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# GENOTYPE-ENVIRONMENT INTERACTIONS AND STABILITY ANALYSES FOR WHEAT AND BARLEY AND CLASSIFYING TESTING SITES USING MULTIVARIATE AND UNIVARIATE TECHNIQUES

A Dissertation

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Doctor of Philosophy

Degree

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DEDICATION

To my wife, Zohreh F. Chabi

Whose love and sacrifice

Have made this work possible

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# ABSTRACT

Judgment of phenotype to evaluate the genetic potential of a genotype is difficult when genotype x environment interactions exist. Identifying the optimum environment where the greatest differentiation between genotypes relative to their genetic potential can be explored is essential. The objectives of this research were to estimate genotype x environment interactions and stability parameters of wheat and barley cultivars tested over 27 years.

This research was conducted on yield performance data of winter wheat and barley genotypes tested at several locations within the state of Tennessee during 1955-1981. Analysis of variance showed that all sources of variation and their interactions were highly significant except the genotype x year interactions for barley. In wheat, the genotype x year component of variance was much larger than that for genotype x location, suggesting that environmental effects associated with years were more important in determining differential genotypic responses.

Stability adaptation analyses indicated that 22% of the wheat genotypes had a deviation from regression close to zero and a regression coefficient not different from unity. Southern-Belle, Roy, and McNair 3001 were the most

stable genotypes with broad adaptation and the best yielding capacity. Twenty-eight percent of barley genotypes were highly stable. Maury, Henry, Tenn 60-38, and Surry were highly stable barley genotypes with broad adaptation and high mean yields.

Factor analysis revealed that Jackson should be considered as a unique location due to its lack of association with other locations. Factor loading indicated interrelationships among Spring Hill, Springfield, Milan, Martin, and Knoxville. Regression techniques indicated that Crossville provided the least desirable conditions for wheat genotypes to reach their genetic potential and be differentiated, while Springfield, Milan, and Greeneville were suggested as the best testing sites, and Milan and Spring Hill were recommended as the most desirable selection sites for wide adaptation.

In barley, regression techniques revealed that Knoxville was the least desirable location for selection and testing purposes. However, subjecting the barley data to factor analysis revealed that Spring Hill, Knoxville, Springfield, and Jackson were loaded heavily on the same factor indicating the existence of interrelationships among them.

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# INTRODUCTION

The importance and implications of genotype x environment (GxE) interactions are widely recognized by plant breeders and geneticists. In a breeding program, the development of cultivars well adapted to a wide range of environments in which the cultivars may be grown is a common objective.

There is a wealth of supporting evidence that genotypes of different crops including barley (Hordeum vulgare L.) and wheat (Triticum aestivum L.) differ widely in their response to varying environmental conditions; that is, a GxE interaction exists. Such statistical interaction results from changes in the relative ranking of the genotypes or changes in the magnitudes of differences between genotypes from one environment to another (Nguyen et al., 1980). Genotype x environment interaction is in some way involved in most problems of quantitative genetics and many problems of plant breeding (Comstock and Moll, 1963). This is due to the fact that selection is based on phenotype; there is potential contribution of genotype x environment interaction effects to phenotype of all quantitative characters; and genetic facts are inferred from observations on phenotype (Comstock and Robinson, 1963). Complex quantitative traits such as yield are

highly influenced by environmental conditions; therefore, the relative yield performance of a genotype often varies across environments (Ntare and Aken'Ova, 1985). The presence of GxE interactions reduces the correlation between phenotype and genotype and makes it difficult to judge the genetic potential of a genotype (Sharma et al., 1987), which in turn often reduces the progress from selection (Comstock and Moll, 1963; Schutz and Bernard, 1967; Nguyen et al., 1980). A significant GxE interaction for a quantitative trait reduces the usefulness of genotype means over all environments for selecting and advancing superior genotypes to the next stage of selection (Pham and Kang, 1988). Robinson and Moll (1959) indicated that GxE interactions must be considered a major factor in any breeding approach.

Maximum level of yield and stability performance are two features desired in agricultural varieties (Qualset and Granger, 1970). Stability of performance refers to minimum variation in the level of performance in response to changing environments. Pawnee wheat, released in 1942, was one of the first widely adapted wheat varieties, which occupied over 11 million acres (13% of the U.S. wheat acreage) (Zdravkov, 1973). Scout wheat and its identified derivatives in 1972 were estimated to occupy 8-9 million of the 53 million acres of wheat in the United States

(Zdravkov, 1973). In view of the available evidence and, as pointed out by Zdravkov (1973), there is no doubt that the prime characteristic of such widely grown varieties is wide adaptation to seasonal variation in regions where they were or still are grown (Schmidt et al., 1973; Rasmusson and Lambert, 1961; Beaver and Johnson, 1981; Skorda, 1973; Nguyen et al., 1980; St. Pierre et al., 1967). Qualset (1968) stated that stability of performance is difficult to assess because genotype or population responses in a large number of environments are required. However, it can be argued that useful comparisons can be made if stability of one genotype or population is measured relative to another (Qualset, 1968).

In a breeding program, the optimum environment for selection is the one in which the genotypes differentiate best. Frey (1964) noted that differentiation between genotypes relative to their genetic potential is greater in favorable environments. Angus and Mancur (1977) reported that the higher yielding environments provide better predictions of the line's performance across environments than predictions from lower yielding environments. It was concluded that, where yield evaluation is restricted to a few locations (such as early generation testing), it may be sensible to utilize test environments which have high potential probabilities of producing relatively high yields

(Angus and Mancur, 1977). This is in agreement with the conclusions made by Frey (1964). Fribourg and Creel (1981) indicated that it is also important for a plant breeder to know whether data from a testing site can be substituted for other site(s). In cases where two sites were highly correlated with each other, one provides the common information if there was a failure at the other.

In making decisions regarding breeding methods, selection programs, and testing procedures, a knowledge of the nature and relative magnitudes of various types of genotype and environment interactions, and the response of individual genotypes with the environment (stability of performance) is needed. In addition it is essential to have a clear picture of the degree of similarity among testing sites.

The data from the variety tests of 57 winter wheat (Triticum aestivum L. em Thell) varieties, and 44 winter barley (Hordeum vulgare L.) varieties conducted by the University of Tennessee Agricultural Experiment Station at several locations across the state were utilized in this study.

The objectives of this study were to:

1. Estimate genotype, and genotype x environment interactions of the wheat and barley cultivars tested;

2. Examine the stability of wheat and barley cultivars tested over 27 years in 8 and 7 locations respectively;

3. To classify testing sites utilizing multivariate and univariate techniques; and

4. Develop and justify, if possible, (a) a stability-adaptation parameter with covariance of site variation removed, (b) a model to characterize the suitability of a site for selection or testing purposes.

# CHAPTER 1

# REVIEW OF LITERATURE

## Genotype x Environment Interactions

In a breeding program, knowledge of genotype x environment interactions is important in making decisions regarding (a) allocation of resources, (b) number of breeding and/or testing programs to use, and (c) choosing the appropriate nursery environment. Plant breeders have two choices. The first is to develop varieties with adaptation to a wide range of environments. These are characterized by low variability across a wide range of environmental conditions. The second choice is to develop several varieties, each one highly adapted to a subarea with relatively uniform environmental conditions. Choosing one or the other depends on the relative magnitude of genotype x year and genotype x location interaction.

Crop varieties differ widely in their response to environment. Some exhibit a specific response to a particular environment; whereas others can be productive in a wide range of environments. Johnson (1968) showed that the capacity of a variety for yielding well in a range of environments has importance equal to that of its yield

potential. Pfahler (1965) and Allard (1961) concluded that regardless of the natural mating system involved, differences of environmental variability among genotypes within a species were found to be a significant factor. Pfahler (1965) indicated that knowledge of the extent of genetic diversity within a particular species is necessary if selection for desirable agronomic characteristics is to be considered.

An understanding of GxE interactions is of considerable importance in establishing objectives in a breeding program. It is helpful in determining the extent to which wide adaptation of cultivars occurs and in identifying areas requiring specific adaptation (Campbell and Lafever, 1980). The importance of genotype x environment interaction to quantitative genetics and plant breeding was reviewed by Finlay and Wilkinson (1963), Comstock and Moll (1963), Matzinger (1963), Allard and Bradshaw (1964), Eberhart and Russell (1966), Johnson (1968), Breese (1969), Freeman and Perkins (1971), Fripp and Caten (1971), Hardwick and Wood (1972).

Allard and Bradshaw (1964) pointed out that higher plants are dynamic living systems in which changes occur constantly from germination to maturity. The pattern of change is rarely the same from genotype to genotype in one environment or for a single genotype grown in different

environments (Allen et al., 1978). Perkins and Jinks (1968b) categorized the response of a line to its environment as follows:

1. The line exhibits no genotype x environment interactions. This means that the reaction of the line to the environmental variation does not differ significantly from that of the average performance of all other lines in the experiment.

2. The line exhibits genotype x environment interactions in which case it falls into one of the following classes:

(a) There is no linear relationship between this interaction and the additive environmental values, that is, only the regression remainder mean square is significant against the residual mean square.

(b) There is a linear regression and this accounts for all of the genotype x environment interactions, that is, the remainder mean square is not significant.

(c) There is a linear regression but this does not account for all the genotype x environment interactions since the remainder mean square is also significant. This last category can be subdivided on the basis of whether the regression mean square is significant, or not significant, when tested against the remainder mean square.

Effects of GxE interaction on efficiency of a breeding program have been widely studied. Comstock and Moll (1963) reported that genotype x environment interactions reduce the correlation between phenotypic and genotypic values and reduces progress from selection. According to Nguyen et al. (1980), progress from selection is reduced due to the presence of large GxE interactions. In early generations such as $F_3$, there are often large numbers of lines tested and consequently few locations can be used, which leads to elimination of promising materials due to the occurrence of large genotype x environment interactions and a small number of sites (Ntare and Aken'Ova, 1985).

Schutz and Bernard (1967) indicated that genotype x environment interactions in reality consist of two parts: one part is due to the difference in genetic correlations from one environment to another and the other part is due to differences in genotypic variances. For the plant breeder who wants to select the best genotypes, the latter part of the interaction is of relatively minor importance (Schutz and Bernard, 1967). Rasmusson and Lambert (1961) found a highly significant variety x year x location interaction which indicated that the varieties tested responded differently when grown in different years and locations.

Considerable attention has been given to the nature and magnitude of the various genotype x environment interaction components in several crop species, such as wheat (Allen et al., 1978; Marais, 1985;, Liang et al., 1966); barley (Allen et al., 1978); cotton (Abou-El-Fittouh et al., 1969b; Miller et al., 1959; Miller et al., 1958); corn (Poneleit and Bauman, 1970; Sprague and Federer, 1951); grain sorghum (Reich and Atkins, 1970); oats (Qualset and Granger, 1970; Grafius and Kiesling, 1960); soybean (Allen et al., 1978; Schutz and Bernard, 1967); smooth bromegrass (Knowles and Christie, 1972); rice (Gomez and DeDatta, 1975); cowpea (Erskine and Khan, 1977); potato (Tai, 1979); and reed canary grass (Barker et al., 1981).

Studies on cotton reported by Miller et al. (1958, 1959, 1962) have indicated that genotype by environmental interactions are important for yield. Miller et al. (1959) postulated that the patterns of rainfall distribution and insect infestation were the primary factors determining the differential varietal response. Abou-El-Fittouh et al. (1969b) reported that the interaction components were important for yield, but relatively less important for the other traits studied. Gomez and DeDatta (1975) showed that crop season and location are some major sources of variation in rice protein content.

Pfahler (1965) concluded that varieties with the highest grain production generally had the lowest amount of variability as measured both by the squared coefficient of variability and the total squared deviation, but the relation between grain production and environmental variability was not consistent. He further pointed out that the populations differed considerably in their response to the different components of environment. An evaluation by a CIAT agronomist (Fellows, 1948) showed a highly significant cultivar-season interaction.

Allen et al. (1978) performed research to determine the type of yield trial environment that would foster maximum progress from selection for wheat, barley, oats, soybean, and flax. They concluded that if any class of environments is eventually established as substantially superior for testing purposes, it will be because the correlation between a genotype relative to a test environment and a genotype relative to the entire population of environments in which a selected genotype would be used was relatively high. In other words, a test site should represent the entire area well.

In order to make variety recommendations, it is essential that varieties be evaluated over an adequate sample of the environments likely to be encountered over the production area in future years (Miller et al., 1959). In a

study estimating the relative magnitudes of the various types of genotype x environment interactions in winter wheat, winter barley, and winter oats in Tennessee, Wu (1978) reported that the GxE interactions were all significant, except genotype x year interaction for oats. The magnitudes of the components were relatively small in relation to genotype components, except genotype x year interactions for wheat and barley. His results indicated that there was an important differential response to specific environmental conditions which was not accounted for by location, but some differential varietal responses might be accounted for by years.

Chabi (1979) in a study estimating genotype x environment interactions and stability parameters for triticale (X Triticosecale Wittmack) across the states of Arkansas, Alabama, and Tennessee, reported that genotype environment interactions were significant for all agronomic traits studied with the exception of grain protein in one location.

Genotypic variance has been found highest in the favorable environments for wheat, barley, oats, flax, and soybean, but the relative magnitude of the variances in the three types of environments were dissimilar from crop to crop (Allen et al., 1978).

In wheat the genotypic variance for the favorable environments has been several times greater than in the unfavorable environments, which is evidence of substantial GxE interaction (Allen et al., 1978). Campbell and Lafever (1980) studied the influence of years upon relative yields at locations. Their results documented the influence of years on genotype x location interactions and support a rather extensive regional testing program within the soft red winter wheat region. They suggested that genotypes being considered for release should be tested over years and that substitution of locations for years should be minimized.

When numbers of replicates and years are kept constant, the expected variance of a variety mean decreases as the number of locations increase (Liang et al., 1966). However, as the number of years and locations increases, the effect of number of years in reducing the expected variance becomes much less important (Liang et al., 1966). He concluded that the number of locations is more effective in decreasing the expected variance of a variety mean than is an increase in number of years, which in turn is more effective than an increase of replicates (Liang et al., 1966). On the other hand, Rasmusson and Glass (1967) indicated that the error component of variance can be as effectively reduced by adding replications as locations.

The greater size of the VxLxY interaction variance has to be due to one or more aspects of the environment for which the pattern of variation among locations differs from year to year (Comstock and Moll, 1963). This can be the case for timing of stress periods relative to physiological stage of plants (Comstock and Moll, 1963).

To develop formulas for obtaining the optimum allocation of numbers of replicates, years, and locations for a given number of varieties and given cost function, Sprague and Federer (1951) have used the relative magnitude of variety x location and variety x year components of variance to the error variance component. They suggested that the optimum distribution of a given number of plots, disregarding costs, would be one replicate per location with an increase in number of locations and years (Sprague and Federer, 1951).

Allard and Bradshaw (1964) stated that if testing is carried out at a number of locations, chances of identifying genotypes adapted to several environments are improved. Horner and Frey (1966) in a study to determine whether the state of Iowa could be divided into logical subareas for making oat varietal recommendations, noted that the optimum patterns of division into 2, 3, 4, and 5 subregions resulted respectively in an 11%, 12%, 30%, and 40% decrease in

the average variety x location component within sections compared to the same statistics for the state as a whole.

A similar study was conducted by Miller et al. (1959) in North Carolina on 15 cotton varieties at 9 locations for a 3 year period. The lack of sizeable variety x location interactions for the state as a whole indicated that there would be little if any advantage to be gained from attempting to divide the state into subareas for breeding and testing purposes.

Liang et al. (1966) evaluated winter wheat, winter barley, and spring oats for a 3 year period in Kansas at 13, 10, and 5 locations respectively. They found significant variety x location interactions for wheat and barley, indicating the state could be divided into subareas. It is suggested that each subarea should be considered as an independent unit in testing the significance of variety x location interaction because the decrease or increase in the magnitude of variety x location mean squares of subareas compared to that of the state as a whole does not always provide the true picture of its significance (Liang et al., 1966).

Dividing the area to uniform subareas has helped to lower GxE interaction substantially. However, in light of numerous studies GxE interaction within subregions over different years remains large.

Eberhart and Russell (1966) stated that since little additional progress can be expected in reducing genotype x environment interactions by the stratification of environments, other methods such as selecting stable genotypes needed investigation.

## Stability

Stability of performance refers to minimum variation in the level of performance in repeated production fields. Generally, stability is known as range of adaptation and also implies minimum genotype x environment interactions.

Qualset and Granger (1970) shared the same view and indicated that maximum level and stability of performance are two features desired in an agricultural variety.

Lerner (1954) stated that homeostasis refers to the property of the organism to adjust itself to variable conditions, or to the self-regulatory mechanisms of the organism which permit it to stabilize itself in fluctuating inner and outer environments.

Allard and Bradshaw (1964) defined a "well buffered" cultivar as one which can adjust its genotypic and phenotypic response to varying environments in such a way that result in high and stable economic return for the location and year.

Wide adaptation is one that consistently gives superior production over a series of environments. The range of adaptation may be defined by climatological features or as a response to other environmental conditions such as incidence of pests or variation in management-directed factors (Qualset and Granger, 1970).

Jinks and Connolly (1975) indicated that selection in good environments relative to those in which the material is usually raised, more likely leads to the high positive correlations between mean performance and sensitivity. They summarized their findings as follows:

a. Selection for high yield in an above average environment leads to selections with above average environmental sensitivity.

b. Selection for low yield in an above average environment leads to selections with below average environmental sensitivity.

c. Selection for high yield in a below average environment will lead to selections with below average environmental sensitivity.

d. Selection for low yield in a below average environment will lead to selections with above average environmental sensitivity.

Heinrich et al. (1983) stated that stability can be the result of genetic heterogeneity, yield component

compensation, stress tolerance, capacity to recover rapidly from stress, or combination of all of these. Reserve remobilization may have an important role in yield of small grains, especially in stress environments (Wych et al., 1982). Wicks et al. (1988) reported that plants adjust to unfavorable environments by adjusting different characters in different genotypes.

Scott (1967) indicated that yields do not depend on "genetic factors" for stability, and have merit only if populations of many genotypes are less subject to environmental influences than populations of fewer genotypes. However, Tan and Tan (1980) evaluated a 7 x 7 diallel (F1's and parents) with their parents for 3 years at 4 locations in bromegrass. They found that the presence of a substantial proportion of variability due to the additive genetic component in the linear response suggests that it should be possible to exploit this fraction of variability in developing high yielding stable cultivars of bromegrass.

Eberhart and Russell (1966) stated that if stability of performance, or the ability to show a minimum of interaction with the environment, is a genetic characteristic, then preliminary evaluation could be planned to identify the stable genotypes.

Grafius and Kiesling (1960) concluded that uniform regional nurseries at locations in several states in a few

years can provide useful information on adaptation of varieties that would require many years if evaluations were restricted to one or only a few locations.

In plant breeding, selection for qualitative traits can be successfully conducted in limited nursery tests while selection for quantitative traits, such as yield, which are strongly influenced by environments should be conducted in several environments (Ntare and Aken'Ova, 1985). Frey (1964) pointed out that, generally, good adaptive capacity means somewhat superior productivity (relative to all strains being tested) of a genotype or population over several environments.

Grain yield and yield stability under environmental stress remain major selection criteria for stress tolerance in many breeding programs (Bruckner and Frohberg, 1987). In a plant breeding program for the small grains, the strains most likely to be retained are those with a satisfactory regional or area mean performance (Horner and Frey, 1966). Not very often is a strain selected because it produces well in a particular niche. Breeders of soybeans in the United States have emphasized wide adaptation in their selection (Schutz and Bernard, 1967).

Different methods have been employed to create stable genotypes of crop species, among which are synthetic varieties, doublecrosses, mixing seed of two or more

hybrids or varieties, and multiline. Possible advantages of a heterogeneous population such as mixtures of different genotypes are greater yield and stability (Reich and Atkins, 1970; Campbell and Lafever, 1980).

Reich and Atkins (1970) examined parentals, F1's, hybrid blends and parental blends of grain sorghum (Sorghum bicolor L. Moench) as sources with different levels of homogeneity and homozygosity to determine which were the most stable in productivity over a range of environments. They reported that hybrid blends or parentals were the most productive and stable populations.

Becker et al. (1982) reported that phenotypic stability generally increased from three-way to top crosses in winter rye (Secale cereale L.). However, they indicated that the differences in average stability between hybrid types were small as compared to the remarkable variability within each type. Although the stability of a double cross comes from a mixture of genotypes, stability also appears to be under genetic control, that is, certain genotype may show greater stability than others (Eberhart and Russell, 1966). Consequently, higher stability may be genetically combined with high yield in a variety. In self-pollinating species, adaptation can be the result of specific genotypes not associated with heterozygosity (Allard, 1961).

Finlay and Wilkinson (1963) concluded even in a uniform edaphic environment a considerable degree of general adaptability will be important, because of the marked fluctuation of climate conditions from season to season. Frey (1964) found that the group of strains selected in the stress area provided a highly significant mean square for environments x strains interactions; whereas the group of strains selected in the nonstress area did not.

The existence of extreme environmental variation emphasizes that the data obtained in any one year or at any one site cannot be considered as an adequate basis for varietal recommendation. Thus, a measure of the relative stability of varieties under a wide range or environmental conditions becomes necessary in determining efficient breeding procedures (Liang et al., 1966).

Finlay (1963) stated that the increasing emphasis on selection from wide adaptation is itself of some interest, because it is in marked contrast to the previously accepted view that only a specifically adapted genotype will be capable of very high yields in a particular environment.

Even if the variance due to heterogeneity among regressions is not significant when tested against the error mean square, the regressions of each genotype mean on the environmental mean for some of the genotypes taken

individually may show the existence of a highly significant regression when tested against their residual mean squares (Perkins and Jinks, 1968a). Therefore, a reliable prediction for these particular genotypes can be made.

Inheritance of linear regression is controlled predominantly by general combining ability (GCA); whereas both GCA and specific combining ability (SCA) are equally important in the expression of deviation (Tan and Tan, 1980). Several methods of measuring stability of performance of genotypes across environments have been developed.

Conventionally and logically a stable genotype does not respond to changing environments, which can be defined as $b_i = 0$. From Eberhart and Russell's (1966) point of view a stable genotype is the one which responds exactly to the changing environments and does not interact with them. Hanson (1970) has defined a stable genotype as one "which has the minimum possible variability when grown in different environments. This genotype must have minimum $b_i$ expected for the improved genotypes in the test and have no contribution to the genotype environment interaction."

Finlay and Wilkinson (1963) stated that the ideal variety having general adaptability is the one with maximum yield potential in the most favorable environment and minimum response to its environment, that is, maximum phenotypic stability (regression coefficient close to

zero). But practically this is usually not the case, since high stability (b close to zero) is associated with very low mean yields. In their view (Finlay and Wilkinson, 1963), the generally adapted varieties balance between two extremes ($b < 1$, and $b > 1$) which is dependent on the particular genotype and range of environments.

Eberhart and Russell (1966) indicated that under conditions such as exist for maize in the United States, the breeder usually wants a variety that does above average in all environments, that has a high mean yield, and unit regression coefficient and deviation from regression close to zero.

Seif et al. (1979) pointed out that when there is an extreme dependence of yield on one factor of the environment, the environmental factor itself may be used as the independent variable in the regression analysis. This brings more meaningful interpretation, in terms of variability in a single environmental factor (Seif et al., 1979).

Finlay (1968) reported that the two components of adaptation, mean yields over all environments and yield stability ($b_i$) were largely independent (in barley) and selection to combine those two components is possible. Whitehead (1988) performed stability analysis on soybean lines and concluded that the superior lines were the ones

that generally had the greatest yield response to changes in environmental conditions which influenced yield. It was indicated that superior soybean lines were "stable" in the sense that they ranked in the top group regardless of the productivity level of the environments (Whitehead, 1988). Kaltsikes and Larter (1970) found that for yield and days to maturity relative performance was not correlated with sensitivity to environment in durum wheat, and concluded that selection for high mean performance is possible without a sacrifice in the ability to perform well in every environment. However, this was not true for height. Campbell and Lafever (1980) reported that neither measure of stability ($b_i$ and ($S^2_{d_i}$) appeared to be correlated to yield level in winter wheat. Similar findings have been reported by Nguyen et al. (1980). Fussell (1982) reported that no significant correlation between environmental stability (regression coefficients) and protein value was found in triticale (Triticosecale Wittmack). In contrast, both positive and negative correlations between mean performance and linear regression have been found in a number of studies (Perkins and Jinks, 1968a; Monein, 1987; Angus and Mancur, 1970; Perkins and Jinks, 1968b).

Yue et al. (1988) have reported negative and significant correlations between yield and stability parameters for maize and sorghum and suggested that high yield and

stability are not mutually exclusive in the range of environments tested. In wheat-Agropyron derivatives, mean grain yields in severe stress areas were found to be correlated with genotypic stability parameters (Monein, 1987).

In the light of literature reviewed, stability of performance is worth examining for each variety throughout the range of environmental conditions that it is expected to be grown.

## Classifying Locations

For a plant breeder it is essential to identify optimum sites for selecting and/or testing preliminary and advanced materials. Frey (1964) mentioned that there are two schools of theory among plant breeders relative to the optimum conditions for testing for adaptation reaction of small grain strains. One theory is that the optimum selection environment would have no particular stresses of nutrients, moisture, etc., and therefore the plant breeder could differentiate between yielding capacities of different strains (Frey, 1964). The other theory is based upon the reasoning that, in a majority of situations of commercial small grain production, the environment stress situation will be in short supply. Therefore, strains with good

productive capacity under stress testing conditions should be those which would be most widely adapted (Frey, 1964). This latter idea is expressed notwithstanding the fact that differentiation of productive capacity itself will be more difficult to assay under stress conditions because the heritability is lower (Frey, 1964).

According to Hamblin et al. (1980), the best testing site is the one at which the yield of the selected genotypes at the test locality consistently corresponds to their yield when grown over the range of environments for which they are intended. Large and significant associations between mean correlation of locations and the environmental indices, suggested that the most useful predictions of the performance were made from the test in the highest-yielding environments (Angus and Mancur, 1977).

Campbell and Lafever (1980) reported that the locations with a relatively high mean correlation coefficient (r) value would be favorable sites for breeding and testing for wide adaptation; whereas, locations with relatively low mean r may require breeding for traits not generally needed for adaptation throughout much of region.

Allen et al. (1978) reported that error variance increased with decreasing stress level of the nursery and was approximately twice as large for the favorable as for the unfavorable environments for wheat, barley, oats, and

flax. They concluded that error and genotypic variances generally became larger with increases in the productivity of the trial environment.

Frey (1964) concluded that differentiation among genotypes relative to their yield capacity is greater in favorable environments. Therefore, he concluded that high yielding environments are preferred for selection of the early generations breeding material.

Angus and Mancur (1977) reported that the higher-yielding environments provided better predictions of the line performance across environments than that from lower yielding environments. Consequently, where yield evaluation is restricted to a few locations (such as early generation testing) it may be sensible to utilize test environments which have good probabilities of producing relatively high yields (Angus and Mancur, 1977).

The study conducted by Frey (1964) supports this conclusion. He found that the adaptation reaction of oat strains was differentiated better in nonstress environments. The optimum environment in which to practice selection obviously is the one which will elicit the greatest differential genetic manifestation for the attribute in question (Frey, 1964). However, defining the optimum environment to differentiate the degree of adaptation characteristics of small grains is difficult, perhaps,

due to different meanings of adaptation reaction under different situations, or several different mechanisms which may be responsible for adaptation reaction (Frey, 1964).

To identify the association between testing sites in Tennessee for small grain, Wu (1978) used correlation techniques. He concluded that the high level of correlation between either Greeneville or Knoxville and most of the other locations would imply that these are the desirable sites for selecting wheat varieties with general adaptation to all of the state, except Jackson and Milan. Conversely, varieties selected at Milan and Jackson would not necessarily be expected to perform well throughout the state. In the same study, it was suggested that the data of all testing locations might be used to predict the variety performance of barley at any other locations. However, the generally low coefficient of determination ($R^2$) among these locations indicated that none of these locations would be the best site for selecting barley varieties with general adaptation (Wu, 1978).

## Techniques

Significant advances have been made in the measurement and understanding of genotype x environment interactions,

stability of genotypes, and classification of environments during the past decade.

Techniques to Measure Stability

Many statistical methods have been proposed, compared, and examined to measure the stability parameters (Eberhart and Russell, 1966; Finlay and Wilkinson, 1963; Francis and Kannenberg, 1978; Gray, 1982; Kang and Miller, 1984; Lin et al., 1986; Ntare and Aken'Ova, 1985; Plaisted and Peterson, 1959; Plaisted, 1960; Shukla, 1972; Perkins and Jinks, 1968b; Fellows, 1948; Chabi, 1979; Seif et al., 1979; Ghaderi et al., 1980; Johnson et al., 1968; Miller et al., 1959; Lamb et al., 1984).

Plaisted-Peterson stability parameter. An early attempt to measure the stability of individual genotypes was made by Plaisted and Peterson (1959). The mean of the estimated variance components of the GxE interaction for all pairs of genotypes that include genotype i is the stability measure for genotype i. This approach requires a combined analysis of variance for each pair of genotypes. When a large number of genotypes are involved, this method becomes very cumbersome

Finlay-Wilkinson stability parameter. Statistical methods to estimate the GxE interactions involve an analysis of variance. Then a significant GxE may be partitioned

into two components by regression coefficient analysis, proposed by Yates and Cochran (1938) and modified by Finlay and Wilkinson (1963), and again later by Eberhart and Russell (1966), and Perkins and Jinks (1968a).

Finlay and Wilkinson (1963) suggested that selection for wide adaptation can be achieved by selection for high mean yields and regression coefficient close to 1.0 (equivalent to 0.0 in the Perkins and Jinks (1968a) method). This technique has been applied widely to a number of crops since its rediscovery by Finlay and Wilkinson (1963). In this approach, known as joint regression, the individual genotype's yield is regressed on the grand mean of all genotypes for each site. The regression coefficient ($b_i$) for each genotype is then taken as its stability parameter. Similar statistics were suggested by Perkins and Jinks (1968a) except that the observed values are adjusted for location effects prior to the regression.

Hill (1975) pointed out that the main advantage of linear regression technique is its proven ability to reduce complex interactions to a series of orderly, linear responses. It was indicated that regression sometimes fails as any other model, but if used correctly, should facilitate the decision making process in particular breeding programs.

Eberhart and Russell parameter. This model provides a means of partitioning the genotype x environment interaction of each genotype into two parts:

a. The variation due to the response of the variety to varying environmental indexes (sum of squares due to regression); and

b. The unexplained deviations from regression on the environmental index.

"This same regression technique was used by Mooers (1921, 1933) in Tennessee for open pollinated corn varieties, although he did not quantify the method as it is now known" (Qualset, 1968).

The parameters are defined with the following model:

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij} .$$

where $Y_{ij}$ is the mean of the $i^{th}$ variety at the $j^{th}$ environment ($i = 1, 2, \ldots, v$; $j = 1, 2, \ldots, n$), $\beta_i$ is the regression coefficient that measures the response of the $i^{th}$ variety to changing environments, $\delta_{ij}$ is the deviation from regression of the $i^{th}$ variety at the $j^{th}$ environment, $I_j$ is the environmental index, and $\mu$ is the mean of $i^{th}$ variety to changing environments.

The regression of each variety on an environmental index and a function of the squared deviations from this

regression provided the estimates of the desired stability parameters.

The environmental index (I) is the mean of all varieties at the $j^{th}$ environment minus the grand mean.

$$I_j = (\Sigma_i Y_{ij}/v) - (\Sigma_i \Sigma_j Y_{ij}/vn)]. \qquad \Sigma_j I_j = 0 .$$

The first stability parameter is a regression coefficient estimated in the usual manner:

$$b_i = \Sigma_j Y_{ij} I_j / \Sigma_j I_j^2 .$$

The appropriate analysis of variance is given in Table A-1. With this model, the sums of squares due to environments and variety x environments are partitioned into environments (linear), varieties x environments (linear) and deviations from the regression model.

The performance of each variety can be predicted by using the estimates of the parameters where $\hat{Y}_{ij} = \bar{X}_i + b_i I_j$ where $\bar{X}_i$ is an estimate of the $\mu_i$. The deviations [$\hat{\delta}_{ij} = (Y_{ij} - \hat{Y}_{ij})$] can be squared and summed to provide an estimate of another stability parameter ($S^2_{d_i}$):

$$S^2_{d_i} = [\Sigma_j \hat{\delta}^2_{ij}/(n-2)] - S^2_e/r$$

where $S_e^2/r$ is the estimate of the pooled error (or the variance of a variety mean at the $j^{th}$ location), r is number of replications, and:

$$\Sigma_j \hat{\delta}_{ij} = [\Sigma_j Y_{ij}^2 - Y_{i/n}^2] - (\Sigma_j Y_{ij} I_j)^2 / \Sigma_j I_j^2 .$$

A desirable genotype is the one with a high mean ($\bar{X}_i$), unit regression coefficient ($b_i = 1.0$) and the deviations from regression as small as possible ($S_{d_i}^2 = 0$).

The hypothesis that there are no significant differences among variety means

$$H_o: \quad \mu_1 = \mu_2 = \ldots \mu_v$$

can be tested approximately by the F test,

$$F \simeq MS_1/MS_3 ,$$

where $MS_1$ is the variety mean square, and $MS_3$ is the pooled deviations.

The hypothesis $H_o: \beta_1 = \beta_2 = \ldots = \beta_v$ for their regressioned on the environmental index can also be tested approximately by the F test, $F \simeq MS_2/MS_3$, where $MS_2$ is the variety by environment (linear) mean square.

The hypothesis that any regression coefficient does not differ from unity can also be tested by the appropriate

t test. An appropriate test of the deviations from regression for each variety can be obtained,

$$F \simeq (\Sigma_j \hat{\delta}^2_{ij}/n-2)/\text{pooled error} .$$

Shukla's stability parameter. Shukla's (1972) parameter ($\delta^2$) is the variance of a genotype across environments, based on the residuals in a two-way classification. In this method the stability parameter is based on the contribution of the genotype to GxE interactions.

Francis and Kanenberg's stability parameter. Francis and Kannenberg (1978) coefficient of each variability ($CV_i$) was suggested to measure the stability.

Powell and Philips stability parameter. Powell and Philips (1984) estimated environmental sensitivity by taking the square root of the variance of yield over sites whenever the use of linear regression proved to be inappropriate.

Increased interest of plant breeders for developing stable cultivars led researchers to examine and compare different stability statistics.

Statistical validity of the stability parameters proposed by Eberhart and Russell (1966) has been examined by several researchers (Lin et al., 1986; Kang and Miller, 1987; Yue et al., 1988; Pham and Kang, 1988).

Pham and Kang (1988) studied rank correlations among several stability statistics using the data from five international maize (Zea mays L.) trials. It was indicated that $b_i$ statistics by Eberhart and Russell (1966) were highly correlated with $b_i$ and $S_i^2$ statistics by Shukla (1972). On the other hand, none of these statistics were consistently well correlated with mean yields.

Ecovalence ($w_i$) developed by Wricke (1962) and stability variance statistics ($\sigma_i^2$) developed by Shukla (1972) ranked genotypes identically (Kang and Miller, 1984). Baldwin (1971) compared five stability models proposed by Plaisted and Peterson (1959), Plaisted (1960), Wricke (1962), Finlay and Wilkinson (1963), and Eberhart and Russell (1966) using five cultivars of alfalfa (Medicago sativa L.) and eleven cultivars of wheat (Triticum aestivum L. em Thell). It was concluded that, of the five models, three resulted in similar rankings. The other two, Eberhart and Russell and Finlay and Wilkinson, resulted in rankings not only different from others but also different from each other.

No significant association between regression coefficient and coefficient of variation (CV) was found by Fussell (1982) in Triticale (Triticosecale Wittmack). Therefore, it was concluded that, the coefficient of

variation should not be used as an indicator of stability index for protein (Fussell, 1982).

The results of an investigation dealing with various methods utilized as the means of estimating stability parameters were presented in a recent publication by Lin et al. (1986). They indicated that if the scientist is concerned about stability over an entire range of environments, CV and $S_i^2$ (Francis and Kannenberg, 1978) are useful. If the scientist is interested in comparing relative stability among the group of cultivars included in the experiment and if the regression model fits the data, $b_i$ (Finlay and Wilkinson, 1963) and $B_i$ (Perkins and Jinks, 1968a) are best. If the data do not fit, or if the residual mean square from the regression are heterogeneous, statistics $W_i^2$ (Wricke, 1962) and $\sigma^2$ (Shukla, 1972) are useful. Johnson and Whittington (1977) applied stability statistics defined by Finlay and Wilkinson (1966) and pointed out that deviation from regression as a measure of stability seems unnecessary, unless the regression is reasonably significant. Yue et al. (1988) have made the same implications and reported that deviation from regression becomes more important in establishing genotypic stability when regressions ($b_i$) were significant. Lin et al. (1986) indicated that regression coefficient ($b_i$) is a relative measure of stability depending on the genotypes

included in the test. So its scope of inference is confined to the test set and should not be generalized unless the genotypes are a representative sample of those grown in the area in question. In their view, deviation from regression ($S_i^2$) proposed by Eberhart and Russell (1966) indicates no more than how good is the fit, but has no direct bearing on the genotype's stability (Lin et al., 1986). However, deviation from regression ($S_i^2$) has been used frequently since it was proposed in 1966.

Breese (1969) strongly recommended the use of deviation from regression for the reason that the variability of any genotype with respect to varying environment can be partitioned into a predictable part (regression) and an unpredictable part which is deviation from regression. He stated that "the term 'stability' should now rather be reserved to describe measurements of unpredictable irregularities in the response to environment as provided by the deviation from regression" (Breese, 1969).

Becker et al. (1982) indicated that deviation from regression is the most appropriate approach to estimate stability in agronomic sense, because it measures the predictability of genotypic reaction to environments.

Yue et al. (1988) compared six stability statistics proposed by Eberhart and Russell (1966), Tai (1979), and

Shukla (1972). They found that the regression coefficient ($b_i$) best estimates genotypic adaptability and deviation from regression ($S^2_{d_i}$) was best for stability. Langer and Frey (1964) regarded the regression coefficient as a measure of response to varying environments and the mean square for deviation is a true measure of production stability. In this regard, Hardwick and Wood (1972) indicated that if a large number of genotypes are used and the between-environments mean squares is significant, any bias would not be serious. The most used selection criteria for high performance and stable genotype are mean yields, regression coefficient of individual genotypes yields on site mean yields, and deviation from regression (Comstock and Moll, 1963; Fellows, 1948; Fox and Rathjen, 1981; Eberhart and Russell, 1969; Finlay and Wilkinson, 1963; Freeman, 1973).

## Techniques to Classify Testing Sites

Different statistical procedures have been applied to classify and characterize testing or selection sites.

Univariate Techniques

Correlation technique. Plant breeders have applied the correlation coefficient of genotypes performance in different environments to determine the nature and the degree of similarity of environments tested (Allen et al., 1978; Fox and Rathjen, 1981; Hamblin et al., 1980; Wu, 1978). Correlation technique measures the closeness of linear relationship between any pair of variables tested.

Regression technique. To characterize the responses of varieties, Finlay and Wilkinson (1963) applied a regression technique. On the bases of the same principle Fox and Rathjen (1981) regressed the yields of all varieties at a particular site against the mean yields of each of the varieties across all sites. In this approach the yields from each site were used as a measure of similarity of site to relate these to their geographic locations. It was reported that the regression coefficient for high yielding sites were highly significant and the overall mean yields of the varieties were dependent on the performance at the high yielding sites (Fox and Rathjen, 1981). In 1971 Wright had discussed the same approach.

Frey (1964) indicated that the optimum environment in which to practice selection obviously is the one which will

elicit the greatest differential genetic manifestation for the attribute in question. It was noted that differentiation between genotypes relative to their genetic potential is greater in favorable environments (Frey, 1964). Therefore, the optimum selection environment is the one at which differentiation among genotypes could be maximized. This may be achieved if the selection environment does not impose any major environmental stress on genotypes tested.

In this regard, yields of the genotypes at a particular site may be regressed on the mean yields of each of the genotypes across all sites. The magnitude of the regression coefficient for a testing site reflects the level of differentiation among genotypes at that testing site. The above average regression value ($b_i > 1$) indicates that genotypes at that environment were more differentiated than the average environment. Therefore, better differentiation among genotypes in such an environment is possible. In contrast, an environment with a regression coefficient less than average ($b_i < 1$) indicates that the genotypes performed more similar to each other. Consequently, less differentiation was achieved.

Generally, higher differentiation is expected to occur in favorable environments. But, this depends on the environments and genotypes involved in the test. Fox and Rathjen (1981) concluded that the regression method was

particularly valuable in illustrating how the mean yields of the varieties were dependent on the results from few sites. This is expected to be true for evaluating the testing sites.

Generally, overall mean yields of a testing site determines the extent to which the genetic potentiality of the genotypes can be explored at that particular site. Therefore, simultaneous consideration of regression coefficient and overall mean yields of testing sites are important in characterizing testing sites. This may be accomplished by plotting regression coefficient against overall mean yields of the testing sites.

A generalized two dimensional scatter diagram and its interpretation is illustrated in Fig. 1. The regression axis may be divided into three sections using plus or minus one standard deviation from the mean regression. One standard deviation above or below the overall mean may be applied to divide the mean yield axis vertically.

Multivariate Techniques

Different multivariate approaches have been applied to provide information relating cultivar response and location effects (Abou-El-Fittouh et al., 1969a; Ghaderi et al., 1980; Shorter et al., 1977; Wu, 1978; Hamblin et al., 1980; Seiler and Stafford, 1985; Orth et al., 1976; Seif et al.,

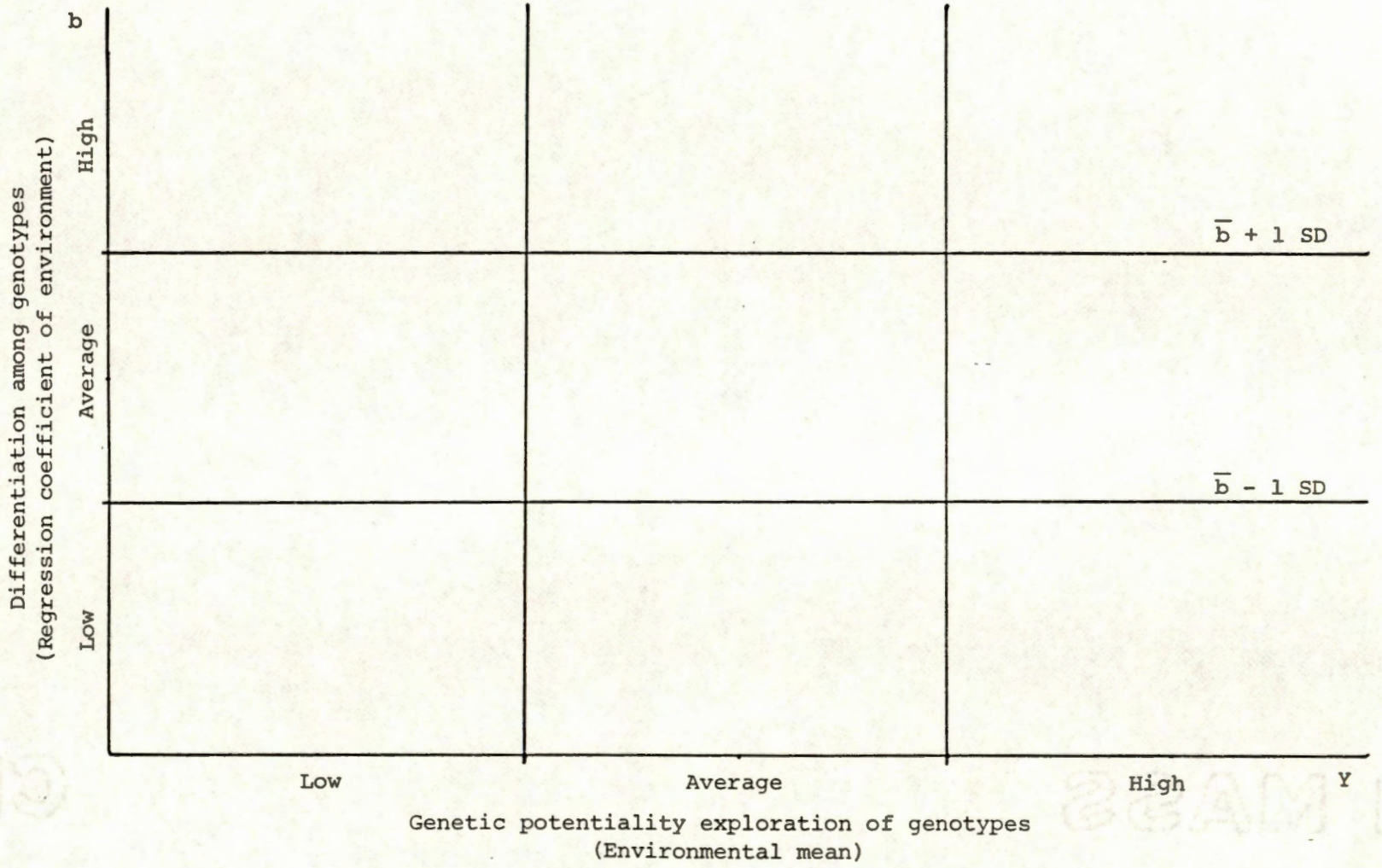



Fig. 1. Generalized diagram of regression coefficient (differentiation) and mean yields of testing sites (genetic potentiality exploration).

1979; Fox and Rathjen, 1981). To find the pattern of interrelationship of variables, and to group the variables most closely interrelated in common factors, the use of factor analysis has been found useful.

Factor analysis techniques have been used by plant breeders to reduce a large number of correlated variables to a small number of uncorrelated main factors. Factor analysis is a considerably more useful technique than simple correlation. It provides groups of variables called "factors" and estimates percentage of contribution of variables to each factor.

Seiler and Stafford (1985) used factor analysis to assess dependence relationship between yield components and morphological characteristics of guar [Cyamposis tetragonoloba (L.) Taub]. They were able to reduce ten variables to four independent factors which adequately accounted for most of the interrelations.

A similar study was conducted by Walton (1972) on spring wheat (Triticum aestiuum L.). Fourteen yield components were divided into four groups of factors which made the largest contribution to yield. They considered factor analysis as a better technique to identify the relationship between variables over multiple regression.

Fribourg and Creel (1981) studied the sequential use of factor analysis and multiple regression techniques in

forage sorghum (Sorghum bicolor L. Moench). They reported that factor analysis reduced the original 38 concomitant variables to 15, and subsequent use of multiple regression reduced the 15 variables to 9.

Orth et al. (1976) utilized factor analysis to investigate the interrelationships of 12 bread quality tests and identified these most closely related to the major factors governing wheat quality.

Using canonical variates analysis, Seif et al. (1979) divided the central west of New South Wales into two uniform subregions for varietal recommendations. It was indicated that test weight data for wheat were used to group locations according to their similarity of GxL effects by cluster analysis (Ghaderi et al., 1980). In their study the area was divided into groups within which the GxL interactions were nonsignificant. They concluded that such an analysis would be useful for the selection of testing sites for early generation testing with wide or narrow adaptability.

Factor analysis. Factor analysis is an approach to explain the relationships among several difficult to interpret correlated variables into few meaningful relatively independent factors. The origins of factor analysis is generally ascribed to Charles Spearman (Harmon, 1976), the author of general intelligence paper (Harmon, 1976).

In multiple regression, the attempt is to explain a single known measured dependent variable through the independent variables. While with factor analysis technique; many variables without causative relationship are to be explained. Factor analysis must be distinguished from component analysis. Since a component is an observable linear combination but a factor is both hypothetical and unobservable (SAS, 1982).

The single most distinctive characteristic of factor analysis is its data-reduction capability, but this should not be taken as the sole rationale for factor analysis (SPSS, 1975). The most common applications of factor analysis are: (a) exploration and detection of patterning of variables to discover new concepts, (b) to construct indices for use as new variables in another analysis, (c) to identify appropriate variables for later analysis from a larger set of variables, and (d) to test the hypothesis about the structuring of variables in terms of the expected number of significant factors and factor loading (SPSS, 1975).

Model. The equation for the common factor model (81):

$$Y_{ij} = X_{i1}b_{1j} + X_{i2}b_{2j} + \ldots + X_{iq}b_{qj} + e_{ij}$$

where

$Y_{ij}$ = the value of the $i^{th}$ observation on the $j^{th}$ variable,

$X_{ik}$ = the value of $i^{th}$ observation on the $k^{th}$ common factor,

$b_{kj}$ = the regression coefficient of the $k^{th}$ common factor for predicting the $j^{th}$ variable,

$e_{ij}$ = the value of the $i^{th}$ observation on the $j^{th}$ unique factor, and

$q$ = the number of common factors.

The assumptions are: (a) the unique factors are uncorrelated with each other and (b) each unique factor is uncorrelated with common factors (SAS, 1982).

Factor analysis involves three main steps: (a) preparation of correlation matrix for the number of variable interested, (b) extraction of orthogonal (independent) factors on the basis of the interrelations exhibited in the data, and (c) rotation of each of these solutions to orthogonal axes.

A common factor is one on which at least two variables are loaded, otherwise it is called unique factor.

Significant loading may be determined in three following steps: (a) identifying the highest value in each row of a rotated factor pattern matrix and marking them,

(b) determining that the lowest absolute value has been marked, and (c) going through the entire rotated factor pattern matrix and mark any value which has a greater absolute value than the value determined in step (b), and has not been previously marked.

The factors may be interpreted and characterized by the variables which have high loadings on the particular factor.

# CHAPTER 2

# MATERIALS AND METHODS

## Data Collection

Each year the University of Tennessee Agricultural Experiment Station conducts yield trials on small grain varieties to evaluate the performance of wheat and barley varieties and experimental lines at the various experiment stations across the state. Data for winter wheat, and winter barley varieties from these performance tests for the years 1955 through 1981 were used in this study. The mean yields for the years each variety was evaluated are shown in Tables A-2 and A-3 for wheat and barley, respectively. Data were provided by the leader of the variety test project, namely Gibson, 1955-1956; Shelby, 1957-1958; Graves, 1959-1981; and Graves, 1979.

Wheat trials were conducted at the Main Station (Knoxville), Tobacco Experiment Station (Greeneville), Plateau Experiment Station (Crossville), Highland Rim Experiment Station (Springfield), West Tennessee Experiment Station (Jackson), Middle Tennessee Experiment Station (Spring Hill), Martin Experiment Station (Martin), and

Milan Experiment Station (Milan). Barley was tested at all stations utilized for wheat except Martin.

The latitude, longitude, and elevation of these eight stations are presented in Fig. 2. They are widely scattered and represent different areas of the state. Each station is situated as to include soil type and climatological representation of that area of Tennessee. The approximate climatic conditions of these stations are shown in Tables 1 and 2.

## Experimental Design

The experimental design used in the variety testing program was a randomized complete block with four replications per testing site. Each plot consisted of 5 or 6 rows, was at least 40 feet long. Seeds were planted using a grain drill or plot grain drill, and harvested by combine. The yield of each plot was measured in bushels per acre. The environments tested were assumed as a random sample of possible environments in the state of Tennessee.

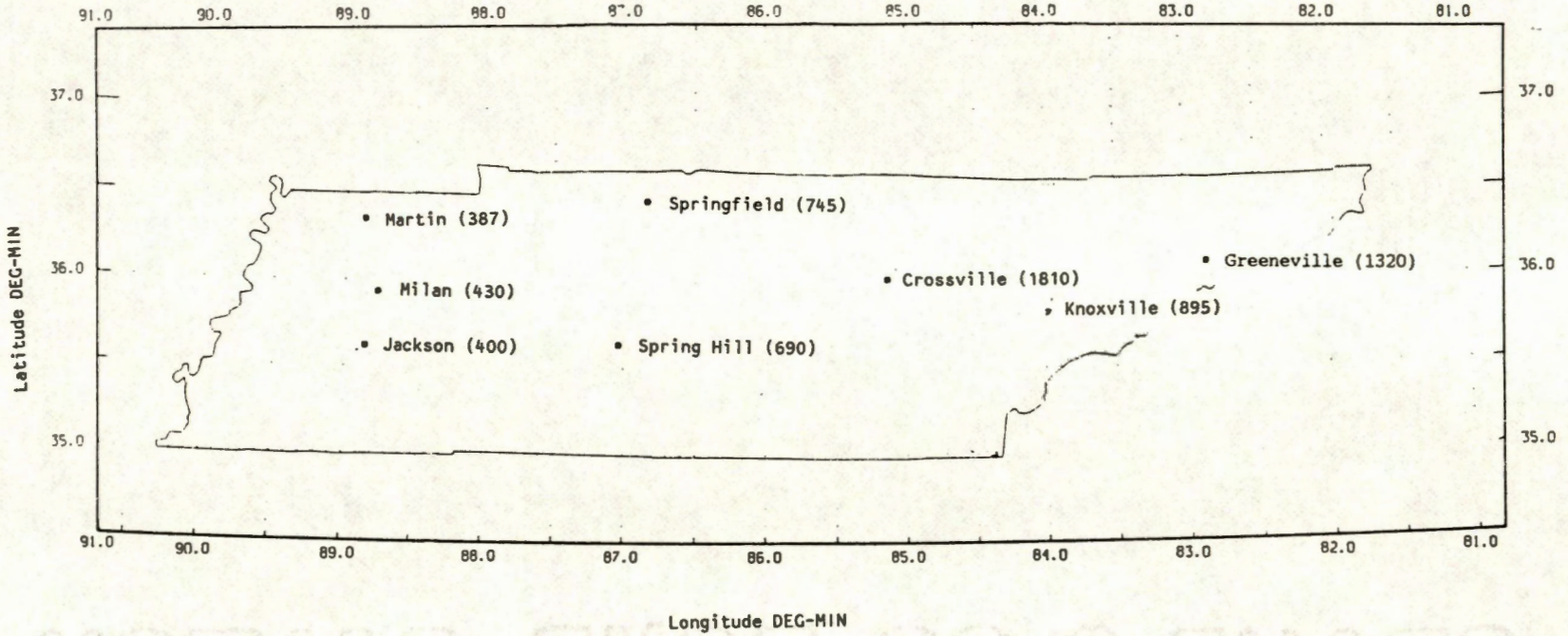



Fig. 2. Map of state of Tennessee and approximate location of testing sites, their latitude, longitude, and elevation (feet in parentheses).

Table 1. Average monthly precipitation (in.) for the small grain growing season (1951-1980).[a]

| Location | Oct. | Nov. | Dec. | Jan. | Feb. | Mar. | Apr. | May | June | Season Total |
|---|---|---|---|---|---|---|---|---|---|---|
| Knoxville (Airport) | 2.73 | 3.78 | 4.59 | 4.65 | 4.18 | 5.49 | 3.87 | 3.71 | 3.95 | 36.95 |
| Springfield | 2.68 | 4.19 | 4.58 | 4.63 | 4.20 | 5.47 | 4.51 | 4.59 | 3.79 | 38.64 |
| Spring Hill[b] | 3.47 | 3.91 | 4.99 | 5.41 | 4.83 | 6.21 | 5.15 | 4.97 | 3.74 | 42.68 |
| Martin | 2.66 | 4.50 | 4.44 | 4.32 | 4.21 | 5.84 | 5.02 | 4.72 | 4.42 | 40.13 |
| Milan | 2.66 | 4.49 | 4.78 | 4.66 | 4.54 | 5.71 | 5.19 | 5.16 | 4.26 | 41.45 |
| Jackson | 2.47 | 4.22 | 4.50 | 4.74 | 4.46 | 5.24 | 5.39 | 4.94 | 3.84 | 39.80 |
| Greeneville | 2.55 | 3.03 | 3.24 | 3.49 | 3.32 | 4.39 | 3.59 | 3.72 | 3.72 | 31.05 |
| Crossville | 3.18 | 4.59 | 5.81 | 5.67 | 4.98 | 6.80 | 5.17 | 4.97 | 4.59 | 45.76 |

[a]Data from the testing site or nearest weather station.

[b]Data from the Columbia Sewage Plant weather station.

Table 2. Mean temperature normals (°F) for the small grain growing season (1951-1980).[a]

| Location | Oct. | Nov. | Dec. | Jan. | Feb. | Mar. | Apr. | May | June | Season Average |
|---|---|---|---|---|---|---|---|---|---|---|
| Knoxville (Airport) | 59.5 | 48.8 | 41.1 | 38.2 | 41.5 | 49.7 | 59.6 | 67.4 | 74.3 | 53.3 |
| Springfield | 58.2 | 46.9 | 38.4 | 34.2 | 37.5 | 46.4 | 57.6 | 65.9 | 73.8 | 51.0 |
| Spring Hill[b] | 59.4 | 48.6 | 41.2 | 37.6 | 41.0 | 48.8 | 59.7 | 67.1 | 74.6 | 53.1 |
| Martin | 60.7 | 49.1 | 40.2 | **36.2**[c] | 40.1 | 49.1 | 60.3 | 68.5 | 76.4 | 53.4 |
| Milan | 59.3 | 48.3 | 40.0 | 36.0 | 39.6 | 48.6 | 59.6 | 67.8 | 75.5 | 52.7 |
| Jackson | 60.2 | 49.1 | 41.0 | 37.0 | 40.6 | 49.1 | 60.3 | 68.3 | 75.8 | 53.5 |
| Greeneville | **57.6** | **47.1** | **39.5** | 36.8 | **39.5** | **47.6** | **57.2** | **65.4** | **72.4** | **51.5** |
| Crossville | **55.0** | **44.6** | **36.1** | **32.3** | **35.1** | **43.6** | **54.6** | **62.3** | **69.1** | **48.1** |

[a]Data from the testing site or nearest weather station.

[b]Data from the Columbia Sewage Plant (nearest weather station).

[c]Two lowest values in each column are in bold type.

## Statistical Analyses

The statistical analyses of the data were computed by the Statistical Analysis System (SAS, 1982) software on an IBM computer. Each crop was evaluated separately.

### Genotype Environment Interactions

Analysis of variance. Conventional analyses of variance were conducted separately on the mean yields of individual genotype x year x location. Data from 57 wheat (Table A-2) and 44 barley genotypes (Table A-3) during the period of 1955-1981 were utilized in analyses of variance. The mathematical model used was

$$Y_{ijk} = \mu + V_i + S_j + V_iS_j + L_k + V_iL_k + S_jL_k + V_iS_jL_k + e_{ijk}$$

where

$Y_{ijk}$ = yield of the $i^{th}$ genotype for the $j^{th}$ year at $k^{th}$ location,

$\mu$ = overall mean yields,

$V_i$ = the effect of the $i^{th}$ genotype (random),

$S_j$ = the effect of the $j^{th}$ year (random),

$V_iS_j$ = the effect of the $i^{th}$ genotype by $j^{th}$ year interaction,

$L_k$ = the effect of $k^{th}$ location (random),

$V_iL_k$ = the effect of $i^{th}$ genotype by $k^{th}$ location interaction,

$S_jL_k$ = the effect of $j^{th}$ year by $k^{th}$ location interaction,

$V_iS_jL_k$ = the effect of $i^{th}$ genotype by $j^{th}$ year by $k^{th}$ location interaction,

$e_{ijk}$ = random error associated with $i^{th}$ genotype for the $j^{th}$ year at $k^{th}$ location.

Since the available computer was not able to perform SAS General Linear Model on the large data set studied, the "absorption" computational technique was used to estimate the variances of main effects and first order interactions. However, it was not possible to obtain the second-order interaction directly, and it was considered to be the residual. The mathematical model used for absorption of variety is shown as an example:

$$Y_{ik} = \mu + S_i + L_k + (S*L)_{ik} + R$$

where

$Y_{ik}$ = mean yields of $i^{th}$ year and $k^{th}$ location,

$\mu$ = overall mean,

$S_i$ = effect of $i^{th}$ year,

$L_k$ = effect of $k^{th}$ locations,

$(S*L)_{ik}$ = interaction of $i^{th}$ year and $k^{th}$ location, and

R = residual term.

Similar absorptions were made separately for the variables location and year in order to calculate estimates of variety and interaction effects. In examining the relative magnitudes of the sources of variation in this study, the size of the error variance was assumed to be small because it was not possible to estimate, since the yields of individual plots were not available and the mean of all replications at each site for each year was used in all computations.

Due to the computation methods used, the estimations were biased; however, the bias should be small due to the number of observations involved.

The generalized forms of the analyses of variance and the expected mean squares are presented in Table A-4. Genotypes, years, and locations were treated as random effects.

## Stability

### Regression Analyses

The significance of differences among genotype means $H_o$: $\mu_1 = \mu_2 = \ldots = \mu_v$ was determined by conventional analysis of variance, both for barley and wheat. Genotype means were found to be statistically different from each other. Therefore, regression analyses were performed to determine the estimates of stability parameters proposed by Eberhart and Russell (1966).

Regression analyses were performed on wheat and barley data considering each location-year as one environment. To obtain more meaningful stability parameters only those wheat genotypes present in the variety trial for at least 16 environments (8 locations, over two years) and barley genotypes present in the variety trial for at least 12 environments (6 locations over two years) were retained for regression analysis. Thirty-six wheat genotypes and 21 barley genotypes met this limiting criterion.

The regression of each genotype mean yields on environmental index and a function of the squared deviations from this regression provided estimates of the individual genotype's stability parameters (Eberhart and Russell, 1966). The mathematical model for these parameters is:

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij} ,$$

where

$Y_{ij}$ = the mean yields of $i^{th}$ genotype at the $j^{th}$ environment,

$\mu_i$ = the mean yields of the $i^{th}$ genotype over all environments,

$\beta_i$ = the regression coefficient that measures the response of the $i^{th}$ genotype to different environments,

$\delta_{ij}$ = the deviation from regression of the $i^{th}$ genotype at the $j^{th}$ environment, and

$I_j$ = the environmental index obtained as the mean of all genotypes at the $j^{th}$ environment minus the grand mean

$[I_j = (\Sigma_i Y_{ij}/v) - (\Sigma_i \Sigma_j Y_{ij}/vn)], \quad \Sigma_j I_j = 0 .$

The first stability parameter measured was linear regression (b-value) of genotype mean yields on the overall entries in each environment (Yates and Cochran, 1938; Finlay and Wilkinson, 1963; Eberhart and Russell, 1966),

$$b_i = \Sigma_j Y_{ij} I_j / \Sigma_j I_j^2 .$$

The performance of each genotype was predicted by using the

estimates of the parameters where $\hat{Y}_{ij} = \bar{X}_i + b_i I_j$ where $\bar{X}_i$ is an estimate of $\mu_i$. The second stability parameter ($\sigma^2_{d_i}$) deviation from regression (Eberhart and Russell, 1966) was estimated for each genotype,

$$S^2_{d_i} = [\Sigma_J \hat{\delta}^2_{ij}/(n-2)] - S^2_e/r$$

where

$S^2_{d_i}$ = deviation from regression for $i^{th}$ genotype,

$\Sigma_j \hat{\delta}^2_{ij} = \Sigma_j (Y_{ij} - \hat{Y}_{ij})^2$

(n-2) = error d.f. for $i^{th}$ genotype in regression analysis,

$\Sigma_j \hat{\delta}^2_{ij}/(n-2)$ = error mean square for $iY^{th}$ genotype in regression analysis,

$S^2_e/r$ = the estimate of the pooled error (or the variance of a variety mean within the $j^{th}$ location), and

$$\Sigma_j \hat{\delta}^2_{ij} = [\Sigma_j Y^2_{ij} - Y^2_{i.}/n] - (\Sigma_j Y_{ij} I_j)^2/\Sigma_j I^2_j .$$

Therefore, the genotype x environment interaction of each genotype was partitioned into two parts: (a) the variation due to the genotype response to varying environmental indexes (sum of square due to regression), and (b) the unexplainable deviations from regression on the environmental index.

The regression of each genotype on environmental index and a function of the squared deviations from this regression provided estimates of the individual genotype's stability parameters.

The hypothesis that the regression coefficient of any genotype does not differ from unity $H_o$: $b_i = 1$ was also tested by use of appropriate t tests (Steel and Torrie, 1960), using the genotype's standard error for regression.

$$t_i = (b_i - 1)/SE_{b_i}$$

where

$b_i = i^{th}$ genotype regression coefficient, and

$SE_{b_i} = i^{th}$ genotype standard error.

The hypothesis that any deviation from regression does not differ from zero was tested by an appropriate F test (Eberhart and Russell, 1966),

$$F \simeq (\Sigma_J \hat{\delta}^2_{ij}/n\text{-}2)/\text{pooled error} .$$

Finally three criteria regression coefficient ($b_i$), deviation from regression ($S^2_{d_i}$) and, overall mean yield were utilized to establish the genotype's stability and yield performance.

## Classifying Testing Sites

### Correlation Coefficient Technique

Correlation techniques were used to measure the closeness of linear relationship between all possible pairs of locations for wheat and barley. Correlation between genotype mean yields at eight locations for wheat data (Table A-2) and six locations for barley data (Table A-3) were computed.

### Factor Analysis

Factor analysis was used to classify the testing sites. Data from eight testing sites for wheat (Table A-2) and six testing sites for barley (Table A-3) were used as variables in factor analysis. Twenty-five wheat genotypes and 28 barley genotypes with observations in all locations were automatically retained by factor analyses, and separately subjected to factor analysis. The equation for the common factor model was:

$$Y_{ij} = X_{i1}b_{ij} + X_{i2}b_{2j} + \ldots X_{iq}b_{qj} + e_{ij}$$

where

$Y_{ij}$ = the value of the $i^{th}$ observation on the $j^{th}$ location,

$X_{ik}$ = the value of $j^{th}$ observation on the $k^{th}$ common factor,

$b_{kj}$ = the regression coefficient of the $k^{th}$ common factor for predicting the $j^{th}$ location,

$e_{ij}$ = the value of the $i^{th}$ observation on the $j^{th}$ unique factor, and

$q$ = the number of common factors.

Two critical assumptions were: the unique factors are uncorrelated with each other, and the unique factors are uncorrelated with the common factors.

The image method of factor analysis was used to determine the maximum number of factors to be retained. Principal factor method of SAS FACTOR procedure was used to extract three factors. In this method the squared multiple correlation coefficients of each variable with all other variables are used as the prior communality estimates. Rotation was necessary for the following reasons: (a) it is possible that the unrotated factors have not given a meaningful patterning of locations, (b) the loadings in the unrotated solution depend heavily on the relative number of locations, and (c) if one location is deleted, the relative loadings on the unrotated factors may change significantly.

Therefore, to simplify the factor structure and to assure the result of this analysis the VARIMAX rotation was performed.

Regression Technique to Characterize the Testing Sites

On the basis of the same principle as regression analysis proposed by Finlay and Wilkinson (1963), yields of all genotypes at a particular site were regressed against the mean yields of each of the genotypes across all sites.

$$Y_{ij} = \mu_i + \beta_i X_j + \delta_{ij} ,$$

where

$Y_{ij}$ = the mean yields of $j^{th}$ genotype at $i^{th}$ location,

$\mu_i$ = the mean yields of the $i^{th}$ location over all genotypes,

$\beta_i$ = the regression coefficient that measures the response of different genotypes in the $i^{th}$ location,

$X_j$ = the mean of $j^{th}$ genotype over all locations.

The regression coefficient (b-value) of location mean yields on the overall locations for each genotype is

$b_i = (\Sigma_j Y_{ij} X_j / \Sigma_j X_j^2$ , and

$\delta_{ij}$ = the random error of the $i^{th}$ location for the $j^{th}$ genotype.

The hypothesis that the regression coefficient of any location does not differ from unity $H_o$: $b_i = 1$, was also tested by the appropriate t test (Steel and Torrie, 1960), using the location standard error for regression.

$$t_i = (b_i - 1)/SE_{b_i} \quad ,$$

where

$b_i$ = $i^{th}$ location regression coefficient, and

$SE_{b_i}$ = $i^{th}$ location standard error.

The regression coefficients for each of the testing sites obtained from regression analysis were plotted against their mean yields to provide two dimensional scatter diagrams as illustrated by Fig. 1 (p. 42).

# CHAPTER 3

# RESULTS AND DISCUSSION

## Analyses of Variance

Twenty-seven years of data (1955-1981) from 57 wheat and 44 barley genotypes tested at agricultural experiment stations of the University of Tennessee were separately subjected to conventional analysis of variance. The Statistical Analysis System (SAS) on IBM was used. The analysis of variance and estimates of the pertinent variance components for the wheat and barley are presented in Tables 3 and 4, respectively. The relative magnitudes of these components indicate the importance of the corresponding source of variation. All sources of variation and their interactions were highly significant ($p < 0.01$) except the genotype x year interaction for barley.

The significant first order interactions (GxL, GxY) indicated that there were changes in the relative order of ranking or differences among genotypes over locations and years, indicating that genotypes tested responded differently in different locations or different years. However, barley did not respond differently from year to year. This

Table 3. Sources of variation with their associated degrees of freedom, mean squares, F values, and variance component estimates for 57 wheat varieties at 8 locations from 1955 through 1981.

| Source of Variation | Degree of Freedom | Mean Square | F | Variance Component |
|---|---|---|---|---|
| Varieties | 56 | 409.52 | 9.67** | .14 |
| Locations | 7 | 1921.48 | 45.38** | .15 |
| Years | 26 | 3258.99 | 76.98** | 1.21 |
| Variety x Location | 350 | 53.47 | 1.26** | 0.10 |
| Variety x Year | 181 | 91.40 | 2.16** | 1.53 |
| Year x Location | 148 | 912.66 | 21.55** | 3.82 |
| Residual | 994 | 42.34 | | |

**Significant at the 1% level of probability.

Table 4. Sources of variation with their associated degrees of freedom, mean squares, F values, and variance component estimates for 44 barley varieties tested at 7 locations from 1955 through 1981.

| Source of Variation | Degree of Freedom | Mean Square | F | Variance Component[a] |
|---|---|---|---|---|
| Varieties | 43 | 479.13 | 2.35** | -0.24 |
| Locations | 6 | 4583.01 | 22.49** | 0.86 |
| Years | 26 | 5830.11 | 28.61** | 4.42 |
| Variety x Location | 217 | 278.08 | 1.36** | .69 |
| Variety x Year | 126 | 177.86 | 0.87 | -.09 |
| Residual | 677 | 203.78 | | |

**Significant at the 1% level of probability.

[a]Negative estimates are assumed to be zero.

might be due to the presence of primarily well adapted barley genotypes in the test.

The significant year and location effects in both crops indicated that there were fluctuations in the environmental conditions throughout the study. These variations among locations and years were mainly due to the presence of differences in soil type, soil fertility, temperature, rainfall, and other environmental factors.

In both crops, the variance component of genotype and location were small in relation to that for year. This is in agreement with previous findings by Wu (1978). For barley the genotype components were negative which are considered to be zero (Allard, 1960). In wheat, the genotype x year component was much larger than that for genotype x location. This indicates that the environmental effects associated with years were more important in determining differential genotype responses than were the environmental effects associated with locations, which is similar to previous findings by Wu (1978). However, the genotype x year component for barley was negative which is considered to be zero (Allard, 1960, p. 95). Perhaps this lack of agreement with previous findings is due to the presence of primarily only well adapted barley genotypes in tests. The significant GxL and GxY interactions caused difficulty in identifying superior genotypes. Therefore,

it was necessary to estimate the stability parameters through regression analysis.

## Stability

Eberhart and Russell (1966) proposed that an ideal genotype is one which has the highest mean yield over a broad range of environments, a regression coefficient ($b_i$) not significantly different from unity, and a deviation mean square ($S^2_{d_i}$) close to zero. According to Langer et al. (1979), the regression coefficient is a measure of a genotype's response to changing environments and the deviation from linear regression is a true measure of production stability. Becker et al. (1982) indicated that the mean square for deviations from regression measures the predictability of genotypic reaction to environments. They regarded it as the most appropriate criterion of phenotypic stability in an agronomic sense.

Stability analyses were performed on wheat and barley data considering each location-year as one environment. To obtain a more meaningful estimate of regression coefficients only 36 wheat and 21 barley genotypes which were present in at least 16 and 12 environments, were retained for stability analysis and are shown in Tables 5 and 6, respectively. According to Eberhart and Russell (1966),

Table 5. Thirty-six wheat genotypes used in the stability analyses, number of environments in which tested and mean yields (bu/A) at each location.

| Genotype | Number of Environments | Locations | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Springfield | Knoxville | Milan | Spring Hill | Crossville | Greeneville | Martin | Jackson |
| Abe | 68 | 42.1 | 42.2 | 48.4 | 48.7 | 35.7 | 45.9 | 42.7 | 33.4 |
| Arthur | 103 | 47.7 | 46.2 | 50.1 | 46.9 | 42.3 | 54.1 | 43.2 | 43.3 |
| Arthur 71 | 38 | 36.8 | 35.4 | 40.3 | 37.6 | 32.2 | 45.6 | 40.2 | 32.6 |
| Beau | 37 | 43.4 | 43.0 | 48.3 | 51.2 | 38.8 | 45.2 | 42.5 | 41.0 |
| Benhur | 21 | 49.3 | 43.7 | 43.0 | 37.3 | 42.7 | 58.5 | 33.7 | 47.7 |
| Blueboy | 49 | 51.6 | 41.9 | 53.5 | 39.9 | 48.3 | **66.0** | 42.9 | **52.3** |
| Coker 68-15 | 34 | 39.8 | 44.4 | --[a] | 36.6 | 28.2 | 58.5 | 37.4 | 46.0 |
| Coker 68-19 | 21 | 49.7 | 44.7 | -- | 30.0 | 40.7 | 56.3 | 35.7 | **57.0** |
| Coker 73-18 | 16 | 51.0[b] | 56.5 | 47.0 | 36.0 | 41.5 | 55.5 | 41.5 | 34.5 |
| Coker 747 | 46 | **58.0**[b] | 53.8 | 54.2 | **58.5** | **51.8** | 58.2 | **54.6** | 37.3 |
| Delta-Queen | 27 | 48.3 | 39.5 | -- | 49.5 | 21.3 | 32.0 | 49.3 | 28.0 |
| Doublecrop | 46 | 47.0 | 44.5 | 49.5 | 52.5 | 38.8 | 45.5 | 42.2 | 34.7 |
| Dual | 29 | 46.5 | 43.3 | -- | 46.9 | 44.4 | 47.9 | 35.0 | 42.4 |
| Hart | 47 | 52.7 | 52.7 | 51.6 | 48.8 | 40.5 | 56.3 | 47.2 | 38.3 |
| Knox | 46 | 49.0 | 39.4 | -- | 41.3 | 39.0 | 48.8 | 35.3 | 48.6 |
| Knox 62 | 53 | 47.5 | 37.4 | 46.0 | 37.1 | 45.6 | 44.7 | 37.0 | 41.1 |
| McNair 1587 | 33 | 53.0 | 45.6 | -- | 38.8 | 36.6 | **64.2** | 40.5 | 42.6 |
| McNair 1813 | 36 | 41.2 | 37.2 | 46.7 | 34.6 | 28.8 | 40.6 | 44.3 | 44.4 |
| McNair 2203 | 28 | 52.8 | 46.8 | -- | 46.3 | 41.5 | 57.8 | 42.5 | **53.0** |
| McNair 3001 | 38 | **60.4** | **56.6** | **55.6** | **58.8** | 38.3 | 52.0 | **65.5** | 48.4 |
| McNair 4823 | 73 | 38.0 | 41.9 | 38.6 | 45.2 | 33.6 | **60.8** | 39.1 | 43.9 |
| McNair 701 | 17 | 35.0 | 21.0 | -- | 29.0 | 17.3 | 24.5 | 29.0 | 29.3 |
| Monon | 89 | 45.0 | 34.8 | 47.0 | 40.0 | 43.1 | 54.7 | 36.0 | 46.5 |
| Oasis | 36 | 38.8 | 42.0 | 45.0 | 46.0 | 37.0 | 49.0 | 44.3 | 32.6 |
| Pioneer-S76 | 30 | 50.5 | 53.0 | 51.7 | 52.8 | 38.3 | 48.5 | 50.0 | 40.8 |
| Pioneer-S78 | 29 | 48.8 | 45.0 | 54.0 | 50.8 | 36.5 | 50.8 | 48.3 | 36.3 |
| Redcoat | 28 | 40.2 | 32.5 | -- | 38.3 | 46.4 | **60.0** | 34.7 | 45.5 |
| Reed | 37 | 39.0 | 35.6 | 50.0 | 36.2 | **52.2** | 54.6 | 35.8 | 35.8 |
| Riley | 16 | 41.5 | 34.5 | 45.0 | 28.0 | **53.0** | 52.0 | 30.5 | 37.0 |
| Roy | 16 | 55.0 | **60.0** | **57.0** | 54.5 | 45.0 | 58.0 | 56.5 | 43.0 |
| Seneca | 53 | 47.2 | 41.9 | 45.0 | 43.8 | 46.8 | 41.4 | 36.4 | 39.6 |
| Southern-Belle | 17 | **71.0** | **63.5** | **57.5** | **60.5** | **53.0** | **58.5** | **68.0** | 45.0 |
| Stoddard | 37 | 42.8 | 48.8 | 48.0 | 43.0 | 38.0 | 45.8 | 37.0 | 31.0 |
| Sullivan | 37 | 48.2 | 44.8 | 53.5 | **53.4** | 39.8 | 43.2 | 43.0 | 37.0 |
| T60-18 | 18 | 37.7 | 32.0 | -- | 39.7 | **54.3** | **58.5** | 29.0 | 36.7 |
| T60-25 | 35 | 49.7 | 36.0 | -- | 42.4 | **52.0** | 55.4 | 38.7 | 45.4 |
| Average | | 47.12 | 43.39 | 49.06 | 43.91 | 40.65 | 51.37 | 41.93 | 40.89 |

[a]No data available.

[b]High yielding genotypes at each location in bold type.

Table 6. Twenty-one barley genotypes used in the stability analyses, number of environments in which tested, and mean yields (bu/A) at each location.

| Genotype Name | Number of Environment | Location | | | | | |
|---|---|---|---|---|---|---|---|
| | | Springfield | Knoxville | Spring Hill | Crossville | Greeneville | Jackson |
| Barsoy | 61 | 68.20 | 52.10 | 47.80 | 52.20 | 64.36 | 57.00 |
| Colonial 2 | 24 | 63.70 | 34.67 | 42.00 | 59.80 | 55.75 | 49.25 |
| Henry | 32 | 59.40 | **58.50** | 58.00 | 60.60 | 66.75 | 50.83 |
| Jackson-No1 | 41 | 63.28 | 56.60 | 51.13 | 45.70 | 34.48 | 50.76 |
| Jefferson | 30 | **72.00**[a] | 50.80 | 57.60 | **69.80** | **79.40** | **63.60** |
| Kenbar | 62 | 69.07 | 52.51 | 60.05 | 55.12 | 51.11 | 59.03 |
| Knob | 24 | 61.75 | 38.50 | 46.75 | 51.00 | 68.00 | 49.50 |
| Maury | 26 | 66.00 | **64.80** | 57.40 | 62.00 | 60.67 | 43.40 |
| Monroe | 20 | 62.00 | **59.50** | 55.50 | 46.00 | 57.00 | 51.50 |
| Penrad | 12 | 67.50 | 44.50 | 34.00 | 52.00 | 61.00 | 37.00 |
| Surry | 32 | 61.80 | **58.67** | 55.33 | 61.20 | **75.25** | 51.33 |
| Tenn 59-15 | 43 | **72.62** | 49.83 | **64.57** | 60.25 | 51.00 | **62.37** |
| Tenn 60-38 | 17 | 61.33 | 47.00 | **61.33** | 52.33 | 61.00 | **74.66** |
| Tenn 61-116 | 12 | 67.50 | 52.50 | 47.50 | **67.00** | 47.50 | 43.50 |
| T65-118 | 12 | **80.50** | 32.00 | 49.50 | 34.00 | **79.50** | 32.00 |
| T60-18 | 12 | **73.00** | 29.50 | 48.00 | 55.50 | **70.00** | 36.00 |
| Upright 50-106-11 | 18 | 68.40 | 51.13 | 53.43 | 44.70 | 30.56 | 56.30 |
| Volbar | 67 | **72.33** | **71.25** | **67.75** | 63.25 | 61.66 | 59.75 |
| Wade | 41 | **73.42** | 50.66 | 60.16 | **73.00** | **70.41** | 50.14 |
| Wong 22 | 13 | 62.95 | 52.20 | 57.75 | 39.85 | 30.76 | 60.30 |
| Watauga | 18 | 71.00 | **58.60** | 47.90 | 36.60 | 31.10 | 60.00 |
| Average | | 67.51 | 50.75 | 53.50 | 54.38 | 57.49 | 52.30 |

[a]High yielding genotypes at each location are in bold type.

yield of each genotype was regressed against site mean yields to obtain the regression coefficient and deviation from regression for each genotype.

As described by Finlay and Wilkinson (1963) the entries' yields were regressed against their overall mean yields at all sites. According to the Finlay and Wilkinson definition, any genotype with a regression coefficient approximating to 1 indicates average stability. When this is associated with mean yields greater than the overall mean yield the genotype is considered to have general adaptation; when the average regression coefficient (b = 1) is associated with low mean yields, the genotype is poorly adapted to all environments. As stated previously, the regression coefficient is a measure of a genotype's sensitivity to environmental changes. Regression values above 1.0 indicate increasing sensitivity to environment (below average stability) and regression values below 1.0 indicate less sensitivity to environment (above average stability) which indicates adaptability to low-yielding environments (Finlay and Wilkinson, 1963).

In this study a genotype with a regression coefficient of 1.00 or greater and relatively low deviations from regression was considered as stable because its yield increases proportionally with environment mean test yield. A genotype was considered unstable if it had a regression

coefficient significantly less than one and relatively high deviation from regression. Overall mean yields of the genotypes, along with regression coefficients, and deviation from regression were used in comparing and evaluating the genotypes' stability and adaptation.

Wheat

The yield performance data for each location for all wheat genotypes included in this stability analysis are shown in Table 5, where the high yield observations in each location are highlighted (bold type). The mean yields, regression coefficients, and deviations from regression of these genotypes are presented in Table 7, in descending order of mean yield. The yields ranged from 24.14 (bu/A) to 59.16 (bu/A) for McNair 701 and Southern-Belle, respectively, indicating that genotypes with a wide range of yielding ability were tested (Table 7). Best yielding genotypes were Southern-Belle, Roy, McNair 3001, and Coker 747 with 59.16, 52.80, 52.55, and 51.77 bu/A mean yields, respectively. The regression coefficient ranged from -0.55 to 3.49. The large variation in the regression coefficients indicated that genotypes responded differently to changing environments (Table 7). The high variation was also indicated by high GxL and GxY interactions (Table 3, p. 64). Half of the wheat genotypes had regression

Table 7. Estimates of phenotypic stability parameters for winter wheat based on grain yield.[a]

| Genotype Name | Mean Yield bu/A | Regression Coefficient ($b_i$) -- on Log(10) data -- | Deviation from Regression ($S^2_{d_i}$) -- on Log(10) data -- |
|---|---|---|---|
| Southern-Belle | 59.16 | 0.87 | 0.000 |
| Roy | 52.80 | 0.91 | 0.000 |
| McNair 3001 | 52.55 | 1.00 | 0.001 |
| Coker 747 | 51.77 | 0.75* | 0.003** |
| Pioneer-S76 | 46.94 | 0.59** | 0.002** |
| Hart | 47.20 | 0.76* | 0.001** |
| McNair 2203 | 45.49 | 0.97 | 0.001* |
| Arthur | 44.87 | 0.75** | 0.001* |
| T60-25 | 44.79 | 1.04 | 0.000 |
| Pioneer-S78 | 44.70 | 0.72* | 0.003** |
| Blueboy | 44.63 | 1.14* | 0.003** |
| Sullivan | 44.57 | 0.55** | 0.001 |
| Coker 73-18 | 43.77 | 0.92 | 0.003** |
| Dual | 43.43 | 0.93 | 0.001 |
| Doublecrop | 43.25 | 0.67** | 0.004** |
| Beau | 43.19 | 0.67** | 0.002** |
| Benhur | 43.00 | 0.74* | 0.000 |
| McNair 1587 | 41.15 | 1.04 | 0.005** |
| Knox | 41.12 | 1.08 | 0.002** |
| Stoddard | 40.99 | 0.79** | 0.000 |
| McNair 4823 | 40.80 | 0.78** | 0.004** |
| Abe | 40.69 | 0.84** | 0.002** |
| Knox 62 | 40.60 | 0.80* | 0.002** |
| Reed | 40.56 | 1.03 | 0.000 |
| Monon | 40.42 | 1.04 | 0.002** |
| Redcoat | 40.42 | 1.05 | 0.003** |
| Oasis | 40.28 | 0.76** | 0.002** |
| T60-18 | 40.23 | 1.07 | 0.000 |
| Seneca | 40.10 | 0.94 | 0.002** |
| Riley | 39.01 | 1.09 | 0.000 |
| Coker 68-15 | 37.47 | 0.99 | 0.004** |
| Arthur 71 | 35.74 | 0.94 | 0.001* |
| Coker 68-19 | 35.20 | 2.39** | 0.021** |
| McNair 1813 | 33.65 | 1.55* | 0.054** |
| Delta-Queen | 27.02 | 3.49** | 0.106** |
| McNair 701 | 24.14 | 1.17 | 0.007** |
| Mean | 42.10 | | |

*,**Significant at 0.05 and 0.01 level of probability, respectively. t and F tests were performed to test the significant differences from one and zero for $b_i$ and $S^2_{d_i}$, respectively.

[a]Genotypes with data from 16 or more environments were included in stability analysis (considering each location-year as an environment).

coefficients statistically different from unity (Table 7). Most of these genotypes showed low responsiveness to environmental changes (that is, low b-value) and a few were highly responsive (high b-value). However, there were 18 genotypes (48%) with the regression coefficient statistically not different from unity (average regression coefficient). Eight of the genotypes (22%) possessed deviations from regression close to zero and an average regression coefficient ($b_i = 1$), indicating good stability performance.

Stability performance. Any genotypes which had (a) zero deviation from regression (stable), and above overall genotype mean yields, or (b) zero deviation from regression and high mean yields at least at one location, were considered as superior genotypes and presented in Table 8. Coker 747 was accepted as a superior genotype in the sense that it performed very well in most of the locations and had high overall mean yields even though its deviation from regression was high. In this table overall mean yields, regression coefficients and deviations from regression for each of the superior genotypes are shown along with their mean yield at each location.

Table 8. Wheat genotypes with superior phenotypic stability parameters and mean yields at each testing site.

| Genotype | Overall Mean Yields (bu/A) | Regression[a] Coefficient ($b_i$) | Deviation[a] from Regression ($s^2_{d_i}$) | Mean Yield (bu/A) | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Spf.[b] | Knox[c] | MLN[d] | SpH[e] | Crss[f] | GRN[g] | MRT[h] | Jack[i] |
| Southern-Belle | 59.16 | 0.87 | 0.000 | 71 | 63 | 57 | 60 | 53 | 58 | 68 | 45 |
| Roy | 52.80 | 0.91 | 0.000 | 55 | 60 | 57 | 54 | 45 | 58 | 56 | 43 |
| McNair 3001 | 52.55 | 1.00 | 0.001 | 60 | 56 | 55 | 58 | 38 | 52 | 65 | 48 |
| Coker 747 | 51.77 | 0.75* | 0.003** | 58 | 53 | 54 | 58 | 52 | 58 | 54 | 37 |
| T60-25 | 44.79 | 1.04 | 0.000 | 49 | 36 | --[j] | 42 | 52 | 55 | 38 | 45 |
| Sullivan | 44.57 | 0.55** | 0.001 | 48 | 45 | 54 | 53 | 40 | 43 | 43 | 37 |
| Dual | 43.43 | 0.93 | 0.001 | 47 | 43 | -- | 47 | 44 | 48 | 35 | 42 |
| Benhur | 43.00 | 0.74* | 0.000 | 49 | 43 | 43 | 37 | 43 | 58 | 34 | 48 |
| Reed | 40.56 | 1.03 | 0.000 | 39 | 36 | 50 | 36 | 52 | 55 | 36 | 36 |
| Riley | 39.01 | 1.09 | 0.000 | 42 | 35 | 45 | 28 | 53 | 52 | 31 | 37 |
| T60-18 | 40.23 | 1.07 | 0.000 | 37 | 32 | -- | 39 | 54 | 58 | 39 | 36 |

[a]Estimated on Log(10) data.

[b]Springfield, [c]Knoxville, [d]Milan, [e]Spring Hill, [f]Crossville, [g]Greeneville, [h]Martin, [i]Jackson.

[j]No data available.

*,**Regression coefficient significantly different from one and deviation from regression significantly different from zero, at 0.05 and 0.01 probability level, respectively.

Southern-Belle, Roy, and McNair 3001 were highly stable as indicated by their having the highest overall mean yields, none or very small deviations from regression and regression coefficients statistically equal to unity (Table 8). T60-25, Dual, Reed, Riley, and T60-18 were highly stable ($S^2_{d_i} = 0$) with average response to changing environments (b = 1) with an average to relatively low mean yields and low deviation from regression. Coker 747, Sullivan, and Benhur were highly stable ($S^2_{d_i} = 0$) with average response to different environmental conditions, regression coefficient less than 1.0 and an average to relatively low overall mean yields (Table 8). Each of these performed well in one or two locations. T60-25 and T60-18 performed well in Crossville and Greeneville. It is interesting that these two genotypes had high yields in two locations with diverse environmental conditions, because Crossville had the lowest and Greeneville had the highest average wheat yield (Table 5). Sullivan with above average yield was highly stable with very low response to environmental changes ($b_i = 0.55$). This genotype performed well in Spring Hill and Milan.

Reed and Riley with below average yield and average response to environmental changes, were highly stable and performed very well in Crossville (poor environment). None

of the top stable genotypes performed very well in Jackson. Coker 68-15, McNair 2203, and Blueboy with 57.0, 53.0, and 52.3 bu/A showed yield advantage over the superior genotypes such as McNair 3001 which yielded 48.4 bu/A in Jackson (Table 5, p. 69). McNair 2203 had higher overall mean yields and better stability performance over Blueboy and Coker 68-15 (Table 7). Therefore, McNair 2203 might be considered as the second choice for Jackson after McNair 3001.

At Greeneville, Blueboy with 66.0 bu/A had the yield advantage over Roy (58.0 bu/A) and Southern-Belle (58.5 bu/A) (Table 5) but it is highly unstable due to a high regression coefficient and significant deviations from regression. Therefore Blueboy may not be recommended as a genotype for Greeneville.

Wheat adaptation pattern. According to the Finlay and Wilkinsen's model (1963) the genotypes' regression coefficients were plotted against their overall mean yields at all sites and presented in Fig. 3. This figure provides a generalized interpretation of the type of adaptability for each wheat genotype based on regression coefficients and average yield performance. Three genotypes showed the combination of broad adaptation and high yielding

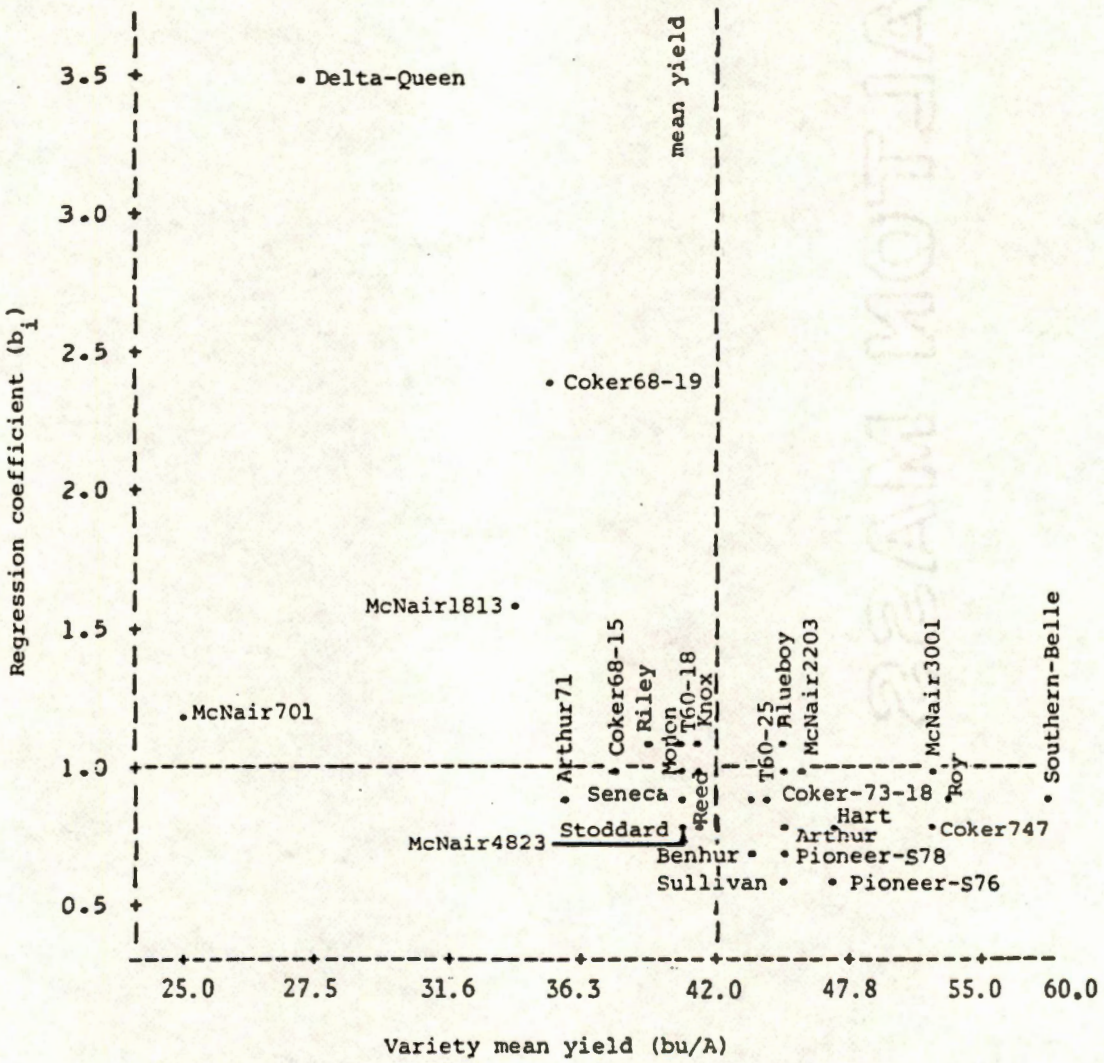



Fig. 3. Relationship of regression coefficients and mean yields of wheat entries as estimate of adaptation.

ability combined. These were Southern-Belle, Roy, and McNair 3001 with regression coefficients close to unity and mean yields of 59.16, 52.80, and 52.55 bu/A, respectively.

There were not any genotypes which would be considered to be adapted to poor environments (low mean yield and regression coefficient of <1.0) as described by Finlay and Wilkinson (1963). Pioneer S76, and Sullivan had the lowest regression coefficients, 0.59 and 0.55, respectively (Table 7), but, they had average yields above overall mean yields (Table 7) and did not perform well in poor locations Crossville and Jackson (Table 5). Delta Queen and Coker 68-19 showed very high regression coefficients and low mean yields (Fig. 3). These are expected to have good adaptation to favorable locations such as Milan, Greeneville, and Springfield. As shown in Table 5, this did not occur. In contrast, several genotypes with broad adaptation ($b_i = 1$) and very high mean yield, performed well in most of the locations. These genotypes were Southern-Belle, Roy, and McNair 3001 (Fig. 3 and Table 5). Coker 747 in spite of having deviations from regression significantly different from 0.0 was among the high yielding genotypes in most locations including a poor location (Crossville) indicating broad adaptation and high yielding ability. However, there was no single genotype which performed well at all

locations. In addition to these three broad adapted genotypes, there were several genotypes which performed very well at specific locations. These were Blueboy at Greeneville and Jackson, McNair 2203 and Coker 68-19 at Jackson, Coker 747 at Spring Hill and Crossville, McNair 1587, McNair 4823, and Redcoat at Greeneville, and T60-18, at Crossville.

As a result there was not any wheat genotype tested with specific adaptation to poor or favorable environments. However, four genotypes, Southern-Belle, Roy, McNair 3001, and Coker 747 might be considered as widely adapted to the state of Tennessee.

It is evident that wheat genotypes responded differently in Jackson and Crossville compared to the rest of the testing sites. There was no single genotype that was ranked highest in all locations. However, Southern-Belle, Roy, and McNair 3001 were suggested as stable genotypes with broad adaptation due to their high mean yields over most of the locations and maximum stability performance. Coker 747 showed a relatively high yield in almost all locations except in Jackson (Table 5). Although Coker 747 had a high deviation from regression (Table 7, p. 73), it might be considered as a top genotype in the sense that it showed high overall mean yields and ranked in the top group in all locations except in Jackson.

Barley

The yield performance data in each location for all barley genotypes utilized in stability analyses are shown in Table 6 (p. 70). In this table the high yield observations for each location were highlighted (bold type).

As shown in Table 6, fourteen genotypes (66%) had very high yield at one or more locations. This reflects the good adaptation of the genotypes tested to one or more locations. None of the barley genotypes appeared as superior in all locations. However, Jefferson, Volbar, T59-15, and Wade performed very well in most of the locations. Overall mean yields, regression coefficients and deviations from regression are presented in Table 9. The mean yields over all locations ranged from 36.76 to 62.85 bu/A for Watauga and Volbar, respectively (Table 9). The overall mean yield was 51.51 bu/A.

More than half of the genotypes (62%) had regression coefficients not significantly different from unity, reflecting that many of the genotypes in the test showed average response to varying environments. Three genotypes responded highly to environmental differences ($b_i > 1$). Among these, only Monroe had an above average mean yield and zero deviation from regression. Only six genotypes (28%) had deviation from regression not different from zero

Table 9. Estimates of phenotypic stability parameters for winter barley grain yield.[a]

| Genotype Name | Average Yield bu/A | Regression Coefficient ($b_i$) -- on Log(10) data -- | Deviation from Regression ($S^2_{d_i}$) -- on Log(10) data -- |
|---|---|---|---|
| Volbar | 62.85 | 0.75** | 0.004** |
| Jefferson | 62.65 | 0.74** | 0.002** |
| Wade | 60.71 | 0.85 | 0.003** |
| Surry | 57.58 | 0.92 | 0.000 |
| Tenn 60-38 | 57.30 | 1.03 | 0.001 |
| Tenn 59-15 | 56.73 | 1.13 | 0.003** |
| Henry | 56.64 | 0.87* | 0.000 |
| Maury | 55.87 | 1.05 | 0.000 |
| Kenbar | 54.79 | 0.78** | 0.005** |
| Monroe | 52.18 | 1.23** | 0.000 |
| Tenn 61-116 | 51.10 | 0.85 | 0.003* |
| Colonial 2 | 50.33 | 0.76* | 0.003** |
| Barsoy | 49.97 | 1.27** | 0.006** |
| Knob | 47.10 | 1.02 | 0.004** |
| T600-18 | 46.62 | 0.99 | 0.009** |
| Upright50-106-11 | 46.10 | 0.80 | 0.009** |
| JacksonNo1 | 45.77 | 0.86 | 0.003** |
| Penrad | 45.44 | 1.11 | 0.000 |
| Wong 22 | 44.14 | 0.76 | 0.009** |
| T65-118 | 41.12 | 2.02 | 0.134** |
| Watauga | 36.76 | 1.87** | 0.066** |
| Mean | 51.51 | 1.00 | |

*,** Significant at 0.05 and 0.01 level of probability, respectively. t and F tests were performed to test the significant differences from one or zero for $b_i$ and $S^2_{d_i}$, respectively.

[a] Genotypes with data from 12 or more environments were included in stability analysis (considering each location-year as an environment).

indicating that 70% of the barley genotypes tested did not show a high level of stability.

Stability performance. All barley genotypes which had (a) above overall mean yields, and high performance at least at one location, or (b) were stable and performed very well in one or more location(s), were included in Table 10. Volbar, Jefferson, and Wade were top yielding genotypes and performed very well in three or more locations, indicating their yielding ability over a relatively wide range of environment. None of these three genotypes showed a low deviation from regression. Therefore they may not be considered as stable genotypes. Surry, Tenn 60-38, Henry, Maury, and Monroe with high to average overall mean yields were highly stable and performed as one of the best genotypes in one or more locations. Most of the stable genotypes (Surry, Tenn 60-38, Henry, and Maury) yielded best in Knoxville (low yielding environment), while most unstable, high yielding genotypes ranked high in a high yielding environment (Springfield). It seems that high stability was a necessity to be able to perform very well in a poor environment (such as Knoxville) while in a favorable environment it was not the case. Among top genotypes (Table 10) only Monroe responded highly to the environmental differences (b = 1.23) whereas, all other top genotypes showed a low to average environmental response (Table 10).

Table 10. Superior barley genotypes phenotypic stability parameters and mean yields at each testing site.

| Genotype Name | Average Yield bu/A | Regression Coefficient ($b_i$) | Deviation from Regression ($S^2_{d_i}$) | Location | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | -- on Log(10) data -- | | Spf.[b] | Knox[c] | SpH[d] | Crss[e] | GRN[f] | Jack[g] |
| Volbar | 62.85 | 0.75** | 0.004** | **72.33**[h] | **71.25** | **67.75** | 63.25 | 61.66 | 59.75 |
| Jefferson | 62.65 | 0.74** | 0.002** | **72.00** | 50.80 | 57.60 | **69.80** | **79.40** | **63.60** |
| Wade | 60.71 | 0.85 | 0.003** | **73.42** | 50.66 | 60.16 | **73.00** | **70.41** | 50.14 |
| Surry | 57.58 | 0.92 | 0.000 | 61.80 | **58.67** | 55.33 | 61.20 | **75.25** | 51.33 |
| Tenn 60-38 | 57.30 | 1.03 | 0.001 | 61.33 | 47.00 | **61.33** | 52.33 | 61.00 | **74.66** |
| Tenn 59-15 | 56.73 | 1.13 | 0.003** | **72.62** | 49.83 | **64.57** | 60.25 | 51.00 | **62.37** |
| Henry | 56.64 | 0.87* | 0.000 | 59.40 | **58.50** | 58.00 | 60.60 | 66.75 | 50.83 |
| Maury | 55.87 | 1.05 | 0.000 | 66.00 | **64.80** | 57.40 | 62.00 | 60.67 | 43.40 |
| Monroe | 52.18 | 1.23** | 0.000 | 62.00 | **59.50** | 55.50 | 46.00 | 57.00 | 51.50 |

[a]Genotypes with data from 12 or more environments were included in stability analysis.

[b]Springfield, [c]Knoxville, [d]Spring Hill, [e]Crossville, [f]Greeneville, [g]Jackson.

[h]High yielding genotypes at each location are bolded.

*,**Significant at 0.05 and 0.01 level of probability, respectively. t and F tests were performed to test the significant differences from one or zero for $b_i$ and $S^2_{d_i}$, respectively.

In contrast, Henry had a low and significant regression coefficient (b = 0.87) and zero deviation from regression. This genotype had a high mean yield (56.65 bu/A) and yielded relatively high in Knoxville. Volbar with the highest overall mean yield (62.85 bu/A) performed very high in Springfield, Knoxville, and Spring Hill and relatively high in other locations. Volbar showed a low response to environment (b = 0.75) and high deviation from regression. Jefferson with similar regression coefficient and deviation from regression to Volbar performed very high in Springfield, Crossville, Greeneville, and Jackson. There was no single genotype which dominated at all locations. However, several top yielding genotypes performed very well in 3 or 4 locations. These were Jefferson, Tenn 59-15, Volbar, Wade, T65-118. None of these have both a regression coefficient of 1.0 and deviation from regression of zero.

Adaptation pattern. To illustrate the type of adaptation, as described by Finlay and Wilkinson (1963), the genotypes' regression coefficients were plotted against their overall mean and shown in Fig. 4. As shown in Fig. 4, Wade, Surry, Tenn 60-38, Tenn 59-15, and Maury were in the broad adaptation zone, due to their high mean yields and regression coefficients near 1.0. Volbar and Jefferson had the highest mean yields but due to the low regression coefficients they were not in the zone of widely adapted

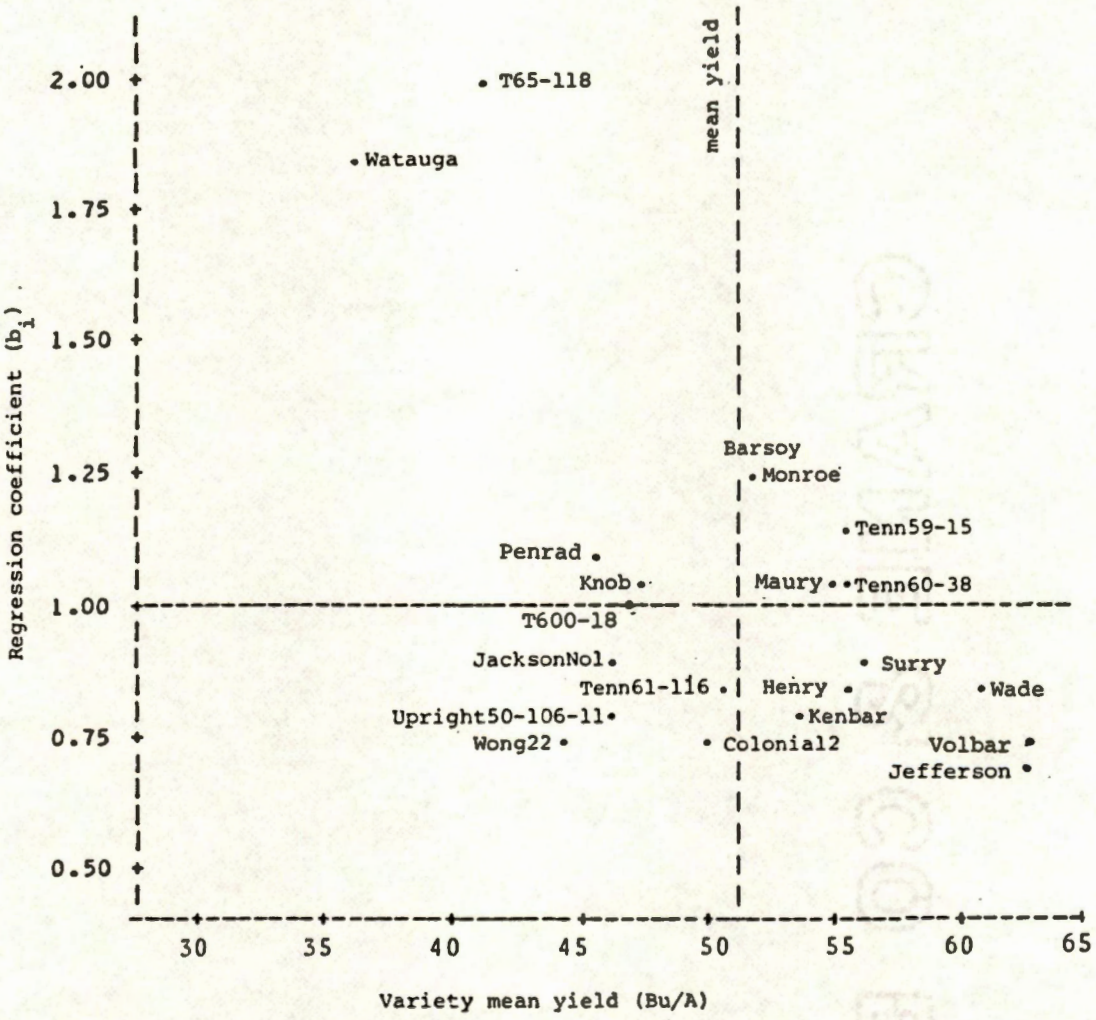



Fig. 4. Relationship of regression coefficient and mean yields of barley entries.

genotype (Fig. 4). These two genotypes ranked as the best genotypes at several locations. On the other hand, T65-118 and Watauga had very high regression coefficients and low mean yields. They might be considered as genotypes with specific adaptation to favorable environments. T65-118 performed very well in environments with high overall mean yields such as Springfield and Greeneville, and performed poorly in Knoxville and Spring Hill where overall mean yields were very low. Both T65-118 and Watauga were unstable (high deviation from regression). Collectively Volbar, Jefferson and Wade were valuable genotypes in the sense that they had the highest overall mean yields and performed very well in one or more locations. This is particularly true of Volbar which performed as the best genotype in Knoxville and Spring Hill, where most genotypes performed very poorly. Maury, Henry, Tenn 60-38, and Surry were recommended as highly stable genotypes with broad adaptation and high mean yields. T65-118 might be considered as a genotype with specific adaptation to favorable conditions.

## Classifying Testing Sites

Three procedures were utilized to classify and characterize the testing sites.

Correlation Technique

Correlation coefficients between genotypes performance in any pair of locations indicate the predictability of genotype performance in any one location for the other location. A desirable location for selecting genotypes with broad adaptation is the one that has high correlations with most of the other locations in the test.

Correlation coefficients for genotypes' yield performance in all possible pairs of locations are presented in Tables 11 and 12 for wheat and barley, respectively. The more relevant correlations will be discussed.

Wheat. Low to moderate correlations were found between locations. In 54% of the cases, correlation of genotype yield performance between locations was less than 0.536. This indicates that genotype yield performance in those pair of locations had limited value for prediction of performance in other locations. Low correlation between Greeneville, Crossville, and Jackson, and other locations suggested that genotypes in these three locations performed differently than at other locations.

Correlation of yields at Springfield with all other locations were significant at the 1% level of probability,

Table 11. Correlation coefficients for yield of winter wheat varieties among 8 locations.

| | Locations | | | | | | |
|---|---|---|---|---|---|---|---|
| | Greeneville | Crossville | Spring-field | Jackson | Spring Hill | Martin | Milan |
| | r | | | | | | |
| Knoxville | 0.281** | 0.186 | 0.617** | 0.107 | 0.676** | 0.740** | 0.615** |
| Greeneville | | 0.539** | 0.578** | 0.312** | 0.300** | 0.075 | 0.158 |
| Crossville | | | 0.536** | 0.333** | 0.079 | 0.100 | 0.023 |
| Springfield | | | | 0.219* | 0.668** | 0.629** | 0.657** |
| Jackson | | | | | 0.093 | 0.219 | 0.203 |
| Spring Hill | | | | | | 0.666** | 0.743** |
| Martin | | | | | | | 0.659** |

*,**Significantly different from zero at 0.05 and 0.01 level of probability, respectively.

Table 12. Correlation coefficients for yield of winter barley varieties among 6 locations.

| | Locations | | | | |
|---|---|---|---|---|---|
| | Greeneville | Crossville | Springfield | Jackson | Spring Hill |
| | r | | | | |
| Knoxville | 0.101 | 0.296 | 0.337* | 0.423** | 0.690** |
| Greeneville | | 0.406** | 0.018 | 0.341* | 0.119 |
| Crossville | | | 0.236 | 0.258 | 0.400** |
| Springfield | | | | 0.511** | 0.617** |
| Jackson | | | | | 0.663** |

*,**Significantly different from zero at 0.05 and 0.01 level of probability, respectively.

except Jackson, which was significant at the 5% level (Table 11). Yields at Knoxville and Spring Hill correlated highly significantly with each other and with all other locations, except with Crossville and Jackson. It is suggested that data from Knoxville can be used for Spring Hill and vice versa due to the similar pattern of association with other locations and with each other.

Yields at Jackson showed low correlations with other locations including those in its vicinity such as Milan and Martin. This indicates that varieties selected at this location may not be expected to perform similarly throughout the state even at nearby locations such as Milan and Martin. Therefore, Jackson should be considered as a unique site regarding wheat yield response. A similar pattern of association was found between Greeneville and Crossville. Crossville and Greeneville were moderately well correlated with each other and with Springfield, and showed low correlations with all other locations. Yields at Martin and Milan were highly correlated with Knoxville, Springfield, Spring Hill, and with each other. Correlations between Martin or Milan and Crossville, Greeneville and Jackson were low which indicates that these two locations had very similar pattern of association with other locations, regarding wheat yield. The high significant correlations of yield between Springfield and all other

locations except Jackson suggests that this location is suitable to select wheat varieties with broad adaptation to most areas of the state, while, selected varieties at Jackson may not be adapted to any other site in the state. These results showed that several pairs of locations had similar patterns of association with other locations. These pairs of locations were Martin, Milan; Knoxville, Spring Hill; Crossville, Greeneville. Therefore, if it were desired to test at fewer locations a choice could be made among Knoxville, Springfield, Milan, or Martin and a second choice could be made among Crossville or Greeneville. Thus the two aforementioned choices with Jackson would result in testing at three locations with little sacrifice of information. As noted, Spring Hill was not included in the suggested list of locations due to its similarity with Knoxville. Certainly Knoxville as Main Station is the first choice. Choosing one or the other from each pair of similar locations depends on other factors including (a) the wheat acreage within each location's area, (b) the location overall mean yields, and (c) the differentiation between genotypes in each location.

Barley. Correlation coefficients between mean yields of barley at six locations are shown in Table 12. Low to

moderate correlations were found between genotype yield performance at different locations. Most of the correlations between locations were less than 0.511 reflecting poor predictability of yield performance from one location to another. The highest correlation coefficient was found between Knoxville and Spring Hill (0.69). There were no negative correlation coefficients between any of the location pairs.

Correlations of yields at Spring Hill with all other locations were highly significant ($p < 0.01$) except Greeneville. Jackson showed highly significant correlation with Knoxville, Spring Hill, and Springfield ($p < 0.01$), a significant correlation with Greeneville ($p < 0.05$), and no correlation with Crossville. Crossville and Greeneville were correlated with each other and showed no correlation with most of other locations. Correlation of yields between Knoxville and Springfield was low but significant. These two locations were highly correlated with Jackson and Spring Hill and not correlated with Greeneville or Crossville indicating a similar pattern of association between these two locations. Data from either of these two should not be used for the other, due to the low level of correlation between themselves ($p = 0.337$). The high correlations between Spring Hill and all of the other locations, except Greeneville, would suggest that Spring

Hill is a desirable location for selecting barley varieties with wide adaptation for most areas of the state of Tennessee, except Greeneville. Results from this study indicate that wheat and barley were different in their yield response to testing sites.

Factor Analysis Technique

The image method of SAS factor procedure was used to determine the adequate number of orthogonal factors to be retained for wheat and barley. The size of the eigenvalues determined the number of orthogonal factors.

Wheat. As shown in Table 13, only three eigenvalues were greater than 1.0 (bold type). Method Principal Factor analysis was applied to classify the eight wheat locations.

As determined by the Image method, three factors were retained. Three relatively independent major factors were identified, which together accounted for 85% of total variation (Table 14). Factor 1 was a robust factor, and was strongly associated with Springfield, Knoxville, Spring Hill, Milan, and Martin (Table 15). Factor 2 which made the second largest contribution (20% of total variation) (Table 14) was composed of Greeneville and Crossville (Table 15). Factor 3 was a unique factor. It accounted for 11% of the total variations (Table 15) and included

Table 13. Eigenvalues estimated by image method for wheat.

| | Factor1 | Factor2 | Factor3 | Factor4 | Factor5 | Factor6 | Factor7 | Factor8 |
|---|---|---|---|---|---|---|---|---|
| Eigenvalues | **24.80**[a] | **3.33** | 0.94 | 0.43 | 0.07 | 0.08 | 0.16 | **1.56** |

[a]Eigenvalues greater than one are in bold type.

Table 14. Variance explained by each factor for wheat by principal factor analysis method.

| | Factor1 | Factor2 | Factor3 |
|---|---|---|---|
| Eigenvalue | 4.2 | 1.6 | 0.87 |
| Portion (%) | 54 | 20 | 11 |
| Cum Portion (%) | 54 | 74 | 85 |

Table 15. Grouping eight testing sites by factor analysis based on 25 wheat genotypes, yield response both prior to and after VARIMAX rotation.

| | Unrotated Factors | | | Rotated Factors | | |
|---|---|---|---|---|---|---|
| | Factor1 | Factor2 | Factor3 | Factor1 | Factor2 | Factor3 |
| A. Springfield | **0.94**[a] | 0.10 | -0.04 | **0.81** | 0.32 | 0.34 |
| B. Knoxville | **0.87** | -0.20 | -0.04 | **0.88** | 0.10 | 0.13 |
| C. Spring Hill | **0.78** | -0.46 | 0.05 | **0.90** | -0.03 | -0.11 |
| D. Crossville | 0.36 | **0.64** | -0.62 | 0.08 | 0.12 | **0.95** |
| E. Greeneville | 0.45 | **0.70** | 0.11 | 0.13 | **0.69** | 0.46 |
| F. Jackson | 0.38 | 0.58 | **0.63** | 0.10 | **0.93** | -0.00 |
| G. Milan | **0.85** | -0.09 | -0.19 | **0.82** | 0.07 | 0.31 |
| H. Martin | **0.89** | -0.28 | 0.15 | **0.93** | 0.18 | -0.06 |

[a]Highest value in each row of rotated and unrotated factors is in bold type.

only Jackson. These results support the findings from the use of the correlation technique, previously discussed.

The orthogonal factors VARIMAX rotation was performed. Rotation caused some shift in factor loading. But there were no shifting to or from factor 1. However, there was an exchange of loading between factor 2 and factor 3. Jackson and Crossville switched their loading factors for both factor 2 and factor 3 (Table 15). More meaningful results were found with factor loading prior to VARIMAX rotation.

Factors 1, 2, and 3 were plotted against each other and illustrated in Figures 5, 6, and 7. As shown in Figure 5, Springfield, Knoxville, Spring Hill, Martin, and Milan loaded high on factor 1, and Jackson loaded heavily on factor 2. Greeneville and Crossville showed low or no loading on either of these two factors. Figure 6 where factor 1 was plotted against factor 3 showed that Crossville loaded high on factor 3. Springfield, Knoxville, Spring Hill, Martin, and Milan remained heavily loaded on factor 1. Figure 7 shows the plot between factor 2 and 3. In this plot Jackson and Crossville loaded heavily on factor 2 and 3 respectively. Again, Greeneville did not have a high loading on any factor. All locations associated with factor 1 did not show loading on either of

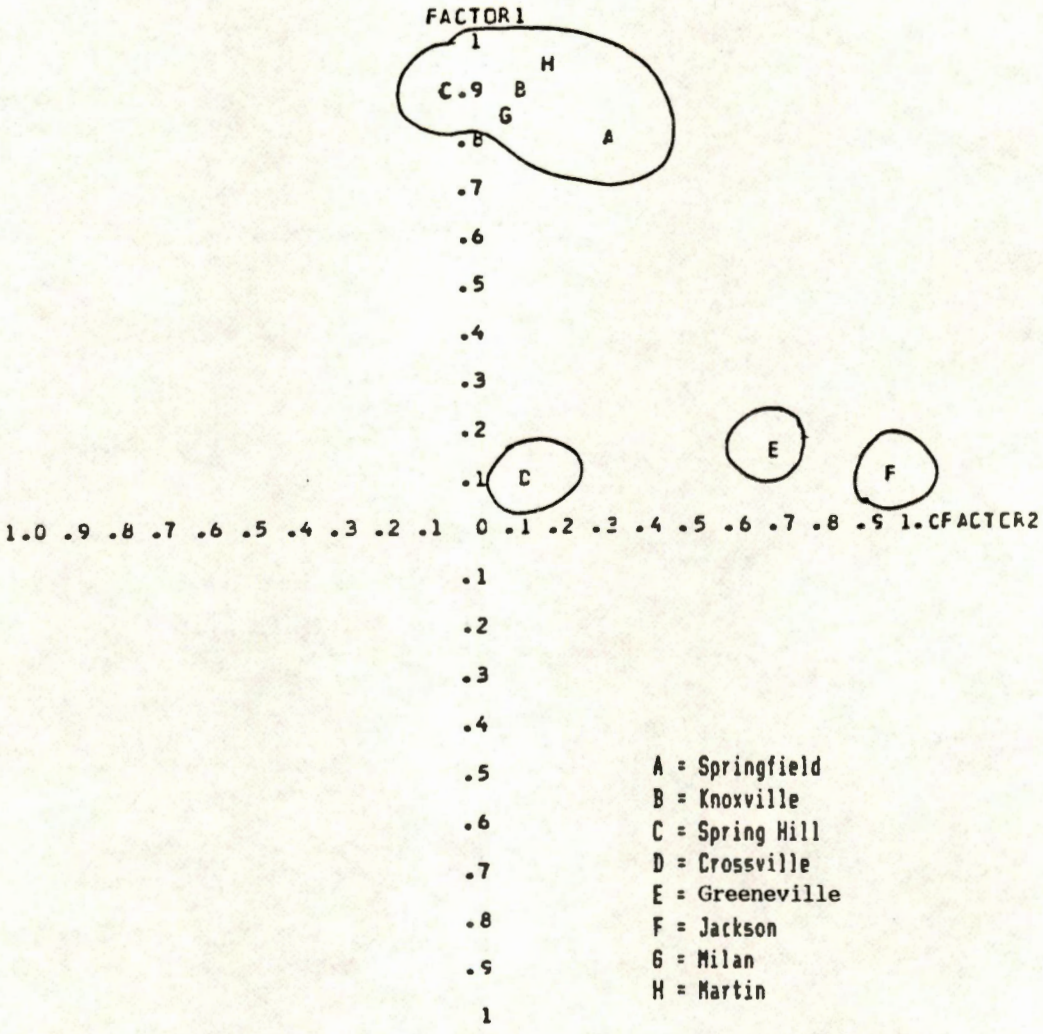



Fig. 5. Relative position of each location in the pair of factor axes 1 and 2 for wheat.

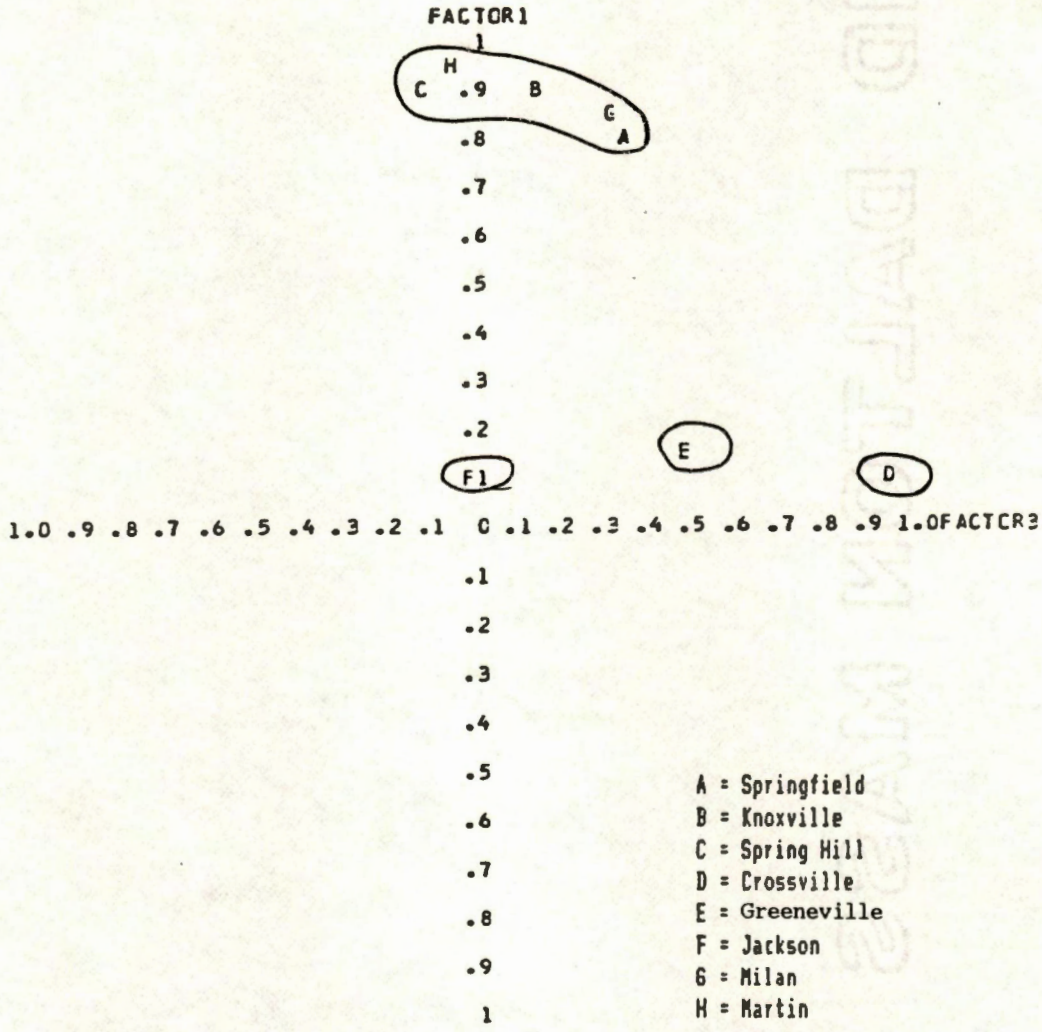



Fig. 6. Relative position of each location in the pair of factor axes 1 and 3 for wheat.

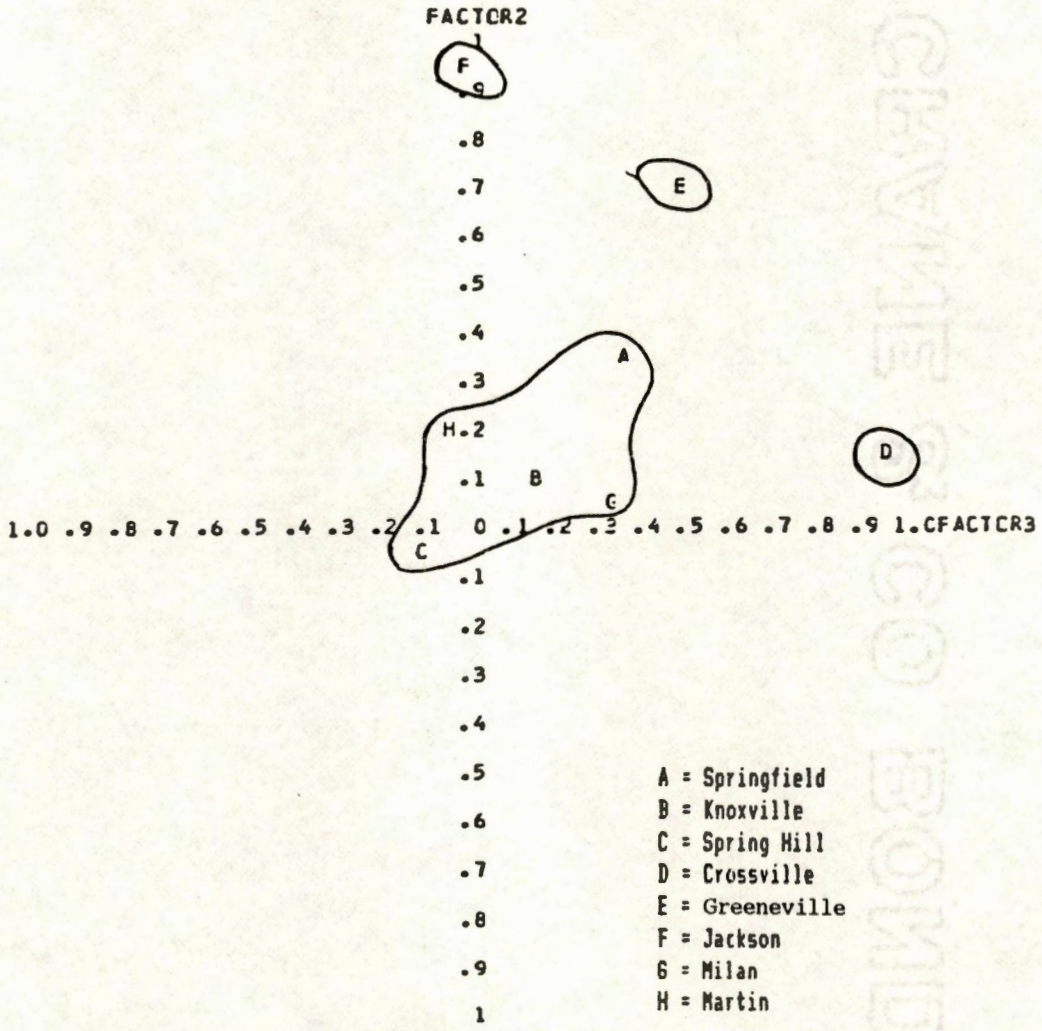



Fig. 7. Relative position of each location in the pair of factor axes 2 and 3 for wheat.

the factors, 2 or 3. It is clear that Fig. 6 illustrated the unrotated factor pattern better than Figs. 5 and 7.

It is evident that wheat genotypes in Springfield, Knoxville, Spring Hill, Martin, and Milan performed similarly in such a manner that they grouped close together and loaded on the same factor. The magnitude and the pattern of association between locations (Table 11, p.89) supports this grouping.

These results are not in complete agreement with the results of the study conducted by Wu (1978). In both studies, however, Jackson performed differently from other locations except for the correlation found between Jackson and Milan in the previous study conducted by Wu (1978). Springfield has always been located at the edge of its cluster toward other clusters while Spring Hill has always been situated at the edge of its cluster far from the other clusters. This may support the indication made earlier regarding the high degree of association between Springfield and all other locations. Therefore it was suggested again that Springfield is a desirable location for selecting wheat varieties with general adaptation to most areas in the state, except Jackson. This conclusion is based on the fact that (a) none of the wheat genotypes had the adaptation broad enough to cover all sites including Jackson (Table 8, p. 75), and (b) correlation coefficient

and factor loading patterns showed that wheat genotypes responded completely differently in Jackson than they did at other locations (Table 11, p. 89, Table 15, and Fig. 6).

Barley. The image method determined that two factors had eigenvalues greater than 1 (Table 16). Therefore, only two factors were retained in factor analysis of the barley data. The results of Principal Factor Analysis indicated that Factor 1 and 2 combined accounted for only 68% of the total variation (Table 17). Factor 1 alone associated with four of the six locations (Table 18) and accounted for 44.4% of the total variation (Table 17). These locations were Springfield, Knoxville, Spring Hill, and Jackson. This result is similar to the result for wheat except Jackson which was shown to be a unique location with the wheat data. Factor 2 consisted of the two remaining locations, Crossville and Greeneville; Factor 2 contributed to 24% of the total variation. Rotation (VARIMAX) did not improve loading weights and did not change the loading pattern of locations. Factor 1 was plotted against factor 2 and is illustrated in Figure 8. It is evident that barley genotypes responded differently in Greeneville and Crossville compared to the other locations. This was also noted in the results from use of the correlation technique.

Table 16. Eigenvalues estimated by image method for barley.

| | Factor1 | Factor2 | Factor3 | Factor4 | Factor5 | Factor6 |
|---|---|---|---|---|---|---|
| Eigenvalues | **6.31**[a] | 0.63 | 0.40 | 0.04 | 0.06 | **1.13** |

[a]Eigenvalues greater than one are in bold type.

Table 17. Variance explained by each factor for barley by principal factor analysis method.

| | Factor1 | Factor2 |
|---|---|---|
| Eigenvalues | 2.66 | 1.41 |
| Portion (%) | 44.4 | 23.6 |
| Cum Portion (%) | 44 | 68 |

Table 18. Grouping six testing sites by factor analysis based on 28 barley genotypes yield response prior and after VARIMAX rotation.

| | Unrotated | | Rotated | |
|---|---|---|---|---|
| Location | Factor1 | Factor2 | Factor1 | Factor2 |
| Springfield | **0.79**[a] | -0.03 | **0.79** | 0.07 |
| Knoxville | **0.72** | -0.12 | **0.73** | -0.02 |
| Spring Hill | **0.92** | -0.04 | **0.92** | 0.08 |
| Crossville | 0.15 | **0.84** | 0.04 | **0.85** |
| Greeneville | 0.13 | **0.81** | 0.02 | **0.82** |
| Jackson | **0.77** | -0.11 | **0.78** | 0.00 |

[a]Highest value in each row of rotated and unrotated factors is bolded.

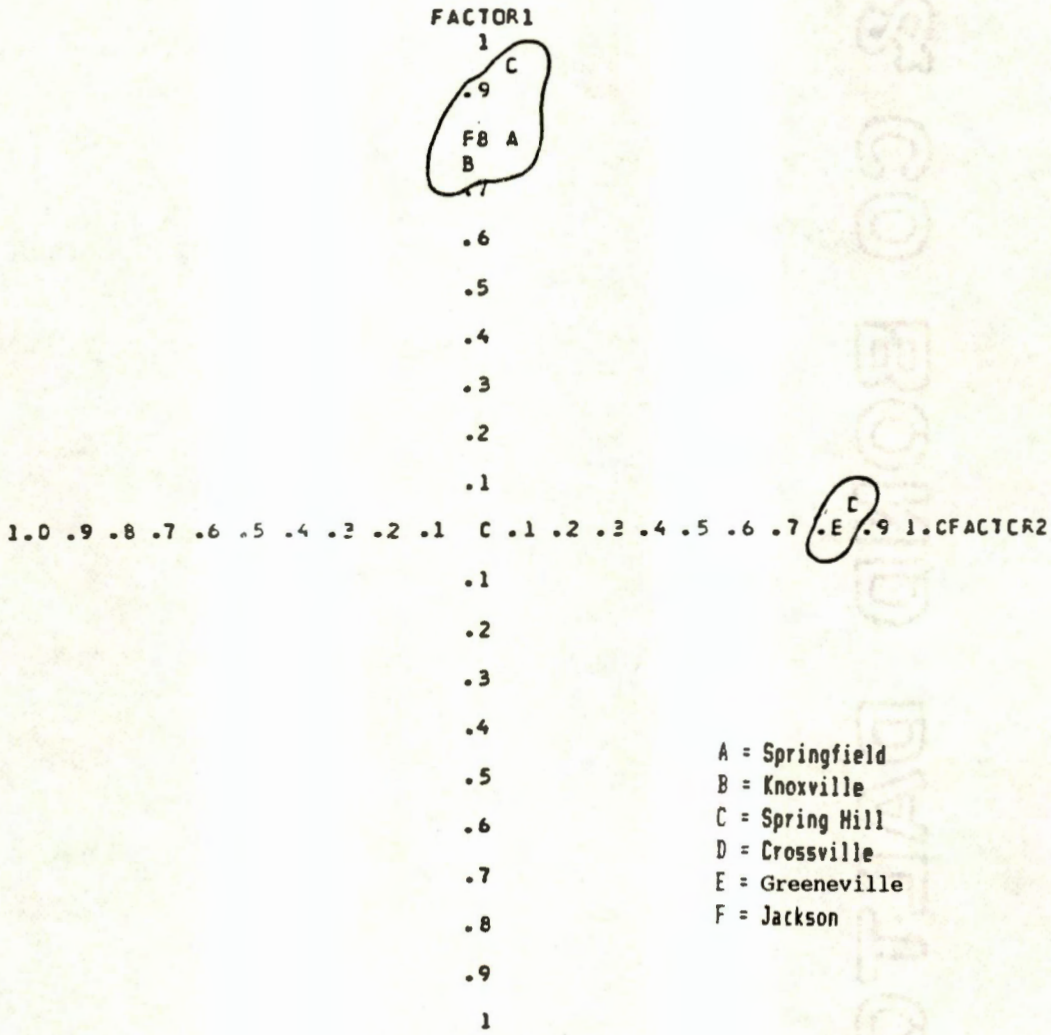



Fig. 8. Relative position of each location in the pair of factor axes 1 and 2 for barley.

Greeneville and Crossville were correlated with each other and showed no correlation with most of the other locations (Table 12, p. 90).

Both studies for wheat and barley showed that Springfield, Knoxville, and Spring Hill performed relatively more similarly than other locations. Jackson was a unique location, and Greeneville and Crossville were grouped together.

To identify the underlying environmental factors which caused barley and wheat genotypes to respond differently in different environments, the climatic (Tables 1 and 2, pp. 51 and 52) and geographic data (Fig. 2, p. 50) from experiment stations or from the nearest weather station to the testing sites were examined. No similar trend was found between monthly precipitation and the wheat and barley yield response in different locations. Greeneville and Crossville were grouped together by factor analysis and were similar in their relationship with other locations. This trend was not shared by average monthly precipitation, and average monthly mean temperatures. It is apparent that elevation (Fig. 2), and to a lesser extent average monthly temperature (Table 2), had similar trends as grouping patterns (Tables 12 and 16) resulted from factor analysis except for wheat in Jackson. Both for wheat and barley, Greeneville and Crossville with low average monthly temperature and highest elevation were loaded on the same

factor away from the rest of the locations. Among these environmental factors, elevations for Crossville and Greeneville were higher than the rest of the locations. This indicates the importance of these environmental factors as a differentiation tool between locations regarding wheat and barley responses. However, the average monthly temperatures for these two locations were not considerably different from other locations. Therefore, it is suggested that elevation was more important regarding genotypes' response to environmental changes and consequently in classification of the testing sites.

Regression Technique

In a breeding program, knowledge of the nature and the response of crop genotypes is important in making decisions regarding (a) allocation of resources, (b) number of breeding and/or testing programs to use, and (c) choosing the appropriate nursery environment.

Frey (1964) indicated that the optimum environment in which to practice selection obviously is the one which will elicit the greatest differential genetic manifestation for the attribute in question. It was noted that differentiation between genotypes relative to their genetic potential is greater in favorable environments (Frey (1964). Angus

and Mancur (1977) reported that the higher yielding environments provide better predictions of the line performance across environments than prediction from lower yielding environments. It was concluded that, where yield evaluation is restricted to a few locations (such as early generation testing) it may be sensible to utilize test environments which have high potential of producing relatively high yields (Angus and Mancur, 1977).

According to Hamblin et al. (1980), the best testing site is the one where the yield of the selected genotypes at the test locality consistently corresponds to their yield when grown over the range of environments for which they are intended.

Allen et al. (1978) concluded that if any class of environments is eventually established as substantially superior for testing purposes, it will be because the correlation between a genotype relative to a test environment and a genotype relative to the entire population of environments in which a selected genotype would be used was relatively high. In other words, a test site should represent the entire area well. It is evident that an optimum testing/selection site should provide the environmental conditions in which (a) the maximum genetic potentiality of the genotypes can be exploited and (b) the highest level of differentiation between genotypes can be achieved.

In addition, the trait in question in an optimum testing site should also consistently correspond to that when grown over a wide range of environments expected to be encountered in the future.

In this regard, yields of the genotypes at a particular site may be regressed against the mean yields of each of the genotypes across all sites. The size of the regression coefficient for a testing site reflects the level of differentiation between genotypes in that testing site. The above average regression value ($b_i > 1$) indicates that genotypes at an environment differentiated more than that at average environment. Therefore better differentiation between genotypes in such environments is possible. In contrast in an environment with a regression coefficient less than average ($b_j < 1$) indicates that the genotypes performed more similarly to each other. Consequently less differentiation was achieved.

Testing site characterization should not be based on their regression coefficients ($b_i$) only. Overall mean yields of each testing site are helpful in determining the extent to which the genetic potential of the genotypes can be explored. Therefore a simultaneous consideration of both regression coefficient ($b_i$) and overall mean yields of testing sites was important in identifying suitable sites for test and/or selection purposes.

A generalized interpretation of the environmental characteristics was illustrated in Fig. 1 (p. 41). The regression axis was divided horizontally into three sections based on plus or minus one standard deviation from mean regression coefficients. One standard deviation above or below the overall mean yields was applied to divide mean yields' axis vertically. Then the regression coefficients of testing sites obtained from regression analysis were plotted against mean yields of corresponding sites.

Wheat. The results of regression analysis for eight locations where wheat genotypes were tested and the appropriate plot are presented in Table 19 and Fig. 9, respectively. The regression coefficients of two locations, Jackson and Springfield, significantly depart from unity (Table 19). Regression coefficient for Jackson was 0.36 and for Springfield was 1.65, indicating a low and high degree of differentiation, respectively. Regarding wheat yields, Jackson was a unique location indicated by correlation coefficient and factor analyses. It had the weakest association with other locations. In contrast, Springfield was the most correlated location to all others in the test. The remaining locations fell in the average zone regarding their regression coefficients. Considering mean yields, Crossville provided the least desirable

Table 19. Means, regression coefficients and their standard deviation for yield of wheat genotypes at eight testing sites.

| Location | Mean Yield (bu/A) | Regression Coefficient ($b_i$) |
|---|---|---|
| Crossville | 39.33 | 0.61 |
| Jackson | 41.34 | 0.36** |
| Martin | 41.88 | 0.93 |
| Knoxville | 42.22 | 0.91 |
| Spring Hill | 44.06 | 1.25 |
| Springfield | 45.71 | 1.65** |
| Greeneville | 48.00 | 1.24 |
| Milan | 50.36 | 0.91 |
| Mean | 44.11 | 1.00 |
| STD | 3.70 | 0.37 |

**Significantly different from 1.0 at 0.01 level of probability by t test.

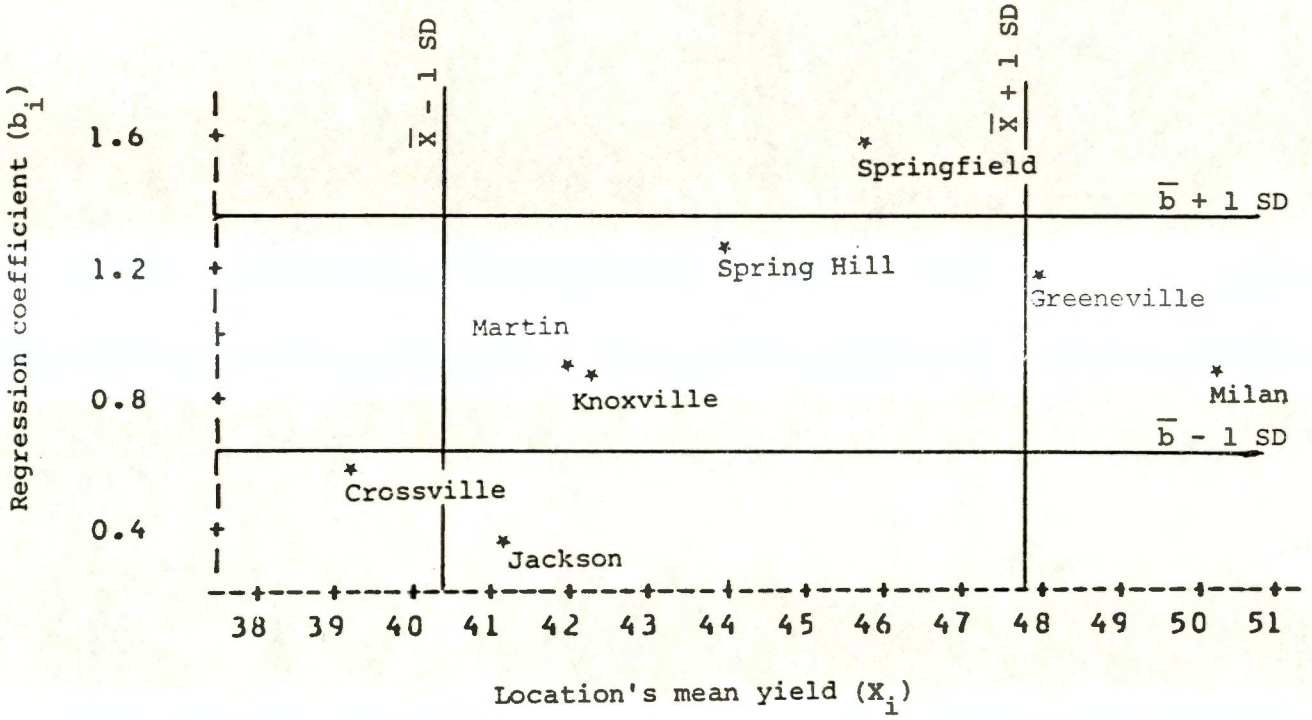



Fig. 9. Relationship of regression coefficient and mean wheat yield of locations.

conditions for genotypes tested to reach their genetic potential. In this respect, Greeneville and Milan had the best environmental conditions among locations tested. Jackson, Knoxville, Martin, Spring Hill, and Springfield fell in the average zone with respect to their mean yields.

As illustrated in Fig. 9, Crossville is situated in a zone where generally the lowest differentiation among genotypes may be obtained. In Crossville, genotypes demonstrated the lowest level of their genetics yield capacity relative to their yields in other sites tested (Fig. 9). It had also a very weak degree of association with other sites (Table 11, p. 89). Therefore, this location is not suitable as a selection or testing site. Jackson is not recommended as a selection or testing site due to very low differentiation between genotypes tested at this location. Martin, Spring Hill, and Knoxville were in the average zone with respect to their regression and mean yields. Springfield had the highest degree of association with other locations (Table 11), provided the best environmental conditions for wheat genotypes to differentiate most, and to perform above average of their genetic potential. Therefore, it might be recommended as a desirable location for testing and selection purposes for wide adaptation. On the other hand, Greeneville and Milan are

in the zone where generally highest genetic potentiality of the tested genotypes may be explored. but the differentiation among genotypes was at the average level. This indicates that in Milan and Greeneville most genotypes performed higher than their own overall mean yields across all sites at the same rate. Among all tested locations, Greeneville, Milan, and Springfield were the best areas for testing purposes. Milan and Greeneville had the same quality with respect to their regression and mean yields, but Milan had a higher degree of association with other locations. Therefore, Milan is a better site for wide adaptation selection.

For selection purpose the level of association between each location and the rest of the tested area is a determining factor. Crossville and Jackson with minimum level of association with the rest of the tested locations (Table 11) and with low level of differentiation and mean yields may not be considered as desirable environments for wide adaptation selection.

Barley. The results of regression analysis for six barley testing sites and the plot between regression

coefficient and mean yields are presented in Table 20 and Fig. 10, respectively. Regression coefficients for all sites significantly departed from unity (Table 20) but only Spring Hill and Jackson had a regression value one standard deviation greater than regression mean, indicating that differentiation between genotypes at these two locations was very high. They also were in the average yield zone. As a result they are desirable sites for barley selection relative to other sites tested. Spring Hill showed a higher degree of association with other sites than any other site tested. Therefore it may be considered as a desirable selection site for wide adaptation. Of course, none of the tested sites proved to be the best site for this purpose. Knoxville was in the average differentiation and low yield zone (Fig. 10). It had also a low degree of association with most other locations in the test. Therefore, it is the least desirable location for selection or testing purposes for barley. Springfield was in the average regression zone and highest mean yield region (Fig. 10), reflecting that most genotypes showed a yield increase relative to their own mean yields. This increase was at the same rate for most of the genotypes tested, as reflected by its average regression coefficient. Therefore, Springfield might be recommended as a testing site, but it may not be suggested as a selection site for broad

Table 20. Means, regression coefficients and their standard deviation for yield of barley genotypes at six testing sites.

| Location | Mean Yield (bu/A) | Regression Coefficient ($b_i$) |
|---|---|---|
| Knoxville | 49.13 | 0.86** |
| Spring Hill | 55.36 | 1.29** |
| Jackson | 56.37 | 1.36** |
| Greeneville | 56.72 | 0.84** |
| Crossville | 57.06 | 0.81** |
| Springfield | 64.88 | 0.87** |
| Mean | 56.59 | 1.00 |
| STD | 5.05 | 0.25 |

*,**Significantly different from 1.0 at 0.01 level of probability by t test.

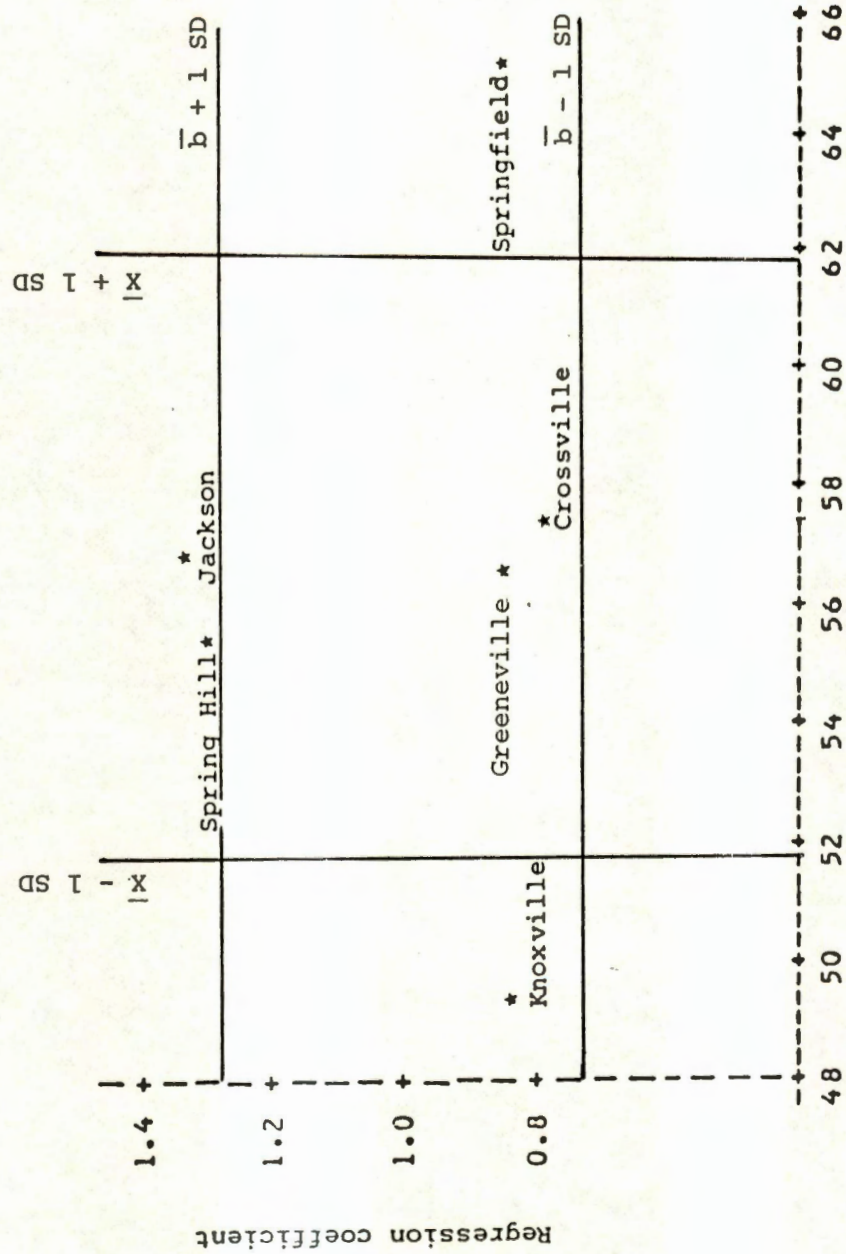



Fig. 10. Relationship of regression coefficient and mean barley yield of locations.

adaptation due to its lack of association with most locations tested (Table 12, p. 90). Greeneville and Crossville were within the average differentiation and average yielding capacity zone, reflecting that the yield response of barley genotypes in these two locations corresponded to their own overall average (Fig. 10). Both of these two locations showed very low to low degree of association with other sites (Table 12). As a result these two sites have an average value for testing purposes and no value as a selection site for wide adaptation.

# CHAPTER 4

## SUMMARY

Data obtained from the variety trials from 1955 to 1981 of 57 winter wheat and 44 winter barley varieties at eight and seven Tennessee Agricultural Experiment Stations, respectively, were used in this investigation to determine the general adaptation or stability of the genotypes tested and the magnitude of genotype x environment interactions. Additionally the desirability of each of each of the Experiment Stations at which the variety trials had been conducted was studied. The variety trials were all conducted utilizing a randomized complete block design with four replications. Although measurements were made on several variables in the variety trials, only the variable yield was utilized in this investigation. The yield of each plot was measured in bushels per acre. The environments were assumed as a random sample of possible environments in the state of Tennessee.

Conventional analyses of variance (ANOVA) were conducted on the mean yields of individual genotypes by year and locations. Results of ANOVA revealed that all sources of variation and their interactions were highly significant except the genotype x year interaction for barley.

The genotype x location and genotype x year interactions were highly significant for wheat while only the genotype x location interaction was highly significant for barley. The genotype x year interaction was not significant for barley which is assumed to be due to the genotypes tested in the barley variety trials being well adapted to the seasons in which tested.

In both crops, the variance component of genotype and location was small in relation to that for year. For barley the genotype components were negative which are considered to be zero. In wheat, the genotype x year component was much larger than that for genotype x location. This indicates that the environmental effects associated with years were more important in determining differential genotype responses than were the environmental effects associated with location. However, genotype x year component for barley was negative which is considered as zero.

Stability parameters were calculated using the models proposed by Eberhart and Russell (1966) and Finlay and Wilkinson (1963). Only wheat varieties which had been in the trial for 16 location-years and barley genotypes which had been in the trials for 12 location-years were retained for use in stability analysis. There were a total of 36 winter wheat and 21 winter barley varieties retained.

In this study a genotype with a regression coefficient of 1.00 or greater and relatively low deviations from regression was considered as stable because its yield increases proportionally with mean test yield in each environment. A genotype was considered unstable if it had a regression coefficient significantly less than one and relatively high deviation from regression. Overall mean yields of the genotypes, along with regression coefficients, and deviation from regression were used in comparing and evaluating the stability and adaptation of the genotypes.

Twenty-two percent of the wheat genotypes had regression coefficients not different from unity and also deviations from regression not different from zero. The outstanding genotypes for stability and adaptation were the varieties of Southern-Belle, Roy and McNair 3001. Other genotypes were identified which had good adaptation for specific locations or testing sites.

Twenty-five percent of the barley genotypes had regression coefficients not different from unity and deviations from regression which were not different from zero. The genotype which stood out as being the most stable were Maury, Henry, Surry, T60-38. These genotypes had broad adaptation as well as high mean yields.

In the classification of the testing sites correlation, factor analysis, and regression techniques were used. For wheat, the correlations among mean yields of eight testing sites revealed that Jackson was a unique location as the yields at that site showed a low correlation or no correlation with the other sites. The high significant correlations of wheat yield between Springfield and all other locations except Jackson suggests that this location is suitable to select wheat varieties with broad adaptation to all sites of the state, while selected varieties at Jackson may not be adapted to any other site in the state. Similar patterns of association were found between Milan, Martin; Knoxville, Spring Hill; Crossville, Greeneville.

The correlations among the sites for barley did not indicate Jackson as being unique. The high correlations between Spring Hill and all of the other locations except Greeneville would suggest that Spring Hill is a desirable location for selecting barley varieties with wide adaptation for most areas of the state of Tennessee, except Greeneville.

Factor analysis resulted in Spring Hill, Springfield, Milan, Martin, and Knoxville being loaded heavily on the same factor for wheat. Also Crossville and Greeneville were associated.

For the barley data, factor analysis indicated that Spring Hill, Knoxville, Springfield, and Jackson were heavily loaded on the same factor. Also Crossville and Greeneville were closely associated.

In regression technique, yields of the genotypes at a particular site were regressed on the mean yields of each of the genotypes across all sites. The size of the regression coefficient for a testing site reflects the level of differentiation among genotypes in the testing site. Overall mean yields of each testing site are helpful in determining the extent to which the genetic potential of the genotypes can be explored. Therefore, a simultaneous consideration of both regression coefficient and overall mean yields of testing site was important in identifying suitable sites for test and/or selection purposes.

For the wheat data, regression technique revealed that Martin, Spring Hill, and Knoxville were in the average zone with respect to their regression and mean yields. Springfield provided the best environmental conditions for wheat genotypes to differentiate most, and to perform above average of their genetic potential. Therefore, it might be recommended as a desirable location for testing and selection purpose for wide adaptation.

For the barley data, regression technique indicated that Knoxville was in the average differentiation and low

yield zone. It had also a low degree of association with most other locations in the test. Therefore, it is the least desirable location for selection or testing purposes for barley. Greeneville and Crossville have an average value for testing purposes and no value as a selection site for wide adaptation. Differentiation between barley genotypes was very high at Spring Hill. This site had highest degree of association with other sites. Therefore, it may be considered as a desirable selection site for wide adaptation.

Based on the results of the classification of testing sites, recommendations can be made regarding the possibility of reducing the number of locations used in the statewide variety testing program. The results of this investigation would indicate that in wheat, conducting the trials at Jackson, Springfield, Spring Hill, Greeneville, and Martin would allow obtaining results which are similar to those obtained from the use of all eight locations. Similar recommendations could be made for the barley variety trials.

Future research efforts should be pursued to enhance the techniques used to estimate the stability of the genotypes and to allow for differentiation of the results from the various locations of the testing sites.

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# APPENDIX

Table A-1. Analysis of variance when stability parameters are estimated.

| Source | d.f. | S.S. | M.S. |
|---|---|---|---|
| Total | nv-1 | $\sum_i \sum_j Y_{ij}^2$ - C.F. | |
| Varieties (V) | v-1 | $\frac{1}{n} \sum_i Y_{i.}^2$ - C.F. | $MS_1$ |
| Environments (Env): | n-1 | | |
| V x Env | (v-1)(n-1) | $\sum_i \sum_j Y_{ij}^2 - \sum Y_{i.}^2/n$ | |
| Env (linear) | 1 | $\frac{1}{v} (\Sigma Y_{.j} l_j)^2 / \sum_j l_j^2$ | |
| V x Env (linear) | v-1 | $\Sigma_i [(\sum_j Y_{ij} I_j)^2 / \Sigma I_{jj}^2]$ - Env(linear)S.S. | $MS_2$ |
| Pooled deviations | v(n-2) | $\sum_i \sum_j S_{ij}^2$ | $MS_3$ |
| Variety[1] | n-2 | $[\sum_j Y_{1j}^2 - (Y_{\frac{1.}{n}})^2] - (\sum_j Y_{1j} l_j)^2 / \sum_j I_j^2$ | |
| ⋮ | ⋮ | ⋮ | |
| Variety v | n-2 | $[\sum_j Y_{vj}^2 - Y_{\frac{v.}{n}}^2] - (\sum_j Y_{vj} I_j)^2 / \sum_j I_j^2 = \sum_j S_{vj}^2$ | |
| Pooled error | n(r-1)(v-1) | | |

Table A-2. Mean yields (bu/A) of 57 winter wheat genotypes at eight testing sites, over 27 years (1955-1981) and four replications.

| Genotype Name | Locations | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Springfield | Knoxville | Milan | Spring Hill | Crossville | Greeneville | Martin | Jackson |
| Abe | 42.1 | 42.2 | 48.4 | 48.7 | 35.7 | 45.9 | 42.7 | 33.4 |
| Ace | 36.5 | 34.0 | --[a] | 41.0 | 49.5 | 64.0 | 35.0 | 35.0 |
| Arthur | 47.7 | 46.2 | 50.1 | 46.9 | 42.3 | 54.1 | 43.2 | 43.3 |
| Arthur 71 | 36.8 | 35.4 | 40.3 | 37.6 | 32.2 | 45.6 | 40.2 | 32.6 |
| Avon | 44.5 | 35.0 | -- | 46.5 | 47.5 | 67.0 | -- | 50.0 |
| Beau | 43.4 | 43.0 | 48.3 | 51.2 | 38.8 | 45.2 | 42.5 | 41.0 |
| Benhur | 49.3 | 43.7 | 43.0 | 37.3 | 42.7 | 58.5 | 33.7 | 47.7 |
| Blueboy | 51.6 | 41.9 | 53.5 | 39.9 | 48.3 | 66.0 | 42.9 | 52.3 |
| Coker 47-27 | 41.8 | 52.5 | -- | 40.4 | 24.3 | 37.8 | -- | 48.8 |
| Coker 65-20 | 52.0 | 36.0 | -- | 30.0 | 48.5 | 44.0 | 37.0 | 45.5 |
| Coker 68-15 | 39.8 | 44.4 | -- | 36.6 | 28.2 | 58.5 | 37.4 | 46.0 |
| Coker 68-19 | 49.7 | 44.7 | -- | 30.0 | 40.7 | 56.3 | 35.7 | 57.0 |
| Coker 73-18 | 51.0 | 56.5 | 47.0 | 36.0 | 41.5 | 55.5 | 41.5 | 34.5 |
| Coker 747 | 58.0 | 53.8 | 54.2 | 58.5 | 51.8 | 58.2 | 54.6 | 37.3 |
| Coker 76-22 | 33.5 | 45.5 | 61.0 | 49.0 | 5.5 | 22.0 | 49.0 | 28.5 |
| Delta-Queen | 48.3 | 39.5 | -- | 49.5 | 21.3 | 32.0 | 49.3 | 28.0 |
| Doublecrop | 47.0 | 44.5 | 49.5 | 52.5 | 38.8 | 45.5 | 42.2 | 34.7 |
| Dual | 46.5 | 43.3 | -- | 46.9 | 44.4 | 47.9 | 35.0 | 42.4 |
| Fulcaster 612 | 37.6 | 39.8 | -- | 42.5 | 35.5 | 34.6 | -- | 45.1 |
| Fulton | 55.0 | 36.5 | -- | 32.0 | 61.0 | 46.5 | 39.5 | 37.0 |
| Genessee | 63.2 | 52.1 | -- | 62.8 | 43.4 | 38.1 | -- | 52.3 |
| Hart | 52.7 | 52.7 | 51.6 | 48.8 | 40.5 | 56.3 | 47.2 | 38.3 |
| Knox | 49.0 | 39.4 | -- | 41.3 | 39.0 | 48.8 | 35.3 | 48.6 |
| Knox 62 | 47.5 | 37.4 | 46.0 | 37.1 | 45.6 | 44.7 | 37.0 | 41.1 |
| Lewis | 35.5 | 19.0 | -- | 25.0 | 34.0 | 52.5 | 38.5 | 44.0 |
| McNair 1587 | 53.0 | 45.6 | -- | 38.8 | 36.6 | 64.2 | 40.5 | 42.6 |
| McNair 1813 | 41.2 | 37.2 | 46.7 | 34.6 | 28.8 | 40.6 | 44.3 | 44.4 |
| McNair 2203 | 52.8 | 46.8 | -- | 46.3 | 41.5 | 57.8 | 42.5 | 53.0 |
| McNair 3001 | 60.4 | 56.6 | 55.6 | 58.8 | 38.3 | 52.0 | 65.5 | 48.4 |
| McNair 4823 | 38.0 | 41.9 | 38.6 | 45.2 | 33.6 | 60.8 | 39.1 | 43.9 |
| McNair 701 | 35.0 | 21.0 | -- | 29.0 | 17.3 | 24.5 | 29.0 | 29.3 |
| Monon | 45.0 | 34.8 | 47.0 | 40.0 | 43.1 | 54.7 | 36.0 | 46.5 |
| Oasis | 38.8 | 42.0 | 45.0 | 46.0 | 37.0 | 49.0 | 44.3 | 32.6 |
| Pennington-23 | 29.0 | 19.0 | -- | 24.5 | 19.0 | 21.0 | 30.0 | 24.0 |
| Pioneer-S76 | 50.5 | 53.0 | 51.7 | 52.8 | 38.3 | 48.5 | 50.0 | 40.8 |
| Pioneer-S78 | 48.8 | 45.0 | 54.0 | 50.8 | 36.5 | 50.8 | 48.3 | 36.3 |
| Redcoat | 40.2 | 32.5 | -- | 38.3 | 46.4 | 60.0 | 34.7 | 45.5 |
| Reed | 39.0 | 35.6 | 50.0 | 36.2 | 52.2 | 54.6 | 35.8 | 35.8 |
| Riley | 41.5 | 34.5 | 45.0 | 28.0 | 53.0 | 52.0 | 30.5 | 37.0 |
| Rosen | 54.5 | 50.5 | 65.5 | 55.0 | 38.5 | 56.5 | 52.0 | 38.5 |

Table A-2 (continued)

| Genotype Name | Locations | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Springfield | Knoxville | Milan | Spring Hill | Crossville | Greeneville | Martin | Jackson |
| Roy | 55.0 | 60.0 | 57.0 | 54.5 | 45.0 | 58.0 | 56.5 | 43.0 |
| Ruler | 43.0 | 42.5 | 30.0 | 41.0 | 36.0 | 53.0 | 34.5 | 20.0 |
| Seneca | 47.2 | 41.9 | 45.0 | 43.8 | 46.8 | 41.4 | 36.4 | 39.6 |
| Southern-Belle | 71.0 | 63.5 | 57.5 | 60.5 | 53.0 | 58.5 | 68.0 | 45.0 |
| Stedler | 37.5 | 24.0 | -- | 24.0 | 41.0 | 44.5 | 37.0 | 44.0 |
| Stoddard | 42.8 | 48.8 | 48.0 | 43.0 | 38.0 | 45.8 | 37.0 | 31.0 |
| Sullivan | 48.2 | 44.8 | 53.5 | 53.4 | 39.8 | 43.2 | 43.0 | 37.0 |
| Tenn 9-17 | 62.5 | 46.5 | -- | 61.0 | 44.5 | 66.0 | -- | 60.0 |
| Tenn 61-35 | 38.0 | 36.5 | -- | 38.5 | 48.5 | 51.0 | 31.0 | 39.0 |
| Thorne | 42.1 | 42.0 | -- | 45.4 | 36.3 | 33.5 | -- | 43.2 |
| Tyland | 43.7 | 47.8 | -- | 51.1 | 42.0 | 39.4 | -- | 50.5 |
| T60-18 | 37.7 | 32.0 | -- | 39.7 | 54.3 | 58.5 | 29.0 | 36.7 |
| T60-25 | 49.7 | 36.0 | -- | 42.4 | 52.0 | 55.4 | 38.7 | 45.4 |
| T65-301 | 36.5 | 28.5 | -- | 37.5 | 37.0 | 53.5 | -- | 55.5 |
| T65-314 | 41.0 | 30.0 | -- | 37.0 | 37.5 | 51.5 | -- | 51.5 |
| Vermillion | 56.5 | 46.4 | -- | 52.0 | 35.8 | 43.0 | -- | 51.0 |
| Vigo | 39.4 | 39.8 | -- | 43.1 | 32.3 | 34.1 | -- | 38.9 |

[a]No data available.

Table A-3. Mean yields (bu/A) of 44 winter barley genotypes at six testing sites, over 27 years (1955-1981) and four replications.

| Genotype Name | Location | | | | | | |
|---|---|---|---|---|---|---|---|
| | Springfield | Knoxville | Spring Hill | Crossville | Greeneville | Jackson | Milan |
| Barsoy | 68.20 | 52.10 | 47.80 | 52.20 | 64.36 | 57.00 | -- |
| Boone | 59.67 | 56.67 | 57.33 | 48.00 | 108.00 | 56.67 | -- |
| Colonial 2 | 63.70 | 34.67 | 42.00 | 59.80 | 55.75 | 49.25 | 55.00 |
| Dayton | 77.31 | 53.63 | 61.82 | 58.92 | 50.89 | 66.26 | -- |
| Decature | 50.00 | 40.00 | 29.00 | 50.50 | 59.00 | 48.00 | -- |
| Dover | 77.00 | 38.50 | 47.50 | 57.50 | 50.00 | 44.50 | -- |
| Harrison | 67.63 | 53.00 | 53.86 | 64.00 | 76.88 | 57.38 | 48.00 |
| Henry | 59.40 | 58.50 | 58.00 | 60.60 | 66.75 | 50.83 | -- |
| Holston | 67.87 | 49.49 | 67.39 | 65.12 | 55.08 | 61.93 | -- |
| Hooded 5-112-38 | 73.35 | 51.25 | 51.68 | 37.53 | 27.93 | 55.08 | -- |
| Hudson | 72.99 | 52.66 | 58.99 | 63.62 | 55.60 | 57.94 | -- |
| Jackson-No1 | 63.28 | 56.60 | 51.13 | 45.70 | 34.48 | 50.76 | -- |
| Jefferson | 72.00 | 50.80 | 57.60 | 69.80 | 79.40 | 63.60 | -- |
| Kenbar | 69.07 | 52.51 | 60.05 | 55.12 | 51.11 | 59.03 | -- |
| Keowee | 70.75 | 50.33 | 57.25 | 54.57 | 65.38 | 57.25 | -- |
| Knob | 61.75 | 38.50 | 46.75 | 51.00 | 68.00 | 45.50 | -- |
| Maury | 66.00 | 64.80 | 57.40 | 62.00 | 60.67 | 43.40 | -- |
| McNair | 59.50 | 27.00 | 30.60 | 36.40 | 39.40 | 34.20 | -- |
| Miller | 73.50 | 56.00 | 61.00 | 71.50 | 84.00 | 88.50 | -- |
| Monroe | 62.00 | 59.50 | 55.50 | 46.00 | 57.00 | 51.50 | -- |
| Penrad | 67.50 | 44.50 | 34.00 | 52.00 | 61.00 | 37.00 | -- |
| Pike | 54.00 | 51.50 | 39.50 | 56.00 | 99.00 | 68.50 | -- |
| Rogers | 52.67 | 41.00 | 36.50 | 67.00 | 47.33 | 41.00 | -- |
| Surry | 61.80 | 58.67 | 55.33 | 61.20 | 75.25 | 51.33 | -- |
| Tenn 54-116 | 86.63 | 69.43 | 77.47 | 63.55 | 58.75 | 77.77 | -- |
| Tenn 59-15 | 72.62 | 49.83 | 64.57 | 60.25 | 51.00 | 62.37 | -- |
| Tenn 59-20 | 85.50 | 63.00 | 85.00 | 70.50 | 68.00 | 96.45 | -- |
| Tenn 60-38 | 61.33 | 47.00 | 61.33 | 52.33 | 61.00 | 74.66 | -- |
| Tenn 60-168-2-3 | 52.00 | 39.50 | 41.50 | 53.50 | 54.00 | 63.00 | -- |
| Tenn 60-19 | 56.33 | 42.33 | 57.67 | 69.67 | 65.00 | 57.00 | -- |
| Tenn 60-34 | 57.25 | 46.00 | 54.67 | 52.25 | 62.67 | 63.25 | -- |
| Tenn 61-116 | 67.50 | 52.50 | 47.50 | 67.00 | 47.50 | 43.50 | -- |
| Tenn 61-119 | 71.00 | 50.00 | 50.00 | 63.67 | 54.67 | 50.67 | -- |
| T65-118 | 80.50 | 32.00 | 49.50 | 34.00 | 79.50 | 32.00 | -- |
| T600-18 | 73.00 | 29.50 | 48.00 | 55.50 | 70.00 | 36.00 | -- |
| Upright 50-106-11 | 68.40 | 51.13 | 53.43 | 44.70 | 30.56 | 56.30 | -- |
| Upright 236-3-146 | 70.45 | 57.80 | 64.65 | 54.05 | 42.35 | 59.95 | -- |
| Upright 58-2 | 90.60 | 63.20 | 65.30 | 68.25 | 78.50 | 87.95 | -- |
| Upright 97-10-11 | 68.13 | 56.80 | 65.17 | 48.47 | 33.03 | 55.78 | -- |
| Volbar | 72.33 | 71.25 | 67.75 | 63.25 | 61.66 | 59.75 | -- |
| Wade | 73.42 | 50.66 | 60.16 | 73.00 | 70.41 | 50.14 | 73.00 |
| Will | 51.00 | 41.00 | 21.00 | 48.00 | 48.50 | 45.00 | -- |
| Wong 22 | 62.95 | 52.20 | 57.75 | 39.85 | 30.76 | 60.30 | -- |
| Watauga | 71.00 | 58.60 | 47.90 | 36.60 | 31.10 | 60.00 | -- |
| Zohra | 80.00 | 30.00 | 44.50 | 57.00 | 54.50 | 49.00 | -- |

Table A-4. Sources of variance and expected mean square.

| Source | Expected Mean Square[a] |
|---|---|
| Year (Y) | $\sigma_3^2 + r\,\sigma_{vy1}^2 + rv\,\sigma_{y1}^2 + r1\,\sigma_{vy}^2 + rv1\,\sigma_y^2$ |
| Location (L) | $\sigma_3^2 + r\,\sigma_{vy1}^2 + rv\,\sigma_{y1}^2 + ry\,\sigma_{v1}^2 + rvy\,\sigma_1^2$ |
| Location x Year | $\sigma_e^2 + r\,\sigma_{vy1}^2 + rv\,\sigma_{y1}^2$ |
| Variety (V) | $\sigma_e^2 + r\,\sigma_{vy1}^2 + r1\,\sigma_{vy}^2 + ry\,\sigma_{v1}^2 + ry1\,\sigma_v^2$ |
| Variety x Year | $\sigma_e^2 + r\,\sigma_{vy1}^2 + r1\,\sigma_{vy}^2$ |
| Variety x Location | $\sigma_e^2 + r\,\sigma_{vy1}^2 + ry\,\sigma_{v1}^2$ |
| Residual: VxYxL | $\sigma_e^2 + r\,\sigma_{vy1}^2$ |
| Residual: Error | $\sigma_e^2$ |

[a] y, 1, v, and r are numbers of years, locations, varieties, and replicates, respectively; $\sigma_e^2$ = error variance; $\sigma_{v1}^2$ = variance due to interaction of varieties; etc.

# VITA

G. Hussein Chabi was born in Busheir, Iran, on January 4, 1945. He received his elementary and secondary education with an honorary title of first rank student in the state of Busheir, Iran. He entered the University of Jundi Shapour, College of Agriculture, in Ahwaz, Iran, and he received a Bachelor of Science degree in agriculture in the spring of 1967.

He joined the Agricultural Extension and Development Corps in 1967 and received an honorary title of "Distinguished Agricultural Extension Member" from the Secretary of Agriculture in 1969. He was employed by the Iranian Tobacco Research Institute during 1969-1978 as an agronomist and head of Tobacco Technology Research Department.

In the spring of 1978, he was granted a sabbatical leave and joined R. J. Reynolds Tobacco Company research department in Winston-Salem, North Carolina. In January 1979, he attended Alabama Agricultural and Mechanical University where he received a Master of Science degree, with a major in plant breeding.

In January 1980 he entered the University of Tennessee in Knoxville to pursue a Doctor of Philosophy degree in

Plant and Soil Science, with a major in plant breeding and genetics. He received his Ph.D. in the spring of 1990.

In the spring of 1983, he joined the Iranian Tobacco Research Institute as the research assistant general manager. The following year he accepted a research and teaching position in the Statistics and Genetics Research Department of the Department of Agriculture.

In the spring of 1985 he was employed by United AgriSeeds, Inc., Wisconsin, as a genetic computing consultant and later as a corn research station assistant manager. In the spring of 1987 he accepted a position with Interstate Seed Company, Wisconsin, as director of corn research. In 1988 he joined Trilogy Consulting Corporation. Wisconsin, as a statistics consultant.

He married the former Zohreh F. Pay of Busheir, Iran in the spring of 1972. In the fall of 1973 and the winter of 1979 he and his wife were blessed with their first and second daughters, Almira and Shabnam, respectively.

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