GENOTYPE BY ENVIRONMENT INTERACTIONS AND LINEAR REGRESSION ANALYSES IN WHEAT GRAIN YIELD

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TABLE OF CONTENTS

LIST OF TABLES

CHAPTER I

INTRODUCTION

Wheat breeding programs in the Great Plains of the United States individually have responsibility for large production areas where extreme regional and seasonal variations in wheat growing environments exist. Because of such variability, genotype by environment interactions are commonly found when experiments for quantitative traits of genotypes are conducted across the environments in the region.

These genotype by environment interactions may cause serious problems in breeding programs; inasmuch as they reduce efficiency and precision of genotype evaluation. The presence of the interactions in an experiment automatically implies reduction in the estimates of genotypic variation upon which genetic advance by selection depends. They may also indicate inconsistencies in the relative performance of genotypes from one environment to another.

Numerous statistical genetical methods have been employed to lessen the difficulties created by genotype by environment interactions. The analysis of variance can provide precise information on the interactions. Such information, when obtained, is useful to plant breeders in designing more effective breeding programs. Methods using simple linear regression of genotype performance on environment effects have been developed to study genotype responses to the environments. If genotype by environment interaction observed in an experiment is proved to be a linear function of environment effects, regression analyses can characterize genotype

response and permit a comparison of genotypes across a series of environments where relative genotype performance is confounded by the interactions.

The chief objectives of this study were to examine genotype by environment interactions for wheat grain yield in Oklahoma and to examine the potential usefulness of the linear regression analysis in the wheat breeding program in Oklahoma.

CHAPTER II

LITERATURE REVIEW

General Considerations of Genotype By Environment Interactions

In dealing with quantitative traits in crop plants, statistical genetical methods are necessary to obtain the type of genetic information that allows for the prediction of genetic advance when selection is practiced under various systems of breeding.[1] For this purpose, the analysis of variance approach, which can separate total variability of phenotypes into variance components arising from the joint action of genotypes and environments, has been adopted and developed by the efforts of early researchers.

The evidence that the genotype interacts with the environment was clearly demonstrated by Immer et al.,[19] who used the analysis of variance to study data from barley yield trials conducted during 1930-1931. Comstock and Moll[10] discussed genotype by environment interactions from a view of statistical genetics and indicated that the interactions may introduce upward bias in estimating genetic variance when the variance was estimated from data collected at one location. As genotypes are tested more extensively, genetic variance will be reduced to some extent by the interaction variance.

Since genotype by environment interactions tend to reduce the estimates of genetic variance, emphasis has been placed on the use of

designs to reduce the magnitude of the interactions in relation to that for genetic variance.

Allard and Bradshaw[2] classified environmental variation into two types: one type was predictable variation arising from the permanent character of locations and the second type was unpredictable variation arising from fluctuations of weather. They suggested that where the predictable variation was large, a region could be divided into a number of different and special environments. In such a region, the development of cultivars adapted specifically to the special environment would be effective. Stratification of a region into homogeneous sub-regions can reduce the interactions within a sub-region. Horner and Frey[18] estimated genotype by location interactions from oat cultivar trials conducted at 9 locations for 5 years. When a region was divided into 2, 3, 4 and 5 sub-regions, that interaction component was reduced by 11%, 21%, 30% and 40%, respectively. Similar results were obtained by Liang et al.[25] who studied the interactions in yield trials of wheat, barley, and oats in Kansas.

However, Allard and Bradshaw[2] stated that when year to year fluctuations as well as three-factor interactions were large, such interactions often remained large within a homogenous sub-region. In such a case, it is essential that tests be conducted in a series of locations over a series of years.

When genotype by environment interactions are present, the performance of genotypes depends on the a particular environment where they are grown. Thus, the relative performance of cultivars in one environment may not be the same in another environment. Such inconsistency results in changes in the absolute differences between gentoypes and often causes

alternation of the order of genotype ranking. This feature of the interaction indicates the difficulty in comparing cultivars across the environments, and it also suggests the need for genotypes better adapted to varying environments.

Since the analysis of variance does not have procedures of testing to compare overall performance of genotypes, attempts to characterize genotype response to environments so as to measure the adaptability and/or stability of a genotype were made by various researchers.[13,14,30,35]

Wricke[35] proposed that among genotypes, the one which interacts least to environments is the most stable and the contribution of a genotype to the interaction sum of squares in a two-way analysis of variance can be a basic measurement of its instability. Plaisted and Peterson[30] suggested a similar approach.

Finlay and Wilkinson[14] suggested a simple linear regression approach. The mean performance of all genotypes in an environment would be a suitable measurement of that environment. They found that much of the genotype by environment interaction could be accounted for by the linear regression of the performance of a genotype on the environmental mean. Thus, the regression coefficients for genotypes could characterize their differential responses to the environments: genotypes with coefficients greater than 1, which is the mean of the coefficients, are adapted to favorable environments, on the other hand, genotypes with the coefficients smaller than 1, are adapted to poor environments.

Eberhart and Russell[13] proposed that in addition to the regression coefficients, the deviation from linear regression would be another important parameter in the regression analysis. They developed a

mathematical model for this analysis and presented a definition for a stable genotype as determined by regression parameters.

Perkins and Jinks[31] discussed linear regression of genotypic components of a genotype into environment components. Their method allows orthogonal partition of genotype by environment interactions into a part due to regression and a part due to deviation, and thus, provides an accurate test as to whether or not the interaction observed in an experiment is a linear function of the environment components.

The linear regression approach has been applied to a number of different crops and different quantitative traits. As far as wheat is concerned, this approach was used by numerous researchers: Bhullar et al.,[4] Brennan and Byth,[6] Campbell and Lafever,[9] De Pauw et al.,[11] Johnson et al.,[20] Kaltsikes and Larter,[22] Pinthus[32], and Walton[34] reported on grain yield while Busch et al.,[7] Ghaderi and Everson[16], and McGuire and McNeal[27] reported on grain quality traits.

In many cases, the linear regression analysis could successfully describe the responses of genotypes to environments. However, it appears that the explanation provided by linear regression is merely empirical; there seems to be no biological or physiological explanation for it.[17] For this reason each experiment should be examined as to whether or not the regression model fits to the data.

The traits examined by regression parameters are heritable. Since the genotype by environment interactions depend on the genotype as well as environment, it follows that the interactions are partly heritable. The heritable portion of the interaction variance can be estimated for any given environment by the linear regression analysis and it can be exploited in breeding programs.[17]

Bucio et al.[8] studied inbred lines of Nicotiana rustica as well as segregating populations derived from crosses of the inbred lines. They estimated the regression parameters of the inbred lines and segregating populations. On the assumption that the genetypic contribution to the interaction component is confined to additive and dominance gene effects, they also computed expected values for the regression parameters of the segregating populations from parental lines. They found that there was good agreement between observed values and expected values.

For regression parameters to be proved as partly heritable and thus, to have any practical value in selection, they would have to be repeatable over years and locations.[3] High repeatability for estimates of regression parameters was reported by Jopp et al.[21] For yield data collected from spring wheat cultivar trials at 15 to 20 locations in the Northern Great Plains, they estimated these parameters each year over 10 years, 1959-1968. They concluded that each cultivar tended to have its own characteristic value for the regression parameters.

On the other hand, poor accordance for regression statistics were reported by Fatunla and Frey.[15] They evaluated nine sets of 20 random lines of oats in two randomly divided sets of seven environments and found that correlation coefficients between regression parameter estimates from the two sets of environments were significant in only one of the nine sets of lines. Their test environments, however, had some differences in treatment of fertilizer and the range of environment mean.

Becker[3] reported high repeatability in maize grain yield but poor repeatability in barley and oat grain yield. Although poor repeatability was found in some cases, it did not contradict the theory that the response pattern determined by the regression parameters is

heritable. The cause of unrepeatability seemingly stems from differences in environments which are assessed to estimate regression parameters.

Knight[23] considered the effect of different environmental conditions on regression parameter estimates. Perkins and Jinks[31] stated that it was essential that the parameters be measured for those environmental factors, whether seasonal, locational or deliberately imposed, that are likely to be the most critical for the material under the conditions in which it will ultimately be grown.

The relationship between the measurements of regression parameters and other statistical measurements, such as genotype mean performance, has been of great interest. If the regression parameters are estimated without serious error, the possibility of selection in breeding programs with respect to the adaptability is expected. Whether such selection for a certain trait is compatible with other existing selection procedures for the same trait depends on the relationship between the measurements of the adaptability and other measurements which have been taken for the selection previously.

Bhullar et al.[4] found no association between mean yield and regression parameters, regression coefficients and deviation, in wheat grain yield. The absence of any relationship between mean performance and regression coefficients has been also reported by Johnson et al.[20] in wheat grain yield, Langer et al.[24] and Pfahler and Linskens[29] in oat grain yield, by Nguyen et al.[28] in tall fescue forage yield, and by McGuire and McNeal[27] in wheat grain quality. For these cases, it should be possible to select genotypes which have higher mean performance and any type of environmental adaptation.[14]

On the other hand, a significant positive correlation between mean performance and regression coefficients was found in wheat grain yield by Brennan and Byth.[6] Similar results were obtained in oat grain and straw yield by Eagle et al.[12] and in plant height of Nicotiana rustica by Perkins and Jinks.[31] With a significant positive correlation, the selection toward higher performance over environments would result in genotypes responsive to improvement in cultural conditions, and genotypes with low responsiveness would be expected to have a lower performance, in general.[6]

Eagle et al.[12] pointed out that when the correlations between mean performance and regression coefficients were highly significant, regression lines tended to converge at a small region. If the region of convergence was outside the range of normal environments, then selection based on mean performance alone would be sufficient because genotypes with higher mean performance would be superior at all levels of environments.

The definitions of stability are many and varied.[17] Becker[3] considered the characteristics of a genotype that showed a constant yield despite the differences in environments as a biological concept of stability, and the characteristics of a genotype to realize the yield expected at the level of productivity of the respective environment as an agronomic concept of stability. A stable genotype, in an agronomic sense, does not interact with environment; thus, the agronomic concept of stability can be measured by the parameter defined by Wricke.[35]

Eberhart and Russell[13] defined a stable genotype as one with the regression coefficient of 1.0 and no deviations from regression. Breese[5] proposed that stability should be measured only by the deviation

from regression. Walton[34] and Pinthus[32] used the coefficient of determination, which is the proportion of the variation in genotype performance attributable to the linear regression. This coefficient could be used instead of the deviation from a regression line. Some of the stability parameters are mutually related. Their relationship was discussed in detail by Becker.[3]

Statistical Models

Analyses of Variance

When a specific combination of years and locations is regarded as an environment, the analysis of variance model for an experiment with the randomized complete block design is given by

$$Y_{ijk} = \mu + g_i + e_j + (ge)_{ij} + r_{jk} + \varepsilon_{ijk}$$

where Y_{ijk} is the observed performance of the ith gentotype at the kth block of the jth environment (i=1, 2, 3, . . . , t; j=1, 2, 3, . . ., s; k=1, 2, 3, . . . , r), μ is the grand mean over all blocks, genotypes and environments, g_i is the additive genetic contribution of the ith genotype, e_j is the additive environmental contributior of the jth environment, $(ge)_{ij}$ is the interaction between the ith genotype and jth environment, r_{jk} is the contribution by the kth block of the jth environment, and ε_{ijk} is the residual variation.

Linear Regression Analyses

Two different approaches of a simple linear regression analysis have been proposed; the Eberhart and Russell approach[13] and the Perkins and Jinks approach.[31]

Their mathematical models for the regression and a combined form with the analysis of variance are given by:

The Eberhart - Russell approach:

$\bar{Y}_{ij.} = \mu + g_i + \beta_i e_j + \delta_{ij}$ (regression)

$Y_{ijk} = \mu + g_i + \beta_i e_j + \delta_{ij} + r_{jk} + \varepsilon_{ijk}$ (a combined form)

The Perkins - Jinks approach:

$\bar{Y}_{ij.} = \mu + g_i + e_j + b_i e_j + \delta_{ij}$ or

$\bar{Y}_{ij.} = \mu + g_i + (1 + b_i) e_j + \delta_{ij}$ (regression)

$Y_{ijk} = \mu + g_i + e_j + b_i e_j + \delta_{ij} + r_{jk} + \varepsilon_{ijk}$ (a combined form)

where β_i is the regression coefficient for the regression of $\bar{Y}_{ij.}$ on e_j. δ_{ij} is the deviation of the ith genotype from its regression line, and b_i is the regression coefficient of the ith genotype for the regression of $(ge)_{ij}$ on e_j. Here, symbols to express parameters have been modified for a comparison of two models from their original and environment indexes used by Eberhart and Russell are replaced by the additive environment components because they are estimated in the same way.

The analysis of variance table for the combined models are shown in Tables I and II respectively for the Eberhart and Russell, and the Perkins and Jinks approaches.

Comparison of Two Approaches. In comparing the two regression models, it is obvious that the parameters used in both approaches have a direct relationship; the Eberhart-Russell β_i and δ_{ij} are equal to the Perkings-Jinks $(1 + b_i)$ and δ_{ij}, respectively. Furthermore, between the two analyses of variance, the sum of squares for the environment linear, heterogeneity of regressions, and pooled deviations of the Eberhart-Russell approach are equal to the sum of squares for the

environments, heterogeneity of regressions, and deviations of the Perkins-Jinks approach, respectively.

In the Perkins-Jinks approach, the interaction source is directly partitioned into the regression and deviation sources. Both regression and deviation terms are orthogonal to other terms in the analysis of variance table; the exact comparison can be made to any term by the means of F tests.

On the other hand, in the Eberhart-Russell approach, partition involves the environment source as well as the interaction source of variation. The regression source, the mean square for the heterogeneity of regressions, seems to be adjusted for the environment source by being corrected for the mean, of which the sum of squares is equal to the environment sum of squares. But this is not so for the deviation source. Thus, in their approach, any F tests which have the mean square for the deviation as numerator or denominator are approximate. For this reason, the Perkins-Jinks approach is more desirable in determining whether the interactions are linear functions of the environment component.

When a comparison of regression and deviations among individual genotypes is intended, it is necessary to divide these variations into parts attributable to individual genotypes. With the Perkins-Jinks approach, this partition is possible arithmetically, but it is invalid statistically, the degrees of freedom attached to the interactions, $(t-1)(s-1)$, are not divisible into t groups.

With the Eberhart-Russell approach, however, it is possible and statistically valid to partition the regression and deviation variation into individual genotypes although these partitioned variations include the environment source besides the interaction source of variation.

Interpretation. In the combined analysis of variance table following the Perkins-Jinks approach, the mean square for the heterogeneity of regressions and the deviations can be tested against the error mean square. If the mean square for the heterogeneity of regressions alone is significant, it can be concluded that, overall, the interactions are satisfactorily explained by the linear regression on the environment component and at least one of the regression coefficients is significantly different from the others. If the deviation mean square alone is significant, there is no simple relationship between the interactions and the environment component. If both items are significant, the mean square for the heterogeneity of regressions should be tested against the deviation mean square to determine whether a significant portion of the variation in the interactions can be explained by the regression. If it is, the linear model would still have predictable value although it is not entirely satisfactory.[31]

Regression coefficients estimated by the Eberhart-Russell model can be compared among genotypes by estimating the approximate standard error from the pooled deviation. If the deviation mean squares for individual genotypes are found to be heterogeneous by Bartlett's test,[33] the standard errors for regression coefficients of individual genotypes should be estimated from their own deviation mean squares and the comparison between genotypes should be made with use of these standard errors.

The deviation mean square measures the departure of actual observation from a fitted regression line. If all assumptions in a simple linear regression statistics were valid in the Eberhart-Russell model, the individual deviation mean square would be the unbiased estimate for the common population variance of genotype mean performance at

each environment: this is the equivalent to the variance of the genotype overall mean performance.[33] The same population variance can be estimated from the pooled error from the combined analysis of variance table as σ_e^2/r. Therefore, although the assumptions for the regression statistics are unlikely to be valid in the Eberhart-Russell approach, the approximate departure of actual observations from the regression lines, which cannot be attributed to chance, could be detected by comparing these two variance estimates.

Biometrical Relationship Between Stability Parameters

The biometrical relationship between various stability parameters was discussed by Becker.[3] Using symbols as shown above, the parameters are interrelated as follows:

Variance about genotype mean performance:

$$\sum_{ijk}(\bar{Y}_{i..} - \bar{Y}_{...})^2 = \beta_i^2 \sum_{ijk} e_j^2 + \sum_{ijk} \delta_{ij}^2$$

$$= \sum_{ijk} e_j^2 + 2(\beta_i - 1) \sum_{ijk} e_j^2 + (\beta_i - 1)^2 \sum_{ijk} e_j^2 + \sum_{ijk} \delta_{ij}^2$$

the Wricke's parameter

$$W_i = (\beta_i - 1)^2 \Sigma e_j^2 + \Sigma \delta_{ij}^2$$

the deviation from the regression line:

$$D_i = \Sigma \delta_{ij}^2$$

the coefficient of determination:

$$r_i^2 = \beta_i^2 \Sigma e_j^2 / \Sigma (\bar{Y}_{i..} - \bar{Y}_{...})^2 \quad \text{or}$$

$$1-r_i^2 = \Sigma \delta_{ij}^2 / \Sigma (\bar{Y}_{i..} - \bar{Y}_{...})^2$$

Since $(\beta_i - 1)^2 \underset{ijk}{\Sigma} e_j^2$ is usually small and the deviation is relatively small compared to the variance about the genotype mean performance, highly positive and negative correlations are expected between the deviation, D_i, and the Wricke's parameter, W_i, and between the deviation, D_i, and the coefficient of determination, r_i^2, respectively.

However, when genotypes with a similar magnitude of deviation are compared, Wricke's parameter estimate tends to be large for the genotype of which regression coefficient is different from 1.0, and the estimate of coefficient of determination tends to be large for the genotype with a large regression coefficient.

Convergence

When the correlation between mean performance and regression coefficients is highly significant, regression lines tend to converge at a small region with varying slopes. The convergence of regression lines can be detected by partitioning the sum of squares for heterogeneity of regression into a part due to convergence and a part due to nonconvergence following the methods suggested by Mandel[26] and Eagle et al.[12] The sum of squares for the convergence is given by,

$$S = r^2 H^2$$

where S is the sum of squares for the convergence, r is a correlation coefficient between mean performance and regression coefficients, and H^2

is the sum of squares for heterogeneity of regression. If mean squares for the convergence is significant when tested against mean squares for the nonconvergence, there is a tendency for regression lines to converge at a point. Such a point can be estimated by,

$$\gamma_o = \mu - 1/\hat{\alpha}$$

where μ is the grand mean and

$$\hat{\alpha} = \sum_i \beta_i(\bar{Y}_{i..} - \bar{Y}_{...}) / \sum_i (\bar{Y}_{i..} - \bar{Y}_{...})^2.$$

CHAPTER III

MATERIALS AND METHODS

Locations and Years

This study used grain yield data collected from wheat yield trials conducted in Oklahoma during 1971-1982. Each year trials were conducted by the Oklahoma Agricultural Experimental Station wheat breeding personnel and data were collected from 4-7 locations. Test locations and years are shown in Table III. The locations were Stillwater, Lahoma, Woodward, Goodwell, Altus, Muskogee, Haskell, and Cordell. At Goodwell, cultivars were tested under both irrigated conditions and dry land conditions.

The tests were abandoned at Goodwell under dry land conditions in 1971, 1974, 1975, 1976, 1978 and 1979 because of drought, and at Altus in 1979 because of severe lodging. Although the Bartlett's test did not determine the heterogeneity of error variance in each environment of analyses, data from Goodwell under irrigated conditions in 1971 were not used in the study because they exhibited exceptionally large error variances. All major wheat growing environments in the state are represented by at least one of these locations each year.

The Goodwell site in the northwestern Panhandle region of Oklahoma, characterized by relatively low annual precipitation, has a Richfield clay loam, a member of the fine, montmorillonitic mesic Aridic Argiustoll. Altus in the southwestern part of the state, characterized

by semi-arid conditions, has a soil complex of Tillman clay loam, a member of the fine, mixed, thermic Typic Paleustolls, and Hollister clay loam, a member of the fine, mixed thermic Pachic Paleustolls. Lahoma in the north central part of the state, representing the largest sheat production area in the state, has a Pond Creek silt loam, a member of the fine, silty, mixed, thermic Pachic Argiustolls. Stillwater in the north central portion of the state, where a main breeding station for wheat is located, has a Norge loam, a member of a Udic Paleustolls. Haskell in the eastern part of the state, receiving a relatively large amount of rainfall compared to the western part of the state, has Taloka silt loam a member of the fine, mixed, thermic Mollic Albaqualfs.

Data were used from 73 individual tests, which comprised location and year combinations in the cultivar yield trials for the 12 years during 1971-1982. Although the same set of cultivars were tested throughout all locations in any one year, the combinations of cultivars changed slightly year by year as older cultivars were dropped off and newer ones were added. In order to analyze year to year variation in the study, a data set for an analysis must be created so as to consist of at least two year periods and a data set consisting of three or four year periods might be preferable. When the number of years in the data set increased, however, the number of cultivars common to all these year periods decreased. Considering this situation, the 12 year data set was divided into four three-year sets as follows: 1971-1973, 1974-1976, 1977-1979, and 1980-1982. Consequently, the 73 location and year combinations for the 12 years were divided into 17, 18, 18, and 20 individual tests for the respective four three-year periods.

Genotypes Analyzed

In any one year, a set of 26-32 genotypes consisting of cultivars, advanced lines and F_1 hybrids were planted all locations. In the early years, cultivars were mostly standard height types. Gradually, they were replaced by semi-dwarf types. Except for four cultivars, Concho, Scout 66, Tam W-101, and Triumph 64, which had been planted for all 12 years, most genotypes were planted for 1-8 years during 1971-1982. Thus, genotypes which were common to all three years of each three-year period were chosen and only those genotypes were used for analyses. The numbers of these gentypes were 12, 15, 15, and 12 in the periods during 1971-1973, 1974-1976, 1977-1979, and 1980-1982, respectively.

Field Practices and Grain Yield

Field practices including pest control, fertilizer application, seedling rates, and planting dates, were equated with good wheat culture in areas where tests were located.

The field layout was a randomized complete block design with four replications at each location throughout all test years. Plots were either four or five rows three m in length. The area harvested for yield determination was either the entire plot or the two center rows of the four row plots. Grain weight was recorded in grams per plot and then was converted to kilograms per hectare for analyses.

Statistical Analyses

Analyses of Variance

A combined analysis of variance was conducted for each of the four sets of the cultivar yield trials with the use of two models. The first was the analysis where a specific combination of years and locations was regarded as an environment. The second was the analysis where genotypes, years, locations, and their interactions were orthogonal terms for which variations were partitioned.

For the first analysis, the data from all locations were used. For the second analysis, however, locations which were common to all three years of each three-year period were chosen and the data from only such locations were subjected to the analysis. Since each year the same set of genotypes were planted at all locations, a deletion of locations so as to create balanced sets of years and locations does not change the number of genotypes analyzed. Tests of significance for all sources of variance in the analyses of variance were made by F tests assuming all effects were fixed in both models.

Linear Regression Analyses

The model presented by Perkins and Jinks[31] was applied to the data from all locations of each of four periods of cultivar trials. The sum of squares for heterogeneity was partitioned into components due to convergence and nonconvergence within each of the four periods following the formulas discussed earlier. The regression coefficients and deviations from regression line were estimated for each genotype by the Eberhart and Russell model.[13] The significance of the deviation from the

regression line was tested by comparing the deviation mean square to the pooled error from the analysis of variance table divided by the number of replications (blocks). The difference of the regression coefficient from other genotypes or the deviation of the regression coefficient from the unity were tested for each genotype by estimating the 95% confidence interval for the regression coefficient with the use of its own deviation mean square. The coefficient of determination and the Wricke's[35] stability parameter were also computed for each genotype.

Some of the cultivars analyzed in one three-year period were also included in the analysis of the following three-year period; i.e., seven cultivars for the two periods, 1971-1973 and 1974-1976, eight cultivars for the two periods, 1974-1976 and 1977-1979, and six cultivars for the two periods, 1977-1979 and 1980-1982. In order to determine the repeatability of the regression analysis, simple correlation coefficients between the regression parameter estimates from these two periods were computed for each of three paired periods. Since ranking is often important in practice and some of the stability parameters studied hereafter are unlikely to have normal distributions, correlation between the regression parameter estimates by ranking was also studied by computing Spearman's rank correlation coefficients.[33]

The same statistical methods were applied to all possible pairs of the stability parameters and cultivar mean yield for each period to examine relationship among these parameters.

The 12 cultivators in the period during 1980-1982 were placed into two groups based on the years when they were released. For a comparison of these two cultivar groups, the sum of the squares for the genotypes, heterogeneity of regressions and deviations from the analysis of variance

table were partitioned into the variations due to the differences between the two cultivar groups and those due to the differences within each of the two groups.

All computations were made by the Statistical Analysis Systems (SAS) at the Oklahoma State University Computer Center.

CHAPTER IV

RESULTS AND DISCUSSION

Analyses of Variance

Mean squares from the analysis of variance for the data from four three-year groups of all location and year combinations are presented in Table IV. Variabilities in the estimates of the effects of each variance source (fixed components of variance), i.e., $\sum_{ijk} g_i^2/(t-1)$, $\sum e_j^2/(s-1)$ and $\sum (ge)_{ij}^2/(t-1)(s-1)$ are presented in Table V.

Mean squares for the differences among genotypes and environments as well as those for genotype by environment interactions were significant at the 0.01 level of probability throughout all four periods of the cultivar yield trials. Significant genotype by environment interactions indicated that cultivars (which will be referred as genotypes in the following) performed differently at least one of the environments with regard to grain yield.

Variability in the estimates of the interaction effects, that is the estimates of variance in unbiased estimates of interaction effects (Table V), was considerably larger than that for genotypes suggesting the difficulty in recognizing differences among genotypes.

Mean squares and variability in the estimates of the effects of each variance source from the analysis of variance for the data from balanced sets of years and locations are presented in Tables VI and VII, respectively.

All variance sources (mean squares) were significant at the 0.01 level of probability in all four periods of the cultivar yield trials. Significant interactions indicated that relative performance of genotypes was not consistent from one environment to another (Table VI).

Variability in the estimates of the location effects was the largest in magnitude among all variance sources indicating that the differences among locations in productivity as measured by average yield were substantial (Table VII).

The variability in the three-factor (genotype by year by location) interaction effects was larger than those for two-factor (genotype by year and genotype by location) interaction effects except the period during 1974-1976, and was generally larger than that for genotype effects.

In two periods during 1971-1973 and 1974-1976, the size of the variability in genotype by year interaction effects was much larger than that for genotype by location effects. However, in the other two periods, the relative sizes of the variabilities in these interaction effects were opposite.

In addition to the large magnitude of the three-factor interactions, inconsistency in the relative magnitude of two two-factor interactions indicated that the differential genotype responses to environments could not be attributed simply to the effects of years or locations.

This is contrary to the results reported by Liang et al.[25] who analyzed wheat yield data in Kansas and found non-significant genotype by year interactions and highly significant genotype by location interac-

tions. In their study, a reduction of the genotype by location interactions was made by dividing the state into sub-areas.

The statistical results in this study, however, suggested that the stratification of the state into sub-areas might be less effective; even after the state was divided into sub-areas according to the similarity in the permanent characteristics of locations, genotype by year interactions within a sub-area would be expected to remain large.

On the other hand, the stratification of the state into sub-areas may have some value to the wheat breeding program of Oklahoma. Based on the results of this study, there were substantial differences in average productivity among areas sampled by test locations. Additionally, excluding locational causes of interactions would tend to reduce the magnitude of the interactions within an area and might allow breeders to concentrate on more specific sources of the interactions in each area. More discussion on the breeding strategies requires consideration of other factors, and consequently, is beyond the scope of the study.

Whatever strategies are taken, however, the statistical genetical methods to recognize genotype responses to environments might be important in the wheat breeding program of Oklahoma since even within a homogenous area, it is expected that substantial interactions would occur.

Linear Regression Analyses

Results of the Linear Regression Analyses

Mean squares for heterogeneity of regression and deviation were estimated by partitioning the sum of squares for genotype by environment interactions. These are presented in Table VIII. Both mean squares when

tested against the pooled error were significant at the 0.01 level of probability throughout all periods of the cultivar yield trials. Mean squares for heterogeneity of regression were significantly greater than those for deviation during 1971-1973, 1977-1979, and 1980-1982.

These results are interpreted as follows:

1. much of the genotype by environment interaction could be explained by the regression of the interaction effects on the environment component,
2. at least one of the regression coefficients was significantly different from others,
3. however, some significant portion of the interaction was not explained by regression.
4. although not entirely satisfactory, the regression analysis could determine the differences in responses to the environments among genotypes.

In the period during 1974-1976 mean squares for heterogeneity of regression were not greater than those for deviation of regression. In this case, characterizing genotypes by regression parameters was not effective although the regression accounted for a significant portion of the interactions.

The estimates of regression parameters, 95% confidence intervals for regression coefficients (β_i), the Wricke's stability parameter, the coefficients of determination, and genotype mean yield over all environments are presented in Tables IX, X, XI, and XII.

The regression coefficients ranged from 0.744 to 1.197, 0.772 to 1.130, 0.739 to 1.243, and 0.802 to 1.256, in four periods of the

cultivar yield trials during 1971-1973, 1974-1976, 1977-1979, and 1980-1982, respectively.

Based on the confidence intervals, there were differences in the regression coefficients among genotypes in all test periods with the exception of the period during 1974-1976. Some genotypes had regression coefficients that differed from unity, with unity being derived from the mean of the coefficients over all genotypes.

Deviation mean squares were significantly greater than zero for most of the genotypes in all test periods, and there were large differences among genotypes for this parameter.

Since the range of confidence intervals is proportional to the standard error of the regression coefficients, which in turn is proportional to the square root of the deviation mean square, the relatively large deviations observed for most of the genotypes prevented the detection of differences in the regression coefficients. This was especially true for the results from the period during 1974-1976 and was in agreement with the results of the previous analysis.

Repeatability of the Regression Analysis

Simple correlation coefficients and Spearman's rank correlation coefficients were computed between two estimates of the regression parameters for the same genotype evaluated in two different periods (Table XIII).

A positive association was observed for all comparisons with the exception of the rank correlation coefficient for the regression coefficients between 1971-1973 and 1974-1976. However, only four out of 12 coefficients were significant at the 0.05 or 0.01 levels of probability.

The cultivars used in the comparisons, along with their parameter rankings are presented in Tables XIV, XV, and XVI. It is readily seen that the ranking of a few genotypes was greatly different between two periods, i.e. the ranking of Scout 66 by the regression coefficient in a comparison between 1971-1973 and 1974-1976. In general, a large change in ranking between two periods was associated with a large magnitude in deviation mean squares or a large change in the estimates of the deviation mean squares. When the deviation is large, the regression line is unlikely to have a predictive value for the genotype concerned. Taking this into account and excluding the genotypes with large deviations from the comparison, the relative order of other genotypes were similar between two periods. Thus, with certain limitations, the regression analysis might have some repeatability over different environments.

Relationship Between Parameters

The empirical relationship between the regression parameters and other stability parameters was examined by computing simple correlation coefficients and Spearman's rank correlation coefficients within each period of the cultivar yield trials (Table XVII).

The results showed that the genotype mean yield (Y_i) generally had a highly significant positive correlation with the regression coefficients (β_i)(0.483-0.891), but no consistent correlation with other parameters.

The regression coefficient and the coefficient of determination (r_i) were positively correlated, in general. Between the regression coefficient and the deviation mean square (D_i), there seemed to be no constant correlation. Similar results were obtained between the regression coefficient and the Wricke's stability parameter (W_i).

As expected, a significantly high correlation among the deviation mean square, the coefficient of determination and the Wricke's parameter was found except for the period during 1980-1982. Since the deviation from the regression line measures the departure of an actual observation from the theoretical model, it is of great importance in the linear regression analysis. Although high correlation was obtained, the coefficient of determination was found to give somewhat different estimates from those of the deviation of regression; therefore, the coefficient of determination might not be equally effective and perhaps should not replace the measurements of the deviation.

The results of the correlation by ranking estimates were almost identical to those found for simple correlation.

Convergence

The sum of the squares of the heterogeneity of regression was partitioned into convergence and non-convergence (Table VIII). The mean square for the convergence was significant throughout all test periods indicating that in general the regression lines tended to radiate from a small region, i.e., the regression lines tended to converge at some point. Such a region was estimated for each test period: -331 kg/ha, -324 kg/ha, 1199 kg/ha, and 616 kg/ha in four periods during 1971-1973, 1974-1976, 1977-1979, and 1980-1982, respectively.

In general the region of convergence was below normal in environmental productivity; this suggested that the genotype with high mean yield tended to be superior at a range of normal environments and thus, the

mean yield for genotypes might be sufficient to determine the genotypes which perform better than others at all environments.

Comparison of Newly Released and Traditional Cultivars

The 12 cultivars analyzed in the periods of the cultivar yield trials during 1980-1982 (Table XII) consisted of eight newly released cultivars (released after 1971): Centurk 78, Payne, Osage, Wings, Tam W-101, Newton, Vona, and Tam 105, and four traditional cultivars: Concho, Scout 66, Triumph and Triumph 64.

In order to compare these two cultivar groups, the sums of the squares for the genotypes, heterogeneity of regression and deviation from the analysis of variance table were partitioned into the variations due to the differences between the two cultivar groups, and those due to the differences within each of the two groups (Table XVIII).

The differences between the two cultivar groups were significant for genotypes, heterogeneity of regression, and deviation at the 0.01 level of the probability. The newly released cultivars tended to have larger regression coefficients and deviations as well as higher mean yield. The heterogeneity of regression was highly significant for newly released cultivars, but was not significant for traditional cultivars. This indicated that newly released cultivars responded inconsistently to the changes of environments, but all traditional cultivars responded similarly and poorly to the improvement of environments.

Discussion on the Linear Regression Analyses

When summarizing the results of the linear regression analysis, it appears that this analysis could adequately explain the differential

response of genotypes to environments in three out of four tests in this study. The parameter estimates for the genotypes given by the regression analysis might be repeatable over years except for genotypes with large deviations. Significant differences in regression coefficients and deviations among genotypes were detected suggesting that the parameter estimates could be used for characterizing the genotype response to environments. Overall, the linear regression analysis might have some practical value in selecting breeding lines of the wheat breeding program of Oklahoma. It must be noted here, however, that there is a case, as the result from the 1974-1976 period in this study, where the linear regression analysis seems to give reliable parameter estimates to some individual genotypes, yet, this method fails to explain the interactions as a whole.

There may be no biological or physiological reason to believe genotype by environment interactions will be a linear function of environments.[17] For this reason, the regression parameters in an experiment must be examined and the overall applicability of this method to the experiment must be considered by constructing a complete analysis of variance table provided by either Eberhart and Russell[13] or Perkins and Jinks;[31] the parameter estimates obtained by simply regressing genotype performances on environmental mean are sometimes misleading.

The correlation between genotype mean yield and regression coefficients was found to be highly significant in general. Geometrically this correlation is interpreted to mean that regression lines converged at a small region of environments with varying slopes. This region was generally at the low end of the scale, usually below the yield range experienced in agricultural practice for wheat in Oklahoma.

The statistical evidence regarding the correlation between genotype mean yield and regression coefficients implies that in terms of germplasm represented by genotypes analyzed in this study, genetic modification toward higher yield will be associated with the improvement of yielding ability mostly under favorable environments. In other words, there is little possibility to develop cultivars with high average yield as well as a wide adaptation as defined by Eberhart and Russell.[13]

Such relationship in genetic control between high mean yield and an adaptability seems to have a broad basis. Results from comparisons between newly released cultivars and traditional cultivars indicated that yield improvement realized by these newer cultivars resulted from the selection of genotypes responsive to more productive environments. If the characteristics of the responses to environments had been inherited independently of that for high mean yield, there would have been the possibility of selecting genotypes with high yield and insensitivity in response to environments. Apparently this did not happen.

There are biological reasons why the improvement of yield under poor environment conditions has not been yet very successful, but our understanding of this problem is limited. One alternative would be to seek different genetic sources of wheat in which the traits of adaptation and yield are independently inherited. This would allow independent manipulation of these traits. Unless such genetic sources are found, regression coefficients estimated by the linear regression analysis are of limited usefulness as suggested by Eagle et al.[12]: selection for wide adaptation would not be achieved by concurrent selection for high mean yield and a regression coefficient of unity. Instead, selection by genotype mean yield over all environments alone could identify genotypes

which were superior at all environments. Based on the results in this study, this selection strategy, that leads selection toward large regression coefficients, might be appropriate in the wheat breeding program of Oklahoma.

Among various definitions of stable genotypes, one given by Breese[5] seems to be the most meaningful for estimating stability of grain yield of wheat in Oklahoma. In this case stability is termed as the measurements of unpredictable irregularities in the response to environment as provided by the deviation from regression.

In consideration of this definition, much is left to be improved: most genotypes studied had large deviations in the analysis. For this purpose, the linear regression analysis still is useful in exploiting stable genotypes.

CHAPTER V

SUMMARY AND CONCLUSION

This study, which examined genotype by environment interactions in wheat grain yield with particular reference to the linear regression analysis, was conducted to provide information which could be useful in dealing with the difficulties created by these interactions in a plant breeding program.

The study used grain yield data from the cultivar yield trials conducted at 4-7 locations each year in Oklahoma during the 12-year-period 1971-1982. The cultivar yield trials were divided into four three-year periods, and data were used for cultivars which were common to all three years of each of four periods.

An analysis of variance was applied to the data set for each period. Statistical results revealed genotype by environment interactions of large magnitude. A balanced set of years and locations was derived for each period and responses were examined further by another analysis of variance model which could separate the effects of years, locations, genotypes and their interactions.

It was found that three-factor as well as two two-factor interactions were highly significant throughout all three-year periods. Among them, genotype by year by location interactions were, in general, larger than the differences among genotypes. The relative magnitudes of genotype by year interactions and genotype by location interactions were inconsistent from period to period.

These results suggested that the interactions were substantial and complex such that stratification of environments would not appear to be effective in the wheat breeding program of Oklahoma.

A linear regression analysis based on the Perkins and Jinks model was applied to the yield data from all locations of each period. This analysis could adequately explain much of the interaction and permitted a comparison of genotypic response to environments by the use of regression parameters. When the same genotypes were evaluated at different three-year periods, this analysis tended to give somewhat different estimates of the parameters to genotypes, especially with the large deviations from regression lines. Except for such irregular genotypes, however, the regression analysis was found to be repeatable. In view of this, linear regression might have some practical value in determining genotype response to environments and in making comparison among genotypes in the wheat breeding program of Oklahoma.

Highly positive correlations were found between regression coefficients and genotype mean yield in all periods of the cultivar yield trials. This correlation resulted in the convergence of the regression lines at a small region, and that region was at an environment generally below normal in productivity levels.

When cultivars were grouped as newly released and traditional types and analyzed from the period during 1980-1982, the newly released cultivars tended to have significantly larger regression coefficients and deviation mean squares as well as higher mean yields.

These results suggested that traditional selection procedures, where selection is practiced on high yield performance at most of the test

locations, resulted in the cultivars performing well under favorable conditions.

High correlations observed between regression coefficients and genotype mean yield suggested that there was little possibility for the independent manipulation of yield and stability across environments, and that selection by use of mean yield alone would be sufficient to develop cultivars which are superior to all environments.

However, most of the cultivars were found to have relatively large deviation from the regression lines. In this sense, the linear regression analysis might offer some help to exploit stable cultivars.

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APPENDIXES

TABLE I

THE ANALYSIS OF VARIANCE TABLE
FOR A COMBINED MODEL BY THE
EBERHART-RUSSELL APPROACH

Sources of Variance	Sum of Squares		d.f.
	Definition	Expectation	
Total	$\sum_{ijk}(Y_{ijk} - \bar{Y}_{...})^2$		tsr-1
Genotype	$\sum_{ijk}(\bar{Y}_{i..} - \bar{Y}_{...})^2$		t-1
Envi. + Geno. x Eniv.	$\sum_{ijk}(\bar{Y}_{ij.} - \bar{Y}_{i..})^2$	$\sum_{ik}(\beta_{ij}^2\sum e_j^2 + \sum_j \delta_{ij}^2)$	ts(r-1)
Regressions pooled	$\sum_{ijk}(\hat{\bar{Y}}_{ij.} - \bar{Y}_{i..})^2$	$\sum_{ik}(\beta_i^2 \sum_j e_j^2)$	t
Environment linear (due to means)	$\sum_{ijk}(\hat{\bar{Y}}_{.j.} - \bar{Y}_{...})^2$	$\sum_{ik}(\bar{\beta}_{.j}^2 \sum e_j^2)$	1
=	$\sum_{ijk}(\bar{Y}_{.j.} - \bar{Y}_{...})^2$	$\sum_{ijk} e_j^2$	
Heterogeneity of regression	$\sum_{ijk}(\hat{\bar{Y}}_{ij.} - \bar{Y}_{i..})^2$		t-1
-	$\sum_{ijk}(\bar{Y}_{.j.} - \bar{Y}_{...})^2$		
Pooled deviations	$\sum_{ijk}(\bar{Y}_{ij.} - \hat{\bar{Y}}_{ij.})^2$	$\sum_{ijk}\delta_{ij}^2$	t(s-2)
Pooled error	$\sum_{ijk}(Y_{ijk} - \bar{Y}_{ij.})^2$		(t-1)s(r-1)
-	$\sum_{ijk}(\bar{Y}_{.jk} - \bar{Y}_{.j.})^2$		

TABLE II

THE ANALYSIS OF VARIANCE TABLE
FOR A COMBINED MODEL BY THE
PERKINS-JINKS APPROACH

Sources of Variance	Sum of Squares	d.f
Total	$\sum_{ijk}(Y_{ijk} - \bar{Y}_{...})^2$	tsr-1
Genotypes	$\sum_{ijk}(\bar{Y}_{i..} - \bar{Y}_{...})^2$	t-1
Environments	$\sum_{ijk}(\bar{Y}_{.j.} - \bar{Y}_{...})^2$	s-1
Geno. x Envi.	$\sum_{ijk}(\bar{Y}_{ij.} - \bar{Y}_{i..} - \bar{Y}_{.j.} + \bar{Y}_{...})^2$	(t-1)(s-1)
Heterogeneity of regressions	$\sum_{ik}(b_i^2 \sum_j e_j^2)$	t-1
Remainder (Deviations)	$\sum_{ijk} \delta_{ij}^2$	(t-1)(s-2)
Pooled error	$\sum_{ijk}(\bar{Y}_{ijk} - \bar{Y}_{ij.})^2 - \sum_{ijk}(\bar{Y}_{.jk} - \bar{Y}_{.j.})^2$	(t-1)s(r-1)

TABLE III

TEST YEARS AND LOCATIONS OF THE CULTIVAR YIELD TRIALS
1971-1982

Locations	Crop Years											
	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982
Stillwater	*	*	*	*	*	*	*	*	*	*	*	*
Lahoma	*	*	*	*	*	*	*	*	*	*	*	*
Woodward	*	*	*	*	*	*	*	*	*	*	*	*
Goodwell												
Irrigated land	+	*	*	*	*	*	*	*	*	*	*	*
Dryland	-	*	*	-	-	-	*	-	-	*	*	*
Altus		*	*	*	*	*	*	*	-	*	*	*
Muskogee	*	*		*	*	*	*					
Haskell								*	*	*		
Cordell												*

*Indicates a year-location of which data was used in analyses
-Indicates that a trial was seeded but not harvested
+Indicates that data was not used because of large error variance

TABLE IV

MEAN SQUARES FROM THE ANALYSIS OF VARIANCE OF ALL LOCATIONS

Sources of Variation	1971-1973		1974-1976		1977-1979		1980-1982	
	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.
		X 10^3		X 10^3		X 10^3		X 10^3
Genotype	11	3484**	14	2160**	14	4786**	11	9482**
Environment	16	67997**	17	34089**	17	73114**	19	51980**
Geno. x Env.	176	639**	238	527**	238	446**	209	771**
Pooled error	561	107	756	124	756	109	660	134

**Significant at the 0.01 level of probability.

TABLE V

FIXED COMPONENTS OF VARIANCE FROM THE ANALYSIS OF VARIANCE OF ALL LOCATIONS

Sources of Variance	1971-1973	1974-1976	1977-1979	1980-1982
	X 10^3	X 10^3	X 10^3	X 10^3
Genotype	50	28	65	117
Environment	1414	566	1277	1080
Geno. x Envi.	133	101	84	157
Pooled Error	107	124	109	144

TABLE VI

MEAN SQUARES FROM THE ANALYSIS OF VARIANCE
OF BALANCED SETS OF YEARS AND LOCATIONS

Sources of Variation	1971-1973		1974-1976		1977-1979		1980-1982	
	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.
		X 10^3		X 10^3		X 10^3		X 10^3
Genotype	11	2565**	14	2160**	14	4757**	11	9295**
Year	2	786**	2	8931**	2	138504**	2	22294**
Location	2	14856**	5	70468**	3	183497**	5	88691**
G x Y	22	890**	28	1607**	28	313**	22	1002**
G x L	22	400**	70	431**	42	759**	55	972**
G x Y x L	44	433**	140	360**	84	418**	110	711**
Y x L	4	5276**	10	20932**	6	10315**	10	26769**
Reps.	27	694**	54	456**	36	285**	54	587**
Pooled error	297	93	756	124	504	125	594	138

**Significant at the 0.01 level of probability

TABLE VII

FIXED COMPONENTS OF VARIANCE FROM THE ANALYSIS OF VARIANCE OF BALANCED SETS OF YEARS AND LOCATIONS

Sources of Variance	1971-1973	1974-1976	1977-1979	1980-1982
	$\times 10^3$	$\times 10^3$	$\times 10^3$	$\times 10^3$
Genotype	69	28	97	127
Year	5	24	577	77
Location	103	391	1019	615
Geno. x Year	66	62	12	36
Geno. x Location	26	26	53	69
Geno. x Year x Location	85	59	73	143
Pooled Error	93	124	125	138

TABLE VIII

MEAN SQUARES FOR HETEROGENEITY OF REGRESSION, DEVIATION, AND CONVERGENCE FROM THE ANALYSIS OF VARIANCE

Sources of Variation	1971-1973		1974-1976		1977-1979		1980-1982	
	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.
		X 10^3		X 10^3		X 10^3		X 10^3
Geno. x Envi.	176	639**	238	527**	238	446**	209	771**
Hetero. of regression	11	1316**	14	514**	14	1547**	11	1633**
Convergence	1	4855	1	1677	1	17198	1	13402
Non-conver.	10	962	13	424	13	342	10	456
Deviation	165	594**	224	528**	224	377**	198	723**
Pooled error	561	107	756	124	756	109	660	134
$F = \frac{MS(Hetero.)}{MS(Devi.)}$		2.215*		0.973		4.103**		2.259*
$F = \frac{MS(Conver.)}{MS(Non\text{-}Conver.)}$		5.047*		3.955*		50.287**		29.390**

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

TABLE IX

STABILITY PARAMETER ESTIMATES
1971-1973

Genotypes	Regression Coefficients	95% confidence intervals for β_i	Deviation Mean Squares	Coefficients of Determination	Wricke's Parameter	Mean Yield
		0.7 0.8 0.9 1.0 1.1 1.2 1.3	X 10^3		X 10^3	(kg/ha)
OK585551	0.744		86**	0.907	11219	2283
Triumph	0.861		109**	0.911	8624	2393
Scout 66	0.940		114**	0.921	7422	2932
Pronto	0.947		168**	0.890	11211	2622
Triumph 64	0.956		63**	0.956	4175	2640
Nicoma	0.961		83**	0.944	6175	2663
Concho	1.040		215**	0.884	13037	2709
TAM W-101	1.070		247**	0.875	16161	3093
Danne	1.108		63**	0.967	5397	2717
Yukon	1.124		209**	0.901	14318	2876
Centurk	1.131		96**	0.953	8437	2853
Caprock	1.197		180**	0.913	13636	2551

**Significant at the 0.01 level of probability

TABLE X

STABILITY PARAMETER ESTIMATES
1974-1976

Genotypes	Regression Coefficients	95% confidence intervals for β_i	Deviation Mean Squares	Coefficients of Determination	Wricke's Parameter	Mean Yield
		0.7 0.8 0.9 1.0 1.1 1.2 1.3	X 10^3		X 10^3	(kg/ha)
Triumph 64	0.772		113**	0.761	9255	2621
Dekalb 582	0.800		62*	0.863	5504	2539
Caprock	0.874		352**	0.567	23134	2691
Concho	0.898		112**	0.813	7582	2726
Rall	0.963		136**	0.805	8731	2862
Homestead	0.996		96**	0.862	6145	2878
TAM W-101	1.014		203**	0.753	13022	2825
TAM W-103	1.030		190**	0.772	12168	2549
Centurk	1.059		73**	0.905	4936	3014
Osage	1.073		70**	0.909	4677	3123
Sage	1.078		73**	0.905	4936	3014
Danne	1.084		80**	0.899	5387	2662
Scout 66	1.101		43	0.945	3126	2761
OK 66V2621	1.128		104**	0.881	7256	2903
Baca	1.130		143**	0.843	9809	2662

*, **Significant at the 0.05 and 0.01 levels of probability

TABLE XI

STABILITY PARAMETER ESTIMATES
1977-1979

Genotypes	Regression Coefficients	95% confidence intervals for β_i	Deviation Mean Squares	Coefficients of Determination	Wricke's Parameter	Mean Yield
		0.7 0.8 0.9 1.0 1.1 1.2 1.3	X 10^3		X 10^3	(kg/ha)
Triumph 64	0.739		71**	0.909	10156	3031
Triumph	0.771		49**	0.940	7492	2906
Dekalb 589	0.878		140**	0.877	10165	3197
Concho	0.918		107**	0.911	7388	2930
Sturdy	0.941		125**	0.911	8267	3166
Centurk	0.990		76**	0.943	4894	3324
Osage	0.999		70**	0.949	4473	3372
Larned	1.010		50*	0.964	3193	3474
Sage	1.024		73**	0.949	4749	3253
Pioneer 940	1.041		67**	0.954	4443	3338
Rall	1.065		27	0.982	2051	3347
Scout 66	1.089		66**	0.959	4481	3292
Lindon	1.146		64**	0.964	5840	3570
TAM W-101	1.147		182*	0.904	13437	3656
Vona	1.243		152**	0.929	14630	3847

*, **Significant at the 0.05 and 0.01 levels of probability

TABLE XII

STABILITY PARAMETER ESTIMATES
1980-1982

Genotypes	Regression Coefficients	95% confidence intervals for β_i	Deviation Mean Squares	Coefficients of Determination	Wricke's Parameter	Mean Yield
		0.7 0.8 0.9 1.0 1.1 1.2 1.3	X 10^3		X 10^3	(kg/ha)
Scout 66	0.802		119**	0.861	11795	3196
Triumph	0.844		133**	0.859	11617	3061
Concho	0.844		179**	0.820	14872	2739
Centurk 78	0.894		99**	0.903	8028	3414
Triumph 64	0.908		188**	0.834	14214	3232
Payne	1.034		134**	0.901	9748	3565
Osage	1.040		151**	0.891	11006	3341
Wings	1.043		225**	0.847	16386	3694
TAM W-101	1.078		221**	0.863	15712	3820
Newton	1.105		135**	0.912	10649	3676
Vona	1.154		186**	0.891	15369	3725
TAM 105	1.256		226**	0.889	21646	3880

**Significant at the 0.01 level of probability

TABLE XIII

CORRELATION OF THE PARAMETER ESTIMATES
FROM TWO SUCCESSIVE TEST PERIODS

Parameters	Between 1971-1973 1974-1976	Between 1974-1976 1977-1979	Between 1977-1979 1980-1982
Regression coefficient			
Correlation coefficient	0.077	0.786**	0.415
Rank coefficient	-0.143	0.548	0.257
Deviation			
Correlation coefficient	0.534	0.634*	0.792*
Rank coefficient	0.357	0.333	0.886**

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

TABLE XIV

CULTIVAR RANKING BY REGRESSION COEFFICIENTS AND DEVIATIONS 1971-1973 VERSUS 1974-1976

Cultivars	β_i		Deviation	
	(I)	(II)	(I)	(II)
Scout 66	1	7	4	1
Triumph 64	2	1	1	5
Concho	3	3	6	4
Tam W-101	4	4	7	6
Danne	5	6	2	3
Centurk	6	5	3	2
Caprock	7	2	5	7

β_i - a regression coefficient for ith cultivar

Deviation - a deviation from regression for ith cultivar

(I) - a period during 1974-1976
(II) - a period during 1977-1979

TABLE XV

CULTIVAR RANKING BY REGRESSION COEFFICIENTS AND DEVIATIONS 1974-1976 VERSUS 1977-1979

Cultivars	β_i		Deviation	
	(I)	(II)	(I)	(II)
Triumph 64	1	1	6	4
Concho	2	2	5	7
Rall	3	6	7	1
Tam W-101	4	8	8	8
Centurk	5	3	4	6
Osage	6	4	2	3
Sage	7	5	3	5
Scout 66	8	7	1	2

β_i - a regression coefficient for ith cultivar
Deviation - a deviation from regression for ith cultivar

(I) - a period during 1974-1976
(II) - a period during 1977-1979

TABLE XVI

CULTIVAR RANKING BY REGRESSION COEFFICIENTS AND DEVIATIONS 1977-1979 VERSUS 1980-1982

Cultivars	β_i		Deviation	
	(I)	(II)	(I)	(II)
Triumph 64	1	4	4	5
Triumph	2	2	1	2
Concho	3	3	5	4
Osage	4	5	3	3
Scout 66	5	1	2	1
Tam W-101	6	6	6	6

β_i - a regression coefficient for ith cultivar

Deviation - a deviation from regression for ith cultivar

(I) - a period during 1977-1979
(II) - a period during 1980-1982

TABLE XVII

CORRELATION BETWEEN PARAMETERS

Parameters		1971-1973	1974-1976	1977-1979	1980-1982
Simple correlation coefficients					
Y_i	β_i	0.579*	0.483	0.891**	0.864**
Y_i	D_i	0.446	0.403	0.343	0.412
Y_i	r_i	-0.094	-0.290	0.245	0.583*
Y_i	W_i	0.215	-0.349	0.253	0.355
β_i	D_i	0.406	-0.262	0.264	0.561
β_i	r_i	0.109	0.553*	0.378	0.523
β_i	W_i	0.270	-0.339	0.075	0.537
D_i	r_i	-0.854**	-0.945**	-0.779**	-0.402
D_i	W_i	0.916**	0.993**	0.857**	0.910**
r_i	W_i	-0.867**	-0.966**	-0.743**	-0.348
Rank correlation coefficients					
Y_i	β_i	0.420	0.359	0.846**	0.902**
Y_i	D_i	0.350	-0.300	0.068	0.594*
Y_i	r_i	-0.056	0.497	0.386	0.413
Y_i	W_i	0.112	-0.477	-0.104	0.448
β_i	D_i	0.273	-0.243	0.043	0.678*
β_i	r_i	0.133	0.607*	0.461	0.391
β_i	W_i	0.266	-0.379	-0.104	0.441
D_i	r_i	-0.853**	-0.900**	-0.800**	-0.378
D_i	W_i	0.888**	0.961**	0.736**	0.867**
r_i	W_i	-0.853**	-0.957**	-0.821**	-0.580*

Y_i, β_i, D_i, r_i, and W_i represent genotype mean yield, regression coefficient, deviation from regression line, coefficient of determination, and Wricke's stability parameter, respectively.

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

TABLE XVIII

MEAN SQUARES FROM THE ANALYSIS OF VARIANCE TABLE FOR A CULTIVAR GROUP COMPARISON, 1980-1982

Sources of Variance	d.f.	Mean Squares
Genotype	11	9482
New versus Old	1	72401 **
New	7	2832 **
Old	3	4026 **
Genotype x Environment	209	771
Heterogeneity of Regression	11	1633
New versus Old	1	11196 **
New	7	899 **
Old	3	157
Deviation	198	723
New versus Old	18	1654 **
New	126	703 **
Old	54	458 **
Pooled error	660	144

**Significant at the 0.01 level of probability

VITA 2

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