DG5 index had positive differentials for all yield traits in the elite population, ranging from 25.6 to 114.3, and should be effective in improving yield in the elite population.

The SW8, RS5, RS8, EWF5, EWF8, BSD5, and BSD8 indices had positive differentials for all yield traits, ranging from 16.0 to 135.7. Therefore, those 7 indices were effective in isolating superior families for the 3 yield traits. The differentials for the fruit quality traits varied for these 7 indices, but in general the differentials were positive. Thus, SW8, RS5, RS8, EWF5, EWF8, BSD5, and BSD8 indices were effective in isolating superior families for all traits studied in the elite population.

In the medium-base population, the SH5 index had positive selection differentials for all traits except color and seedcell size, which were 0 (Table 5). The DG5 index had negative selection differentials for all traits except for fruit shape; therefore, it was ineffective in isolating superior individuals for fruit quality. The remaining indices had positive differentials for all the yield traits. Their selection differentials for some quality traits were negative, varying among the indices. Based on selection differentials, the SW8, RS5, RS8, EWF5, EWF8, BSD5, and BSD8 indices should be effective in isolating superior families for all traits studied in the medium-base population.

In the wide-base population, all indices had positive differentials for most of the 8 traits evaluated, except for the DG5 index. The DG5 index had negative differentials for 5 (marketable and early yield, percentage of culls, shape, and overall performance) out of the 8 traits (Table 6). All indices except SH5, DG5, and BSD5 had negative differentials for seedcell size. However, all indices except DG5 were effective in selecting superior families from the wide-base population.

Based on the selection differentials, it appears that RS5, EWF5, and BSD5 were the most effective selection indices for isolating superior families in the 3 populations of interest. The SH5 index performed well in the medium-base and wide-base populations, but had negative selection differentials in the elite population. The problems encountered with the SH5 index in the elite population may be due to poor estimates of genetic and phenotypic variances and covariances used to construct the index. Poor estimates of these parameters adversely affect the reliability of the Smith–Hazel index, as was shown by Lin (8), Williams (21), and Young (22). However, that explanation does not seem likely in this case, because estimates were satisfactory in the medium-base and wide-base populations. Genotypic and phenotypic variances for these populations were reported in Strefeler and Wehner (13).

Another possible cause of poor performance for the SH5 index in the elite population may be the existence of colinearity among traits used in this study. Colinearity among traits may result in b-values that are not representative of the relative importance of each trait (E. Eisen, personal communication). Thus, the effectiveness of the index to identify superior individuals may be reduced. Furthermore, the index actually may function to lower the means of the traits after selection. Although traits were eliminated during calculation of the SH5 index in an attempt to alleviate this problem, some traits exhibiting colinearity (early yield and shape, seedcell size and shape) were still present in the modified index for the elite population because we considered it essential to select for those traits.

The problems encountered in this study in the construction of the SH5 index demonstrated the problems associated with developing this index for use as a method of selecting superior individuals and families. These problems also indicate the need for a multiple-trait selection index that is easier to develop and use without sacrificing the ability of that index to select superior individuals or families from a population.

The best indices of those measured were the RS5, RS8, and BSD5, since they had the highest overall selection differentials. However, all of the indices except the DG5 and BSD8 performed very well in this study and any of those would be effective for use in breeding programs. The superior performance of the 5-trait indices indicate that improvement of the 8 traits studied can be achieved by measuring fewer traits. Thus, a savings of time and effort for population improvement of fruit yield and fruit quality would result.

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In Vitro Production of Jojoba Liquid Wax by Zygotic and Somatic Embryos

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Abstract. **Zygotic embryos of jojoba (*Simmondsia chinensis* Link) accumulated liquid wax in vivo from 10 mg dry weight to maturity (800 mg dry weight) with relatively constant proportions of 36 to 46 carbon length wax esters. Immature zygotic embryos (initial dry weight, 1.6 ± 0.5 mg SE), cultured on a semisolid basal medium supplemented with 15% sucrose for 10 weeks, reached 64.7 ± 20.5 mg SE dry weight and produced 50% wax, an efficiency twice that of in vivo zygotic embryos of the same size. Somatic embryos (initial dry weight, 0.3 mg) cultured on semisolid basal media containing 9% sucrose for 12 weeks averaged 92.5 ± 32.7 mg SE dry weight with 20% wax, 74% of the efficiency of zygotic embryos in vivo of the same size. The proportion of wax esters accumulated by zygotic and somatic embryos produced in vitro was similar to that of in vivo-produced wax.**

Seed metabolites of cacao can be produced in vitro by proliferation and development of somatic embryos (2), but because these embryos did not reach full maturity, lipid quality was not equivalent to commercial cocoa butter (3).

Rost et al. (11) first attempted to produce jojoba liquid wax in vitro by culturing callus derived from mature seed. The percentage of wax decreased from 55% to 2% as the dry weight of the callus increased. Studies by Lee and Thomas (5) and Wang and Janick (14) have shown that zygotic embryos of jojoba cultured on semisolid media produced liquid wax in response to high sucrose concentrations, with maximum production per gram dry weight at 20% to 21% sucrose. We have reported (13) the proliferation of somatic embryos of jojoba from embryogenic-competent callus incubated on a basal medium containing 4.5 μM (2,4-dichlorophenoxy)acetic acid (2,4-D) with development proceeding when 2,4-D is withdrawn. This study concerns the pattern of in vivo and in vitro accumulation of storage lipids (liquid wax) in zygotic and somatic embryos of jojoba.

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Materials and Methods

Culture media

Basal medium consisted of the following substances: inorganic salts according to Murashige and Skoog (6) and 0.5 mM-myo-inositol, 4 μM nicotinic acid, 2.4 μM pyridoxine–HCl, 0.3 μM thiamine–HCl, 26.6 μM glycine and 1 g·liter^{-1} casein hydrolysate. Media were supplemented with various concentrations of sucrose as indicated. Agar-gelled medium (8 g·liter^{-1}, Difco Bacto-agar) was poured into petri dishes (60 × 15 mm, Falcon), 12.5 ml per dish, after autoclaving at 121°C and 1.1 kg·cm^{-2} (15 psi) for 15 min. Liquid medium was distributed into culture tubes (25 × 150 mm, 10 ml media/tube) and covered with plastic closure (Kaputs, Bellco) before autoclaving.

Culture environment

Cultures were maintained at a constant temperature of 25°C with low intensity illumination (45 μmol·s^{-1}·m^{-2} photosynthetic active radiation) from cool-white fluorescent lamps for 16 hr daily. Liquid cultures were maintained on a rotary apparatus (Rollodrum, New Brunswick) at 15 rpm.

Plant material

Zygotic embryos in vivo. Jojoba capsules from native stands in Arizona were received by mail from 20 Apr. to 10 July 1983.