SELECTION INDICES FOR YIELD AND QUALITY TRAITS IN SWEET CORN

MUHAMMAD JAWAD ASGHAR[1] AND SYED SADAQAT MEHDI[2]

[1]Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad, Pakistan
[2]Virtual University, Lahore, Pakistan.

Abstract

The efficiency of three selection indices, viz., Smith-Hazel index (SHI), Desired gain index (DGI) and Base Index (BI) was compared for the improvement of an open pollinated sweet corn (*Zea mays* L. *Saccharata*) population. The data of genetic studies on various yield and quality traits among S_1 families were used to construct these selection indices. Smith-Hazel index was found to be the most efficient in improving the aggregate genotype of yield traits for most of the selection strategies. Base index proved to be more efficient as compared to Smith-Hazel index in the improvement of aggregate genotype for five out of six selection strategies of quality traits. Both smith-hazel and Base indices were found useful for the improvement of sweetness and sweet flavour for all the selection strategies. When selection was confined to eight yield and four quality traits simultaneously, Base index proved to be more efficient as compared to Smith-Hazel index and desired gain index in improving the aggregate genotype for almost all the selection strategies.

Introduction

Sweet corn (*Zea mays* L. *Saccharata*) is one of the most popular vegetable grown in the US. It currently ranks second in farm value for processing and fourth for fresh market among vegetable crops. Sweet corn is used as fancy maize and each cob gives roughly 22% of the daily requirement for Vitamins A and C, Magnesium and Iron. In Pakistan, little research work has been conducted on sweet corn. Sweet corn yield has been certainly increased through different recurrent selection schemes (Ali & Saleh, 2003; Tanveer, 1989; Younis, 1989).

Population improvement of a crop is the primary objective of a plant-breeding program. However, the progress in any breeding program depends primarily upon the genetic diversity and the effectiveness of the selection procedure involved. Studies have been previously reported on genetic diversity among genotypes (Cheema *et al*., 2004), interrelationships among various plant traits (Arshad *et al*., 2004) and selection criteria in segregating populations (Sarwat *et al*., 2004). Besides other selection method used for the population improvement, selection indices are considered as an aid to the breeder for simultaneous selection of multiple traits (Smith, 1936). This tool can help the breeder in spotting the desirable genotype/family of a crop species in a population improvement program. Smith (1936) and Hazel (1943) illustrated the procedure for constructing a selection index that gives maximum advance from selection. Selection indices provide useful information about which traits to be combined (Banziger & Lafitfe, 1997). Selection indices have been an effective selection criterion to increase grain yield in corn (Modarresi *et al*., 2004). More recently, Rabiei *et al*., (2004) have studied the nature of relationships between yield traits and rice grain shape for developing selection indices in rice breeding programs and reported that selection indices would be an effective selection criterion to improve rice grain shape. Many other Researchers have used selection indices as an effective selection criterion in their breeding programs on different crops (Vikram & Roy, 2003; Xie *et al*., 1998 and Dolan *et al*., 1996). However, the conditions

determining the usefulness of an appropriate selection index may vary with individual plant breeder.

The present study was conducted on an open pollinated sweet corn population with the objectives, a) to obtain the estimates of components of variance and covariance for various yield and quality traits and thus calculate the predicted gains from S_1 family section for these traits, and b) to construct three different types of selection indices among S_1 families in order to compare their relative efficiency.

Materials and Methods

The experimental material consisted of one hundred S_1 families which were derived from an open-pollinated population of sweet corn by selfing the S_0 plants at random. These S_1 families were planted in a modified randomized complete block design with three replications where each block contained 25 S_1 families. The experimental unit consisted of a single row plot of 3.5 m length with plants spaced 30 cm apart and having 60 cm distance between rows. Yield traits measured on plot mean basis were days to silking, plant height (cm), cob length (cm), cob diameter (cm), number of grain rows per cob, number of grains per row, 100-grain weight (g) and grain yield per plant (g). Two random plants from each plot were selected for organo-leptic evaluation of quality traits (Table 1) described by Marshall (1987) like seed quality, pericarp tenderness, sweetness, sweet flavour, shank softness and shank wetness. Separate analyses of variance and covariance of all plant traits and pairs of traits were carried out by following the procedures described by Steel & Torrie (1984) (Table 2).

The genetic components of variance and covariance were calculated using expected mean squares as outlined by Robinson *et al.*, (1951) by dividing S_1 families mean squares and S_1 families mean cross products with number of replications, respectively. The genetic and phenotypic covariances were calculated among yield and quality traits separately and also among all plant traits simultaneously.

Estimates of broad-sense heritability on S_1 family mean basis were calculated for each trait using variance components as follows:

$$h^2_{(BS)} = \hat{\sigma}^2_g / \hat{\sigma}^2_p$$

where

$$h^2_{(BS)} = \text{the broad-sense heritability in fraction,}$$

Significance of broad-sense heritability was tested by calculating its respective standard error (S.E of h^2) on plot mean basis outlined by Lothrop *et al.*, (1985) as under:

$$\text{S.E of } h^2 = \text{S.E } (\hat{\sigma}^2_g) / \hat{\sigma}^2_p$$

$$\text{S.E } (\hat{\sigma}^2 g) = \sqrt{\frac{2}{C^2} \left\{ \sum \frac{MSi^2}{dfi + 2} \right\}}$$

where

$$\begin{aligned}
C &= \text{the coefficient of components in the expected mean} \\
&\quad \text{squares,} \\
MSi &= \text{mean square for the ith trait and} \\
dfi &= \text{degrees of freedom for the ith trait.}
\end{aligned}$$

Table 1. Relative scores (statistical scale) for seven indicated quality traits of 100 S₁ families of Sweet corn.

Character	Score		
	0	**1**	**2**
Seed Quality	Poor	Normal	Good
Pericarp tenderness	Tender	Medium	Tough
Sweetness	Low	Medium	Sugary
Sweet Flavour	No	Little	High
Shank softness	Soft	Normal	Tougher
Shank wetness	Dry	Normal	Wetter

Table 2. Format of analysis of variance and covariance of S₁ families with 'b' blocks, 'r' Replicates per block and fᵢ S₁ families in the ith block.

Sources of variation	Degrees of freedom	Mean square	Expected mean square	Expected mean cross product
Blocks	$(b-1)$			
Replicates / Blocks	$b(r-1)$			
Families / Blocks	$b\left(\sum f_i -1\right)$	MS_2	$\sigma^2 e + r\sigma^2 g$	$\sigma e + r\,\sigma g$
Error	$(r-1)\,b(\sum f_i -1)$	MS_1	$\sigma^2 e$	σe
Total	$(r\,b\sum f_i -1)$			

Where

$\sigma^2 g$ = the genetic variance, $\sigma^2 e$ = the environmental variance, σg = the genetic covariance, σe = the environmental variance.

Construction of selection indices:

The estimates of genotypic and phenotypic variance and heritability for each trait and covariance for each pair of traits obtained among S₁ families of sweet corn population were used for construction of three selection indices viz., Smith-Hazel index (SHI) (Smith, 1936 & Hazel, 1943), Desired gain index (DGI) (Pesek & Bakar, 1969) and Base index (BSI). The efficiency of these three indices for improving sweet corn population by S₁ family selection was compared based on expected gain in the individual primary trait and the aggregate genotype for yield and quality traits.

Six yield traits viz., cob length (CLEN), cob diameter (CDIA), number of grain rows per cob (RCOB), number of grains per row (GROW), 100-grain weight (GRWT) and grain yield per plant (GYLD) were included as primary traits in 8 selection strategies. Whereas days to silking (DSLK) and plant height (PLHT) were considered as secondary traits. The secondary traits were given zero economic values or desired grains for their improvement, because no genetic improvement was needed for these traits in sweet corn population under study. The vector of relative economic weights and desired gains for primary and secondary traits are presented in Table 3. Desired gains of 10 percent were set for CLEN, CDIA, RCOB, GROW and GRWT; and 20 percent for GYLD (Table 3).

Similarly, four quality traits, viz., seed quality (SQLT), pericarp tenderness (PTEN), sweetness (SWTN) and sweet flavor (SWTF) were included as primary traits in six selection strategies. Whereas shank softness (SHKS) and shank wetness (SHKW) were considered as secondary traits. Desired gains of 10% were set for SQLT, PTEN and SWTF; and 20% for SWTN. Zero economic values or desired gains were set for secondary traits (SHKS and SHKW) (Table 3).

Six yield traits and four quality traits mentioned were included simultaneously as primary traits in eight selection strategies, whereas days to silking (DSLK) and plant height (PLHT) were considered as secondary traits and were given zero economic values or desired gains. The vector of relative economic values and desired gains for primary and secondary traits remained same (Table 3).

Choice of different selection strategies is necessary to pick the index having fewer traits with better gains, because inclusion of many traits in the index results in smaller gains of each individual trait. Therefore, a series of indices was constructed for sweet corn population to maximize the genetic gain (Table 4).

Genotypic and phenotypic variance-covariance matrices were developed to aid calculation of index coefficients (Table 6). Estimated indices were calculated by the method described by Smith (1936). The index coefficients were estimated from the following relationship:

$$B \quad = \quad V_P^{-1}. \, V_g . \, a$$

where,

$$
\begin{aligned}
b \quad &= \quad \text{the the vector of bi 's.} \\
V_P^{-1} \quad &= \quad \text{the inverse of phenotypic variance-covariance matrix, and} \\
V_g \quad &= \quad \text{genotypic variance-covariance matrix, and} \\
a \quad &= \quad \text{the vector of relative economic values}
\end{aligned}
$$

Desired gain indices were computed by the method given by Pesek & Baker (1969). The weighing factors (bi's) were obtained as:

$$b \quad = \quad V_g^{-1} . \, h$$

where,

$$
\begin{aligned}
b \quad &= \quad \text{the the vector of bi 's.} \\
V_g^{-1} \quad &= \quad \text{the inverse of genotypic variance-covariance matrix, and} \\
h \quad &= \quad \text{the vector of desired gains.}
\end{aligned}
$$

Base index proposed by Williams (1962) was constructed for different selection strategies to improve plant traits of sweet corn population. Base index uses the economic weight as index weight.

Expected gain in each trait by index selection was calculated by using the formula given by Finney (1962) as:

$$\Delta gi \, b \quad = \quad K \, (GB)i \, /\sqrt{b' \, P \, b}$$

where,

$$
\begin{aligned}
\Delta gi \quad &= \quad \text{the genetic gain in the ith trait,} \\
K \quad &= \quad \text{the standardized selection differential at 10\% selection} \\
& \qquad \text{intensity (1.755) ,} \\
G \quad &= \quad \text{the genotypic variance-covariance matrix,} \\
b \quad &= \quad \text{the vector of index coefficients,} \\
(GB) \, I \quad &= \quad \textit{i}\text{th element of the column vector GB,} \\
b' \quad &= \quad \text{the transpose of b, and} \\
p \quad &= \quad \text{the phenotypic variance-covariance matrix.}
\end{aligned}
$$

Table 4. List of indices (selection strategies) constructed to maximize gain in sweet corn population for various yield and quality traits and the traits included in those indices.

Index #	Yield traits
IY_1*	DSLK, PLHT, CLEN, CDIA, RCOB, GROW, GRWT, GYLD.
IY_2	DSLK, PLHT, CLEN, CDIA, RCOB, GRWT, GYLD.
IY_3	DSLK, PLHT, CLEN, CDIA, GROW, GRWT, GYLD.
IY_4	DSLK, PLHT, CLEN, RCOB, GROW, GRWT, GYLD.
IY_5	DSLK, PLHT, CDIA, RCOB, GROW, GRWT, GYLD.
IY_6	DSLK, PLHT, CLEN, CDIA, GRWT, GYLD.
IY_7	DSLK, PLHT, RCOB, GROW, GRWT, GYLD.
IY_8	DSLK, PLHT, GRWT, GYLD.
	Quality traits
$IQ_1§$	SHKS, SHKW, SQLT, PTEN, SWTF, SWTN.
IQ_2	SHKS, SHKW, SQLT, PTEN, SWTN.
IQ_3	SHKS, SHKW, SQLT, SWTF, SWTN.
IQ_4	SHKS, SHKW, PTEN, SWTF, SWTN.
IQ_5	SHKS, SHKW, PTEN, SWTN.
IQ_6	SHKS, SHKW, SWTF, SWTN.
	Yield and Quality traits simultaneously
$IYQ_1ξ$	DSLK, PLHT, CLEN, CDIA, RCOB, GROW, GRWT, GYLD, SQLT, PTEN, SWTF, SWTN.
IYQ_2	DSLK, PLHT, RCOB, GROW, GRWT, GYLD, SQLT, PTEN, SWTF, SWTN.
IYQ_3	DSLK, PLHT, GROW, GRWT, GYLD, SQLT, PTEN, SWTF, SWTN.
IYQ_4	DSLK, PLHT, GRWT, GYLD, SQLT, PTEN, SWTF, SWTN.
IYQ_5	DSLK, PLHT, GRWT, GYLD, SQLT, SWTF, SWTN.
IYQ_6	DSLK, PLHT, GRWT, GYLD, PTEN, SWTF, SWTN.
IYQ_7	DSLK, PLHT, GRWT, GYLD, SQLT, SWTN.
IYQ_8	DSLK, PLHT, GRWT, GYLD, SWTN.

(* = Index of yield traits, § = Index of Quality traits and ξ = Index of Yield and Quality traits simultaneously)

The aggregate genotype was equal to the sum of predicted responses in traits included in selection strategy. The relative efficiency of selection strategies were expressed by their genotypic values in terms of their genetic standard deviations.

Results and Discussion

Genetic parameters:

The genotypic and environmental variances for different yield and quality traits among S_1 families of sweet corn along with their heritabilities are given in Table 5. In general, the estimates of all the components of variance were larger for yield traits as compared to quality traits. The estimates of genotypic variance were smaller than their respective phenotypic variance for all plant traits evaluated in sweet corn population. Likewise the estimates of genetic variance were greater than the estimates of environmental variances for all the yield traits except grain yield per plant which showed smaller genetic variance. In contrast the estimates of genetic variance for all the quality traits were smaller than the environmental variance. However, shank softness resulted in greater estimate of genetic variance as compared to its respective environmental variance estimate.

The estimates of genetic variance were significant for all the yield and quality traits as their absolute magnitudes exceeded twice their respective standard errors. These statistics revealed that significant genetic variability existed among S_1 families of sweet corn population. These results are in agreement with the findings of Walters *et al*., (1991).

Table 5. Estimates of genetic variance, environmental variance and broad-sense heritability for yield and quality traits among S_1 families of sweet corn population.

Traits #	$\sigma^2 g$	$\sigma^2 e$	h^2
DSLK	$6.5309^+ \pm 1.6804$	4.7395	$0.5795^+ \pm 0.1491$
PLHT	$88.2668^+ \pm 19.2048$	42.6967	$0.6740^+ \pm 0.1466$
CLEN	$1.8511^+ \pm 0.3718$	0.7033	$0.7247^+ \pm 0.1456$
CDIA	$0.3041^+ \pm 0.0748$	0.2001	$0.6033^+ \pm 0.1484$
RCOB	$1.1985^+ \pm 0.2051$	0.2269	$0.8402^+ \pm 0.1438$
GROW	$9.123^+1 \pm 2.4163$	4.7053	$0.6597^+ \pm 0.1747$
GRWT	$2.7280^+ \pm 0.5100$	0.7969	$0.7739^+ \pm 0.1447$
GYLD	$17.9698^+ \pm 7.3738$	29.2948	$0.3802^+ \pm 0.1561$
SQLT	$0.0908^+ \pm 0.0308$	0.1104	$0.4515^+ \pm 0.1532$
PTEN	$0.0419^+ \pm 0.0215$	0.0931	$0.3104^+ \pm 0.0531$
SWTN	$0.0456^+ \pm 0.0193$	0.0777	$0.3698^+ \pm 0.1565$
SWTF	$0.0354^+ \pm 0.0173$	0.0739	$0.3239^+ \pm 0.1583$
SHKS	$0.1103^+ \pm 0.0305$	0.0930	$0.5425^+ \pm 0.1500$
SHKW	$0.0894^+ \pm 0.0276$	0.0925	$0.4915^+ \pm 0.1517$

$\pm$ = Standard error value.

$^+$ = The estimate of genetic variance / broad-sense heritability differs significantly from zero as its absolute magnitude exceeded twice its respective standard error.

The estimates of broad sense heritability for all plant traits recorded form S_1 families of sweet corn population were found significant (Table 5) as their absolute value exceeded twice their respective standard errors. This indicated the presence of heritable genetic variation among S_1 families for various yield and quality traits in sweet corn population. The estimates of broad-sense heritability for yield traits ranged from 0.38 to 0.84 (for grain yield per plant and number of grain rows per cob, respectively). Similarly for quality traits, the estimates of broad-sense heritability ranged from 0.31 to 0.54 (for pericarp tenderness and shank softness, respectively).

All the yield traits with high estimates of genetic variance and low estimates of environmental variance resulted in large significant heritabilities except grain yield in which case, low estimate of genetic variance and high estimate of environmental variance resulted in lowest value for heritability ($h^2 = 0.38$). Similar estimates of heritability for grain yield ($h^2 = 0.33$) were also reported by Ayala Osuna & Churata (1995). Low estimate of heritability for grain yield suggested that direct selection for this trait in the proceeding generations would not be effective. Higher estimates of broad-sense heritability among yield traits were observed for cob length ($h^2 = 0.72$) and 100-grain weight ($h^2 = 0.77$). Number of grain rows per cob was the most heritable trait with the value of 0.84 among yield traits.

Among the quality traits, low estimates of genetic variance and high estimates of environmental variance for seed quality, pericarp tenderness, sweetness, sweet flavour and shank wetness resulted in low but significant heritabilities. In contrast, high estimate of genetic variance and low estimate of environmental variance for shank softness resulted in largest estimate of heritability ($h^2 = 0.54$). Shank wetness was ranked second highest with the value of 0.49 among quality traits. Where as seed quality exhibited low value of heritability ($h^2 = 0.45$). However, lowest estimates of broad sense heritability were noted for pericarp tenderness ($h^2 = 0.31$), sweetness ($h^2 = 0.37$) and sweet flavour ($h^2 = 0.32$). Lower heritability estimates for sensory traits (sweetness, sweet flavour and pericarp tenderness) revealed that further improvement for these traits through simple selection schemes would be ineffective. Since the inheritance of sweetness and pericarp

tenderness is controlled by sugary (su) and Waxy (wx) genes, when present in recessive condition, respectively (Andrew *et al.*, 1944). Therefore, the effect of these genes would be more pronounced in homozygous condition.

However, from the results presented in Table 5, it can be concluded that most of the yield and quality traits are better heritable which implies that the proportion of total variation due to average effect of genes for these traits was of a reasonable magnitude; hence this would play a pivotal role in a selection scheme.

Selection indices: Genotype and phenotypic variance covariance matrices used in the calculation of selection indices are given in Table 6.

Yield traits: In general, out of three selection indices, Smith-Hazel index was the most efficient in improving the aggregate genotype of yield traits for all the selection strategies (Table 7). These results are in agreement with the findings of Wells & Kofoid (1986). Smith-Hazel index was superior to base index in the improvement of predicted gain in the aggregate genotype in all the selection strategies except IY_5 and IY_7, where in the base index was superior to both Smith-Hazel and desired gain index. Crosbie (1980) and Dolan (1996) also predicted similar responses for Smith-Hazel and base index. The aggregate genotype was negative for the selection strategy IY_5 using desired gain index and it was due to cob length which showed negative estimate of predicted gain which is undesirable. Therefore, selection for the traits included in this selection strategy is not feasible.

When selection was for all eight yield traits simultaneously (IY_1), predicted gains were greatest using Smith-Hazel index. This is evident in the aggregate genotype (Table 7). However, desired gain index was efficient for the improvement of number of grain rows per cob, but the aggregate genotype was low. Selection for the eight yield traits at a time is not justifiable.

When selection was focused to six yield traits simultaneously (IY_6 and IY_7), the aggregate genotype was greatest using Smith-Hazel index for IY_6, whereas the predicted gains were maximum using base index for IY_7. Smith-Hazel index predicted similar responses for yield traits in IY_7, but aggregate genotype was slightly reduced. Smith-Hazel index and base index were useful in improving grain yield for IY_6 and IY_7. The desired gain index had maximum predicted gain for grain yield but the aggregate genotype was low. However, the same index with IY_8 selection strategy involving selection of four traits simultaneously was the most efficient in improving yield traits and it maximized gain in aggregate genotype. Mock & Bakri (1976) also suggested the use of desired gain index because they observed difficulty in assigning meaningful economic values to the traits selected.

Quality traits: In general, base index proved to be more efficient as compared to Smith-Hazel and desired gain indices in the improvement of aggregate genotype in almost all selection strategies of quality traits in sweet corn population (Table 8). The exception to this generalization was the selection strategy IQ_5 where in, Smith-Hazel index was more efficient than base index. This could be due to the fact that selection was confined to only pericarp tenderness and sweetness (Table 8).

Both Smith-Hazel index and base index were found useful for the improvement of sweetness and sweet flavour for all the selection strategies. But undesirable correlated responses were predicted, for pericarp tenderness in all six selection strategies. However, desired gain index was useful for improving pericarp tenderness in IQ_1, IQ_2, IQ_4 and IQ_5. Smith-Hazel index proved to be the most efficient in improving seed quality with selection strategy IQ_2 than any other index.

When selection was confined to four traits simultaneously (IQ_5 and IQ_6) the predicted gains for quality traits were greatest using Smith-Hazel index in IQ_5 and base index in IQ_6. Both these indices maximized predicted gains for sweet flavour in IQ_6 and for sweetness in IQ_5 and IQ_6. But negative undesirable correlated responses were predicted for pericarp tenderness in both the selection strategies. However, Smith-Hazel and base indices were useful in improving seed quality with the selection strategy IQ_6 and desired gain index was useful for improving pericarp tenderness in IQ_5. Base index as stated by Suwantaradom *et al.* (1975), in which relative economic weight (values) are used *per se* as index coefficients (b-values) was 95 and 97 percent as efficient as Smith-Hazel index. They suggested that S_1 family testing would be preferable as compared to S_2 testing for increased predicted gains.

Yield and quality traits simultaneously: Out of three selection indices, base index proved to be most efficient in the improvement of aggregate genotype for almost all the selection strategies (Table 9). However, exceptions to this generalization were the selection strategies IYQ_1, IYQ3 and IYQ_7 where in Smith-Hazel index was the most efficient in improving the aggregate genotype. Both Smith-Hazel and base indices were useful in improving the predicted gains for cob length, number of grains per row, grain yield and seed quality in all the selection strategies. These indices were also useful for improving sweetness and sweet flavour in IYQ_1, IYQ_2, IYQ_3 and IYQ_6. Desired gain index had maximum gains for sweetness in IYQ_5, IYQ_7 and IYQ_8 but the aggregate genotype was low. These results indicated that both Smith-Hazel and base indices were superior to desired gain index in improving the aggregate genotype and the predicted gains for the individual traits. Present findings are in agreement with those of Chisi *et al.*, (1996), Dolan *et al.*, (1996), Eta-Ndu & Openshaw (1992).

When selection was for all the twelve traits simultaneously (IYQ_1), predicted gains were greatest using Smith-Hazel index. This is evident in the aggregate genotype (Table 9). Selection for all the twelve traits at a time is not justifiable since it would require a lot of efforts and time which breeder always lacks. A selection index with many traits is likely to have low heritability (Bernardo & Yu, 2007). Moreover, the predicted gains by using Smith-Hazel index and base index were negative and undesirable for number of grain rows per cob, 100-grain weight and pericarp tenderness for IYQ_1 and IYQ_2 selection strategies. However, desired gain index predicted reasonable responses for all the traits in same selection strategies. This index was most efficient for the improvement of number of grain rows per cob, 100-grain weight and pericarp tenderness, but the aggregate genotype was low.

When selection was focused to seven traits simultaneously (IYQ_5), aggregate genotype was greatest for yield and quality traits using desired gain index. The Smith-Hazel index was useful for improving cob length, cob diameter number of grains per row and sweet flavour in IYQ_5 selection strategy but the aggregate genotype was small.

When selection was confined to only five traits (IYQ_8), the aggregate genotype for yield and quality traits, individually using Smith-Hazel index was greatest. Similar response was predicated for all these traits by using desired gain index with selection strategy IYQ_8. However, the aggregate genotype was slightly reduced. The predicted gains for number of grain rows per cob using all the three indices and pericarp tenderness using Smith-Hazel and desired gain indices were negative in the selection strategy IYQ_8. However, base index was useful in improving pericarp tenderness for the selection strategy IYQ_8.

The superiority of selection indices over other methods of selection and of one index over another mainly depends upon the accurate estimates of genotypic and phenotypic variances and covariances and relative economic values or desired gains specified for different traits. Their successful application to complex multiple-trait improvement also depends upon the judgment of the breeder himself as indicated by Mehdi (1986).

The information generated from the present study taking into account the reliability of predicted response of an index as well as its expected genetic gain might be helpful to determine the importance of various yield and quality traits to the sweet corn breeder, and finally to evaluate recurrent S_1 family selection scheme with respect to the predicted progress possible through index selection for achieving specific goals.

References

Arshad, M., A. Bakhsh and A. Ghafoor 2004. Path coefficient analysis in chickpea (*Cicer arietinum* L.) under field conditions. *Pak. J. Bot*., 36(1): 75-81.

Ali, E.S. and G.B. Saleh. 2003. Response of two cycles of phenotypic mass selection and heritability on two tropical sweet corn (*Zea mays* L. Saccharata) populations. *Asian J. Pl. Sci*., 2(1): 65-70.

Andrew, R.H., R.A. Brink and N.P. Neal. 1944. Some effects of the waxy and sugary genes on endosperm development in maize. *J. Agric. Res*., 69: 355-371.

Ayala Osuna, J. and B.G. Churata. 1995. Estimates of genetic parameters in the maize composite (*Zea mays L*). Arquitetura. *Centro de investigaciones Fitoecogeneticas de Pairumani*: 769-779 (Pl. Br. Abst.67 (4): 3478; 1997).

Banziger, M. and H.R. Lafitte. 1977. Efficiency of secondary traits for improving maize for low-nitrogen target environments. *Crop Sci*., 37: 1110-1117.

Bernardo, R. and J. Yu. 2007. Prospects for genome wide selection for quantitative traits in maize online publication. *Crop Sci*., 47: May-June, 2007.

Cheema, A.A., M. Rashid, M. Ashraf and Z.U. Qamar. 2004. Genetic divergence in rice collections. *Pak. J. Bot*., 36(3): 557-565.

Chisi, M., P.J. Bramel-Cox, M.D. Witt, M.M. Claassen and D.J. Andrews. 1996. Breeding for grain yield stability using full-sib family recurrent selection in Sorghum. *Crop Sci*., 36 (5): 1083-1087.

Crosbie, T.M., J.J. Mock and O.S. Smith. 1980. Comparison of gains predicted by several selection methods for cold tolerance traits of two maize populations. *Crop Sci*., 20: 649-655.

Dolan, D.J., D.D. Stuthman, F.L. Kolb and A.D. Hewings. 1996. Multiple traits selection in a recurrent selection population in Oat (*Avena sativa* L.). *Crop Sci*., 36(5): 1207-1211.

Eta-Ndu, J.T. and S.J. Openshaw. 1992. Selction criteria for grain yield and moisture in maize yield trials. *Crop Sci*., 32(2): 332-335.

Finney, D. J. 1962. Genetic gain under three methods of selection. *Gent. Res*. (Camb.), 3: 417-423.

Hazel, L.N. 1943. Genetic basis for constructing selection indices. 1943. *Genetics*, 28: 476-490.

Lothrop, J.E., R.E. Atikins and O.S. Smith. 1985. Variability for yield and yield components in IAPIR grain sorghum random mating population. I. Means, variance components and heritabilities. *Crop Sci*., 25: 235-240.

Marshall, S.M. 1987. *Corn chemistry and technology*: 431-445. Crookham Company Caldwell, Idaho, USA.

Mehdi, S.S. 1986. *Predicted response to S_1 selection for yield and disease resistance traits in two sunfower populations*. Ph.D. Thesis, South Dakota State Univ., Brookings, SD, U.S.A.

Mock, J.J. and A.A. Bakri. 1976. Recurrent selection for cold tolerance in maize. *Crop Sci*., 16: 230-233.

Modarresi, M., M.T. Assad and M. Kheradnam. 2004. Determining selection indices in corn hybrids (*Zea mays* L.) to increase grain yield. *J. Sci. & Tech. of Agric. and Natural Resources*, 7(4): 71-82.

Pesek, J. and R.J. Bakar. 1969. Desired improvements in relation to selection indices. *Can. J. Pl. Sci.*, 49: 803-804.

Rabiei, B., M. Valizdah, B. Ghareyazie and M. Moghaddam. 2004. Evaluation of selection indices for improving rice grain shape. *Field Crops Res.*, 89(2-3, 8): 359-367.

Robinson, H.B., R.E. Comstock and P.H. Harvey. 1951. Genotypic and phenotypic correlations in corn and their implications in selection. *Agron. J.*, 43: 283-287.

Sarwar, G., M.S. Sadiq, M. Saleem and G. Abbas. 2004. Selection criteria in F_3 and F_4 population of mungbean (*Vigna radiata* (L.) Wilczek). *Pak. J. Bot.*, 36(2): 297-310.

Smith, H.F. 1936. A discriminant function of plant selection. *Ann. Eugenics*, 7: 240-250.

Steel, R.G.D., J.H. Torrie and D.A. Dick. 1997. *Principles and procedures of Statistics – A biometrical approach*. McGraw Hill Book Co. Inc., New York, USA.

Suvantaradon, K., S.A. Eberhart, J.J. Mock, J.C. Owens and W.D. Guthrie. 1975. Index Selection for several yield traits in $BSSS_2$ maize population. *Crop Sci.*, 15: 827-833.

Tanveer, H. 1989. *Genetic improvement of sweet corn through mass selection*. M.Sc. (Hon.) Agri. Thesis. Deptt. Pl. Br. Genet., Univ. Agri. , Faisalabad, Pakistan.

Vikram, A. and D. Roy. 2003. Selection of characters for constructing selection index in ground nut (*A. hypogea* L.). *Legume Res.*, 26(2): 137-139.

Walters, S.P., W.A. Russell and K.R. Lamkey and P.R. White. 1991. Performance and inbreeding depression between a synthetic and three improved populations of maize. *Crop Sci.*, 31(1): 80-83.

Wells, W.C. and K.D. Kofoid. 1986. Selection indices to improve an intermating population of spring wheat. *Crop Sci.*, 26: 1104-1109.

Williams, J.S. 1962. The evaluation of a selection index. *Biometrics*, 18: 375-393.

Xie, C., S. Xu and J.A. Mosjidis. 1998. Multistage selection indices for maximum genetic gain and economic efficiency in red clover. *Euphytica*, 98(1-2): 75-82.

Younis, M. 1989. *Comparison of half-sib, full-sib and S_1 family selection for improving an open-pollinated sweet corn population*. M.Sc. (Hons) Agri. Thesis. Deptt. Pl. Br. Genetic. , Univ. Agri., Faislabad.