

# ANALYSIS OF MULTI-ENVIRONMENTAL YIELD TRIALS FOR TESTING ADAPTABILITY OF CROP GENOTYPES

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## ABSTRACT

Methods of analysis of genotype x environment (GE) interaction that provide stability parameters defined in an agronomically sound way would be useful for the evaluation of wide adaptability of crop genotypes. However, each of such reported methods has its own advantages and disadvantages. This paper proposes an efficient and simple method of evaluating wide adaptability and stability of crop genotypes. Deviation of the yield of each plot from the environmental mean is computed and an analysis of variance is performed on these deviations. Thus, the additive environmental effect and overall mean are zero so that they are not included in the model. Genotypes are selected for adaptability using mean deviation across environments ( $D$ ) and a stability parameter derived by partitioning GE interaction variance into components, one corresponding to each genotype ( $s^2$ ). Provisions have been made to detect genotypes giving consistently superior yield across all environments despite their stability. The methodology and the use of  $s^2$  in comparison to  $\theta$  (interaction variance),  $w^2$  (ecovalance) and  $\sigma^2$  (stability variance) are explained on soybean [*Glycine max* (L.) Merr.] yield trials. The parameter,  $s^2$  perfectly correlated with  $w^2$  which is an index number and characterized genotypic stability of soybean similar to  $\sigma^2$  which tends to give more significant results than  $s^2$ .

**KEY WORDS :** Adaptability, Cultivar, Deviation, Environment, Genotype X Environment interaction variance, Stability

## INTRODUCTION

Adaptability of a crop genotype is described as its ability to perform well in diverse environments. Flinn and Garrity (1986) defined yield stability as the performance of a genotype with respect to environmental variability over time at a given location while Evenson *et al.* (1978) defined adaptability as the performance

of a genotype with respect to environmental variability over locations. In contrast, we define adaptability of a genotype as a function of mean productivity and production stability across environments. Stability of a genotype is defined as a function of yield variation due to changing environmental factors across either locations or seasons or both. Our explicit distinction between adaptability and stability is in agreement with most workers (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Perkins and Jinks, 1968; Shukla, 1972) who have made an implicit distinction between these two concepts in the methodologies developed to test adaptability and stability of crop genotypes.

When genotype x environment (GE) interactions are present, it is important to analyse them and utilize the results in evaluating wide adaptability of crop genotypes. Four different methods have been reported for analysis of GE interaction. They are (i) multivariate analysis methods, such as cluster analysis (Lin and Thompson, 1975; Lin, 1982; Lin and Butler, 1990), principal component analysis (Williams, 1952; Gollob, 1968; Johnson and Graybill, 1972; Kroonenberg and Basford, 1989), factor analysis (Grafius and Kiesling, 1960), and principal co-ordinate analysis (Gower, 1966), (ii) relative scoring or ranking method (Das, 1982), (iii) regression methods (Yates and Cochran, 1938; Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Perkins and Jinks, 1968; Tai, 1971) and (iv) variance component methods (Plaisted and Peterson, 1959; Plaisted, 1960; Wricke, 1962; Shukla, 1972).

The choice of the method of analysis of GE interaction should be based on the use to be made of the results. The results of multivariate analysis may not be useful in identifying genotypes with wide adaptability and stability defined in an agronomically sound way. Lin *et al.* (1986) indicated that for an agronomic concept of stability, a genotype is considered to be stable if its response to environments parallels the mean response of all genotypes tested in those environments. Fripp and Caten (1971), Fripp (1972) and Hardwick and Wood (1972) pointed out that when a large number of genotypes is used to quantify the environment in terms of crop response, any bias which results should not prove serious.

The method of relative ranking can detect any genotype with significantly superior yield in all environments, a property lacking in regression and variance component methods. However, this method needs relatively more replications in each environment for the within-environment genotypic mean separation to be effective. Conducting multi-environmental genotypic trials with large number of replications would be expensive and laborious. Furthermore, the method of ranking is comparatively less informative since it does not provide any useful stability parameter.

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The linear regression coefficient or the yield response parameter in the regression method can be effectively used to test adaptability of genotypes only if the linear regression lines of genotypes converge at a point within the given environmental space (Eagles *et al.* 1977). Non-convergence indicates a positive correlation between yield response and mean yield parameters, thus allowing only mean yield to be used in genotypic evaluation. Characterization of genotypes based on regression coefficient may not be very effective if only a small fraction of the interaction sum of squares can be accounted for by heterogeneity among linear regressions. Thus, it might be useful to have methods that partition GE interaction variance into components, one corresponding to each genotype (Baker, 1969).

Mean variance components computed for each genotype from pairwise GE interaction variances (Plaisted and Peterson, 1959) are biased since they contain a portion of the total interaction variance component in addition to the interaction of individual genotypes with environments. The stability variance parameter for each genotype estimated by Shukla (1972) is not statistically independent and it can be negative as it is a difference of two sums of squares. Since the distribution of this parameter is not clear, tests of homogeneity of the estimates are approximate. Wricke (1962) estimated a stability parameter called "ecovalance" and no test of significance has been developed for this parameter so that it is merely an index number.

The purpose of this paper is to present an efficient method of evaluating wide adaptability of crop genotypes using a stability parameter derived by partitioning GE interaction variance into components, one corresponding to each genotype. Application of the proposed method to soybean [*Glycine max* (L.) Merr.] yield trials is illustrated on a comparative basis with some of other variance component methods.

## METHODS

Genotypes to be tested are grown in a randomized complete block design over several locations and /or seasons (environments). Environments can be fixed or random. After collecting yield data, a mean (average over all genotypes and blocks) for each environment is computed. This allows an estimate of the differences among environments.

Deviation (d) of the yield of each plot from its environmental mean is computed as,

$$d_{ijk} = Y_{ijk} - \bar{Y}_j$$

where,  $d_{ijk}$  is the yield deviation of the  $i^{\text{th}}$  genotype in the  $k^{\text{th}}$  block in the  $j^{\text{th}}$  environment from the  $j^{\text{th}}$  environmental mean (average over all genotypes and blocks),  $Y_{ijk}$  is the yield of the  $i^{\text{th}}$  genotype in the  $k^{\text{th}}$  block in the  $j^{\text{th}}$  environment and  $\bar{Y}_j$  is the mean of the  $j^{\text{th}}$  environment. Hereafter, these deviations will be referred to as plot deviations. The plot deviations with positive and negative signs are arranged in a two-way table where environments head the columns and genotypes front the rows. Each cell of the two-way table would contain a number of plot deviations corresponding to the number of blocks. Mean for each cell ( $\bar{d}_{ij}$ ) is calculated and included within parenthesis. Hereafter, these cell means will be referred to as genotypic deviations. Because the sum over genotypic deviations for each environment

$$\left( \sum_{i=1}^p \bar{d}_{ij} \right)$$

is zero, the additive common effect of environments and hence its overall mean will be zero. However, the mean of genotypic deviations across environments for each genotype ( $D_i$ ) would estimate the average effect of that genotype and be either positive, negative, or zero.  $D_i$  is calculated as

where,  $n$  = number of environments.

$$D_i = \sum_{j=1}^n \bar{d}_{ij} / n$$

Perkins and Jinks (1968) regressed the genotypic deviations on additive environmental effect. The present method differs in that it performs an analysis of variance on the plot deviations. The statistical model for the analysis is given below. The analysis of variance is presented in Table 1.

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**Table 1: Analysis of variance of the plot deviations from the environmental means**

| Source             | df               | SS                                                                                                                                    | MS                             |
|--------------------|------------------|---------------------------------------------------------------------------------------------------------------------------------------|--------------------------------|
| Total              | pnq-n            | $\sum_{i=1}^p \sum_{j=1}^n \sum_{k=1}^q d_{ijk}^2$                                                                                    |                                |
| Bks/Environment(E) | n(q-1)           | $\sum_{j=1}^n \sum_{k=1}^q d_{jk}^2 / p$                                                                                              |                                |
| Genotype (G)       | p-1              | $\sum_{i=1}^p d_{i..}^2 / nq$                                                                                                         | MS(G) <sup>†</sup>             |
| GE                 | (p-1)(n-1)       | $\sum_{i=1}^p \sum_{j=1}^n d_{ij.}^2 / q - \sum_{i=1}^p d_{i..}^2 / nq$                                                               | MS(GE)                         |
| GE <sub>1</sub>    | n-1 <sup>‡</sup> | $[\sum_{j=1}^n d_{1j.}^2 - \frac{(\sum_{j=1}^n d_{1j.})^2}{n}] / q$                                                                   | MSGE <sub>1</sub> <sup>*</sup> |
| ...                | ...              | ...                                                                                                                                   | ...                            |
| GE <sub>p</sub>    | n-1              | $[\sum_{j=1}^n d_{pj.}^2 - \frac{(\sum_{j=1}^n d_{pj.})^2}{n}] / q$                                                                   | MSGE <sub>p</sub>              |
| Pooled error       | n(q-1)(p-1)      | $\sum_{i=1}^p \sum_{j=1}^n \sum_{k=1}^q d_{ijk}^2 - \sum_{j=1}^n \sum_{k=1}^q d_{jk}^2 / p - \sum_{i=1}^p \sum_{j=1}^n d_{ij.}^2 / q$ | MS(E)                          |

<sup>†</sup> If environments are random 'MS(G)' is tested against the 'MS(GE)' and if environments are fixed 'MS(G)' is tested against the pooled error.

<sup>‡</sup> The df n-1 for each genotype is approximate

<sup>\*</sup> Variance of the deviations of each genotype [MSGE<sub>1</sub> to MSGE<sub>p</sub>] is tested against the pooled error.

## Model

The statistical model is

$$d_{ijk} = G_i + GE_{ij} + B(E)_{kj} + e_{ijk}$$

where,  $d_{ijk}$  is the yield deviation of the  $i^{\text{th}}$  genotype in the  $k^{\text{th}}$  block (replicate) from the  $j^{\text{th}}$  environmental mean;  $G_i$  is the effect of the  $i^{\text{th}}$  genotype;  $GE_{ij}$  is the interaction effect of the  $i^{\text{th}}$  genotype with the  $j^{\text{th}}$  environment;  $B(E)_{kj}$  is the effect of the  $k^{\text{th}}$  block in the  $j^{\text{th}}$  environment;  $e_{ijk}$  is the random error component and  $i = 1 \dots p$ ,  $j = 1 \dots n$ , and  $k = 1 \dots q$ .

The additive common effect of environment and hence the overall mean are forced to be zero, and thus are not included in the model. The genotypic deviations include the additive genotypic effect, a constant, plus the GE interaction effects. The block effect remains in the model as blocks within environment because blocks in a given environment include the effects that are found in the GE interaction unique to that environment. In this model, the individual GE interaction effect of the  $i^{\text{th}}$  genotype with the  $j^{\text{th}}$  environment is of little interest; however, the GE interaction variance supplies a parameter that indicates the existence of differential genotypic response to environments. The GE interaction variance can be partitioned into components, one corresponding to each genotype ( $s_i^2$ ). The stability parameter,  $s_i^2$  or simply the variance in genotypic deviations, for each genotype is computed as,

$$s_i^2 = \left[ \sum_{j=1}^n d_{ij.}^2 - \frac{(\sum_{j=1}^n d_{ij.})^2}{n} \right] / q(n-1)$$

The distribution of  $s_i^2$  would approximate chi-square distribution. However, the  $s_i^2$ 's are not independent, but the mean of  $s_i^2$ 's over all genotypes becomes equal to the mean squares for GE interaction and the distribution of the variance ratio of  $s_i^2$  and the random error term with  $n-1$  and  $n(q-1)(p-1)$  degrees of freedom (df), respectively would have a F distribution if the number of genotypes in the test is large. Shukla (1972) addressing on a similar point in detail used  $np(q-1)df$  for error term in his analysis. Because this term also includes the block effect, this is not the appropriate error term in our analysis involving randomized

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complete block design. Thus we separate block effect with  $n(q-1)$  df and use  $n(q-1)(p-1)$ df for pooled error term.

The interaction term is tested for significance against the pooled error. If it is non-significant, genotypes are selected for their adaptability solely based on mean deviation parameter (D). This mean deviation parameter can be compared to the mean yield parameter as follows: (i) mean deviation in yield includes only the average effect of the genotype, while mean yield includes the overall mean (a constant) plus the average effect of the genotype and (ii) both parameters are perfectly correlated among genotypes such that a mean separation of genotypes based on mean deviation in yield is identical to that of mean yield.

If GE interaction term is significant, interaction variance or the  $s_i^2$  for each genotype is computed. Each genotype's  $s_i^2$  is tested against the pooled error by a F test to see whether it is different from zero. Since the average effect of a genotype is a constant, a significant  $s_i^2$  of a genotype indicates a significant GE interaction effect for the genotype. Non-significant  $s_i^2$  of a genotype indicates that the genotype does not interact with the environments in an unpredictable manner, and thus as the environment improves the performance of the genotype improves in a predictably proportional manner.

### Selection criteria

The genotypes with positive deviations over all environments are noted from the genotypic deviations. Any zero deviation would be considered as positive. A genotype with positive deviations over all environments indicates its consistent performance in relation to environmental means. Although positive deviations in all environments is generally expected to be associated with the significantly highest D in a set of genotypes tested over several environments, this may not be always the case since D is an average value. On the other hand, the significantly higher D if not associated with positive deviations over all environments is expected to give comparatively higher  $s_i^2$  value which may be significant. However, higher  $s_i^2$  values are not expected to be always associated with the genotypes having both positive and negative deviations. For example, genotypes with significantly highest D's and positive deviations over all environments are also expected to associate with higher  $s_i^2$  values due to their disproportionate higher yields in some environments. Such genotypes would be the most adaptable genotypes in a set of genotypes grown in several environments, although they

may not satisfy the requirements for agronomic stability due to higher  $s_i^2$  values. They would be eliminated if the selection is performed for significantly higher D with non-significant  $s_i^2$ . In contrast, selection for the significantly highest D only, may involve the risk of selecting genotypes giving relatively poor yields (less than the environmental mean) in some environments, though they are significantly superior on the average. Such genotypes can be discriminated over those with significantly highest D's giving consistently superior yields in all environments only by the consideration of the association of the significantly highest D with positive deviations in all environments despite the agronomic stability ( $s_i^2$ ). Although such genotypes may be rare, provisions must be made to detect them if present in adaptability tests.

The selection for genotypic adaptability is performed in the following order : (i) select for significantly highest D with positive deviations over all environments regardless of  $s_i^2$  (ii) select simultaneously for significantly higher D and non-significant  $s_i^2$  and (iii) selection only for non-significant  $s_i^2$  would identify most stable genotypes in the test. Selection for such higher stability is useful since genotypic stability is considered to be under genetic control although care must be taken not to select genotypes with overall low productivity. Such stable genotypes could be used as parents in crossing programmes.

#### Application of the proposed method<sup>1</sup>

Application of the proposed method will be illustrated using seed yield data of 18 soybean genotypes of maturity group five that were grown in six environments (data obtained from the Virginia soybean Variety Evaluation Tests in 1989, Reese *et al.*, 1990). The six environments included full-season plantings at Blackstone, Orange, Painter, Suffolk, and Warsaw and a double-crop planting at Painter. In each environment, all 18 genotypes were planted in a randomized complete block design with three replications. An analysis of variance was performed on soybean seed yield in each environment and the experimental error variances among the six environments were found to be homogeneous based on Hartley's maximum F test. Environments were assumed to be fixed since they are permanent research stations in different physiographic regions of the state.

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<sup>1</sup>Mention of certain private genotypes to the exclusion of others does not infer any recommendation by Virginia Polytechnic Institute & State University.

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A combined analysis of variance was performed on plot deviations and  $s^2$  corresponding to each genotype was estimated upon the significance of the GE interaction term in the analysis. Based on the classification of stability statistics by Lin *et al.*, (1986), the stability parameter,  $s^2$  may be classified in the group with stability parameters of  $\theta$  (Plaisted and Peterson, 1959),  $w^2$  (Wricke, 1962), and  $\sigma^2$  (Shukla, 1972). Therefore,  $w^2$ ,  $\theta$  and  $\sigma^2$  were also estimated for the purpose of comparison. The correlation coefficient of the associations of  $s^2$  with  $w^2$ ,  $\theta$  and  $\sigma^2$  were also estimated.

## RESULTS AND DISCUSSION

Results from the combined analysis of variance performed on the plot deviations of seed yield from the environmental means are presented in Table 2.

**Table 2 : Combined analysis of variance for plot yield (Mgha<sup>-1</sup>) deviations of 18 soybean genotypes grown in six environments**

| Source                 | df  | MS                  |
|------------------------|-----|---------------------|
|                        |     | x 10 <sup>-2†</sup> |
| Total                  | 318 |                     |
| Blocks/Environment (E) | 12  | 26.83               |
| Genotypes (G)          | 17  | 129.15**            |
| GE                     | 85  | 22.85*              |
| Pooled error           | 204 | 11.02               |

\*,\*\* significant at the 0.05 and 0.01 probability levels, respectively.

† multiply the reported value by this to get the actual number.

The stability parameters of  $s^2$  and  $\sigma^2$ , corresponding to each genotype were tested for significance against the pooled error. However, the stability parameters of  $w^2$  and  $\theta$  were used as index numbers. Since environments were assumed to be fixed, the mean square (MS) for genotypes was tested against the pooled error. A Duncan's New Multiple Range (DNMR) test was performed on mean deviations (D) of genotypes. D,  $s^2$ ,  $\sigma^2$ ,  $w^2$ , and  $\theta$ , for each genotype are presented in Table 3.

**Table 3 : Adaptability and stability parameters of D,  $s^2$ ,  $\sigma^2$ ,  $w^2$ , and  $\theta$  for each of 18 soybean genotypes grown in six environments**

| Genotype         | D <sup>†</sup>      | $s^2$   | $\sigma^2$         | $w^2$  | $\theta$ |
|------------------|---------------------|---------|--------------------|--------|----------|
|                  |                     |         |                    |        |          |
|                  |                     |         | x 10 <sup>-2</sup> |        |          |
|                  | Mg ha <sup>-1</sup> |         |                    |        |          |
| Deltapine 415    | 30.6 A              | 18.60   | 19.49              | 93.00  | 11.06    |
| FFR 544          | 29.4 A              | 24.95*  | 26.79*             | 120.50 | 13.97    |
| Stanford HT 5248 | 27.5 AB             | 27.60*  | 31.56**            | 141.70 | 16.21    |
| Hutcheson        | 24.1 AB             | 16.91   | 19.78              | 90.21  | 10.76    |
| Essex            | 24.0 AB             | 9.67    | 10.25              | 46.98  | 6.18     |
| Toano            | 23.9 AB             | 20.22   | 22.40              | 101.10 | 11.91    |
| V85-5344         | 20.8 AB             | 24.92*  | 26.50*             | 119.20 | 13.83    |
| V84-1797         | 8.5 ABC             | 44.59** | 50.06**            | 223.90 | 24.92    |
| Deltapine 105    | 1.7 BCD             | 26.11*  | 29.07*             | 130.60 | 15.04    |
| TN5-85           | 0.4 BCDE            | 20.79   | 23.05              | 103.90 | 12.21    |
| Pioneer 5482     | - 4.0 CDE           | 24.90*  | 26.40*             | 118.80 | 22.18    |
| Bay              | - 4.5 CDE           | 13.23   | 14.57              | 66.18  | 8.22     |
| Vance            | - 15.6 CDEF         | 14.46   | 15.95              | 72.33  | 8.86     |
| V84-1787         | - 18.5 DEF          | 23.07   | 25.65*             | 115.40 | 13.43    |
| V85-4000         | - 20.3 DEF          | 14.76   | 16.29              | 73.83  | 9.03     |
| V85-1197         | - 24.0 EF           | 35.03** | 40.29**            | 180.50 | 20.32    |
| Forrest          | - 38.3 F            | 2.66    | 2.67               | 13.29  | 2.62     |
| Cordell          | - 65.7 G            | 26.13*  | 29.08*             | 130.60 | 15.04    |

\*,\*\* Significant at the 0.05 and 0.01 probability levels, respectively.

† D's with the same letter are not significantly different based on the 0.05 probability level (DNMR Test)

Several observations can be made to illustrate the value of our method. Cordell and Forrest have significantly lower D's than others so would be rated as poorly adapted by all methods. However, Forrest has very low  $s^2$ ,  $w^2$ ,  $\sigma^2$ , and  $\theta$  and would be rated highly stable based solely on consistent performance. No single genotype with the significantly highest D associated with positive deviations over all environments is found in this test. Thus, the top non-significant group of

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genotypes based on the DNMR test can be used for within-group genotypic selection for adaptability based on stability parameters. Within that group,  $s^2$  and  $\sigma^2$  of Deltapine 415, Hutcheson, Essex, and Toano are not significantly greater than the error variance so that these four genotypes could be considered the most adapted group of genotypes in the test. These genotypes are also associated with lower  $w^2$  and  $\theta$  values than that of others in the group. The remaining four genotypes in the top group in mean deviation, having significant  $s^2$  and  $\sigma^2$ , and comparatively higher  $w^2$  and  $\theta$  values would be considered somewhat more risky to grow, in spite of their overall high yield. All the other genotypes included in the test are considered less adapted than the above group of eight genotypes due to significantly lower D. Cordell appeared to be an exceptional genotype in the test because its  $\sigma^2$  as well as  $s^2$  are significant and  $w^2$  and  $\theta$  are comparatively large while having the significantly lowest D values.

V84-1797 and V85-1197 can be evaluated with more confidence as unstable genotypes in the test since their  $S^2$ 's as well as  $\sigma^2$  are highly significant. They also have comparatively large  $w^2$  and  $\theta$  values. This appears to be a reflection of their being selected for resistance to specific diseases rather than for general adaptation.

The characterization of genotypic stability using  $w^2$  and  $\theta$  is subjective because these parameters are merely index numbers without any test of significance. The correlations between both,  $s^2$  and  $w^2$  ( $r = 0.99$ ) and  $s^2$  and  $\theta$  ( $r = 0.93$ ) are significant at the 0.1% probability level. The correlation between  $s^2$  and  $w^2$  appears perfect and thus it justifies the use of  $s^2$  over  $w^2$  since  $s^2$  has a test of significance. Although the correlation between  $s^2$  and  $\sigma^2$  ( $r = 0.93$ ) is significant at the 0.1% probability level,  $\sigma^2$  for each genotype is always somewhat higher than the  $s^2$ . The stability evaluation of the genotypes using  $\sigma^2$  is similar to that of  $s^2$  except with V84-1779 where  $\sigma^2$  is significant while  $s^2$  is not in the present example. Thus, there is a tendency to get more significant  $\sigma^2$ 's than  $s^2$ 's because  $\sigma^2$  values are always higher than  $s^2$  values. Therefore,  $s^2$  may be considered as a more conservative stability parameter than  $\sigma^2$ . Conservative approaches are important when the tests for significance are approximate. In addition  $s^2$  never has negative values, its F test for testing significance is not approximate and its estimation is simpler.

### Characteristic features of the proposed method

The proposed method has made provisions to detect genotypes giving consistently superior yields in all the environments tested, with a greater assurance. The method has the ability to detect such genotypes because a genotype with the

significantly highest D is selected for adaptability regardless of  $s^2$  only if it is associated with positive deviations over all environments.

The proposed method does not assume linear response of GE interaction to improving environments. The environments can be either fixed or random and no prior knowledge of environments is needed. Furthermore, this method is simple and has a F test for testing significance.

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