

Application of a stability statistic to international maize yield trials

M. S. Kang¹, D. P. Gorman¹ and H. N. Pham²

¹ Department of Agronomy, Louisiana Agricultural Experiment Station, Louisiana State University Agricultural Center, Baton Rouge, LA 70803-2110, USA

² CIMMYT, Apdo. Postal 6-641, 06600 Mexico D.F., Mexico

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Summary. Genotype \times environment (GE) interaction encountered in experiments complicates genotype selection and varietal recommendation. The integration of yield and stability of genotypes into a single parameter may make selection and recommendation easier. Kang developed a rank-sum method that allows selection for both yield and the stability variance statistics (σ_i^2 or s_i^2) of Shukla. The objective of this research was to compare the rank-sum selection method to selection based on yield alone in five international maize (*Zea mays* L.) yield trials. Ranks were assigned for yield (the highest mean yield received a rank of 1) and for σ_i^2 and s_i^2 (the lowest value received a rank of 1). The yield and σ_i^2 ranks and/or the yield and s_i^2 ranks for each genotype were summed. Each trial contained two reference entries (REs). Yield rank or rank-sum of each genotype was compared to yield rank or rank-sum of the best RE (BRE). GE interaction was significant for all trials. Heterogeneity in the GE interaction due to the linear effect of a covariate (differences in fertility and/or cultural practices) was significant in Trials 1, 2, and 5. Overall, in all trials, 29 genotypes were selected on the basis of yield alone. On the basis of σ_i^2 and yield rank-sum, 32 genotypes were identified, with 11 being lower yielding than the 29 yield-based selections. On the basis of s_i^2 and yield rank-sum, 31 genotypes were selected, with 11 being lower yielding than the yield-based selections. Obviously, yield is sacrificed when the rank-sum method is used in the selection process. However, selection based on yield alone may not be adequate when GE interaction is significant because of testing in diverse environments.

Key words: Genotype \times environment interaction – Stability – Maize – *Zea mays* – Heterogeneity

Introduction

A large and significant genotype \times environment (GE) interaction effect often hinders researchers' ability to select high-yielding genotypes in breeding programs and to recommend varieties to farmers. Furthermore, GE interaction has been shown to reduce progress from selection (Comstock and Moll 1963). Selection and recommendation of varieties may become more difficult because of a large GE interaction when testing is done in diverse environments, e.g., in regional trials and at international locations. This problem may be enhanced due to the fact that, in most variety testing programs, varietal recommendations are generally based solely on yield. Several reports (Hühn 1979; Kang and Miller 1984; Kang and Martin 1987; Kang and Pham 1991) have stressed the importance of the use of stability analysis in selecting and recommending genotypes. There are many statistical procedures for stability analyses and some of these have been compared (Pham and Kang 1988).

A promising procedure may be one that integrates yield and stability for selection and recommendation. Simultaneous selection for yield and stability has been proposed by some investigators (Hühn 1979; Eskridge 1988; Kang 1988b; Lin and Binns 1988). Hühn (1979) proposed the use of two statistics (S_i^3 and S_i^6) that combine yield and stability. The S_i^6 statistic was associated more with yield than with stability, whereas the reverse was true for S_i^3 (Kang and Pham 1991; Léon 1986). Lin and Binns' (1988) P_i statistic was defined as the distance mean square between a cultivar's response and the maximum response averaged over all locations. Kang (1988b) developed a rank-sum method that combines yield and stability into a single parameter. The highest mean yield receives a rank of 1, whereas the lowest stability variance (σ_i^2) of Shukla (1972) receives the rank of 1. The two

values are then summed and the lowest rank-sum is considered the most desirable.

These three methods of combining stability and yield have been empirically tested and compared (Kang and Pham 1991). Kang's (1988b) method that assigns equal weight to yield and stability was intermediate to Hühn's (1979) statistics (S_i^3 and S_i^6) in selecting genotypes, whereas as the P_i method did not prove advantageous to either method (Kang and Pham 1991). Kang and Pham (1991) state that the rank-sum method may be a compromise.

The use of Kang's (1988b) rank-sum method may make genotype selection and varietal recommendation easier and more refined. The fact that GE interactions are encountered in most yield trials justifies a comparison of the rank-sum method of selection to selection based on yield alone. Therefore, the objective of this research was to apply the rank-sum selection method to CIMMYT's five international maize (*Zea mays* L.) yield trials.

Materials and methods

Data from CIMMYT's international maize yield trials were used in this study. Information on genotypes and locations is provided in Table 1. A randomized complete block design, with four replications per location, was used for each trial. Analysis of variance was performed (SAS 1985) for each trial, and GE interaction was partitioned into heterogeneity and residual according to Shukla (1972). The stability statistics, σ_i^2 and s_i^2 , assignable to each genotype [s_i^2 calculated following removal of heterogeneity due to environmental index (Z_j) from GE interaction variance ($Z_j = \bar{X}_{j..} - \bar{X}_{..}$, where $\bar{X}_{j..}$ is the mean of all genotypes in the j^{th} location and $\bar{X}_{..}$ is the overall mean)] were calculated via the BASIC program of Kang (1988a). The environmental index measures differences in the effects of fertility and/or cultural practices.

Ranks were assigned for yield and for σ_i^2 and s_i^2 . The rank-sum method of Kang (1988b) was used. The highest mean yield received a rank of 1, whereas the lowest value for σ_i^2 or s_i^2 received a rank of 1. A lower stability statistic implies a more stable genotype. The yield and σ_i^2 ranks and/or the yield and s_i^2 ranks for each genotype were summed. Each trial contained two reference entries (REs). Yield rank or rank-sum of each genotype was compared to the yield rank or rank-sum of the best RE (BRE), and genotypes with a value smaller than that of the BRE were selected.

Table 1. Genotypes and test locations for five international maize yield trials

| Trial | Genotypes | Locations |
|-------|---|------------------------------|
| 1 | 14 open-pollinated, experimental varieties (EV) | 39 locations in 21 countries |
| 2 | 23 EV | 46 locations in 27 countries |
| 3 | 16 EV | 23 locations in 13 countries |
| 4 | 18 EV | 25 locations in 15 countries |
| 5 | 12 EV | 17 locations in 10 countries |

Results and discussion

Genotype-by-environment interaction was significant in all trials (Table 2). However, heterogeneity or nonadditivity due to the linear effect of the covariate (environmental index) was significant in Trials 1, 2, and 5. Data for mean yield, σ_i^2 , s_i^2 , yield rank, and rank-sum of each genotype are presented. A significant σ_i^2 indicates an unstable genotype. However, the s_i^2 value for a particular genotype may be nonsignificant after the removal of the effect of the environmental index from GE interaction. A well-adapted genotype would be one with a low stability variance (σ_i^2) and a high mean yield.

On the basis of the BRE (genotype 13's yield) in Trial 1, genotypes 8, 10, and 12 would be selected (Table 3). Based on the rank-sum method of σ_i^2 and yield, no genotype was selected, and based on s_i^2 and yield, only genotype 6 would be selected. Selection of this genotype was due to much lower s_i^2 value after removal of the effect of the environmental index from the GE interaction. In Trial 2, based on the BRE yield, 15 genotypes (6 and 8–21) would be selected. Fifteen genotypes (2, 3, 5, 8–15, 17–19, and 21) would also be selected based on the rank-sum of σ_i^2 and yield (Table 4). Bases on s_i^2 and yield, 14 genotypes (2, 3, 5, 8–12, 14, 15, 17–19, and 21) would be selected. In Trial 2, all genotypes selected in the above three cases were not necessarily the same. This indicates changes in the rank-sum of genotypes due to differences in the two stability-variance statistics before and after use

Table 2. Analyses of variance for yield (tons ha^{-1}) for five international maize trials

| Trial | Source of variation | df | Mean square |
|-------|-------------------------------|-------|-------------|
| 1 | Genotype \times environment | 494 | 0.583 ** |
| | Heterogeneity | 13 | 0.800 * |
| | Residual | 481 | 0.577 ** |
| | Pooled error (σ_o^2) | 1,495 | 0.397 |
| 2 | Genotype \times environment | 990 | 0.520 ** |
| | Heterogeneity | 22 | 1.760 ** |
| | Residual | 968 | 0.492 * |
| | Pooled error (σ_o^2) | 3,036 | 0.319 |
| 3 | Genotype \times environment | 330 | 0.725 ** |
| | Heterogeneity | 15 | 0.700 |
| | Residual | 315 | 0.727 ** |
| | Pooled error (σ_o^2) | 1,005 | 0.465 |
| 4 | Genotype \times environment | 391 | 0.426 ** |
| | Heterogeneity | 17 | 0.506 |
| | Residual | 374 | 0.422 ** |
| | Pooled error (σ_o^2) | 1,224 | 0.340 |
| 5 | Genotype \times environment | 176 | 0.787 ** |
| | Heterogeneity | 11 | 1.335 ** |
| | Residual | 165 | 0.750 ** |
| | Pooled error (σ_o^2) | 561 | 0.414 |

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

Table 3. σ_i^2 's, s_i^2 's, and means for yield (tons ha^{-1}) from international maize Trial 1

| Geno-type | σ_i^2 | s_i^2 | Mean yield (tons ha^{-1}) |
|----------------|----------------|----------------|------------------------------|
| 1 | 0.368 (14) | 0.380 (14) | 4.53 (13) |
| 2 | 0.378 (16) | 0.391 (16) | 4.30 (14) |
| 3 | 0.436 (14.5) | 0.449 (14.5) | 4.54 (11.5) |
| 4 | 0.457 (14) | 0.452 (14) | 4.57 (10) |
| 5 | 0.536 (18.5) | 0.553 (20.5) | 4.54 (11.5) |
| 6 | 0.603* (15) | 0.495 (10) | 4.68 (5) |
| 7 | 0.610* (17) | 0.597* (17) | 4.67 (6) |
| 8 | 0.579* (12) | 0.581* (13) | 4.75 (3) |
| 9 | 0.704** (19.5) | 0.676** (19.5) | 4.66 (7.5) |
| 10 | 1.045** (16) | 1.038** (16) | 4.76 (2) |
| 11 | 0.569* (15.5) | 0.534 (14.5) | 4.66 (7.5) |
| 12 | 0.964** (14) | 0.859** (14) | 4.81 (1) |
| 13 (RE) | 0.520 (10) | 0.534 (11) | 4.70 (4) |
| 14 (RE) | 0.518 (14) | 0.534 (16) | 4.65 (9) |
| σ_o^2 + | 0.397 | 0.397 | |

Values in parenthesis are rank-sum for σ_i^2 and s_i^2 and rank for yield

*.** Significant at the 5% and 1% level, respectively, and indicates unstable genotype

(RE)=Reference entry

+ Pooled error

Table 4. σ_i^2 's, s_i^2 's, and means for yield (tons ha^{-1}) from international maize Trial 2

| Geno-type | σ_i^2 | s_i^2 | Mean yield (tons ha^{-1}) |
|----------------|----------------|----------------|------------------------------|
| 1 | 1.059** (46) | 0.831** (46) | 3.45 (23) |
| 2 | 0.296 (22) | 0.241 (21) | 3.97 (20) |
| 3 | 0.381 (24) | 0.390 (26) | 4.12 (18) |
| 4 | 0.856** (44) | 0.713** (43) | 3.53 (22) |
| 5 | 0.255 (20) | 0.244 (21) | 4.07 (19) |
| 6 | 0.663** (32) | 0.663** (32) | 4.28 (11) |
| 7 | 0.459* (29) | 0.471* (30.5) | 4.15 (17) |
| 8 | 0.565** (20.5) | 0.576** (22.5) | 4.36 (5.5) |
| 9 | 0.343 (16) | 0.352 (17) | 4.28 (11) |
| 10 | 0.363 (12) | 0.367 (13.5) | 4.34 (7) |
| 11 | 0.475* (15.5) | 0.462* (13.5) | 4.44 (2.5) |
| 12 | 0.626** (19) | 0.567** (17) | 4.55 (1) |
| 13 | 0.568** (27) | 0.597** (28) | 4.30 (10) |
| 14 | 0.439* (10.5) | 0.441* (12.5) | 4.44 (2.5) |
| 15 | 0.342 (8.5) | 0.337 (9.5) | 4.36 (5.5) |
| 16 | 0.806** (35) | 0.798** (36) | 4.26 (14) |
| 17 | 0.444* (17) | 0.326 (11) | 4.33 (8) |
| 18 | 0.449* (22) | 0.440* (21) | 4.28 (11) |
| 19 | 0.457* (15) | 0.466 (16) | 4.38 (4) |
| 20 | 0.637** (34) | 0.653** (34) | 4.24 (15) |
| 21 | 0.518** (23) | 0.471* (22.5) | 4.32 (9) |
| 22 (RE) | 0.398 (28) | 0.367 (27.5) | 3.84 (21) |
| 23 (RE) | 0.571** (32) | 0.545** (31) | 4.20 (16) |
| σ_o^2 + | 0.319 | 0.319 | |

Values in parenthesis are rank-sum for σ_i^2 and s_i^2 and rank for yield

*.** Significant at the 5% and 1% level, respectively, and indicates unstable genotype

(RE)=Reference entry

+ Pooled error

Table 5. σ_i^2 's, s_i^2 's, and means for yield (tons ha^{-1}) from international maize Trial 3

| Geno-type | σ_i^2 | s_i^2 | Mean yield (tons ha^{-1}) |
|----------------|----------------|----------------|------------------------------|
| 1 | 1.078** (27) | 1.117** (27) | 5.10 (12) |
| 2 | 0.406 (12.5) | 0.405 (12.5) | 5.21 (10.5) |
| 3 | 0.887** (16) | 0.751 (14) | 5.30 (5) |
| 4 | 1.412** (30) | 1.290** (30) | 5.08 (14) |
| 5 | 0.637 (16) | 0.634 (16) | 5.25 (9) |
| 6 | 0.493 (14.5) | 0.519 (15.5) | 5.21 (10.5) |
| 7 | 0.268 (16) | 0.285 (16) | 5.03 (15) |
| 8 | 0.467 (5.5) | 0.494 (6.5) | 5.35 (2.5) |
| 9 | 1.062** (21) | 0.949** (21) | 5.27 (8) |
| 10 | 1.077** (20.5) | 1.073** (20.5) | 5.29 (6.5) |
| 11 | 0.762* (25) | 0.752* (26) | 5.01 (16) |
| 12 | 0.774* (16.5) | 0.767* (17.5) | 5.29 (6.5) |
| 13 | 1.042** (13) | 0.838* (13) | 5.43 (1) |
| 14 | 0.732* (10.5) | 0.738* (10.5) | 5.35 (2.5) |
| 15 (RE) | 0.573 (10) | 0.464 (7) | 5.32 (4) |
| 16 (RE) | 0.529 (18) | 0.550 (19) | 5.08 (13) |
| σ_o^2 + | 0.465 | 0.465 | |

Values in parenthesis are rank-sum for σ_i^2 and s_i^2 and rank for yield

*.** Significant at the 5% and 1% level, respectively, and indicates unstable genotype

(RE)=Reference entry

+ Pooled error

of the covariate. Seven genotypes (1, 2, and 6–10) would be selected based on BRE yield in Trial 5 (Table 7). The rank-sum of σ_i^2 or s_i^2 with yield selected the same ten genotypes (1–10) in Trial 5. This was due to the significant and large values of σ_i^2 and s_i^2 , relative to the other genotypes, for the REs in Trial 5.

Genotypes that were judged stable (nonsignificant s_i^2) after use of the covariate (environmental index) included genotypes 6 and 11 in Trial 1 (Table 3), genotype 17 in Trial 2 (Table 4), and genotypes 1 and 6 in Trial 5 (Table 7). The use of this covariate in stability analyses may help breeders to identify the underlying cause of the GE interaction.

There were two trials (3 and 4) in which the heterogeneity was not significant. Therefore, selections based on s_i^2 and yield give no additional information over the rank-sum of σ_i^2 and yield. In Trial 3, three genotypes (8, 13 and 14) would be selected on the basis of BRE yield (Table 5). The rank-sum of σ_i^2 and yield selected only genotype 8. In Trial 4, only genotype 16 would be selected based on BRE yield, whereas 6 genotypes (1, 2, 9, 11, 15, and 16) would be selected based on the rank-sum of σ_i^2 and yield (Table 6). The high stability -variance statistics for the BRE allowed more genotype to be selected under the rank-sum method in Trial 4.

In all trials, 29 genotypes were selected on the basis of yield alone. The rank-sum of σ_i^2 and yield selected 32

Table 6. σ_i^2 's, s_i^2 's, and means for yield (tons ha^{-1}) from international maize Trial 4

| Geno-type | σ_i^2 | s_i^2 | Mean yield (tons ha^{-1}) |
|----------------|--------------|---------|------------------------------|
| 1 | 0.265 | (8) | 0.268 (10) 4.69 (6) |
| 2 | 0.304 | (7) | 0.306 (9) 4.72 (3) |
| 3 | 0.572* | (25) | 0.597* (25) 4.64 (9) |
| 4 | 0.419 | (18) | 0.435 (19) 4.64 (9) |
| 5 | 0.555* | (29) | 0.530* (28) 4.51 (14) |
| 6 | 0.533* | (22) | 0.556* (24) 4.64 (9) |
| 7 | 0.618** | (22) | 0.606* (22) 4.70 (5) |
| 8 | 0.629** | (30.5) | 0.658** (30.5) 4.57 (12.5) |
| 9 | 0.315 | (16) | 0.238 (12) 4.59 (11) |
| 10 | 0.270 | (20) | 0.251 (20) 4.44 (17) |
| 11 | 0.363 | (14) | 0.380 (15) 4.67 (7) |
| 12 | 0.497 | (28) | 0.520 (29) 4.49 (16) |
| 13 | 0.328 | (21) | 0.286 (20) 4.50 (15) |
| 14 | 0.372 | (20.5) | 0.376 (19.5) 4.57 (12.5) |
| 15 | 0.240 | (5) | 0.250 (6) 4.71 (4) |
| 16 | 0.448 | (12) | 0.456 (13) 4.87 (1) |
| 17 (RE) | 0.443 | (28) | 0.434 (27) 4.34 (18) |
| 18 (RE) | 0.539* | (16) | 0.454 (13) 4.78 (2) |
| σ_o^2 + | 0.340 | | 0.340 |

Values in parenthesis are rank-sum for σ_i^2 and s_i^2 and rank for yield

*.** Significant at the 5% and 1% level, respectively, and indicates unstable genotype

(RE)= Reference entry

+ Pooled error

Table 7. σ_i^2 's, s_i^2 's, and means for yield (tons ha^{-1}) from international maize Trial 5

| Geno-type | σ_i^2 | s_i^2 | Mean yield (tons ha^{-1}) |
|----------------|--------------|---------|------------------------------|
| 1 | 0.726* | (9) | 0.680 (10) 4.48 (2) |
| 2 | 1.444** | (14) | 1.482** (15) 4.44 (3) |
| 3 | 0.365 | (12) | 0.320 (12) 3.96 (10) |
| 4 | 0.332 | (10) | 0.310 (10) 3.98 (9) |
| 5 | 0.452 | (14) | 0.490 (14) 3.93 (11) |
| 6 | 0.745* | (13) | 0.622 (10) 4.28 (5) |
| 7 | 0.759* | (16) | 0.752* (16) 4.23 (7) |
| 8 | 0.548 | (10) | 0.586 (10) 4.26 (6) |
| 9 | 0.676 | (7) | 0.640 (8) 4.53 (1) |
| 10 | 0.630 | (9) | 0.634 (10) 4.43 (4) |
| 11 (RE) | 1.628** | (24) | 1.258** (23) 3.75 (12) |
| 12 (RE) | 1.149** | (18) | 1.227** (18) 4.19 (8) |
| σ_o^2 + | 0.414 | | 0.414 |

Values in parenthesis are rank-sum for σ_i^2 and s_i^2 and rank for yield

*.** Significant at the 5% and 1% level, respectively, and indicates unstable genotype

(RE)= Reference entry

+ Pooled error

genotypes, with 11 being lower yielding than the 29 yield-based selections. Furthermore, 31 genotypes were selected by the rank-sum of s_i^2 and yield; 11 of those genotypes were lower yielding than the 29 yield-based selection. Obviously, yield is sacrificed when the rank-sum method (combining either stability-variance statistic with yield) is used in the selection process. However, a farmer may be willing to sacrifice some yield if he is guaranteed that a variety will produce consistently from year to year. Selection based on yield alone may not always be adequate when GE interaction is significant. The use of this rank-sum method is an alternative when testing is done in diverse environments.

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