

ESTIMATING STABILITY AND SELECTION INDEX¹

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ABSTRACT

The two stability parameters suggested by Eberhart and Russell (3), namely the coefficient of the regression of yield on the environmental index (b) and the standard deviation from the regression (S_d), are combined into a single measure of stability. A tentative suggestion is made to further incorporate this measure of stability and average yield into a single selection index.

INTRODUCTION

A genotype of a given crop should perform well under a rather wide range of environmental conditions before it is recommended for licensing. Stability in yield, therefore, has been one of the objectives sought by breeders.

According to Perkins and Jinks (6) two main approaches have been used to specify, estimate and correct for effects of environmental variation and genotype - environmental interaction in experimental and practical breeding. One, based on fitting models, specifies the contributions of genetic, environmental and genotype - environmental interactions to generation means and variances and allows for the contributions of additive, dominance and epistatic gene action to the genetic and interaction components. This approach has been used by Bucio Alanis (1) and Bucio Alanis and Hill (2). The other one is a purely statistical analysis originally proposed by Yates and Cochran (7) and adopted by Finlay and Wilkinson (5) and further developed by Eberhart and Russell (3). They calculated the regression of yield on the environmental index. The index for each environment was estimated by the average of the yield of all genotypes in that environment. A stable genotype was defined as one with $b = 1$ and $S_d^2 = 0$, b and S_d^2 representing the regression coefficient and the mean square of the deviations from regression, respectively.

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Freeman and Perkins (4) pointed out some of the statistical weaknesses in the techniques used especially regarding estimation of the environmental index. They noted that environmental index for a given environment cannot be a function of the mean of the replications of a genotype in that environment because the regression of the mean yield of the same genotype on environmental index is being considered. They suggested a number of ways to resolve the problem. From a practical point of view, however, the problem is of little consequence when a large number of genotypes are being tested.

DISCUSSION

Stability

The two estimates, b and S_D^2 , proposed by Eberhart and Russell (3), are indeed of practical importance to breeders. The method, however, has one drawback. It furnishes two separate estimates of stability, namely b and S_D^2 . This would make the selection for stable genotypes quite subjective. To circumvent this problem the procedure with the following steps is suggested :

- 1) For each environment the environmental index and the means for the genotypes in that environment are estimated following the method used by Eberhart and Russell (3).
- 2) Using the following modified regression model,

$$Y_i = \beta'_0 + X_i + \epsilon'_i$$

in which

Y_i = the observed mean for the genotype in the i th environment,

β'_0 = intersection of the regression line with the Y axis,

X_i = the value of the environmental index for the i th environment, and

ϵ'_i = a random variable, $N(\mu'_i, \sigma_{Y,X})$ with $\mu'_i = (\beta_1 - 1) X_i$, in which β_1 corresponds

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to the regression line of $Y_i = \beta_0 + \beta_1 X_i + \epsilon_i$ for the same data. $\sigma_{Y, X}$ is the same for both models.

A line with the slope of 1 is fitted to the data for each genotype so that $\sum \epsilon_i^2$ is minimum. It can be shown that $\sum \epsilon_i^2$ is minimum when $\beta_0' = \bar{Y} - \bar{X}$.

- 3) Stability (St) is thus defined as the standard deviation from this regression line, namely

$$St = \sqrt{\frac{\sum (Y_i - \hat{Y}_i)^2}{n - 1}}$$

where

\hat{Y}_i = the estimated mean (based on slope of 1) for the genotype in the *i*th environment and

n = the number of environments.

St can also be calculated as follows, which is more adapted to machine calculation:

$$St = \sqrt{S_Y^2 + S_X^2 - 2S_{YX}}$$

where S_Y^2 , S_X^2 and S_{YX} represent variance of Y, variance of X and covariance of Y and X, respectively. A low value of St indicates high stability. The St's can be adjusted for differences between the mean yields (\bar{Y} 's) if the regression of St on \bar{Y} is significant in the population of genotypes concerned.

The theoretical limitations of the method are obvious. It cannot, for example, distinguish between two genotypes with the same high values for St as A and B in Fig. 1a and C and D in Fig. 1b; or between two genotypes with the same low values of St as E and F in Fig. 1c. This lack of distinction, however, is not of any practical consequence to breeders.

In cases such as in Fig. 1a and 1b, the genotypes are undesirable due to their slopes

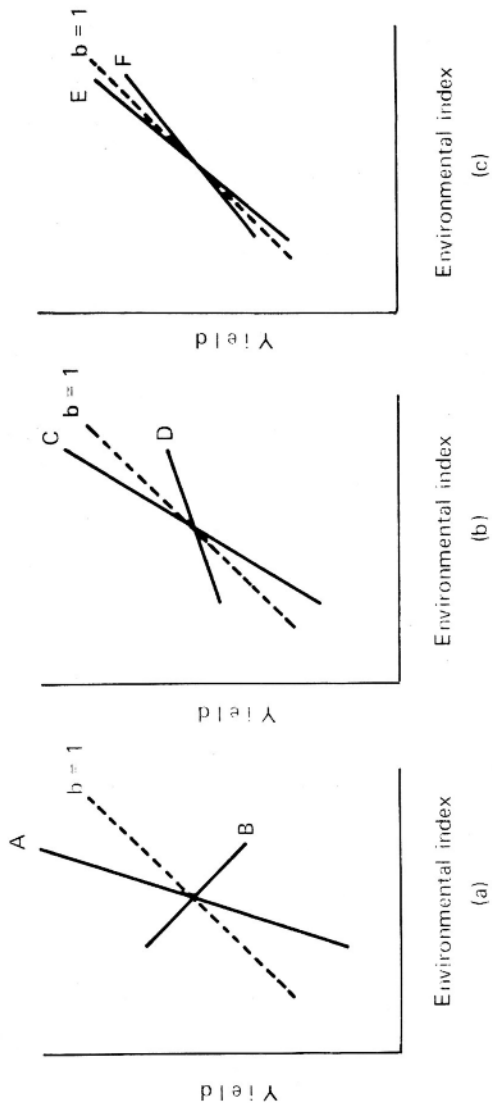


Fig. 1. Three hypothetical cases representing genotypes with equal values for St having different slopes.

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being far from 1 and would be eliminated by the breeder anyway. In the case of Fig. 1c, to the writers knowledge no distinction has been made regarding the relative desirability of genotypes such as E and F. In the case of any personal preference however, the value of b can be considered.

Selection Index

In actual selection, the breeder is concerned with high average yield (\bar{Y}) as well as high stability (i.e. low St). Thus the two estimates (\bar{Y} and St) should be incorporated into a single selection index.

Different methods can be devised by breeders for calculating the selection index depending on the relative emphasis given to \bar{Y} and St . A tentative suggestion consists of the following steps :

- 1) For each environment, the maximum yield (attained by any genotype) is determined. Thus M_i would be the maximum yield in the i th environment.
- 2) A hypothetical genotype is assumed with a yield equal to M_i in the i th environment. The regression line, with the slope of $b = 1$ of this genotype on the environmental index is determined.
- 3) The estimated yield for the hypothetical genotype is calculated from the regression, namely by :

$$\hat{H}_i = \bar{H} + (X_i - \bar{X})$$

where

\hat{H}_i = the estimated yield of the hypothetical genotype in the i th environment,

X_i = the environmental index for the i th environment,

\bar{H} = the mean yield for the hypothetical genotype and

\bar{X} = the mean environmental index.

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- 4) The selection index (SI) for a given genotype is calculated by :

$$SI = \sqrt{\frac{A-B}{n}}$$

in which

$$A = \sum (Y_i - \hat{H}_i)^2$$

$$B = \sum (Y_i - \hat{H}_i) \text{ for } Y_i > \hat{H}_i$$

with

n = the number of environments and

Y_i = the yield of the given genotype in the i th environment.

In fact, SI more or less measures the deviation of the yield of a given genotype from the estimated yield of the hypothetical genotype. Thus, low values of SI indicate the superiority of the corresponding genotypes.

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