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Derivation and Improvement of the Selection Index and Estimation of Potential for Further Improvement

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Introduction

A SELECTION INDEX is a useful concept for improving several traits simultaneously. It is also useful for enhancing the effectiveness of selection for one trait by suitably incorporating information on one or more secondary traits.

Selection index

Both the traits to be included in the current project, and the form of the selection index (SI), were decided by a consensus of the breeding and physiology staff involved in the project. The model components for the large segregating populations were derived from the simple measurements of TE using SPAD chlorophyll meter readings (Nageswara Rao *et al*. 2001, Sheshayee *et al*. 2002), total dry matter, and pod and kernel yield at final harvest following Wright *et al*. (1996). Various options for the form of the index were considered.

In traditional indices the coefficients would involve estimates of either phenotypic, or phenotypic and genetic, variances and covariances. It is essential that these estimates be derived from the material to be selected; in our case, this meant the $F_{2:3}$ and $F_{2:4}$ families. These variances and covariances would differ between crosses or sites; and, among the unreplicated F_3 progenies, the phenotypic variances would be inseparable from the genotypic estimates. We considered a simple index using the sum of standardised values of HI, TE and T, but this assumes a normal distribution of each trait. There are no such assumptions if standardising with median and range, but the range was vulnerable to the extreme values measured.

The final choice of index used the quartile range (3rd quartile to 1st quartile), which satisfies the need for both simplicity and robustness.

The three traits (T, HI and TE) were combined into the selection index:

$S = \sum_j (x_j - med_j)/SIQR_j$

where:

$SIQR_j$ = semi-inter-quartile range = $\{Q_{3(j)} - Q_{1(j)}\}/2$
Q_3 = third quartile
Q_1 = first quartile

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In our case, there are j = 3 traits (T, HI and TE) included in the index. The index, S, was based on the median (med) and the (SIQR) to ensure selection was not being influenced by extreme values and to give equal weight to each trait. The index, S, was used to select the top 10% of $F_{2:3}$ families to get 50 $F_{2:4}$ families in each cross, and the top 10% (or 20% in Australia) in the $F_{2:4}$ experiments.

Measurement of outcome of selection

Analysis of Variance (REML) was used to predict means and estimate the variance components and their corresponding standard errors (se) due to: Environment, σ_E^2; Genotype, σ_G^2; Genotype x Environment, σ_{GE}^2; and Error, σe^2. Using the progeny means, selection methods were compared using the criterion frequency of trait-based (T) and empirical (E) genotypes in the top 5% and 10% of high-yielding genotypes.

Measurement of Potential Further Improvement

Genetic variances were computed for the progenies selected by each selection method. The predicted selection efficiency under selection method T, relative to selection method E, was estimated using the concept of response to selection, computed as:

$RE_T = R_T/R_E$

where:
$R_T = i_T\, h_T\, s_{GT}$ = Response to selection under T
$R_E = i_E\, h_E\, s_{GE}$ = Response to selection under E.

This gives the efficiency of T relative to E as:

$RE_T = \{i_T/i_E\}\ \{h_T/h_E\}\ \{s_{GT}/s_{GE}\}$
$RE_T = \{h_T/h_E\}\ \{s_{GT}/s_{GE}\}$ for $i_T = i_E$

where:
i = selection intensity
h = square root of heritability
s_G = genetic standard deviation.

For selection method T to be superior to E, RE_T should exceed unity. This can happen when any one of these conditions hold:

1. $h_T > h_E$ for $s_{GT} = s_{GE}$
2. $s_{GT} > s_{GE}$ for $h_T = h_E$
3. $\{h_T/s_{GT}\} > \{h_E/s_{GE}\}$.

The above formulation of relative efficiency assumes the genotype effects within the selection method are random. This is true because the selected progenies are really a subset of a much larger set of possible selections.

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