THE AREA UNDER THE FUNCTION: AN INDEX FOR SELECTING

DESIABLE GENOTYPES

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The linear regression approach has been widely used for selecting high yielding and stable genotypes targeted to several environments. The genotype mean yield and the regression coefficient of a genotype's performance on an index of environmental productivity are two main stability parameters. Often, using both can complicate the breeder's decision when comparing high yielding, less stable genotypes with low yielding, stable genotypes. This study proposed to combine the mean yield and regression coefficient into a unified desirability index ($D_i$). $D_i$ is defined as the area under the linear regression function divided by the difference between the two extreme environmental indexes. $D_i$ is equal to the mean of the $i$th genotype across all environments plus its slope multiplied by the mean of the environmental indexes of the two extreme environments (symmetry). Desirable genotypes are those with a large $D_i$. For symmetric trials the desirability index depends largely on the mean yield of the genotype and for asymmetric trials the slope has an important influence on the desirability index. The use of $D_i$ was illustrated by a 20 environments maize yield trial and a 25 environments wheat yield trial. Three maize genotypes out of nine showed $D_i$ that were significantly larger than a hypothetical, stable genotype. These were considered desirable, even though two of them had slopes significantly greater than 1.0.
Key Words: Genotype x environment interaction, Adaptation, Stability, Desirability Index.
INTRODUCTION

Differential genotypic responses to varied environmental conditions are known, in the classical sense, as genotype-environment interactions (GEI). Their most important effect in plant breeding is to complicate the identification of superior genotypes for general adaptation and for specific environments.

The most widely used method for selecting high yielding and stable genotypes is the linear regression fitted by least squares. It was first proposed by Yates and Cochran (1938) for analyzing a barley yield trial and used by Finlay and Wilkinson (1963) to examine the adaptation of several hundred barley genotypes. A genotype's stability is shown by its proportional response to the environmental index (regression coefficient). It is considered to be relatively stable if it has a regression line whose slope is near to 1.0. In general, this is a good criterion for selecting a genotype or a group of genotypes targeted to several environments.

Eberhart and Russell (1966) used the linear regression approach for assessing genotypic yield stability. They proposed pooling the sum of squares for environments and GEI and subdividing it into a linear effects between environments, a linear effect for genotype-environment, and a deviation from regression. The deviation from the regression line of each genotype is considered another
stability parameter. A stable genotype has slope equal to one plus a small deviation from regression. However, deviation from regression has been criticized because biological and algebraic interdependencies exist between the slopes and the sum of squares due to deviations from regression (Hardwick and Wood, 1972; Westcott, 1986).

Several authors have pointed out the statistical and biological limitations of regression analysis (Freeman, 1973; Hill, 1975; Westcott, 1986; Lin et al., 1986; Crossa, 1990). Although a genotype's slope is the primary stability parameter, not all stable genotypes are desirable, since mean yield is also an important parameter. Often these two parameters complicate a breeder's decision when comparing high yielding, less stable genotypes with low yielding, stable genotypes (Crossa, 1988).

In general, the regression model is used to partition the overall response pattern of a genotype into two components: yield performance and stability. However, an analytical method for examining the total behavior of a genotype across the tested environments should consider both of these components simultaneously.

The main objective of this study was to present a simple statistical method for selecting genotypes. The procedure is called the "area under the function" and combines the two principal parameters (regression coefficient and mean yield) which describe genotype performance into a unified desirability index. The method was illustrated with examples
from an international maize (Zea mays L.) trial and an international wheat trial (Triticum aestivum L. em Thell.) distributed by the International Maize and Wheat Improvement Center (CIMMYT).

**METHODOLOGY FOR DEVELOPING A GENOTYPIC DESIRABILITY INDEX**

From a breeding perspective, a practical problem of the regression approach is how to reconcile and utilize the two most important parameters, slope and mean yield. Often a high yielding genotype is not stable (β significantly different from 1.0) or a genotype with β=1.0 may show poor yield response.

**Relationship between slope and mean yield production of the i^th genotype and a standard genotype**

In this section we examine different situations where the response pattern of a specific genotype, given by its slope and mean yield, is compared with the response of a stable genotype. Consider an experiment where "g" genotypes (i=1,2,...,g) are evaluated in "e" environments (j=1,2,...,e). The function that estimates the yield of the i^th genotype is

\[ Y_i = f_i(I) \]

where \( f_i(I) = u_i + \beta_i I \); \( u_i \) is the mean yield of the i^th genotype over all environments and is estimated by \( Y_i \); \( \beta_i \)
is the regression coefficient of the $i^{th}$ genotype on the environmental index ($I_j$) and is estimated by $b_i$. The environmental index is the mean of an environment minus the grand mean ($Y_{j} - Y_{..}$).

Let the function that estimates the yield of a standard genotype "s" be defined by

$$Y_{s} = f_{s}(I)$$

where $f_{s}(I) = u + I$; $u$ is the mean of all genotypes in all the environments and is estimated by the overall mean ($Y_{..}$). By definition, the standard genotype is stable because $\beta_{s} = 1$.

The relationships between the two parameters, slope and mean yield production, under the models $Y_{i}$ and $Y_{s}$ can be displayed in a diagram where phenotypic values of the $i^{th}$ genotype and the standard genotype are regressed on the environmental indexes ($I_a$ being the lowest yielding environment and $I_b$ the highest yielding environment). Figure 1 displays six hypothetical cases. In case 1 the $i^{th}$ genotype is unstable ($b_i$ greater than 1.0); however it can be considered a desirable genotype because its yield production is better than that of the standard genotype in all environments (Fig. 1A). In case 2 the $i^{th}$ genotype is unstable ($b_i$ less than 1.0) and its yield is lower than the standard genotype in all environments (Fig. 1B). Note that in both cases GEI exists but without change in genotypic performance across environments. In cases 3 and 4 the $i^{th}$ genotype is unstable ($b_i$ is greater than 1.0 in Fig. 1C and less than 1.0 in Fig. 1D) and yield is higher than that of
the standard genotype in some high and low yielding environments, respectively. Both cases show genotypic rank change across environments. In case 5 the $i^{th}$ genotype is stable ($b_i=1.0$) and more productive than the standard one (Fig. 1E), whereas in case 6 the $i^{th}$ genotype is stable ($b_i=1.0$) and yield is lower than that of the standard genotype (Fig. 1F). When both genotypes are stable ($b=1.0$; case 5 and case 6), it is clear that the $i^{th}$ genotype would be desirable only if it shows better yield performance than the standard one (Case 5). Clearly the response of the $i^{th}$ genotype in Fig. 1A is much more desirable than the response in Fig. 1E. It represents a response to favorable environments and also superiority in stress environments.

For the cases where the $i^{th}$ genotype is unstable but more productive than the standard genotype in all environments (Case 1) or unstable and more productive than the standard genotype in only some environments (Case 3 and Case 4) the decision as to whether or not the $i^{th}$ genotype should be selected is not clear. For these cases it would be useful to obtain an index that includes both stability parameters.

The desirability index of the $i^{th}$ genotypes expressed as

the area under the linear function

Desirability index
The area ($A_i$) under the linear function gives a combined estimate of the influence of $Y_i$ and $b_i$. Because $A_i$ is an area, it should be converted to a unit of measurement that is easier to interpret. By the fundamental theorem of calculus dividing $A_i$ by the distance between the two extreme environment indexes ($I_a$ and $I_b$) we obtain the desirability index ($D_i$): $D_i = A_i/(I_b - I_a)$. This value represents the mean expected yield of the $i^{th}$ genotype expressed in performance units when tested in any of the environments between $I_a$ and $I_b$.

The area under the linear function ($A_i$) is the integral of $f_i(I)$ over the range of the tested environments ($I_a, I_b$) such that

$$D_i = \frac{\int_{I_a}^{I_b} f_i(I) d(I)}{I_b - I_a} = \frac{\int_{I_a}^{I_b} (Y_i + b_i I) d(I)}{I_b - I_a} =$$

$$= \frac{[\int_{I_a}^{I_b} Y_i d(I) + b_i \int_{I_a}^{I_b} I d(I)]}{I_b - I_a} =$$

$$= \frac{[\int_{I_a}^{I_b} Y_i d(I) + b_i \int_{I_a}^{I_b} I d(I)]}{I_b - I_a} =$$

Therefore,

$$D_i = \frac{Y_i + (b_i)C_1}{I_b - I_a}$$

where $C_1 = (I_b + I_a)/2$ is the mean of the two extreme environmental indexes and defines the asymmetry of the distribution of environmental indexes around zero ($C_1 = 0$ for complete symmetry). The contribution of the slope to the desirability index increases with asymmetry.
Similarly, the desirability index ($D_s$) of the standard genotype is defined as the area under its linear function ($A_s$) divided by the difference between the two extreme environmental indexes ($I_b - I_a$):

$$D_s = A_s / (I_b - I_a)$$

where $A_s$ is the integral of $f_s(I)$ over the range of environments such that

$$I_b = \int f_s(I) \, d(I) / (I_b - I_a)$$

and

$$I_a = \int (Y.. + I) \, d(I) / (I_b - I_a)$$

where $C_1$ is the same as above.

According to these results, the desirability index of a genotype depends on its mean yield, the slope of the regression line, and the asymmetry ($C_1$) of the experiment. When the two extreme environmental indexes approach complete symmetry — that is $I_a = I_b$ — then $C_1 = 0$ and $D_i$ and $D_s$ depend only on $Y_i$ and the overall mean ($Y..$), respectively. In this case, the slopes of the genotypes' regression lines do not influence the desirability index, thus the desirable genotypes are those with higher mean yields (higher $D_i$). However, when the two extreme environmental indexes are asymmetric ($C_1$ tends to be different than 0), two different cases are possible: 1) when $I_a < I_b$ and $C_1 < 0$, then $D_i$ and $C_1$ are inversely related. For two genotypes with the same mean
yield the regression line of the desirable one (with higher $D_i$) will have a smaller slope ($b_i$); 2) $I_a < I_b$ and $C_1 > 0$; then $D_i$ and $C_1$ are directly related. For two genotypes with the same mean yield, the one with greater slope will have a greater $D_i$.

The desirability index of a genotype with quadratic or cubic responses can be calculated. For a quadratic response the corresponding coefficient are calculated as $(I_b^3 - I_a^3)/3$, whereas for a cubic pattern its coefficient is $(I_b^4 - I_a^4)/4$.

Comparing the area under the function of the $i^{th}$ genotype with a constant: Hypothesis testing

A linear model testing methodology (Draper and Smith, 1966) is used to test hypotheses about the parameter $D_i$ and its comparison with $D_s$. Let the vector $C$ be $(C_1, C_2)$ and the vector $b$ be $(Y_i, b_i)$; then $D_i$ can be written as

$$D_i = C' b$$

and the variance of $D_i$ is estimated by

$$S^2_{D_i} = (C' (I' I)^{-1} C) (MSE/r)$$

where MSE is the pooled error, $r$ is the number of replicates, and $I$ is a matrix containing ones in the first column and the environmental indexes in the second column.

To test the null hypothesis $H_0: D_i = D_s$, we use the following $F$ test

$$F_C = MS_{HO}/MSE$$
where $\text{MSHo} = (C'\beta_i - D_s)^2 / S^2_{\text{Di}}$. The value $F_c$ is compared with the $F$ value from the table with one degree of freedom ($1, df\ error$).

As pointed out in the previous section, those genotypes with values of $D_i$ that are significantly larger than $D_s$ are the most desirable.

**Trial 1**

A maize experimental variety trial (EVT 16) provides a simple illustration of the use of the area under the model for characterizing desirable genotypes. The trial had 9 genotypes tested in 20 international environments in a randomized complete block design with 4 replicates. The response variable was grain yield (kg ha$^{-1}$).

The highest yielding genotypes are 4, 5, 6, and 9 (Table 1). Of these, genotypes 6 and 9 are stable (slopes not significantly different from 1.0), whereas genotypes 4 and 5 were unstable (slopes significantly greater than 1.0). The asymmetry of this trial is $C_1 = 226$ ($I_a = -2,206$ kg ha$^{-1}$ and $I_D = 2,658$ kg ha$^{-1}$). Therefore, the desirability index for the $i$th genotype is $D_i = Y_i + (b_i)(226)$. The overall mean of the experiment was 4,858 kg ha$^{-1}$ and the desirability index for the standard genotype was $D_s = 5084$ kg ha$^{-1}$. Genotypes 2, 4, 5, 6, and 8 have values of $D_i$ that were significantly different from those of the standard genotype (Table 1). Of these, genotypes 4, 5, and 6 were superior because they had
values of $D_i$ that were significantly larger than the standard genotype. In contrast, genotype 8 had the lowest mean yield response and the lowest $D_i$.

The response pattern of the 9 genotypes given by their regression coefficients and mean yields was compared with the response of the hypothetical standard genotype ($b=1.0$; Figs. 2 to 10). Deviations from the average response can also be seen from these graphs. Genotypes 1 and 2 represent reference case 6, but only the latter had values of $D_i$ significantly smaller than $D_s$. Genotype 3 corresponded to case 4, but $D_i$ is not different from $D_s$ (Table 1). Genotypes 4 and 5 belong to Case 3; they had slopes greater than one (Table 1) and a $D_i$ that was significantly larger than $D_s$. Case 5 is typified by genotype 6, which showed the highest mean yield and therefore the largest desirability index.

Genotypes 7 and 8 fall into case 4; however, the latter had a slope that was less than 1.0 and a $D_i$ significantly smaller than $D_s$ (Table 1). Genotype 8 not only had a low $D_i$ but has large deviations from regression (Fig. 9). Although genotype 9 belongs to case 3, its $D_i$ does not differ significantly from $D_s$.

For this trial, mean yields were the predominant factor contributing to $D_i$ and were highly correlated to the desirability index. However, for trials with higher asymmetry than that of EVT 16, the slope of the regression line will have a greater influence on $D_i$ and thus the
results of ranking genotypes on mean yield should differ from a ranking based on $D_i$.

**Trial 2**

This data come from a elite spring wheat trial (ESWYT 8) that included 18 genotypes planted in 25 international environments in a randomized complete with 3 replicates. Grain yield is the response variable (kg ha$^{-1}$).

Genotype 5 has the highest mean yield but it is unstable because has a slope significantly different from one ($b_i=1.10$). Genotype 5 has the highest $D_i$ (6343 kg ha$^{-1}$) followed by genotypes 9 and 4 with $D_i$'s of 6114 and 6180 kg ha$^{-1}$, respectively. Genotype 15 has a relatively high mean yield (4660 kg ha$^{-1}$) but according to its slope ($b_i=1.16$) it is unstable. The asymmetry of this trial is $C_1=1218$ ($I_a=-3546$ kg ha$^{-1}$ and $I_b=5982$ kg ha$^{-1}$), that is, trial 2 is about five times more asymmetric than trail 1. The desirability index for the $i$th genotype is $D_i = Y_i + (b_i) (1218)$, whereas $D_s=5870$ kg ha$^{-1}$.

For this trial, both parameters mean yields and slope were important factors contributing to $D_i$. Results of ranking genotypes on mean yield differ from a ranking based on $D_i$. For example genotype 9 was ranked second based on mean yield and third based on $D_i$; genotype 4 ranked third based on mean yield and second based on $D_i$; genotype 15 ranked 10th based on mean yield and 5th based on $D_i$. 
Conclusions

The desirability index, expressed as the area under the regression function, attempts to quantify what most plant breeders actually do, that is, to use both the mean yield and the regression coefficient for determining the desirability of a genotype. This index can facilitate the breeder's decision when selecting superior genotypes especially when high yielding genotypes have slope greater than one (i.e., genotypes 4 and 5 on the maize trial). For trials where the environmental indexes are fairly symmetric (trial 1), the genotypic desirability index is highly dependent on the mean yield. In this case, superior genotypes selected by their mean yield or by the desirability indexes are the same. However, for trials with a more asymmetric such as trial 2, distribution of environmental indexes, the slope of the regression line is an important factor, and therefore selecting on the basis of mean yield will identify different genotypes from those selected using the desirability index.

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REFERENCES


Table 1. Mean yield ($Y_i$) (kg ha$^{-1}$), slope of the regression line ($b_i$) and desirability index ($D_i$) in kg ha$^{-1}$ of 9 maize genotypes ($g_i$) at 20 environments (trial 1).

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Yield</th>
<th>$b_i$</th>
<th>$D_i$</th>
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<td>4840</td>
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<td>1.31*</td>
<td>5514++</td>
</tr>
<tr>
<td>12</td>
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<td>1.23*</td>
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</table>

*, ** Significant at the 5% and 1% probability level, respectively.

+, ++ Significantly different from $D_s$ at the 5% and 1% probability level, respectively.