GENOTYPE*ENVIRONMENT INTERACTION AND APPLICATION

by

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B.S., Henan Agricultural University, China, 1981

A MASTER'S THESIS

submitted in partial fulfillment of the

requirements for the degree

MASTER OF SCIENCE

Department of Agronomy

KANSAS STATE UNIVERSITY

Manhattan, Kansas

1987

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I would like to dedicate this thesis to my wife, Xu Qiang, and my son, Liu Suang-Suang.

ACKNOWLEDGMENTS

I would like to express my sincere appreciation to my co-major professors, Drs. Thomas S. Cox and Rollin G. Sears, for their guidance, helpful suggestions, encouragement and patience. Appreciation is also extended to my committee member, Dr. Arlin M. Feyerharm, for the review of the manuscript and his constructive comments.

I am especially indebted to Dr. James P. Shroyer for providing the county demonstration plot data and Mr. Ted L. Walter for allowing me use the Kansas Winter Wheat Variety Performance Test data.

And finally, my deepest gratitude goes to my parents and grandparents for being a constant source of affection and inspiration; to my wife, Xu Qiang, for her encouragement, support and untiring patience; and to my younger brother, Liu Ben-Qun, for his encouragement, and support.

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LITERATURE REVIEW

The phenomenon of genotype by environment interaction has long been recognized. About one thousand years ago, the Chinese agronomist Ja SeYu in his famous work Qi Men Yaw Shoe indicated that some kinds of crops can grow very well in dry weather, while others can't. He noted that peasants may increase yield by selecting good seeds, and by building irrigation systems. Because they were recorded in Chinese, Ja's observations have not been well known outside of China. Fisher and Mackenzie (1923) published their paper about potato production and indicated that "the yields of different varieties under different manurial treatments are better fitted by a product formula than by a sum formula". From that time, the existence of genotype-environment (G*E) interaction has received much attention by many scientists.

Research on the complicated of G*E interaction may be conducted in the field, greenhouse, or laboratory. As genetists sometimes divide genes into main-effect genes and micro-effect genes, we can also divide ecological factors into main-effect factors (such as temperature, soil type, or elevation) and micro-effect factors. The latter would be defined as factors whose individual effects are too small to be detected but whose cumulative effect is large. Research at the greenhouse or laboratory level is concerned most often with main-effect factors. However, field level research is concerned with both main-effect and micro-effect factors.

Field level research on G*E interaction, which is the subject of this review, can be divided into three types:

a. Analysis of variance for data from multiple-location and multiple-year field experiments.

b. Regression of individual yields on an environmental index, often the mean yield of all cultivars for each site.

c. Multivariate analysis.

Immer et al (1934) used analysis of variance to analyze barley data and determine G*E interaction. Sprague and Federer (1951) suggested that variance components might be used to partition the effects of genotypes, environments, and their interaction by equating the observed mean squares in the analysis of variance to their expections using a random model. They proposed that the following mathematical model can represent this kind of experiment.

$$Y_{ij} = \mu + G_i + E_j + (GE)_{ij} + \epsilon_{ijk}$$

Where Y_{ij} is the yield of genotype i in environment j; μ is the overall mean; G_i is the genotypic effect; E_j is the environment effect; $(GE)_{ij}$ is the G*E interaction effect; and ϵ_{ijk} is a random error effect. A genetic variance component analysis was developed by Mather and Jones (1958). Further discussions of the ANOVA method in the study of G*E interaction are found in Comstock and Moll (1963), and Hanson (1964). Such an analysis of variance is the first step in any study of G*E interaction. Through this kind of analysis it may be determined whether or not the interaction exists. The disadvantage of this method is that

no information about the individual genotypes is obtained.

Plaisted and Peterson (1959) developed a mean variance component for pairwise G*E interaction. The mean of the estimated variance components of the G*E interaction for all pairs of genotypes that include genotype i was considered to be the stability measure for genotype i. Plaisted (1960) proposed a similar variance component as another stability parameter. In that analysis one genotype i was deleted from the entire set of data and the G*E interaction variance from that subset was the stability index for genotype i.

Wricke (1962,1964,1965) developed the concept of ecovalence to solve this problem. Ecovalence was defined as the ratio of the interaction sum of squares contributed by each individual genotype to the total interaction sum of squares:

$$EV_i = SS(GE)_i \; / \; SS(GE)$$

where $SS(GE)_i = \sum_{j=1}^{q} (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})^2$ was the environmental sum of squares within genotype i, $SS(GE) = \sum_{i=1}^{p} \sum_{j=1}^{q} (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})^2$ was the total environmental sum of squares within genotypes, and j represented the environments. The final dot represented replications. A large EV_i value indicated low stability.

An approach similar to Wricke's ecovalence was given by Shukla (1972) . He defined a variance σ_i^2 , called a "stability variance", as a stability parameter. It can be estimated by the following equation (Ehrenberg 1950):

$$\sigma_i^2 = \frac{p}{(p-2)(q-1)} \sum_{j=1}^{q} (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})^2 - \frac{SS(GE)}{(p-1)(p-2)(q-1)}$$

where p and q represent the numbers of genotypes and environments, respectively. As with the EV_i value, a large value indicated low stability. Hinkelman (1974) gave a method to test the significance of difference between σ_i^2's.

The regression approach to evaluating stability was proposed originally by Yates and Cochran (1938). They indicated that the average over all genotypes for a particular trial, and a measure of the expected genotypic response to the varying environmental conditions, is obtained by plotting individual genotype values against the trial means. Finlay and Wilkinson (1963), using a method similar to that of Yates and Cochran, defined the regression coefficient (b) of the yield of an individual cultivar on the mean yield of all cultivars as a stability parameter. With b=1 , a cultivar was considered to have average stability; b>1 indicated below-average stability; and b<1 indicated above-average stability. Eberhart and Russell (1966) considered Finlay and Wilkinson's b to be a "response" parameter and defined the mean square for the deviations from regression (S_d) as a stability parameter. Perkins and Jinks' (1968) regression coefficient and residual mean square were similar to Finlay and Wilkinson's "b" and Eberhart and Russell's "S_d" respectively, except that the observed values were adjusted by the location effect before the regression was performed.

Therefore, the mean b value over all genotypes was 0 instead of 1 as in the other analysis. Tai (1971) defined another two stability parameters, α and λ. α equaled Eberhart and Russell's regression coefficient minusone and λ was estimated by the following equation,

$$\hat{\lambda}_i = \frac{\sigma^2_{eg} + \sigma^2_e}{\sigma^2_e}$$

where σ^2_{eg} was the variance component for deviations from linearity for genotype i and σ^2_e was the error variance. Tai defined the perfectly stable cultivar as having $(\alpha, \lambda)=(-1,1)$, and the cultivar of average stability as having $(\alpha, \lambda)=(0,1)$.

The regression approach is based on the assumption that the G*E interaction is a linear function of an environmental index(I_j):

$$(G*E)_{ij} = B_i I_j + \varepsilon_{ij}$$

The regression methods have been criticized, mainly because the independent variable and dependent variable are inevitably correlated, especially when there are only few genotypes in an experiment (Freeman and Perkins, 1971; Hardwick and Wood, 1972; Miezan, Milliken and Liang, 1979).

Application of principal component analysis in the study of G*E interactions was developed by Gollob (1968) and Mandel (1969,1971). Principal component analysis is a useful method for the categorization of environmental conditions and for the classification of cultivars for yield stability. Perkins (1972)

used multiple regression of the principal component on climatic parameters. Goodchild and Boyd (1975) tried to interpret the principal component in terms of seasons and locations . The disadvantage of the principal component analysis is that the components do not necessarily have any direct relationship to known environmental factors.

Another multivariate method is cluster analysis. The main purpose of cluster analysis is to reduce the impact of a G*E interaction through stratifying genotypes or environments into groups, so that interactions within groups are minimized. Several methods have been proposed to achieve this objective . Horner and Frey (1957) used a divisive cluster method to separate environments into homogeneous groups . Abou-El-Fittouh et al (1969) defined homogeneous regions for cotton cultivar tests by cluster analysis (Sokal and Michener , 1958) . They used a distance coefficient and a correlation coefficient as dissimilarity measures and a variable group clustering strategy.

Mungomery et al (1974) employed an unstandardized squared Euclidean distance as a dissimilarity measure, using an unweighted group average link clustering strategy. The calculations were done using the general agglomerative algorithm of Lance and Williams (1967). Byth et al (1976) used a variance-standardized squared Euclidean distance as a dissimilarity measure to classify environments in the 4th International Spring Wheat Nursery.

Gower (1966, 1967) gave a review of cluster methods. He pointed out that distance can be defined in many ways, so a cluster definition must be relative to the particular measure of distance chosen, and that the lack of a precise definition of a cluster will not stop people from using methods of cluster analysis. Corrnack (1971) listed 10 different dissimilarity measures and 8 different clustering strategies.

Lin and Thompson (1975) used their dissimilarity index, based on the test statistics for a joint regression of a pair of genotypes, on the data of Yates and Cochran (1938). Lin (1982) proposed a dissimilarity measure for a pair of genotypes to be the squared distance between them, adjusted for the average effects of genotypes. Ramey and Rosielle (1983) modified Lin's method by minimizing the total sum of squares for G*E interaction within clusters at each fusion cycle.

Johnson (1977) used cluster analysis to evaluate the yield and stability of a set of maize hybrids. He used a weighted Euclidean distance as measure of similarity and maximum distance between clusters as a clustering metric. Ghaderi et al (1980) used cluster analysis to classify environments and genotypes in wheat, with a distance coefficient as a dissimilarity measure and a complete linkage clustering strategy. Fox and Rosielle (1982) proposed a standardized distance and concluded that standardization was the most effective procedure for reducing the influence of environment main effects on squared Euclidean distance measures of dissimilarity.

Lin et al (1986) presented a comprehensive summary of cluster analysis used in research of G*E interaction. They divided cluster methods into two major classes of similarity measure: unicriterion and multicriterion. For unicriterion there are four groups: (1) Euclidean distance, (2) standardized distance, (3) dissimilarity index, and (4) correlation coefficient.

Research on G*E interaction has several practical purposes:

a. to find good methods to determine areas for crop cultivar recommendations ;

b. to find the genetic basis of yield stability and the ways of breeding to improve it ;

c. to take advantage of G*E interaction in managing cultivar performance and production fields.

d. to augment estimates of genetic gain from long-term experiments.

The first purpose, cultivar recommendation, becomes more and more important as cultivars become more elite, and possibly more specialized. Horner and Frey (1957) and McCain and Schultz (1958) gave the methods to determine areas for oat and corn cultivar recommendations, respectively.

Yield stability is partially genetically controlled, and selection for yield stability can be effective (Scott,1967). Genotypes as well as environments may be classified according to their G*E interaction (Johnson, 1982).

The third purpose of G*E research isto increase the efficiency ofcultivar performance experiments. Sprague and

Federer (1951) discussed the determination of the optimum number of years, locations and replications for obtaining the maximum gain in performance through selection , according to the genetic variability among the lines being tested . Another method of how best to determine test site and number of test years was given by Hanson (1964).

There are essentially three ways of evaluating long-term genetic gain achieved by breeding programs: (1) growing cultivars or lines from different eras in common environments, (2) expressing data from trials grown over many years as percentages of the value of a long-term check, and (3) comparison of estimated marginal means (such as least-square means) with year effects removed.

Comparisons of modern and long-term check cultivars in experiments conducted over many years is a popular method of estimating long-term genetic gain. Frey (1971) estimated the cumulative genetic gains from U.S. wheat breeding programs at 35 to 50% over 70 years. Similar results were obtained by Schmidt (1984) and Schmidt and Worrall (1984). Duvick (1977) grew both old and modern maize hybrids released during the period 1939 through 1971 in a common experiment. The result showed that the total yield gain contained a 57%-60% proportion due to breeding.

Majerus and Bramel-Cox (1986) indicated that there were no significant genetic gains in grain sorghum yields from 1960 to 1985 under dryland environments in Kansas, when yields were expressed as percentage of a long-term check, the hybrid RS610.

The concept of least square means (LSM) has been defined by Harvey (1975) and Searle et al (1980). Rodgers et al (1983) used this method to evaluate the proportion of U.S. spring oats yield increase due to genetic gain.

MATERIALS AND ANALYSIS METHODS

Analyses were performed on four data sets. One set of long-term wheat yield data was from the Southern Regional Performance Nursery (SRPN). The data covered 49 locations in Montana, Colorado, South Dakota, Nebraska, Kansas, Oklahoma, Texas, Missouri, Illinois, Indiana, Ohio and Washington; 122 winter wheat lines subsequently released as cultivars; and years between 1935 and 1985, inclusive. Within a given year, all cultivars were evaluated at all SRPN locations, but cultivars and locations included in the SRPN changed from year to year. Another data set came from the Kansas Winter Wheat Variety Performance Test (VPT; Walter,1977-1986), which was unbalanced between and within years.

A third set comprised four years of data from county demonstration plots grown around Kansas. Finally, there were data from a set of 36 cultivars released between 1874 and 1986 evaluated together at three locations in Kansas in 1986 (The "Old Timers" trial).

The methods used to analyze the data included analysis of variance, regression analysis, and cluster analysis. A significant G*E interaction, as evaluated in the analysis of variance, was considered a necessary condition for further analysis. The following model was used to represent the long term data:

$$X_{ijk}=\mu+Y_k+G(Y)_{ik}+GL(Y)_{ijk}+L(Y)_{jk}+\varepsilon_{ijk}$$

where X_{ijk} is the performance of cultivar i in location j and year k; μ was the overall mean; Y_k was the year effect; $G(Y)_{ik}$, $GL(Y)_{ijk}$, and $L(Y)_{jk}$ were the effects of genotype, genotype by

location and location, all within years; ε_{ijk} was the error term. Effects within years were used because some long-term data are unbalanced between years but balanced within years.

In addition to the stability parameters proposed and/or used by others, the yield stability of cultivar within a geographical region was estimated for these data sets by computing a coefficient of variation for the location by year interaction within region and cultivar.

Comparisons of the genetic gains obtained from the following estimates were compared: (1) cultivar means from The"Old Timers" trial, (2) LSMs from SRPN data, (3) all yield data converted to a percentage of the appropriate long-term check. Genetic gains were estimated by regressing cultivar means on the years of release.

APPENDICES A, B, C, and D give the SAS programs used for calculating 10 types of stability parameters (Table 1), the correlations among experiment stations and the county demonstration plot means, cluster analysis of the experiment stations and the counties without a seed variable, and the cluster analysis with experiment stations as seeds.

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Chapter 1

YIELD STABILITY

INTRODUCTION

As the scope and efficiency of crop breeding programs have been increased and as more organizations and individuals have become involved in breeding, more and more new cultivars have been released. In choosing among the many available cultivars, farmers want not only high yield but also stability. Yield stability is an important characteristic which has been paid much attention both formally by breeders and informally by farmers. However, the concept of crop yield stability is by no means unambiguous; it has been defined in many ways, depending on how scientists have approached the problem. The statistics used to parameterize these various concepts are also numerous. This leads many breeders to wonder which stability statistics should be used for their particular problems.

According to Lin et al's (1986) summary, there are three kinds of yield stability concepts:

1) A genotype is considered to be stable if its among-environment variance is small.

2) A genotype is considered to be stable if its response to environments is parallel to the mean response of all genotypes in the trial.

3) A genotype is considered to be stable if the residual mean square from the regression model on the environmental index (which is computed asthe overallmean of genotypes in an environment) is small.

Corresponding to these three concepts there are four groups of statistical methods (Table 1). Group A includes variance of each genotype across all given environments and Francis and Kannenbert's (1978) coefficient of variation. Group B includes four types of stability variances. Plaisted and Peterson' (1959) mean variance component for a genotype was defined as the mean of the estimated variance components for genotype by environment (G*E) interaction over all pairs of genotypes that include that genotype. A large variance value indicated low stability. Plaisted (1960) proposed a similar variance component as another stability parameter. In that analysis one genotype i was deleted from the set of data, and the G*E interaction variance from that subset was the stability index for genotype i. A large variance value indicated high stability.

Wricke's (1962, 1964, 1965) "ecovalence" was defined in several ways. Butit is generally considered that the sum of squares of G*E interaction effects for genotype i across all environments is the stability parameter for genotype i. A large ecovalence value indicated low stability. Shukla (1972) defined a "stability variance" as a stability parameter. The unbiased estimate of this variance can be obtained by the formula (Table 1) given by Ehrenberg (1950).

Group C includes commonly used regression methods. Finlay and Wilkinson (1963) defined the regression coefficient of observations on environmental index, defined as the difference between the marginal mean of the environment and overall mean.

The difference between Finlay and Wilkinson's model and Perkins and Jinks's(1968) model is that Perkins and Jinks adjusted the observationsby environmental effects before regression. The regression methods have been criticized, mainly because the independent variable and dependent variable inevitably are correlated (Freeman and Pekins, 1971; Hardwick and Wood, 1972; Miezan, Milliken and Liang, 1979). Group D includes residual mean squares from the regression slopes in Group C.

The purpose of this chapter is to define yield stability, discuss the usefulness of the various parameters for estimating yield stability, and use these parameters to evaluate the stability of winter wheat cultivars.

Table 1 A summary of equations for the ten stability statistics (reprinted from Lin et al., 1986)

Group	Equation	Authors or users
A	$S_i^2 = \sum_{j=1}^{q} (X_{ij} - \bar{X}_i)^2/(q-1)$	
	$CV_i = S_i/\bar{X}_i \times 100$	Francis and Kannenbert (1978)
B	$\theta_i = \frac{p}{(p-1)(q-1)} \sum_{j=1}^{q} (X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X})^2 + \frac{SS(GE)\dagger}{(p-1)(q-1)}$	Plaisted and Peterson (1959)
	$\theta_{(i)} = \frac{p}{(p-1)(p-2)(q-1)} \sum_{j=1}^{q} (X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X})^2 + \frac{SS(GE)}{(p-2)(q-1)}$	Plaisted (1960)
	$W_i^2 = \sum_{j=1}^{q} (X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X})^2$	Wricke (1962)
	$\sigma_i^2 = \frac{p}{(p-2)(q-1)} \sum_{j=1}^{q} (X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X})^2 - \frac{SS(GE)}{(p-1)(p-2)(q-1)}$	Shukla (1972a)
C	$b_i = \sum_{j=1}^{q} (X_{ij} - \bar{X}_i)(\bar{X}_j - \bar{X}) / \sum_{j=1}^{q} (\bar{X}_j - \bar{X})^2$	Finlay and Wilkinson (1963)
	$\beta_i = \sum_{j=1}^{q} (X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X})(\bar{X}_j - \bar{X}) / \sum_{j=1}^{q} (\bar{X}_j - \bar{X})^2$	Perkins and Jinks (1968)
D	$\delta_i^2 = \frac{1}{(q-2)} \{ \sum_{j=1}^{q} (X_{ij} - \bar{X}_i)^2 - \beta_i^2 \sum_{j=1}^{q} (\bar{X}_j - \bar{X})^2 \}$	Eberhart and Russell (1966)
	$\delta_i^2 = \frac{1}{(q-2)} \{ \sum_{j=1}^{q} (X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X})^2 - \beta_i^2 \sum_{j=1}^{q} (\bar{X}_j - \bar{X})^2 \}$	Perkins and Jinks (1968)

$\dagger SS(GE) = \sum_{i=1}^{p} \sum_{j=1}^{q} (X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X})^2$

METHODS

Analyses were performed on two data sets. One set of long-term wheat yield data was from the Southern Region Performance Nursery (SRPN). The SRPN is a breeders' cooperative trial in which potential cultivars are evaluated, usually before it is decided whether to release them. Only those lines eventually released as cultivars were included in these analyses. The data covered the years between 1935 and 1985.Within a given year, all cultivars were evaluated at all SRPN locations, but cultivars and locations included in the SRPN changed from year to year. Sixteen locations selected in Kansas (Hays, Garden City, Colby, Hutchinson and Manhattan), Colorado (Fort Collins, Walsh, Burlington and Akron), Oklahoma (Stillwater, Altus and Goodwell), and Texas (Dallas, Chillicothe and Bushland) were included in the yield stability analyses.

Another data set came from the Kansas Winter Wheat Variety Performance Test (VPT; Walter, 1977-1986), which is unbalanced between and within years. The data covered 14 locations in Kansas, and year between 1977 and 1986. The basic data observation used in the analysis was a mean annual yield for each cultivar and location calculated over all replications at the location.

APPENDIX A gives the SAS program used for calculating 10 types of stability parameter (Table 1).

Because the data sets were unbalanced, least squares means (LSM) were estimated for each cultivar by using SAS GLM (general

linear model) procedure (SAS Institute, 1985) to represent the yield potential.

RESULTS

Comparisons of Different Stability Statistics

A good yield stability parameter should fulfill the following assumptions:

1) The yield stability parameter should not contain any fixed effects. "Instability" is analogous to the concept of "risk" in economics. Suppose one cultivar produces 4000kg/ha yield under one fertilizer level and 6000kg/ha under another fertilizer level. We cannot say that this cultivar is not stable, because the yield variation is caused mostly by a fixed fertilizer effect. The yield variation can be closely predicted using appropriate statistical procedures. Stability of yield is concerned with the unpredictable part of yield variation.

2) Yield stability parameters should be independent among cultivars. If parameters of different genotypes are not independent, then the parameters are not unbiased estimates.

3) In practical terms, a parameter should represent yield stability in a way which is meaningful to, and easily understood by, both breeders and farmers.

Variance and coefficient of variation of each genotype across all given environments in Group A (Table 1) are estimated independently among genotypes. But the parameters contain fixed environmental effects. For example, suppose the data being analyzed include winter wheat yields at locations from eastern and western Kansas. There are consistent differences in rainfall,

elevation, soil type etc. between locations in the two regions. Variance and CV's will not be very informative for breeders and farmers, who are most interested in maximum yield in a given environment for a given set of inputs. Low variance is often associated with a relatively low yield.

The first term in each of the formulas in Group B is the G*E interaction associated with individual genotype i; the second term is the G*E interaction associated with the whole experiment. In the first term, fixed environmental effects are removed, so no fixed effects are included in the parameters. But the parameters are not independently estimated among genotypes because each estimate depends in part on the G*E interaction for all genotypes.

Group C includes commonly used regression methods. Aside from the fact that the slope of a particular cultivar's regression line depends on the specific set of cultivars with which it is tested, the regression analysis fails to provide very useful information for the farmer, who raises crops at the same location every year. For example, suppose we have an experiment that includes 5 locations and two cultivars (Table 2). Figure 1 is the plot of the data. For both 1 and 2 the conditions improve from location A to location E. Cultivar 1 is more productive in good conditions but less productive in stress conditions. From Fig.1 it is obvious that the farmers in location D and E should choose only cultivar 1; and they do not care what happens to cultivar 1 at location A and B. The slope cannot represent yield

stability because it contains fixed environment effects.

Table 2 Data

Environment	Variety 1	2	Environment index
A	20	30	25
B	30	35	32.5
C	40	40	40
D	50	45	47.5
E	60	50	65

Table 3 Data

Environment	Variety 1	2	3	4
A	25	30	20	30
B	30	25	30	20
C	35	40	40	50
D	40	35	50	40

Table 4 Analysis result from Table 4 data (residual mean squares from regression slopes)

Variety combination	Variety 1	2	3	4
1,2,3,4	12.5	12.5	50.0	50.0
1,2,3	2.9	26.5	11.8	----
1,2,4	26.5	2.5	----	11.8

Table 5 Summary of four groups of stability statistics listed in Table 1

Group	Independent or not among genotypes	Contain fixed effect or not
A	yes	yes
B	no	no
C	no	yes
D	no	?

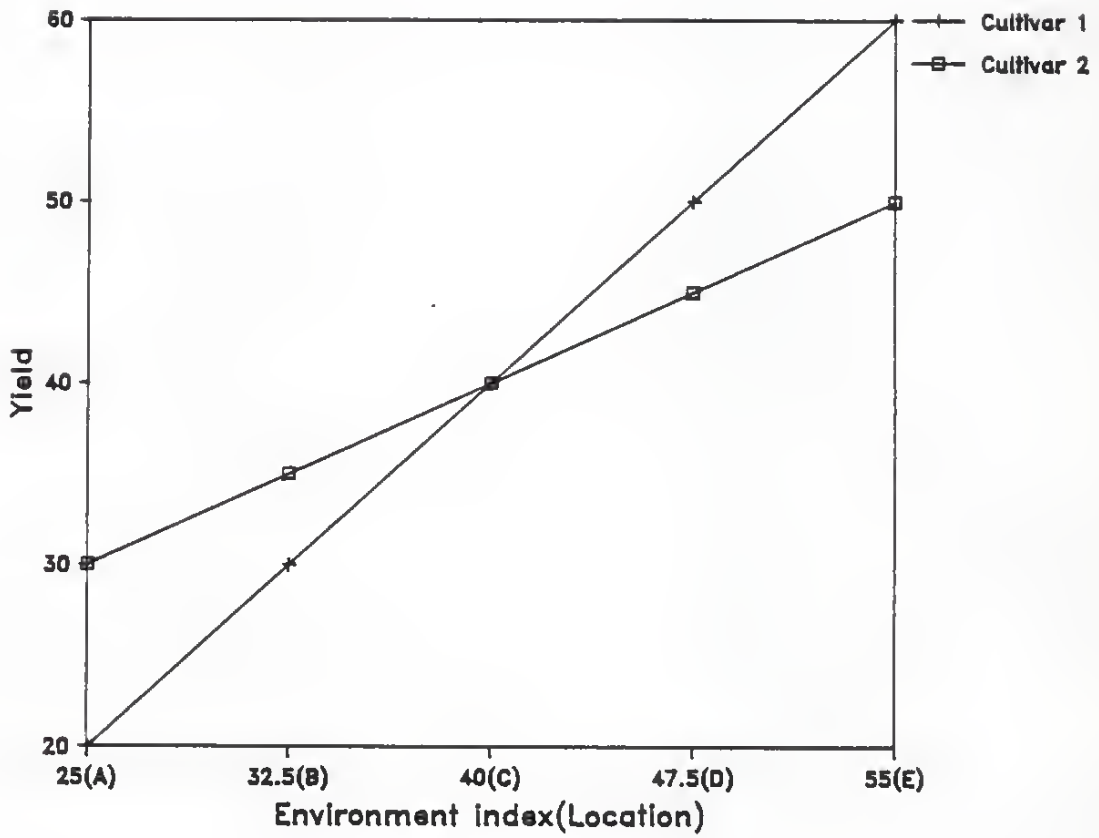
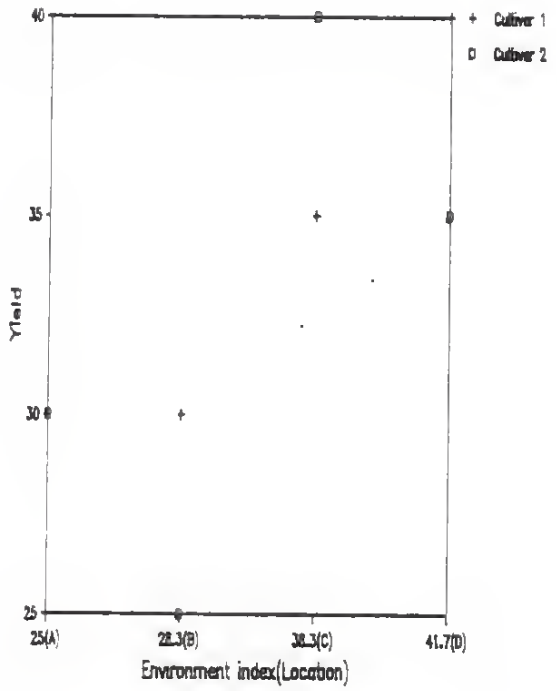
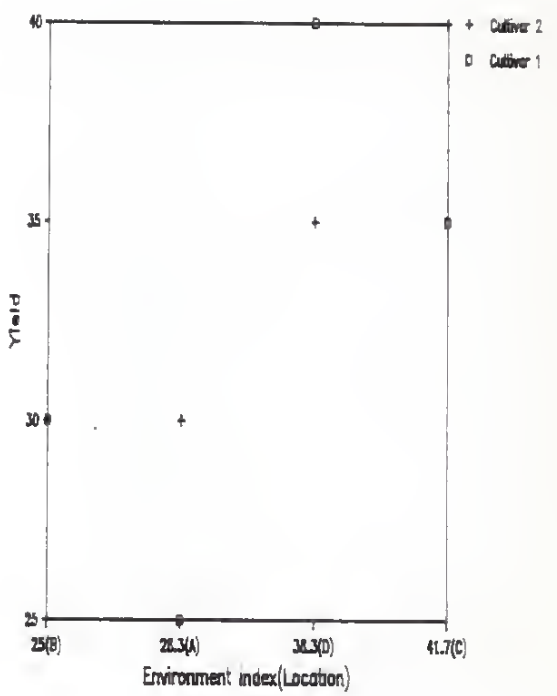


Figure 1 Plot of data in Table 2, the environmental index is the mean of all cultivars in the indicated environment.





2a cultivar combination 1,2,3

2b cultivar combination 1,2,4

Figure 2, a:Plot of data in Table 4. The environmental index is the mean over cultivars 1,2 and 3. b: Plot of data in Table 4. The environmental index is the mean over cultivars 1,2 and 4.

Group D includes residual mean squares from the regression slopes in Group C. Table 4 gives the residual mean squares from the regression model when different combinations of the data in Table 4 are included. Even more than regression coefficients, residual mean squares strongly depend on the cultivar combination tested. Figure 2 gives plots of cultivar combinations 1,2,3 and 1,2,4. From these two plots we can see that the reason for the changes of residual mean squares is that the environmental order changes. In combination (1,2,3), the environmental order is A, B, C and D. But in combination (1,2,4), the order is B, A, D and C. So the residual mean squares of cultivars 1 and 2 are not completely due to themselves but very much effected by cultivars 3 and 4. Similar results could occur even for a test involving a large number of cultivars, especially when cultivars with very different adaptation characteristics are included. The residual mean squares cannot accurately represent yield stability.

Table 5 summarizes the four groups of stability statistics in terms of independence and inclusion of fixed effects. Perkins and Jinks's (1968) adjustment using environmental effects does not eliminate the fixed-environment effects on the regression slope. It is not statistically different from Finlay and Wilkinson's model.

In Table 6 are presented 10 different kinds of stability parameter estimates for cultivars in the SPRN data from year 1982 to 1985. Table 7 gives the rank coefficient of correlation among different stability statistics. Correlation coefficients within

Groups C and D are all unity. So in statistical terms Finlay and Wilknson's (1963), Eberhart and Russell's (1966), and Perkins and Jinks's (1968) models are identical. Correlation coefficients within Group B are also unity, except that correlation coefficients between Plaisted's (1960) and others are negative one. There is no statistical difference among Group B estimates. The CV is not related to any other estimates. The variance is strongly related to the regression approach, indicating that the response of genotypes to improving environments is primarily linear. Group B estimates are related to Group D estimates.

Table 6 Ten stability parameters listed in Table 1 computed from SPRN data (1982--1985)

Year	Cultivar	Stability estimate					
		S_i^2	CV_i	δ_i^2	bi	δ_i^2	β_i
1982	Kharkof	25.0	1081.5	572.1	0.71	572.1	-0.28
	Scout 66	44.4	1335.2	384.9	0.98	384.9	-0.01
	Sage	39.9	1321.0	204.6	1.00	204.6	0.00
	Arkan	45.4	1492.9	416.2	1.10	416.2	0.10
	Chisholm	44.4	1557.4	421.3	1.15	421.3	0.15
	Centura	38.6	1352.1	218.4	1.02	218.4	0.02
	Siouxland	31.3	1198.0	519.9	0.83	519.9	-0.16
	Rodeo	38.9	1451.1	355.8	1.08	355.8	0.08
	Pony	40.5	1443.3	351.9	1.07	351.9	0.07
1983	Kharkof	24.6	534.8	343.8	0.46	343.8	-0.53
	Scout 66	29.0	842.0	346.0	0.85	346.0	-0.14
	Sage	31.4	998.3	346.8	1.03	346.8	0.03
	Arkan	28.4	1033.9	346.8	1.07	346.8	0.07
	Chisholm	33.8	1210.8	517.5	1.21	517.5	0.21
	Centura	27.6	888.4	254.7	0.93	254.7	-0.06
	Siouxland	30.1	1103.1	376.5	1.14	376.5	0.14
	Rodeo	29.9	1068.1	306.1	1.12	306.1	0.12
	Pony	30.6	1087.4	316.6	1.14	316.6	0.14
1984	Kharkof	39.4	1014.2	538.3	0.72	538.3	-0.27
	Scout 66	37.9	1257.1	230.8	1.03	230.8	0.03
	Tam 105	38.1	1316.6	196.5	1.08	196.5	0.08
	Tam 107	36.6	1295.9	227.1	1.06	227.1	0.06
	Tam 108	38.6	1374.9	184.0	1.13	184.0	0.13
	Stallion	37.6	1271.4	435.0	1.00	435.0	0.00
	Thunderbird	34.7	1181.0	241.7	0.96	241.7	-0.03
	Victory	34.4	1178.9	209.2	0.97	209.2	-0.02
1985	Kharkof	35.6	723.4	602.8	0.48	602.8	-0.51
	Scout 66	24.8	740.2	259.7	0.80	259.7	-0.19
	Tam 105	35.3	1034.6	493.7	1.05	493.7	0.05
	Thunderbird	27.8	1015.1	353.1	1.10	353.1	0.10
	Victory	25.9	915.5	269.5	1.01	269.5	0.01
	Century	27.6	1060.9	493.2	1.09	493.2	0.09
	Trailblazer	27.7	1011.2	296.7	1.11	296.7	0.11
	Dodge	27.3	988.2	281.0	1.09	281.0	0.09
	Sumner	28.9	986.4	436.5	1.02	436.5	0.02
	Norkan	32.2	1078.9	292.7	1.20	292.7	0.20

Table 6 continued

Year	Cultivar	Stability estimate			
		θ_i	$\theta_{(i)}$	W_i^2	σ_i^2
1982	Kharkof	353882	160814	8512782	546950
	Scout 66	180991	210212	2672911	151771
	Sage	124206	226436	754821	21975
	Arkan	204975	203359	3483038	206591
	Chisholm	219888	199098	3986772	240678
	Centura	128051	225337	884727	30766
	Siouxland	271348	184395	5724967	358301
	Rodeo	176222	211574	2511810	140869
	Pony	173901	212238	2433415	135564
1983	Kharkof	287297	148421	5973611	426173
	Scout 66	163423	183813	2229864	143033
	Sage	153895	186535	1941902	121254
	Arkan	156038	185923	2006667	126153
	Chisholm	252567	158343	4923991	346790
	Centura	125688	194595	1089422	56781
	Siouxland	174600	180620	2567668	168581
	Rodeo	147065	188487	1735484	105643
	Pony	152965	186801	1913801	119129
1984	Kharkof	278070	72634	6050056	483505
	Scout 66	91516	134818	826545	48213
	Tam 105	89190	135594	761420	42786
	Tam 107	93397	134191	879220	52602
	Tam 108	96118	133284	955425	58953
	Stallion	163378	110864	2838691	215892
	Thunderbird	94140	133944	900029	54336
	Victory	86134	136612	675852	35655
1985	Kharkof	398472	145838	10269907	651106
	Scout 66	149860	207991	1767372	91728
	Tam 105	227880	188486	4435657	267273
	Thunderbird	168193	203408	2394361	132978
	Victory	136493	211333	1310225	61653
	Century	229753	188018	4499719	271488
	Trailblazer	150406	207855	1786050	92957
	Dodge	143606	209555	1553478	77656
	Sumner	198810	195754	3441450	201865
	Norkan	160179	205412	2120293	114947

Table 7 Rank correlation coefficient among different statistics computed from SRPN data

Statistics	Year	Var.	Group B	Group C	Group D
CV	82	.27	.11	.21	.09
	83	.89**	.13	.85*	.60+
	84	.04	.55	-.12	.44
	85	.01	.72*	-.31	.71*
Var.	82		.58+	.98**	-.41
	83		.38	.99**	.41
	84		.73*	.98**	-.69+
	85		.44	.91**	-.14
Group B	82			.72+	.95**
	83			.49	.62+
	84			.85*	.95**
	85			.75*	.91**
Group C	82				-.57
	83				.29
	84				-.82*
	85				-.50

+=significant different from zero at 0.10 level
*=significant different from zero at 0.05 level
**=significant different from zero at 0.01 level

A New Concept of Yield Stability

None of the previously proposed stability statistics can meet the requirements of independence and absence of fixed effects outlined in the previous section. We propose the following new criterion for stability: a genotype is considered to be stable in a certain region if the coefficient of variation for location by year interaction for that genotype is small. This coefficient can be estimated by the following equation:

$$CV_i = \sqrt{\sum_{i}^{n} \sum_{j}^{p} (\bar{Y}_{ijk} - \bar{Y}_{ij.} - \bar{Y}_{i.k} + \bar{Y}_{i..})^2} / Y_{i..} * 100$$

where i=1,2,....,n indicates the genotype, j=1,2,....,p indicates the year, and k=1,2,....,q indicates the location. Y_{ijk} is the observed yield of genotype i in location k and year j. $\bar{Y}_{ij.}$, $\bar{Y}_{i.k}$, and $\bar{Y}_{i..}$ are the corresponding means. This parameter is estimated independently and without fixed location and year effects. Long-term varietal trials are usually unbalanced, but this statistic can be computed easily using standard statistical analysis packages.

This stability parameter is shown in Table 8a for cultivars in the VPT from 1977 to 1986, and in Table 8b for cultivars in the SRPN (5 locations in Kansas) from 1960 to 1985. The rank correlation coefficients between this parameter and the previous four types of parameter are shown in Table 9. Variance of genotype overall environments and the regression slopes were negatively correlated with this parameter. This can be explained if some of the cultivars included both in Table 6 and Table 8b might be sensitive to fixed-environment effects, but not

sensitive to random effects.

The second column in Table 8a and 8b gives yield mean (Least square means) of each cultivar in VPT and SRPN respectively. The correlation coefficients between mean yields and the CVs are -.25(ns, VPT) and -.26(ns, SRPN). The rank correlation coefficient between the CVs from VPT and SRPN is -.09(ns) based on 16 common cultivars. The reason may be that the data sets covered different sets of years and locations. When the analyses are based on the five common locations (Manhattan, Colby, Hutchinson, Hays and Garden City) in the VPT and SRPN, the rank correlation coefficient is .77** (df=12). The regression coefficient of the CV on the year of the cultivar release are not significant (b=.27 for both VPT and SRPN data).

In VPT data hybrids Bounty 310, 203 and 301 and cultivar Chisholm had high yield and stability. In SRPN data Pony, Newton, Vona and Chisholm were top cultivars. Vona and Newton, however, appeared as highly unstable in the VPT data, which included many more observations for these cultivars than did SRPN data. Vona is considered by wheat breeders and growers to be highly unstable, and Newton's yields are often unpredictable because of its susceptibility to the two foliar diseases leaf rust and Septoria leaf blotch. During the three years that Newton was tested in the SRPN, it was resistant to prevalent leaf rust populations, and Septoria leaf blotch did not cause significant losses at most locations. The examples of Vona and Newton illustrate the importance of adequate number s of observations and knowledge of

specific growing conditions.

Table8a Coefficientof variation for location by year interaction within genotype (VPT, 1977-86)

Cultivar	Yield mean (LSM,kg/ha)	CV (%)	Year of release	No. of locations	Evaluation years
LANCOTA	3069	17.6	75	16	77-78
SCOUT	3122	19.6	63	16	77-78
GAGE	3135	18.9	63	16	77-78
SCOTT-66	3142	19.6	67	16	79-86
WINGS	3202	21.0	77	16	81-82
OSAGE	3283	20.7	74	16	77-78
BUCKSKIN	3303	23.0	73	16	77-81
CENTURK	3376	19.7	71	16	77-79
CENTURK 78	3430	25.8	78	16	78-82,84-85
SAGE	3450	22.7	73	16	77-80
BENNETT	3457	28.0	78	16	78-80,82
LARNED	3457	23.3	76	16	77-83,85-86
CHENEY	3510	21.9	76	16	78-80
NEWTON	3604	25.3	77	16	77-86
HAWK	3685	25.9	82	16	81-85
PAYNE	3705	21.7	77	16	78-80
VICTORY	3711	25.2	85	16	85-86
VONA	3738	26.5	76	16	78-85
SIOUXLAND	3772	19.9	84	16	85-86
ARKAN	3825	19.2	82	16	82-86
MUSTANG	3946	17.8	84	16	84-86
THUNDERBIRD	3953	19.5	85	16	85-86
TAM 108	3979	21.4	85	16	84-86
COLT	4020	21.7	83	16	84-85
TAM 107	4073	23.0	85	16	84-86
BOUNTY 202	4180	21.1	.	16	84-86
BOUNTY 301	4321	16.8	.	16	84-86
BOUNTY 100	4408	21.5	.	16	83-84
BOUNTY 205	4475	24.2	.	16	85-86
CHISHOLM	4489	18.4	83	16	84-85
BOUNTY 310	4515	15.0	.	16	83-84
BOUNTY 203	4850	18.3	.	16	84-85

Table 8b Coefficient of variation for location by year interaction within genotype (SRPN, 1960-85)

Cultivar	Yield mean (LSM, kg/ha)	CV (%)	Year of release	No. of locations	Evaluation years
KIRWIN	2760	30.3	73	4	71-72
PRONTO	2847	19.3	70	4	71-72
SANDY	2881	24.5	79	4	78-79
HAIL	2954	46.2	82	4	80-81
SCOUTLAND	2994	30.4	70	4	70-71
W-335	3055	9.5	75	5	74-75
EAGLE	3055	21.7	71	4	71-72
TRISON	3061	8.0	73	4	72-73
HOMESTEAD	3061	21.9	73	4	72-74
SCOUT 66	3068	28.1	67	5	65-85
TAM 101	3075	21.6	73	4	72-73
TAM 105	3095	30.3	79	5	76-78,84-85
CHENEY	3102	8.5	76	4	75-76
BACA	3149	12.9	73	4	72-73
ARTHER	3169	23.9	82	4	80-81
CLOUD	3169	33.5	73	4	72-73
RALL	3189	22.2	76	5	73-75
PLAINSMAN 5	3202	33.4	74	4	79-80
ARKAN	3209	20.1	82	4	81-83
LANCOTA	3229	22.5	75	4	72-74
LARNED	3229	5.4	76	5	74-76
BUCKSKIN	3249	20.6	73	4	71-73
SENTINEL	3252	8.8	73	4	72-73
CHANUTE	3276	14.3	69	4	70-71
PAYNE	3276	14.0	77	4	75-76
POLO DURO	3289	13.3	69	4	70-71
ROCKY	3309	18.1	78	4	78-79
SATANTA	3316	4.4	69	4	70-71
CENTURK	3336	29.8	71	5	68-71
SIOUXLAND	3336	27.2	84	4	81-83
SAGE	3339	23.6	73	5	72-83
CENTURA	3363	23.2	83	4	82-83
YUKON	3383	10.0	69	4	70-71
BRULE	3430	15.7	82	4	78-79
VONA	3457	6.2	76	4	75-76
OSAGE	3470	17.7	74	4	72-73
HAWK	3478	28.3	82	4	80-81
RODEO	3497	25.0	85	4	82-83
TAM-103	3510	21.6	78	4	71-72
NEWTON	3517	12.8	77	4	76-78
CHISHOLM	3530	18.7	83	4	82-83
PONY	3557	13.5	85	4	82-83
THUNDERBIRD	3731	22.3	85	5	84-85

Table 9 Rank correlation coefficient between the CV (Table 8b) and the previously four types of stability estimates (Table 6)

Group(Table 1)	Rank correlation coefficient with the CV for location*year interaction
Group A	
CV	-0.08
Var.	-0.78*
Group B	0.50
Group C	-0.77*
Group D	0.39

DISCUSSION

Evenson et al (1978) discussed the distinction between genotype stability and adaptability. A genotype is said to be stable if, at a given location, its yield varies little from year to year. On the other hand, a genotype is said to be adaptable if its average yield over years at a given location varies little across locations. The distinction is important, because a farmer who has to decide whether to adopt a cultivar is interested only in the stability of the cultivar at his or her location for a given yield level, or, conversely, in how much risk can be tolerated. The yield potential of the genotype at other locations is not important to the farmer.

The slopes from the regression models appear to give estimates of adaptibility, but in fact they do not. The reason is that the environmental index (the mean yield over all genotypes at a given location) is not a unique estimate suitable to every genotype. If we use this mean yield to represent the environment, we ignore genotype by environment interaction. But why are breeders interested in these slopes? A possible reason is that many breeders hope to develop a universally adaptated cultivar that can cover a large geographical area. Actually, this approach is undesirable with regard to the need for further genetic improvement and diversity. Genotype by environment interaction is widespread, but developing a widely adaptable cultivar to reduce G*E effects is not the best way to solve this problem. Researching G*E interaction and developing a series of

cultivars adapated to different ecological conditions may simultaneously increase efficiency of breeding programs and enhance genetic diversity.

Usually stability analysis is treated as G*E interaction analysis. This may not be quite right. Stability effects may be related to G*E interaction, but there is a difference between these two phenomena. If experiments cover a wide environmental range, most of the G*E interaction may be due to fixed effects such as rainfall, temperature, soil type, disease etc.. Stability should not be defined relative to fixed effects.

The use of location by year interaction within genotype and region as an indicator of stability method has been proposed. The method appears to have advantages. The first advantage is that the parameter is independent of the performance of other genotypes. The second is that the parameter does not contain any fixed environmental effects. It is a true estimate of "risk". The third advantage of this parameter compared with the regression approaches is that it is easy to understand and to compute. The parameter can be thought of as the percentage of the yield due to random effects.

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Chapter 2

WINTER WHEAT YIELD INCREASE DUE TO GENETIC GAIN

INTRODUCTION

Yield change over time consists of three parts. The first part is genetic change (G), the second is environmental change (E), and the third is change due to genotype by environment interaction (G*E). If we consider change to be positive then the above parts become improvements or gains. We can use the following model to represent yield increase (YG).

$$YG=GG+EI+(GG*EI)$$

where GG is genetic gain, EI is environment improvement and GG*EI is the interaction between these two effects. When we evaluate long-term genetic gain we should be concerned not only with GG but also GG*EI, because GG*EI is important for increasing the efficiency of a breeding program.

Three methods may be used to eliminate environmental effects and obtain estimates of long-term genetic gain:

1) By growing cultivars or lines from different eras in a common environment. The problems of this method are that long storage or regeneration of old cultivars may influence the results and that a special experiment is needed.

2) By expressing all values in a multiple-year, unbalanced data set as percentages of the value of a long-term check. One criticism of this method is that the long-term check may change genetically because of selection, drift, or seed mixture (Worrall and Cox, 1986). Another problem is that modern cultivars may have very different adaptation characteristics from the long-term check (which is usually by necessity a very old cultivar).

Therefore, there could be a strong G*E effect, and old cultivar may not be a good index of environment for the new ones.

3) By comparing estimated marginal means, such as least squares means (Harvey, 1975) or, synonymously, population marginal means (Searle,Speed and Milliken, 1980) with year effect removed. The problem of this method is that a seriously unbalanced data set can result in low accuracy of the estimates.

Comparisons of modern and long-term check cultivars in experiments conducted over many years is a popular method of estimating long-term genetic gain. Frey (1971) estimated the cumulative genetic gains from US breeding programs at 35 to 50% over 70 years in wheat. Similar results were obtained by Schmidt (1984) and Schmidt and Worrall (1984).

Feyerherm, Paulsen and Sebaugh (1984) estimated that the hard red winter wheat increase ranged from 193 to 416 kg/ha in the U.S. from 1954 through 1979 by using a differential yield ability (DYA), which can be established by computing the mean of differences in yields between a given cultivar and a check cultivar over years and locations within a geographical region of mutual adaptability.

Majerus and Bramel-Cox (1986) found that there were no significantly genetic gains in grain sorghum yield from 1960 to 1985 under dryland environments in Kansas, when yields were expressed as percentages of a long-term check, the hybrid RS610. Miller and Kebede (1984) estimated increase in grain sorghum yield at an annual rate of 7%/year, including a 1 to 2% increase

accounted for genetic improvement.

Duvick (1984) grew both old and modern commercial maize hybrids released during the period of 1950 to 1980 in a common experiment. The result showed that the increase in yield attributable to genetic improvement averaged 92 kg/ha per year.

The concept of least square means (LSM) has been defined by Harvey (1975) and Searle et al (1980). Rodgers et al (1983) used this method to evaluate the proportion of US spring oats yield increase due to genetic gain.

The purpose of this chapter is to compare the genetic gain estimated from different methods and different experiments and to obtain accurate estimates of winter wheat yield increases resulting from breeding programs in the Great Plains.

METHODS

The data included: (1) mean yields of 34 cultivars (released 1933-1986), evaluated in 1986 at Manhattan, Hutchinson, and Hays, Kansas, with 3 replicates at each location (the "Old Timers" trial). (2) least square means, corrected for confounding environment effects, for all lines from the Kansas locations of the 1970-85 Southern Regional Performance Nursery (SPRN) that were eventually released as cultivars. Manhattan and Hutchinson represent the eastern half of Kansas and Hays, Colby and Garden City the western half. (3) least square means for cultivars in the 1977-86 Kansas Variety Performance Test (VPT). Powhattan, Manhattan, Ottawa, Parsons, Hutchinson, Belleville and Hesston represented the eastern half Kansas, and Hays, St. John, Colby, Tribume and Garden City the western half. There were both dryland and irrigated plots at St. John, Colby, Tribume and Garden City. These irrigated stations represented irrigated western Kansas.

In SRPN data, all of the cultivars in a given year were tested over a common set of locations, but the composition of locations usually differed from year to year. The data were balanced within years but unbalanced among years. VPT data were unbalanced both within and among years. The numbers of locations and cultivars each year in the data sets are summarized in Table 1. The cultivars used in genetic gain evaluation are summarized in Table 2. The data did not include all entries in SRPN. Some entries that produced high yield were not released as cultivars, so they were not considered to have contributed to genetic gain.

The basic observation used in the analysis was a mean annual yield for a cultivar at a given location calculated over all replicates. Least square means were obtained by using the SAS GLM procedure with the MODEL of YIELD=CULTIVARS YEAR. Means were regressed on year of the variety released. The regression analysis on "Old Timers" data did not include Turkey or Kharkof. The reason is that there was a large gap between 1874 and 1900, the years of release for Turkey and Kharkof, respectively, and 1933, the year that the next cultivar in the "Old Timers" trial, Cheyenne, was released.

All yield data in VPT and SRPN were converted to a percentage of the appropriate long-term check cultivar's yield, and graphs were constructed on that basis. Overall mean yields without check cultivars, check cultivar means, and the percentage were regressed on year of evaluation.

All pairwise correlation coefficients between different experiments based on the means of common cultivars were obtained.

Table 1 Number of locations and cultivars per year in the Old Timers trial, SRPN (1935-85), and VPT (1977-86) data set

Data set	Number per year	
	Cultivars	Locations(in Kansas)
Old Timers trial(1986)	34	3
SRPN(in Kansas)	7--17	1--5
VPT(including irrigated plots)	11--36*	14--16

* Some cultivars grown only at very few stations were not counted.

Table 2 Cultivars used in genetic gain evaluation

Cultivar	VPT	SRPN	Old Timers trial	Year of release
KHARKOF	.	.	X	00
CHEYENNE	.	.	X	33
RED CHIEF	.	.	X	40
COMANCHE	.	.	X	42
PAWNEE	.	.	X	43
WICHITA	.	.	X	44
PONCA	.	.	X	51
BISOM	.	.	X	56
TASCOSA	.	.	X	59
STURDY	.	.	X	60
WARRIOR	.	.	X	60
KAW-61	.	.	X	61
GAGE	X	.	.	63
LANCER	.	.	X	63
SCOUT	X	.	.	63
TRIUMPH 64	.	.	X	64
SCOUT 66	X	X	X	67
SHAWNEE	.	.	X	67
CHANUTE	.	X	.	69
POLO DURO	.	X	.	69
SATANTA	.	X	.	69
YUKON	.	X	.	69
PRONTO	.	X	.	70
SCOUTLAND	.	X	.	70
CENTURK	X	X	.	71
EAGLE	X	X	.	71
WRANGLER	X	.	.	71
BACA	.	X	.	73
BUCKSKIN	X	X	.	73
CLOUD	.	X	.	73
HOMESTEAD	.	X	.	73
KIRWIN	.	X	.	73
SAGE	X	X	.	73
SENTINEL	.	X	.	73
TAM 101	.	X	.	73
TRISON	.	X	.	73
OSAGE	X	X	.	74
PLAINSMAN 5	.	X	.	74
LANCOTA	X	X	.	75
W-335	.	X	.	75
CHENEY	X	X	.	76
LARNED	X	X	X	76
RALL	.	X	.	76
VONA	X	X	X	76
NEWTON	X	X	X	77
PAYNE	X	X	.	77

Table 2 Continue

CENTURK 78	X	.	X	78
ROCKY	.	X	.	78
SANDY	X	X	.	78
TAM 103	.	X	.	78
TAM 105	.	X	.	79
ARCHER	X	.	.	82
ARKAN	X	X	X	82
ARTHER	.	X	.	82
BRULE	X	X	X	82
HAIL	.	X	.	82
HAWK	X	X	X	82
CENTURA	.	X	.	83
CHISHOLM	X	X	X	83
MUSTANG	.	.	X	84
SIOUXLAND	X	X	X	84
PONY	X	X	.	85
RODEO	.	X	.	85
STALLION	X	.	X	85
TAM 107	X	.	X	85
TAM 108	X	.	X	85
THUNDERBIRD	X	X	.	85
VICTORY	X	X	X	85
1957	.	.	X	86
CENTURY	X	X	X	86
DODGE	X	X	X	86
NORKAN	X	X	X	86
SUMNER	.	X	.	86
TRAILBLAZER	.	X	.	86

RESULTS

The statistical model used in estimating the least-square means for grain yield is evaluated in Table 3. Genotype and year sums of squares were all highly significant for all data sets.

All pairwise correlation coefficients between locations or regions within experiments were all highly significant (Table 4). But the coefficients within regions (eastern Kansas and western Kansas) between experiments were not all large or significant. Therefore, relative yields of cultivars differed among data sets.

Yield trends for SRPN data in eastern Kansas and western Kansas are shown in Fig.1. The long-term check cultivar, Kharkof, was used in the SRPN during the period 1935 to 1985. Coefficients of regression of mean yield, check yield, and mean yield as percentage of check on year of evaluation are given in Table 5. There were large intercepts in eastern Kansas, but small slopes. The regression coefficient for Kharkof were significant both in eastern and western Kansas.

Though Kharkof may have changed in genetic composition (Worrall and Cox, 1986), it is likely that experimental conditions or other ecological factors have improved Kharkof's yield since 1935. If Kharkof has changed genetically, then the mean yield adjustment by Kharkof cannot remove environmental effects. This illustrates the main problem with using long-term checks to evaluate genetic gain. The coefficients of determination from the regression model ranged from .05 to .45.

The low coefficient means that only a small proportion of total variation of the dependent variable (mean yield, Kharkof yield or mean yield/Kharkof) due to the independent variable (year), probably because of large year-to-year fluctuations in the environment, superimposed on slow, gradual improvement of cultivars and/or management of experiments.

Yield trends for VPT data in eastern, western(dryland), and western(irrigated) Kansas are shown in Fig.2. The long-term check, Newton, was included in VPT during the period of 1977 to 1986. The regression slopes of the relative percentage yield on year of evaluation were significant in eastern and western(irrigated) Kansas (Table 6). Both coefficients of determination were relatively large. The mean yield in eastern Kansas has not increased since 1977, but because of the decrease in Newton's yield, a significant estimate of genetic gain in this region was obtained. Newton's original resistance to leaf rust (caused by Puccinia recondita) is no longer effective, and the incidence of speckled leaf blotch (caused by Septoria tritici) has increased in recent years. Several more recently released cultivars have better resistance to these two diseases; other new cultivars are as susceptible as Newton but perhaps more productive in other respects. Either type of cultivars would contribute to genetic gain.

The coefficients of regression of the least squares means or "Old Timers"s trial means on year-of-release were all highly significant (Table 7), indicating that genetic gain truly

occurred in both eastern and western Kansas. The coefficients ranged from 7.4 to 44.5. This means that due to breeding programs, wheat yield in Kansas increased 7.4 to 44.5 kg/ha/year. In terms of percentage of overall mean yield, the coefficients ranged from 0.5 to 1.5%. There was greater genetic advance when evaluation was in eastern Kansas, or at irrigated sites in western Kansas (20.0 to 44.5 kg/ha), than there were in dryland western Kansas (7.4 to 27.6 kg/ha).

Table 3 Mean squares from analysis of variance of grain yield for genotype and year

Source	SPRN				VPT			
	Eastern KS		Western KS		Eastern KS		Western KS	
	df	MS	df	MS	df	MS	df	MS
Year	14	37481**	14	295609**	9	3030075**	9	8734596**(d)
							9	3948324**(i)
Genotype	48	54385**	51	40562**	55	25260**	54	121535**(d)
							55	634744**(i)
Residual	137	1818	316	1910	89	7429	88	35095 (d)
							81	13311 (i)

Notes: (d)=dryland
(i)=irrigated
**=significant at 0.01 level

Table 4 Correlation coefficient between different regions andexperiments(E-KS=eastern Kansas, W-KS=western Kansas, (dry)=dryland, (irr)=irrigated)

	SPRN		VPT			Old Timers		
	E-KS	W-KS	E-KS	W-KS (dry)	W-KS (irr.)	Man.	Hutc.	Hays
SPRN								
E-KS	1.00	.49**	-.23	-.16	.48*	.64**	.50	.23
W-KS		1.00	-.10	.50*	.68**	.18	.10	.10
VPT								
E-KS			1.00	.54**	.35**	.48	.60**	.45
W-KS(dry)				1.00	.74**	-.19	-.05	.07
W-KS(irr.)					1.00	-.04	.18	-.23
Old Timer								
Man.						1.00	.89**	.67**
Hutc.							1.00	.72**
Hays								1.00

*=significant at 0.05 level
**=significant at 0.01 level

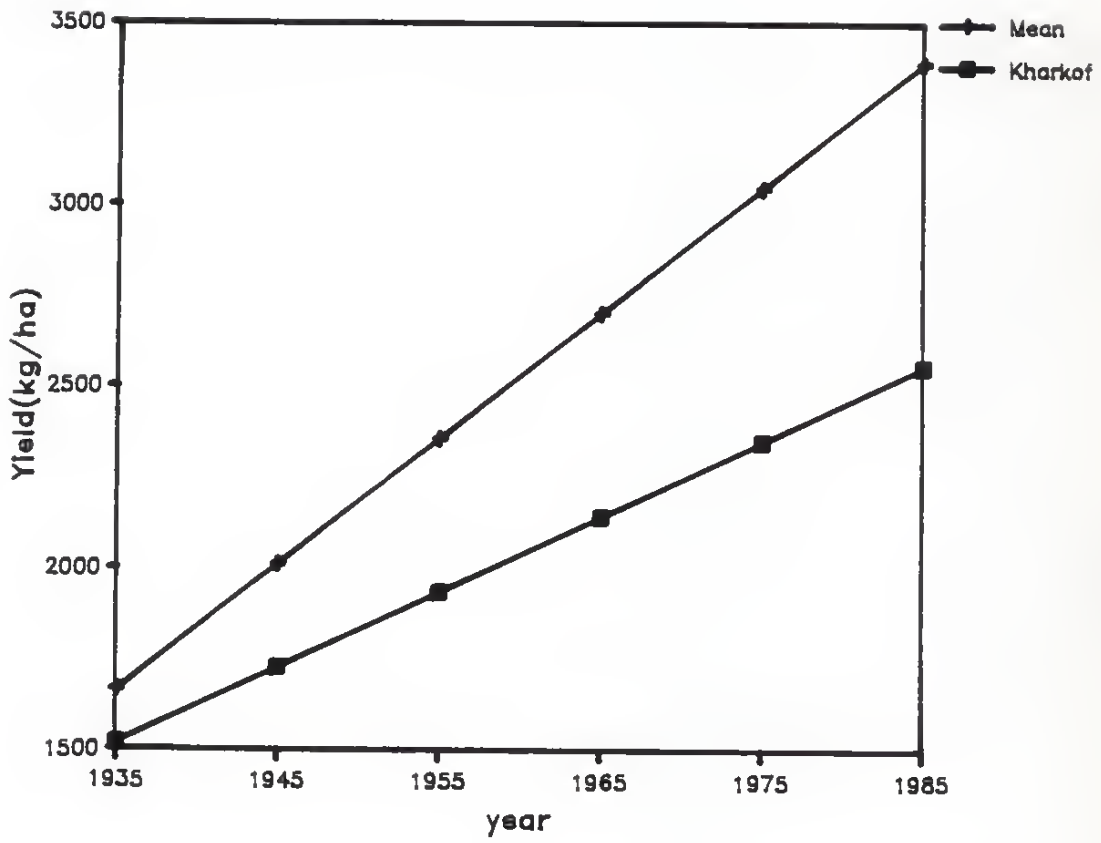

Figure 1a Regressions of mean yield and Kharkof(check) yield on on year (eastern Kansas SRPN, 1935-85)

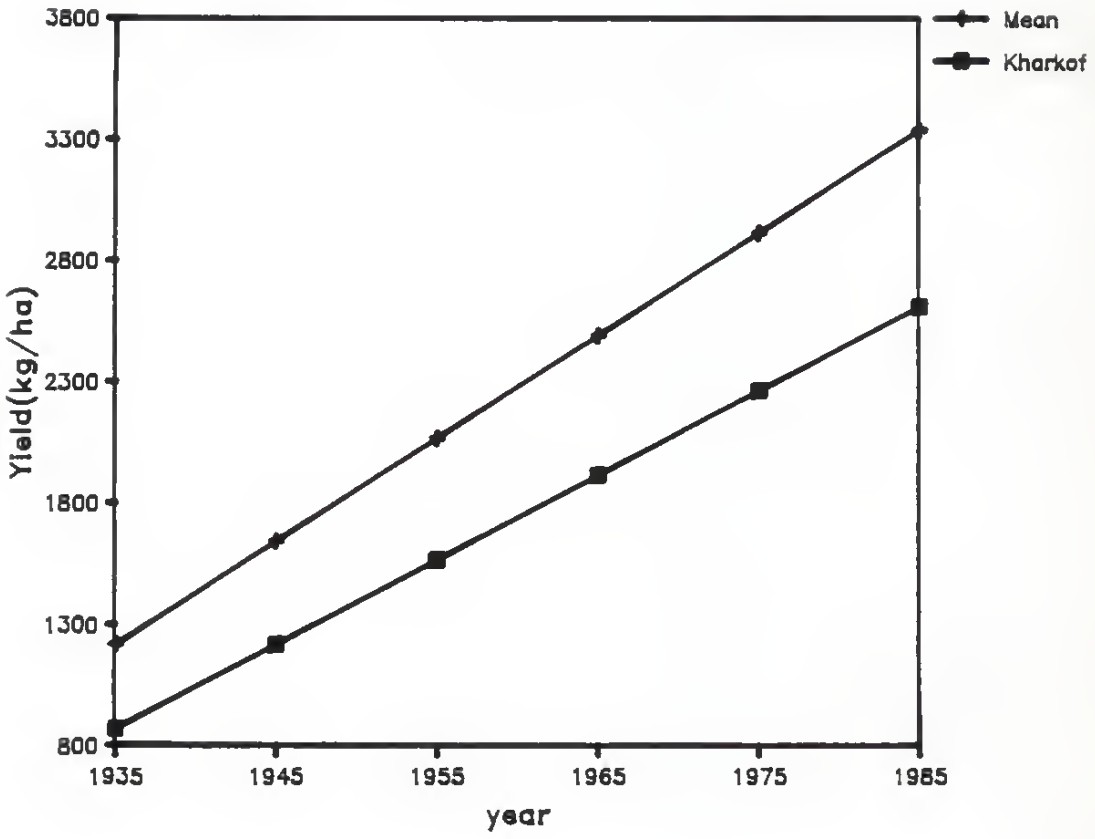

Figure 1b Regressions of mean yield and Kharkof(check) yield on year (western Kansas SRPN, 1935-85)

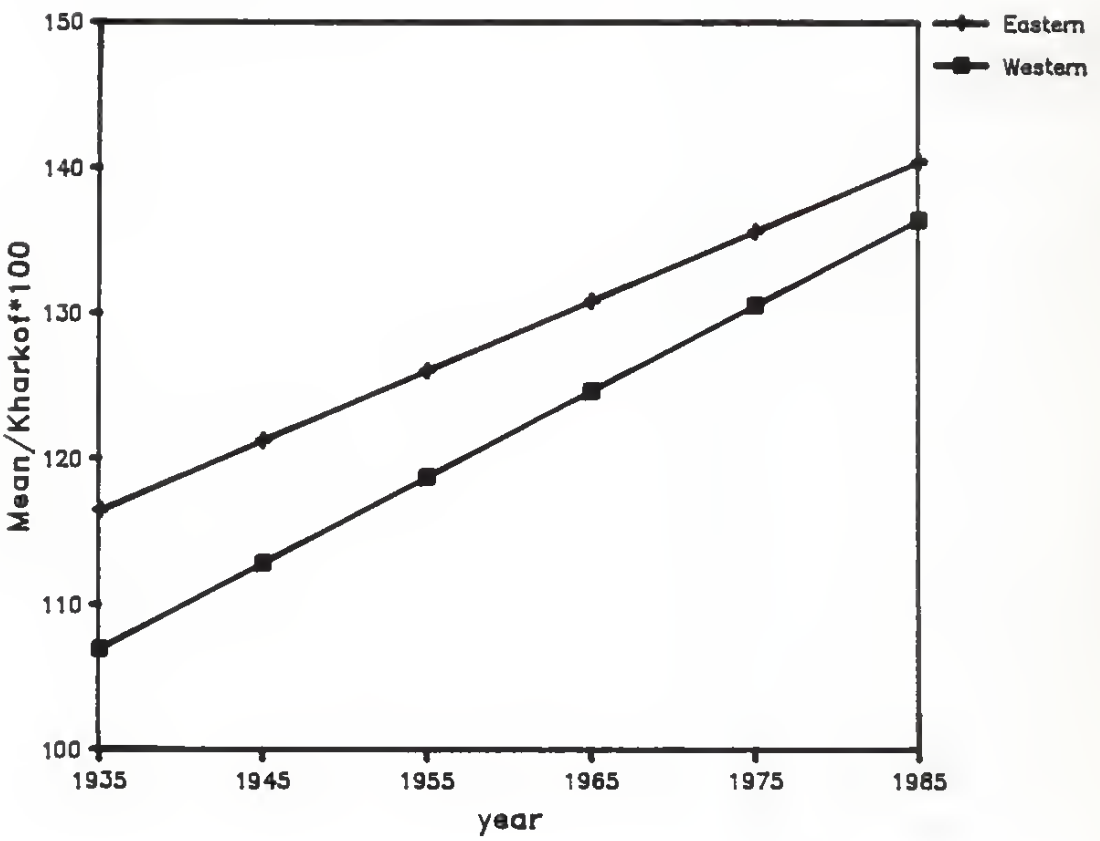

Figure 1c Regressions of mean yield as a percentage of Kharkof on year in Kansas (SRPN, 1935-85)

Table 5 Regressions of mean yield, check (Kharkof) yield and mean yield as percentage of check on year (SRPN, 1935-85)

Dependent variable	Region					
	Eastern Kansas			Western Kansas		
	Intercept	Slope	R^2	Intercept	Slope	R^2
Mean yield	1665.5 (.00)*	34.5 (.00)	.37	1216.7 (.00)	42.4 (.00)	.45
Kharkof yield	1519.2 (.00)	20.7 (.00)	.19	868.2 (.00)	34.8 (.00)	.45
Mean yield /Kharkof	116.4 (.00)	.48 (.12)	.05	106.9 (.00)	.59 (.02)	.11

* significant level in parentheses.
R^2=coefficient of determination due to regression model.
Unit=kg/ha.

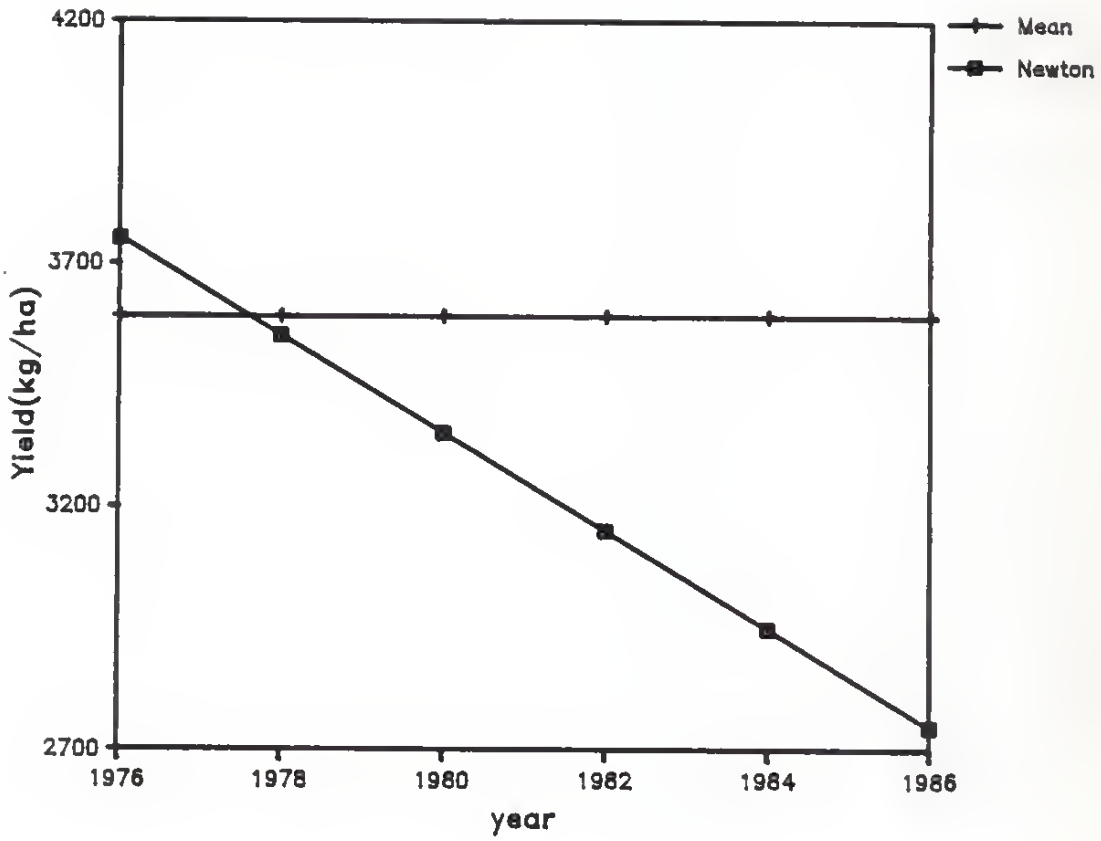

Figure 2a Regressions of mean yield and Newton (check) yield on year, eastern Kansas (VPT, 1977-86)

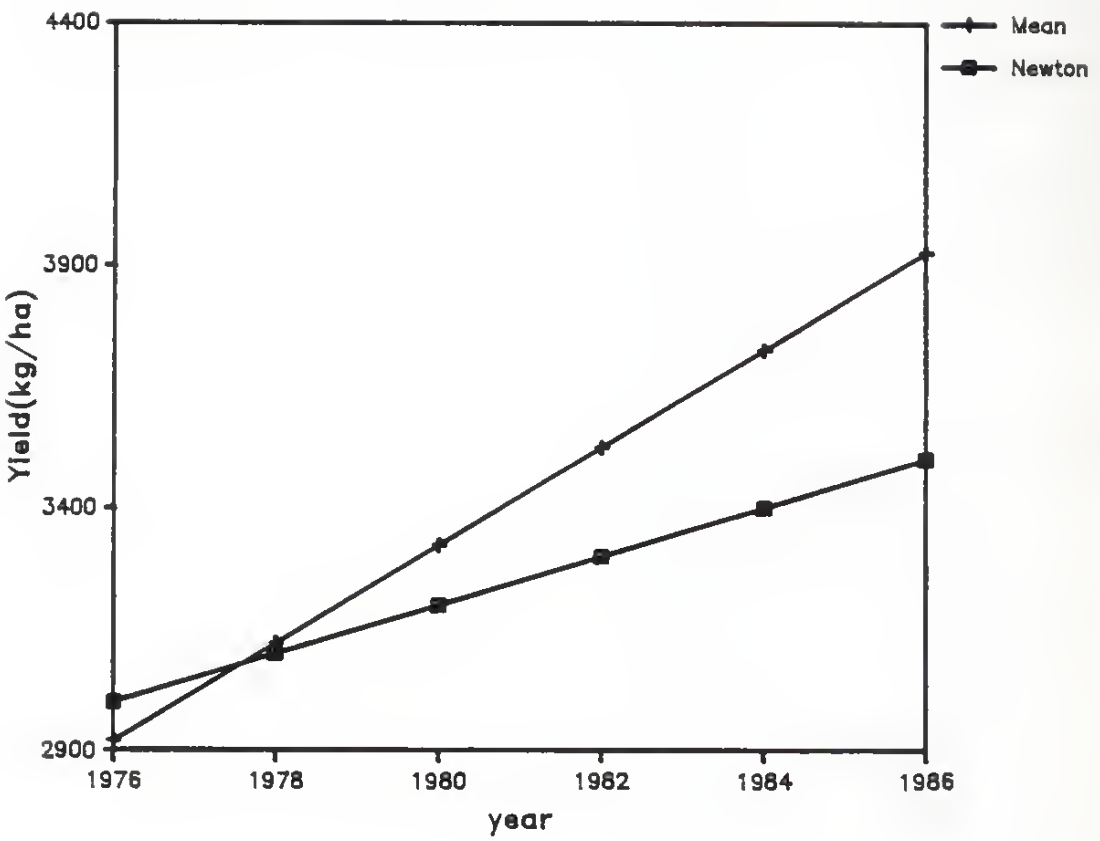

Figure 2b Regressions of mean yield and Newton (check) yield on year, western(dryland) Kansas (VPT, 1977-86)

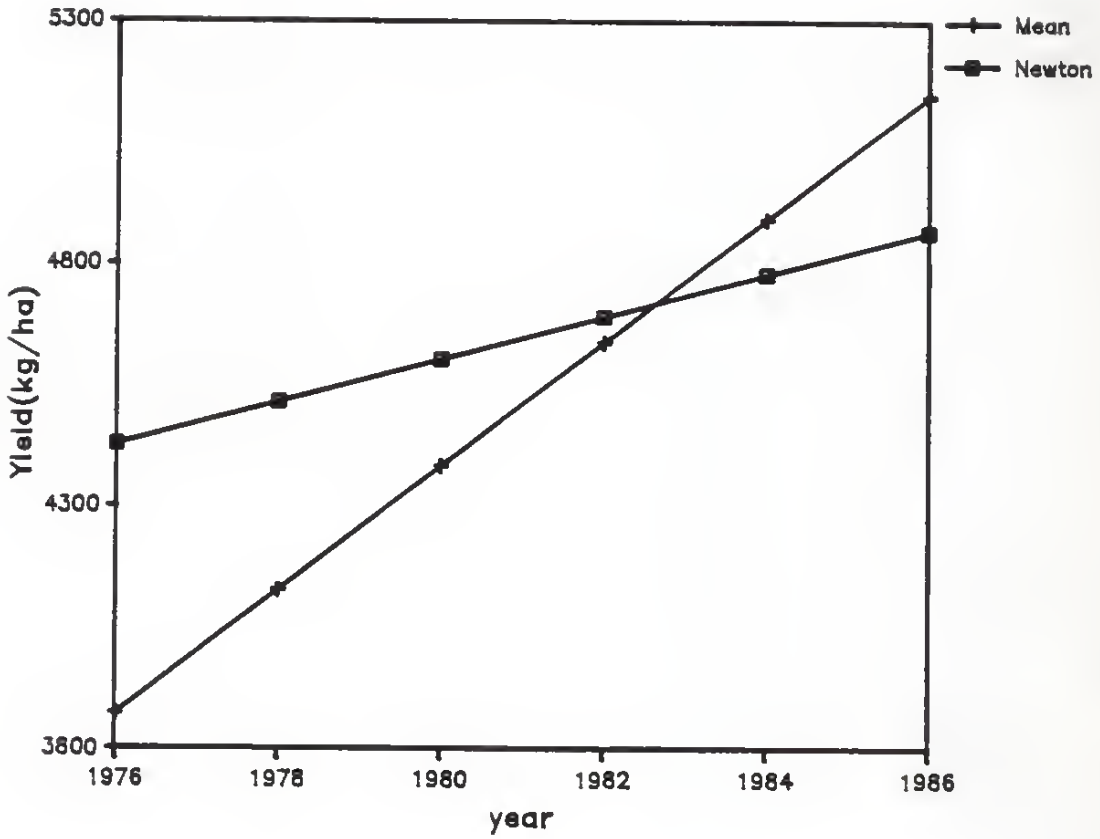

Figure 2c Regressions of mean yield and Newton (check) yield on year, western(irrigated) Kansas (VPT, 1977-86)

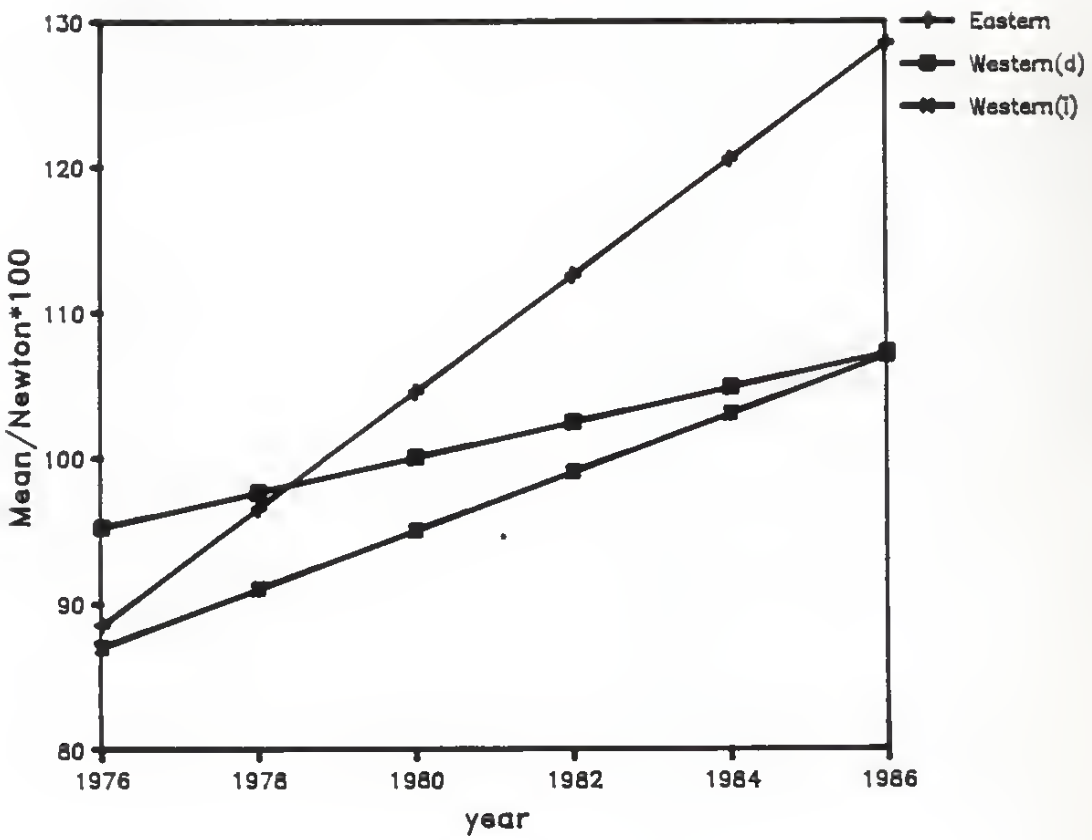

Figure 2d Regressions of mean yield as the percentage of check (Newton) on year in Kansas (VPT, 1977-86)

Table 6 Regressions of mean yield, Newton (check) yield and mean yield as the percentage of check on year (VPT,1977-86)

Dependent variable	Region					
	Eastern Kansas			Western Kansas		
	Intercept	Slope	R^2	Intercept	Slope	R^2
Mean yield	3591.2	.00	.00	2921.3	100.5	.17 (dry)
	(.48)*	(.98)		(.46)	(.23)	
				3873.3	127.3	.36 (irr.)
				(.25)	(.07)	
Newton yield	3752.0	-100.5	.19	3000.3	49.6	.05 (dry)
	(.09)	(.21)		(.89)	(.56)	
				4426.5	44.0	.07 (irr.)
				(.81)	(.46)	
Mean yield /Newton yield	88.5	4.0	.54	95.2	1.2	.15 (dry)
	(.07)	(.02)		(.97)	(.26)	
				87.3	2.0	.61 (irr.)
				(.19)	(.00)	

* significant level in parenthese
R^2=coefficient of determination due regression model

Table 7 Genetic improvement in yield in kg/ha/year (as percent of overall mean in parentheses) estimated from regression of cultivar yield (LSM) on year of release for three data sets (Man.=Manhattan, Hutch.=Hutchinson, (dry)=dryland, (irr.)=irrigated)

Data set	Year of release	Yield increase per year in kg/ha			
		Eastern KS		Western KS	
		Slope	R^2	Slope	R^2
Old Timer	1933-86	27.6 (Man.) (1.5%)	.61**	7.4 (Hays) (0.5%)	.45**
		31.0 (Hutch.) (1.0)	.73**		
SRPN	1967-86	35.1 (1.0%)	.25**	27.6 (0.8%)	.41**
VPT	1963-86	20.0 (0.6%)	.18*	18.2 (dry) (0.6%)	.06(ns)
				44.5 (irr.)	.27**

R^2=coefficient of determination due regression model
**=significant at 0.01 level
*=significant at 0.05 level
(ns)=not significant

DISCUSSION

In summary, long-term genetic gain estimates from different data sets or using different estimation methods did not give entirely consistent results.

From VPT data, using mean yields adjusted by check (Newton) method, wheat yield increase 4 percent of Newton each year in eastern Kansas, and 2 percent in western(irrigated) Kansas due to genetic improvement from 1977 to 1986. There was no significant genetic gain in western(dryland) Kansas. Using the same method to analyze SRPN data, yield increased .59 percent of Kharkof each year in western Kansas from 1935 to 1985. The coefficient of determination due to the regression model was very low (.11), so the result may be not dependable. There was no significant genetic gain in eastern Kansas.

Genetic gains were also estimated by using regression of cultivar least squares means on the year of release. For VPT data, yield increased 20.0 kg/ha/year due to breeding program in eastern Kansas, 44.5 in western(irrigated) from 1963 to 1986. There was no significant genetic gain in western(dryland) Kansas. From SRPN data, yield increased 35.1 kg/ha/year due to genetic improvement in eastern Kansas, 27.6 in western Kansas.

From the "Old Timers" trial, yield increased 27.6, 31.0 and 7.4 kg/ha/year from 1933 to 1986 due to breeding program, when evaluation was at Manhattan, Hutchinson, and Hays respectively. Compared to other two methods, growing cultivars from different eras in a common experiment is a more direct method evaluating

long-term genetic gain, but there are disadvantages. The "Old Timers" trial sampled only three locations and, so far, only one year, whereas the use of long-term data sets involves many more environments. Also, genetic gain estimates from the "Old Timers" trial may include genotype*environment interaction effects, since modern management practices were used to evaluate cultivars from all eras.

Evaluation in different regions may result in different genetic gain estimates, the main reason being G*E interaction. If a large genetic gain estimate is obtained in a region, this means that the breeding programs were efficient for that region. But growing cultivars in their appropriate niches within the region can result in even greater actual improvement through genotype*environment interaction effect.

Genetic improvement has usually been more important when yield levels were high, and other technological or ecological factors have been more important when initial yield was low (Evans, 1980). The problem is how to improve this situation. With the low price of seed relative to fertilizers and other agricultural chemicals, genetic improvement is the cheapest way for a farmer to increase grain yield. Breeders should pay much more attention to low yield areas. This means that not only do we need breeding programs for specific ecological stress factors such as drought, but also that we need breeding programs for specific regions, each of which is a complete ecological system.

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Chapter 3

COMPARISON OF CULTIVAR YIELDS FROM THE KANSAS WINTER WHEAT PERFORMANCE TESTS AND COUNTY DEMONCIRATION PLOTS IN KANSAS

INTRODUCTION

A practical purpose of research on genotype by environment (G*E) interaction is to increase the efficiency of cultivar performance experiments. Sprague and Federer (1951) and Hanson (1964) discussed how to determine the optimum number of experimental locations, years and replications in order to obtain the most information with the least cost. But their discussions were not concerned with how the experiment stations relate to the areas they serve usually, their surrounding geographical regions. This question is very important to breeders, extension personnel and farmers. The ecological environment of a breeding experiment is directly related to the efficiency of the breeding program. If the conditions under which cultivars are grown at an experiment stations are very different from those in the area it serves, then selection procedures at, and cultivar recommendations by, experiment stations become irrelevant.

Cluster analysis has been used to reduce the impact of G*E interaction through stratifying environments or genotypes into groups so that interactions within groups are minimized. Several methods have been proposed to achieve this objective. Horner and Frey (1957) used a divisive cluster method to separate environments into homogeneous groups. Abou-Ei-Fittouh et al (1969) define homogeneous regions for cotton cultivar tests by cluster analysis (Sokal and Michener, 1958). They used a distance coefficient and a correlation coefficient as dissimilarity measures and a variable group clustering strategy.

SAS (SAS Institute, 1985) is a popular statistical package. Several kinds of cluster analysis can be conducted by using SAS procedures CLUSTER, FASTCLUS, VARCLUS, IPFPHC, OVERCLUS, AND ACECLUS.

The purpose of this chapter will be to compare the Kansas Winter Wheat Performance Test (VPT) data with county demonstration plot data in Kansas, and arrive at some conclusions about the relationship between cultivar performance on experiment stations and farms.

METHODS

Analyses were performed on two data sets. One data set came from the Kansas Winter Wheat Variety Performance Test (VPT) (Walter, 1982-1986), which is unbalanced between and within years. The data covered 14 locations in Kansas and years between 1983 and 1986. There were both dryland and irrigated plots at St. John, Tribune, Colby, and Garden City. Table 1 shows the locations and their code in the data set. The basic data observation used in the analysis was a mean annual yield for each cultivar and location calculated over all replications at the location.

Another data set came from county demonstration plots grown around Kansas. Most of the plots were unreplicated. In some counties, there might be more than one locations each year, so the mean yield over the locations in the county was used as a basic observation. Fig.1 shows the counties and the experiment stations, and their codes in the two data sets.

The methods used to analyze the data included analysis of variance, correlation analysis, cluster analysis and factor analysis. The analysis of variance on the county demonstration plot data was based on the following model.

$$Y_{ij} = \mu + V_i + L_j + (V*L)_{ij}$$

Where Y_{ij} was the yield of cultivar i in location j; μ was overall mean; V_i was cultivar effect; L_j was county effect; and $(V*L)_{ij}$ was cultivar by location interaction effect. Because the data were unreplicated at locations, cultivar by location interaction

mean squares were used to test the cultivar and location effects. The analysis of variance was performed year by year, because the data came from different locations from year to year in the same county. SAS GLM(general linear model) procedure was used to do the analysis because the data were unbalanced.

Pairwise correlation coefficients among all 12 experiment stations and 44 counties were calculated year by year, based on grain yield of common cultivars. The numbers of common cultivars varied from pair to pair, ranging from 9 to 92 (including all four years). The cluster and factor analysis were based on the mean correlation matrix.

SAS VARCLUS procedure was used to do cluster analysis (SAS Institute, 1985). The information contribution of each experiment station and county was assumed equal. The VARCLUS procedure is based on the principle of a oblique component analysis related to multiple group factor analysis (Harman, 1976). By default, VARCLUS begins with all variables in a single cluster. It then repeats the following steps:

1) A cluster is chosen for splitting. The selected cluster has either the smallest percentage of variation explained by its cluster component or the largest second eigenvalue.

2) The chosen cluster is split into two clusters by finding the first two principal components, performing an orthoblique rotation (raw quartmax rotation on the eigenvectors), and assigning each variable to the rotated component with which it has the higher squared correlation.

3) Variables are iteratively reassigned to clusters to maximize the variance accounted for by the cluster components. The reassignment may be required to maintain a hierarchical structure.

VARCLUS procedure allows inclusion of initial seed variables. Each variable listed in the SEEDS statement initially becomes the sole member of a cluster, and every final cluster contains a seed. A cluster analysis was conducted with the experiment stations as seed variables. Because the sample numbers (common cultivars) were not equal in the correlation matrix, the results might not be very accurate. But as Gower (1966) mentioned, the lack of a precise definition of a cluster will not stop people from using methods of cluster analysis. This result still can give valuable information.

SAS FACTOR procedure was used to do the factor analysis (SAS Institute, 1985) on the correlation matrix. A unweighted least squares method was initialized with the prior communality for each variable as its squared multiple correlation with all other variables, and a varimax rotation.

Table 1 Experiment stations and codes in VPT data

Code	Experiment station
STNE1	Powhattan
STNE2	Manhattan
STEC1	Ottawa
STSE1	Parsons
STC1	Hays
STNC1	Belleville
STSC1	Hesston
STSC2	Hutchinson
STSC3	St. John (dryland)
STSC4	St. John (irrigated)
STNW1	Colby (dryland)
STNW2	Colby (irrigated)
STWC1	Tribune (dryland)
STWC2	Tribune (irrigated)
STSW1	Garden City (dryland)
STSW2	Garden City (irrigated)

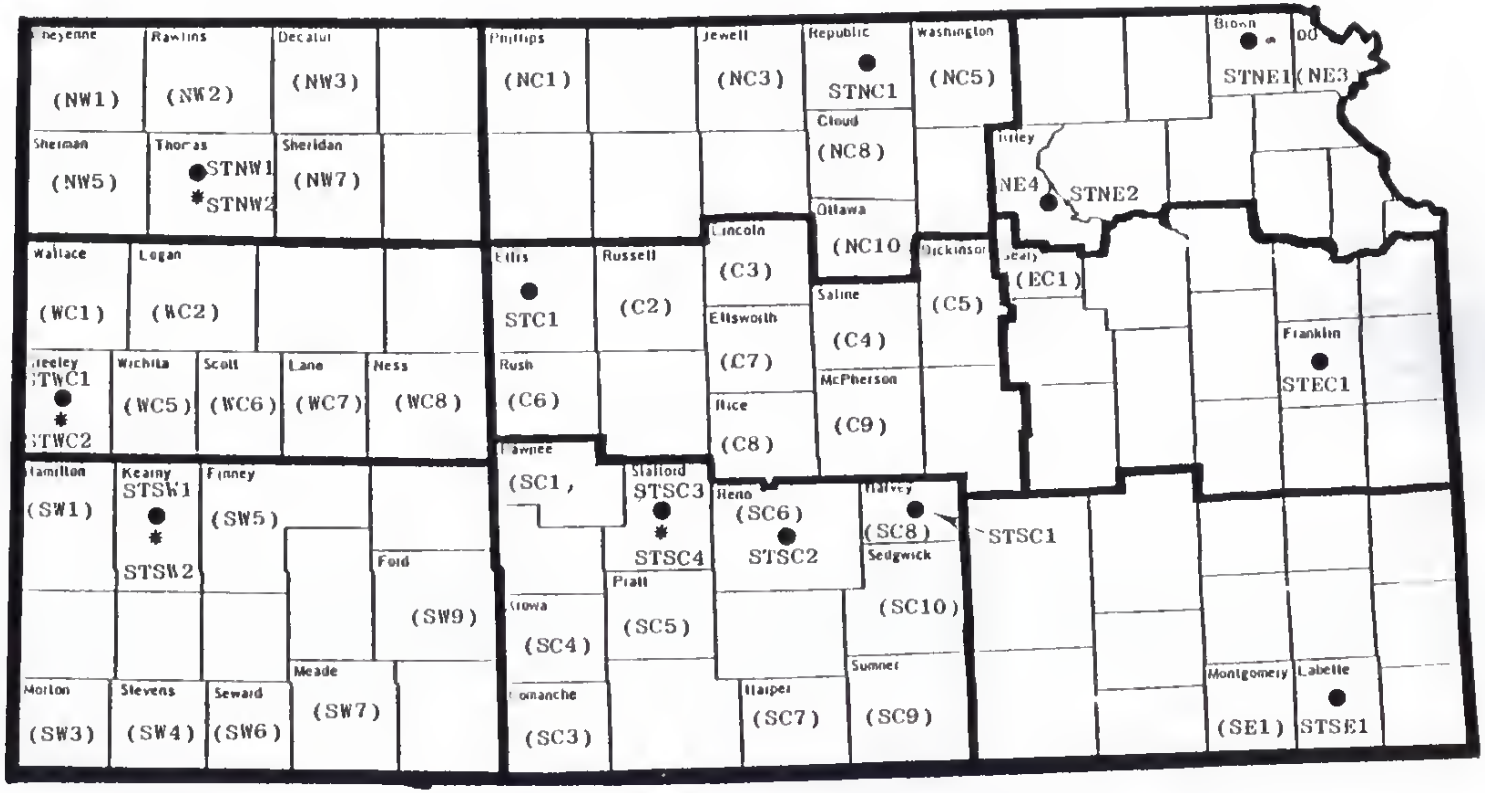


Figure 1 Map of Kansas. Crop reporting districts. Counties and experiment stations included in the data sets
●:experiment station
✱:irrigated plot

RESULTS

The analysis of variance on the county demonstration plot data indicated that cultivar yields were a significant source of variation when tested against cultivar by location interaction (Table 2). Large mean squares from the county effect term indicated that the environments are highly heterogeneous. Significant cultivar mean squares indicated that even though county demonstration plot data are often criticized because of lack of experiment precision, some valuable information may be obtained from them.

Table 3 gives the average correlation coefficients between cultivar grain yield in the performance tests and in the respective surrounding counties. The surrounding counties were determined by crop reporting districts (Fig.1). The correlation coefficients were the overall means of the correlation coefficients between the experiment stations and the counties in the same district. There were only one or two counties involved in the same districts with the Powhattan, Manhattan, Ottawa, and Persons stations, so the results for these four stations may not be representive. All correlation coefficients were 0.52 or less. There are two possible reasons for this. One was that the environments were highly heterogeneous even within small regions in Kansas. Another was that the crop reporting districts may not follow ecological distributions. Extremely low correlations between the irrigated experiment plots, except Colby(irrigated), might result from the fact that

there were few irrigated plots in the county demonstration data.

The cluster analysis based on the correlation matrix among all experiment stations and counties together gave unexpected results (Fig.2). If these locations were classified into nine clusters, some clusters contained several experiment stations, but others contained only counties. For example four experiment stations-Ottawa(STEC1), St. John(dryland)(STSC3), St. John(irrigated)(STSC4) and Tribune(irrigated)(STWC2)- were in one cluster, while four counties-Lincoln(C3), McPherson(C9), Doniphan(NE3) and Montgometry(SE1)- were all in another. An ideal result would be that each cluster contain one experiment station and the surrounding counties.

When we used the experiment stations as cluster seeds, clusters did not follow any geographical distribution (Table 4). There was no county in either the Parsons, St. John(irrigated) or Tribune(irrigated) clusters. For the irrigated stations this is reasonable, and also it is reasonable for Parsons(STEC1), because there was only one county included in the data near Parsons(Fig.1). All other clusters contained counties, but did not correspond to geographical regions.

Figure 3 gives the result of cluster analysis including only experiment stations. If these stations were classified into two clusters, there was a clear division between eastern and western Kansas, except that Hesston(STSC1) was classified into the western group. St. John clustered in eastern Kansas, despite its reputation for drought stress. If more than two clusters were

classified, there was more splitting in eastern than in western Kansas. This indicated that the environments were more heterogeneous in eastern than in western Kansas.

Fig.4 gives the results of the factor analysis based on the correlation matrix, with a unweighted least squares method (SAS Institute, 1985). Ninety-five percent of the total variation could be explained by the first three rotated factor patterns. Again as the results from the cluster analysis, this did not follow geographical distribution.

Table 2 Mean square from analysis of variance of the grain yield in county demonstration plot data

Source	Year							
	1983		1984		1985		1986	
	df	MS	df	MS	df	MS	df	MS
County	27	1226.4	31	2477.6	38	1959.3	37	4123.7
Cultivar	68	130.2	67	79.9	77	186.0	83	162.4
Error(county by cultivar)	413	31.6	579	40.4	713	46.5	719	48.4

Notes: All county and cultivar mean squares are highly significant.

Table 3 Mean correlation coefficient between variety yield in experiment stations and respective surrounding counties

Experiment station	Mean correlation	Number of counties
Powhattan	.07	2
Manhattan	.30	2
Ottawa	.36	1
Parcons	.27	1
Hays	.40	8
Belleville	.49	5
Hesston	.13	9
Hutchinson	.31	9
St. John (dryland)	.22	9
St. John (irrigated)	.13	9
Colby (dryland)	.50	5
Colby (irrigated)	.52	5
Tribune (dryland)	.46	6
Tribune (irrigated)	.10	6
Garden City (dryland)	.39	7
Garden City (irrigated)	.05	7

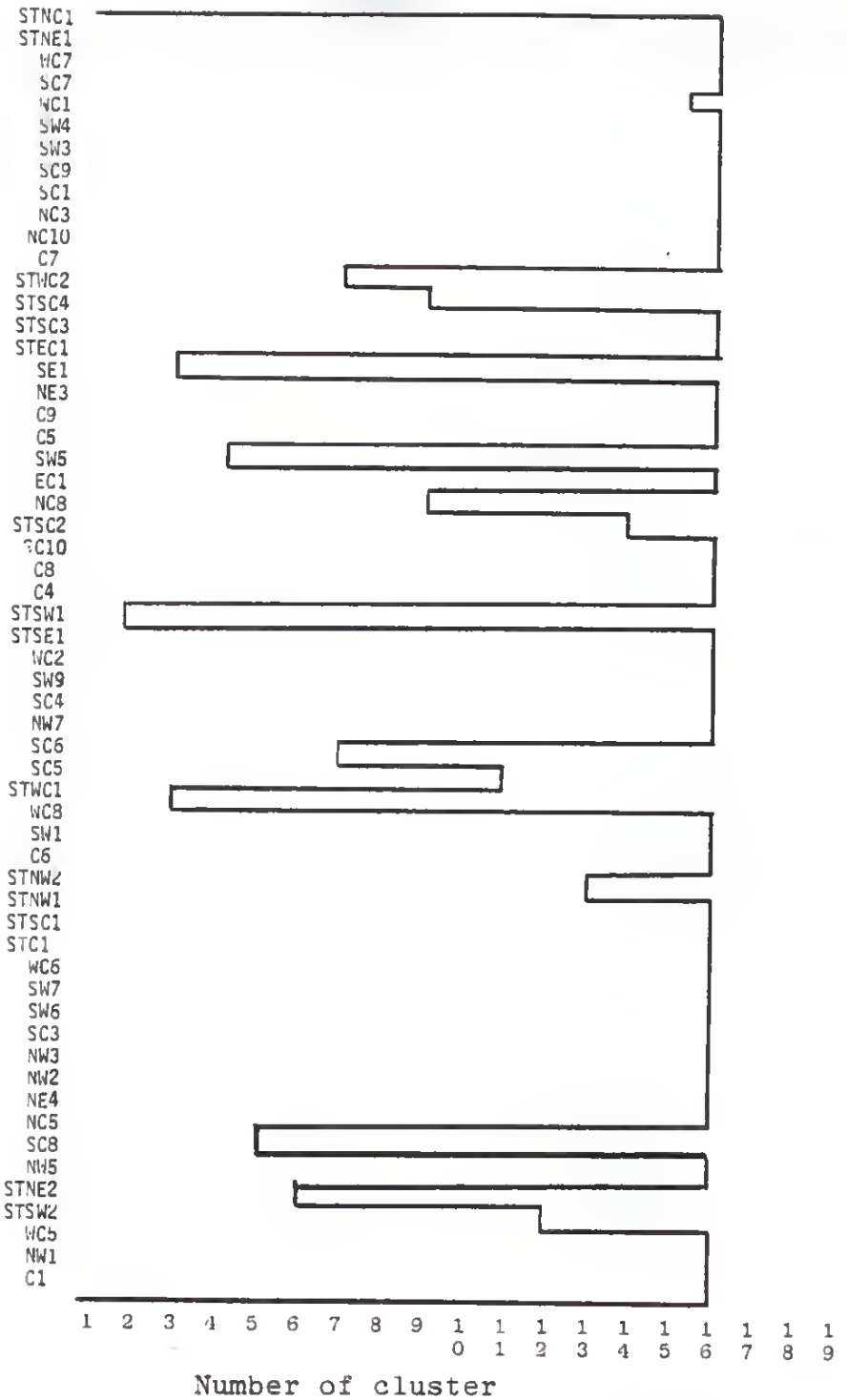


Figure 2 Cluster analysis with all experiment stations and counties. Between two lines without other lines are in same cluster.

Table 4 Results of cluster analysis using experiment stations as cluster seeds

Cluster	Experiment station	County
1	STNE1	C4, C8, NC3, SC1, SC10 SC9, WC7
2	STNE2	C6, NC8, SW5
3	STEC1	SC4, SW9
4	STSE1	------
5	STC1	NC5, NE4, NW3, NW7
6	STNC1	C9, SC7, SE1
7	STSC1	NE3, SC6, WC5
8	STSC2	C5, EC1, NC10
9	STSC3	C7, SC3
10	STSC4	-------
11	STWC1	SW1, SW3, SW4, WC1, WC8
12	STWC2	--------
13	STNW1	NW2, SW7, WC6
14	STNW2	SC8, SW6
15	STSW1	NW1, WC2
16	STSW2	C2, NW5, SC5

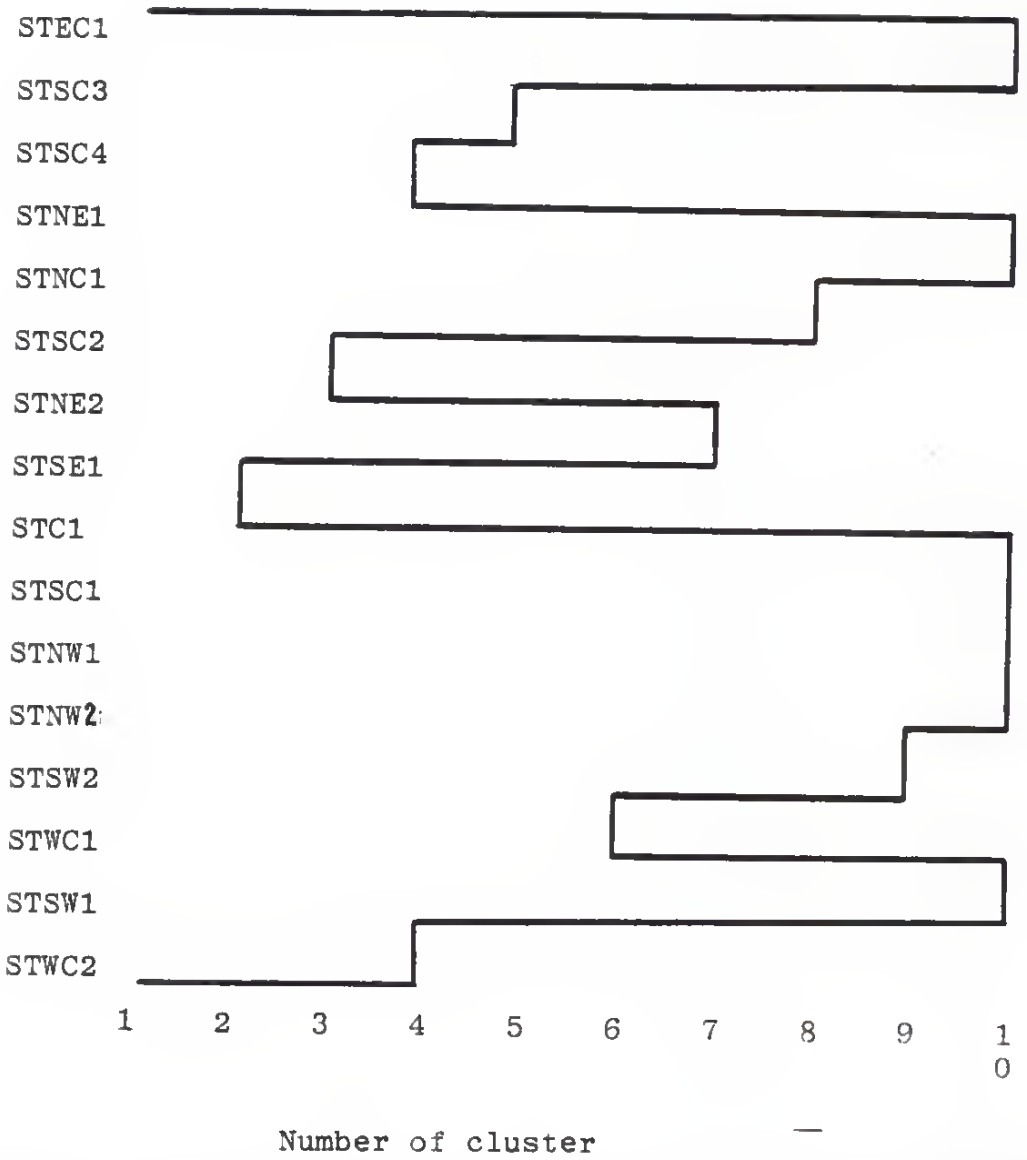
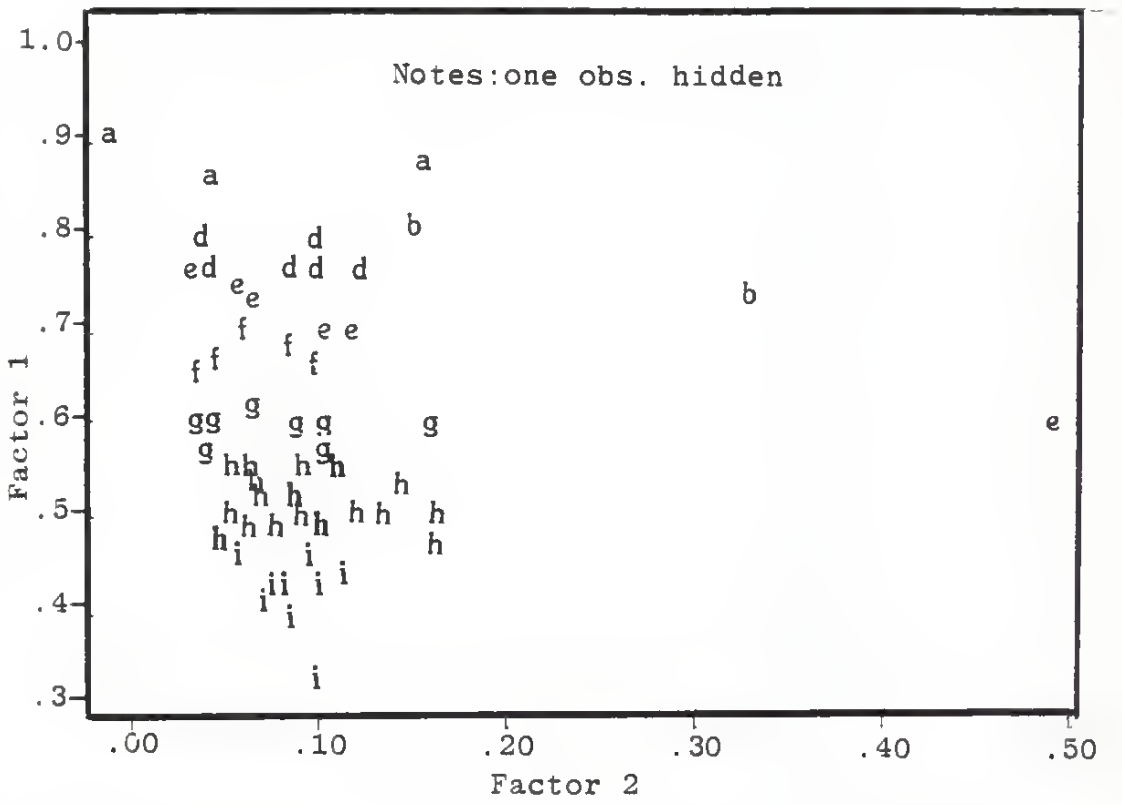


Figure 3 Cluster analysis with only experiment stations. Between lines without other lines are in same cluster.



symbol	factor 3	symbol	factor 3	symbol	factor 3
a	.27-.47	e	.60-.67	h	.80-.87
b	.47-.53	f	.67-.73	i	.87-.93
d	.53-.60	g	.73-.80		

Figure 4 Factor analysis based on the correlation matrix. Contour plot factor 1 * factor 2 = factor 3. In the plot, "a" included counties SW4, NE3 and C2; "b" counties SW5 and SW7; "d" counties WC5, SW2, EC1, WC6, SE1 and SC9; "e" counties SC8, SW6 and SC5 and stations STSW2, STNE1 and STNW2; "f" counties NW5, NW1, C6, and NW7, and station STSC4; "g" counties SC3, SW9, C9, SC1, SC3, WC8, and NC5, and stations STWC2 and STEC1; "h" counties WC7, SC10, SC7, NC8, SC6, NW3, C7, WC2, SW3, NE4, AND SW1, and stations STSC3, STSC2, STNE2, STNW1, STC1, SWC1, and STSW1; "i" counties C8, WC1, NW2, C4, NC10, and C5, and stations STSC1, STSE1, and STNC1.

DISCUSSION

In summary, relative performance of winter wheat cultivars was different in experiment station plots and surrounding county demonstration plots. The reasons may be the different management practices; heterogeneity of environments even within small regions; or lack of correspondence between crop reporting districts and ecological distributions in Kansas. The environments were more heterogeneous in eastern than in western Kansas.

There are two type of ecological factors, natural and artificial. Each effects cultivar performance both in experiment stations and on farm. Natural factors include rainfall, temperature, soil type, elevation, etc.; these are usually very hard for humans to control. The artificial factors include irrigation, fertilizing, Tillage, cultivar choice, planting date, or other farm management practices. The purpose of an experiment station is to show the farmers how to use artificial factors to improve natural factors. So it is very important that the experiment station should be under a natural environment similar to the area it serves. For cultivar performance experiments, this is even more important, because of the existence of G*E interaction.

The environments are strongly heterogeneous in Kansas. Increasing the efficiency of cultivar performance experiments is very important. A complete experiment station survey and comparison with the surrounding counties are suggested. Because

of the year by year cumulative effects, the environments on some old experiment stations may be very different from the areas they serve.

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APPENDICES

Appendix A. SAS program for computing 10 kinds of stability parameters

```
options ls=130 ps=60 nodate;
libname liu 'a:';
data aa;
 infile 'a:stb';
 input yr v 1 y;
run;
proc sort;
 by v yr;
run;
proc means noprint maxdec=2;
 by v yr;
 var y;
 output out=b1 mean=m1 cv=cv std=std;
run;
proc print data=b1;
run;
proc sort data=aa;
 by yr 1;
run;
proc means data=aa noprint maxdec=2;
 by yr 1;
 var y;
 output out=b2 mean=m2;
run;
data b2;
 set b2;
 keep yr 1 m2;
run;
data b3;
 merge aa b2;
 by yr 1;
run;
proc sort data=b3;
 by v yr;
run;
proc reg data=b3 outest=b4;
 model y=m2;
 by v yr;
run;
proc print data=b4;
run;
data b4(rename=(m2=b1));
 set b4;
 keep v yr _sigma_ b1;
run;
proc sort data=b3;
 by yr v;
run;
```

```
proc sort data=b1;
 by yr v;
run;
data b5(keep=v yr l y m1 m2);
 merge b3 b1;
 by yr v;
run;
proc means data=aa;
 by yr;
 var y;
 output out=b6 mean=m;
run;
data b7(keep=v yr l y m1 m2 m);
 merge b5 b6;
 by yr;
run;
data b7(keep=v yr yy m2);
 set b7;
 yy=y-m1-m2+m;
run;
proc datasets;
 delete aa b2 b3 b5 b6;
 save b1 b4 b7;
run;
proc sort data=b7;
 by v yr;
run;
proc reg data=b7 outest=b8;
 model yy=m2;
 by v yr;
run;
proc print data=b8;
run;
data b8(rename=(_sigma_=s2);
 set b8;
 keep v yr s2 m2;
run;
proc sort data=b7;
 by yr v;
run;
proc means data=b7 noprint maxdec=2;
 by yr;
 var yy;
 output out=b9 n=n uss=ssge;
run;
proc means data=b7 noprint maxdec=2;
 by yr v;
 var yy;
 output out=b10 n=n1 uss=ige;
run;
data b11(keep=v yr n2 n1 ssge ige);
```

```
 merge b9 b10;
 n2=n/n1;
 by yr;
run;
proc sort data=b11;
 by v yr;
run;
data b11;
 set b11;
 w1=(n2/(2*(n1-1)*(n2-1))*ige+ssge/(2*(n1-1)*(n2-1));
 w2=-n2/((n2-1)*(n2-2)*(n1-1))*ige+ssge/((n2-2)*(n1-1));
 w3=ige;
 w4=n2/((n2-2)*(n1-1))*ige-ssge/((n2-1)*(n2-2)*(n1-1));
run;
proc print data=b11;
run;
data b12;
 merge b1 b4 b8 b11;
 by v yr;
 keep yr v cv std _sigma_ b1 m2 s2 w1 w2 w3 w4;
run;
proc sort data=b12;
 by yr;
run;
proc datasets;
 delete b1 b4 b7 b8 b9 b10 b11;
 save b12;
run;
data liu.s2;
 set b12;
run;
proc corr data=b12;
 by yr;
 var cv std _sigma_ b1 m2 s2 w1 w2 w3 w4;
run;
```

APPENDIX B SAS program for calculating of the correlation matrix for the VPT and county demonstration plot data

```
options ls=130 ps=60;
data ab;
 infile 'a:c1';
 input r $ yr v $ yy;
 if r='NC8' then r='nc8';
 if r='SC8' then r='sc8';
 if r='WC7' then r='wc7';
 if yy=0 then delete;
 if yr<80 then delete;
 if yy>1000 then yy=yy/67.11;
 if yr<100 then l=1;
 if yr>100 then yr=yr/10;
 l=(yr-floor(yr))*10;
 yr=floor(yr);
 if l=0 then l=1;
run;
data bb;
 infile 'a:data4';
 input v $ snel sne2 secl ssel sncl snc2 sscl ssc2 ssc3 ssc4
   snel sne2 swcl swc2 ssel sse2;
 yr=83;
run;
data cc;
 infile 'a:data5';
 input v $ sne2 secl ssel sncl snc2 sscl ssc2 ssc3 ssc4 snwl
   snw2 swc2 sswl ssw2;
 yr=84;
run;
data dd;
 infile 'a:data6';
 input v $ snel sne2 secl ssel sncl snc2 sscl ssc2 ssc3 ssc4
   snwl snw2 swcl swc2 sswl ssw2;
 yr=85;
run;
data ee;
 infile 'a:data7';
 input v $ sne2 ssel sncl snc2 sscl ssc2 ssc3 ssc4 snwl snw2
   swcl swc2 sswl ssw2;
 yr=86;
run;
data bcde;
 set bb cc dd ee;
 run;
proc sort data=bcde;
 by yr v;
run;
```

```
proc sort data=ab;
 by r yr v;
run;
proc means data=ab noprint;
 by r yr v;
 var yy;
 output out=aa mean=y;
run;
proc datasets;
 delete ab bb cc dd ee;
 save aa bcde;
run;
data t1(rename=(y=c2)) t2(rename=(y=c4)) t3(rename=(y=c5))
  t4(rename=(y=c6)) t5(rename=(y=c7)) t6(rename=(y=c8))
  t7(rename=(y=c9)) t8(rename=(y=ec1)) t9(rename=(y=nc10))
  t10(rename=(y=nc2)) t11(rename=(y=nc3)) t12(rename=(y=nc5))
  t13(rename=(y=nc8)) t14(rename=(y=nc9)) t15(rename=(y=ne3))
  t16(rename=(y=ne4)) t17(rename=(y=nw1)) t18(rename=(y=nw2))
  t19(rename=(y=nw3)) t20(rename=(y=nw5)) t21(rename=(y=nw7))
  t22(rename=(y=sc1)) t23(rename=(y=sc10)) t24(rename=(y=sc3))
  t25(rename=(y=sc5)) t26(rename=(y=sc6)) t27(rename=(y=sc7))
  t28(rename=(y=sc8)) t29(rename=(y=sc9)) t30(rename=(y=se1))
  t31(rename=(y=sw1)) t32(rename=(y=sw2)) t33(rename=(y=sw3))
  t34(rename=(y=sw4)) t35(rename=(y=sw5)) t36(rename=(y=sw6))
  t37(rename=(y=sw7)) t38(rename=(y=sw9)) t39(rename=(y=wc1))
  t40(rename=(y=wc2)) t41(rename=(y=wc3)) t42(rename=(y=wc4))
  t43(rename=(y=wc5)) t44(rename=(y=wc6)) t45(rename=(y=wc7))
  t46(rename=(y=wc8));
 set aa;
 if r='c2' then output t1;if r='c4' then output t2;
 if r='c5' then output t3;if r='c6' then output t4;
 if r='c7' then output t5;if r='c8' then output t6;
 if r='c9' then output t7;if r='ec1' then output t8;
 if r='nc10' then output t9;if r='nc2' then output t10;
 if r='nc3' then output t11;if r='nc5' then output t12;
 if r='nc8' then output t13;if r='nc9' then output t14;
 if r='ne3' then output t15;if r='ne4' then output t16;
 if r='nw1' then output t17;if r='nw2' then output t18;
 if r='nw3' then output t19;if r='nw5' then output t20;
 if r='nw7' then output t21;if r='sc1' then output t22;
 if r='sc10' then output t23;if r='sc3' then output t24;
 if r='sc5' then output t25;if r='sc6' then output t26;
 if r='sc7' then output t27;if r='sc8' then output t28;
 if r='sc9' then output t29;if r='se1' then output t30;
 if r='sw1' then output t31;if r='sw2' then output t32;
 if r='sw3' then output t33;if r='sw4' then output t34;
 if r='sw5' then output t35;if r='sw6' then output t36;
 if r='sw7' then output t37; if r='sw9' then output t38;
 if r='wc1' then output t39; if r='wc2' then output t40;
 if r='wc3' then output t41; if r='wc4' then output t42;
 if r='wc5' then output t43; if r='wc6' then output t44;
```

```
 if r='wc7' then output t45; if r='wc8' then output t46;
run;
data tt;
 merge t1 t2 t3 t4 t5 t6 t7 t8 t9 t10 t11 t12 t13 t14
   t15 t16 t17 t18 t19 t20 t21 t22 t23 t24 t25 t26 t27 t28 t29
   t30 t31 t32 t33 t34 t35 t36 t37 t38 t39 t40 t41 t42 t43 t44
   t45 t46 bcde;
 by yr v;
run;
proc sort data=tt;
 by yr;
run;
proc datasets;
 delete aa  dcde t1 t2 t3 t4 t5 t6 t7
   t8 t9 t10 t11 t12 t13 t14 t15 t16 t17 t18 t19 t20 t21 t22 t23
   t24 t25 t26 t27 t28 t29 t30 t31 t32 t33 t34 t35 t36 t37 t38 t39
   t40 t41 t42 t43 t44 t45 t46;
 save tt;
run;
proc print data=tt;
run;
proc corr data=tt ;
 var c2--ssw2;
run;
```

APPENDIX C SAS program for cluster analysis with whole correlation matrix and with only experiment stations

```
//*++ VMMSG LOG PRINT REGION 1000K TIME 2,2
/*SERVICE UNATTENT
// EXEC SAS
//LIU DD DSN=DSJQS.AAA111A1,UNIT=SYSDA,DISP=SHR
//SYSIN DD *
DATA AA(TYPE=CORR); SET LIU.AAA111A1;
PROC VARCLUS NOPRINT OUTTREE=TREE;
  VAR C2--SSW2;
PROC TREE;
PROC VARCLUS NOPRINT OUTTREE=TREE;
  VAR SNE1--SSW2;
PROC TREE;
```

APPENDIX D SAS program for cluster analysis with seeds of experiment stations

```
//*++ VMMSG LOG PRINT TIME  ,50 REGION 600K
/*SERVICE UNATTENT
// EXEC SAS
//LIU DD DSN=DSJQS.AAA111A1,UNIT=SYSDA,DISP=SHR
//SYSIN DD *
PROC VARCLUS DATA=LIU.AAA111A1(TYPE=CORR) INITIAL=SEED;
 VAR C2-- SSW2;
 SEED SNE1 SNE2 SEC1 SSE1 SNC1 SSC1 SNC2 SSC2 SSC3 SSC4 SNW1 SNW2 SWC1
  SSW1 SSW2 SWC2;
```

GENOTYPE*ENVIRONMENT INTERACTION AND APPLICATION

by

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B.S., Henan Agricultural University, China, 1981

AN ABSTRACT OF A MASTER'S THESIS

submitted in partial fulfillment of the

requirements for the degree

MASTER OF SCIENCE

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KANSAS STATE UNIVERSITY

Manhattan, Kansas

1987

A good yield stability parameter should fulfill three assumptions: (1)does not contain any fixed effects, (2)is independent among cultivars, and (3)can represent yield stability in a way which is meaningful to, and easily understood by, both breeders and farmers. None of the previously proposed stability statistics can meet the requirements.

A new concept of yield stability was defined as: A genotype is considered to be stable in a certain region if the coefficient of variation for location by year interaction for that genotype is small. This coefficient can be estimated by the following equation:

$$CV_i = \sqrt{\sum_{i}^{n} \sum_{j}^{p} (\bar{Y}_{ijk} - \bar{Y}_{ij.} - \bar{Y}_{i.k} + \bar{Y}_{i..})^2} \; / Y_{i..} * 100$$

where i=1,2,....,n indicates the genotype, j=1,2,....,p indicates the year, and k=1,2,....,q indicates the location. Y_{ijk} is the observed yield of genotype i in location k and year j. $\bar{Y}_{ij.}$, $\bar{Y}_{i.k}$, and $\bar{Y}_{i..}$ are the corresponding means. This parameter is estimated independently and without fixed location and year effects. Long-term varietal trials are usually unbalanced, but this statistics can be computed easily using standard statistical analysis packages. This parameter can be thought of as the percentage of the yield variation due to random effects.

Three methods, including to grow cultivars from different eras in a common environment; to express all values in a multiple-year, unbalanced data set as percentages of the value of a long-term check; and to compare estimated the least squares

means (corrected for confounding environment effects), to evaluate the winter wheat yield gain due to genetic improvement. Long-term genetic gain estimates from different data set or using different estimation methods did not always give consistent results. Genotype*environment interaction effect is a main problem for accurate long-term genetic gain estimate.

Relative performance of winter wheat cultivars was different in experiment station plots and surrounding county demonstration plots, either because of different management practices or because of heterogeneity of environments even within small regions in Kansas.