A COMPARISON OF STATISTICAL METHODS TO DESCRIBE GENOTYPE x ENVIRONMENT INTERACTION AND YIELD STABILITY IN MULTI-LOCATION MAIZE TRIALS

BY

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DECLARATION

I herby declare that this thesis, prepared for the degree *Magister Scientiae Agriculture*, which was handed in by myself, to the University of the Free State, is my own original work and has not been handed in previously to any other university/faculty. All sources of materials and financial assistance used for the study have been duly acknowledged. I also agree that the University of the Free State has the sole right to publication of this thesis.

Signed on the 30th of November 2004 at the University of the Free State, Bloemfontein, South Africa.

Martin J. A. Alberts

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DEDICATION

I dedicate this piece of work to my Maker who must get all the honour for giving me the ability and strength to complete this work, also to my late parents who raised me with love and dedication, they would have loved to see me finish this study.

It is also dedicated to my wife, Anina, and my family who encouraged me with love and sacrifice, to finish this work.

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CHAPTER 1

Introduction

Maize is the main grain crop grown in the Republic of South Africa and is produced on about 3.2 million hectares. Maize is produced in a basic triangle starting at Belfast in the east to the Lesotho Highlands in the south, Setlagoli in the west and back to Belfast. A small area in KwaZulu-Natal and irrigation schemes on the banks of South Africa's major rivers, the Vaal and Orange in the far west is also of importance. The average total crop per annum is about 7 million metric tons. Most of this production is used internally and only small amounts are exported. White maize is mostly used for human consumption, mainly milled as a meal which is then cooked to be eaten as porridge, or as grits. Yellow maize is used as animal feed in the dairy, pork, poultry and feedlot industries. The distribution between white and yellow maize is 60% to 40% respectively.

The soil and climatic conditions vary in extremes from shallow loamy to clay soils in the east to deep sandy soils with a restrictive layer at 1.2 - 2.0 meters and fluctuating water table (north western Free State) and sandy loam soils in the west.

The rainfall per annum varies from 300mm in the far west to 650mm per annum in the east. Rainfall is extremely variable and erratic during the season and over years. High spring and summer temperatures, with low humidity, and prolonged periods without rain, lead to serious drought and heat stress. The average long

term yield per hectare in South Africa varies between 2.2 to 3.2 tons per hectare and is an indication of the variation in environmental conditions.

The seed market in South Africa is strongly directed at the commercial farmer. They are planting 100% hybrid seed and are highly advanced in production technology, such as conservation tillage, traffic control and planting at higher densities. The small or subsistence farming sector is emerging strongly and is planting without or with small amounts of fertilizer. These farmers are planting open pollinated varieties or low-cost 3- and 4-way hybrids.

Farmers and scientists want successful new maize hybrids that show high performance for yield and other essential agronomic traits. Their superiority should be reliable over a wide range of environmental conditions but also over years. The basic cause of differences between genotypes in their yield stability is the occurrence of genotype-environment interactions (GEI).

Multi-location trials play an important role in plant breeding and agronomic research. Data from such trials have three main objectives: a) to accurately estimate and predict yield based on limited experimental data; b) to determine yield stability and the pattern of response of genotypes across environments; and c) to provide reliable guidance for selecting the best genotypes or agronomic treatments for planting in future years and at new sites (Crossa, 1990).

A number of parametric statistical procedures have been developed over the years to analyze genotype x environment interaction and especially yield stability over environments. A number of different approaches have been used, for example joint regression analysis and multivariate statistics, to describe the performance of genotypes over environments. To date considerable differences of opinion still exist between the leading protagonists of the different statistical approaches as to

the best and most suitable procedure to be used for a specific data set or production region.

The objective was to carry out these analyses on a multi-year, multilocation data set generated in the most important maize growing areas of South Africa for the period 2001 to 2003. This study aimed to determine which of these methodologies best suit stability analyses on maize planted in South Africa and also discuss certain statistical and biological limitations. Several similar studies have recently been done in South Africa and other African countries on other crops like wheat (Purchase, 1997, 2000), linseed (Adugna and Labuschagne, 2002) and Ethiopian mustard (Kassa, 2002).

The objectives of this study were:

- To compare the various statistical methods of analysis with new statistical approaches to determine the most suitable parametric procedure to evaluate and describe maize genotype performance under dry land multi-location trials, in the maize producing areas of South Africa,
- To study the different stability statistics and measures and determine the most suitable method for a wide range of maize genotypes and environments in South Africa,
- To assess South African maize hybrids for adaptation using multivariate statistical analysis (AMMI).

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CHAPTER 2

Literature study

2.1 Introduction

The phenotype of an individual is determined by both the genotype and the environment, these two effects are not always additive which indicates that genotype x environment interactions (GEI) are present. The GEI result in inconsistent performances between the genotypes across environments. Significant GEI results from the changes in the magnitude of differences between genotypes in different environments or changes in the relative ranking of the genotypes (Falconer, 1952; Fernandez, 1991). Peto (1982) defined these two forms of GEI as qualitative (rank changes) and quantitative (absolute differences between genotypes). GEI makes it difficult to select the best performing and most stable genotypes and is an important consideration in plant breeding programs because it reduces the progress from selection in any one environment (Hill, 1975;Yau, 1995).

South Africa with its very diverse climatic conditions and soil types escalates the problem of GEI even further. To overcome this problem, the universal practise of scientists in most crops when selecting genotypes, is to plant them in yield (performance) trials over several environments and years to ensure that the selected genotypes have a high and stable performance over a wide range of environments. The assessment of genotype performance in genotype x location x year experiments is often difficult because of the presence of location x year interaction (environmental effects) (Lin and Binns, 1988a).

Crossa (1990) pointed out that data collected in multilocation trials are intrinsically complex having three fundamental aspects: structural patterns, non-structural noise, and relationships among genotypes, environments, and genotypes and environments considered jointly.

Pattern implies that a number of genotypes respond to certain environments in a systematic, significant and interpretable manner, whereas noise suggests that the responses are unpredictable and un-interpretable. The function of experimental design and statistical analyses of multilocation trials is thus to eliminate and discard as much of this unexplainable noise as possible.

Plant Breeders generally agree on the importance of high yield stability, but there is less accord on the most appropriate definition of “stability” and the methods to measure and to improve yield stability (Becker and Léon, 1988).

2.2 Concepts of stability

The terms phenotypic stability, yield stability and adaptation are often used in quite different senses. Different concepts and definitions of stability have been described over the years (Lin *et al.*, 1986; Becker and Léon, 1988).

Lin *et al*. (1986) identified three concepts of stability:

Type 1: A genotype is considered to be stable if its among-environment variance is small. Becker and Léon, (1988) called this stability a static, or a biological concept of stability. A stable genotype possesses an unchanged performance regardless of any variation of the environmental conditions. This concept of stability is useful for quality traits, disease resistance, or for stress characters like winter hardiness. Parameters used to describe this type of stability are coefficient of variability (CV_i) used by Francis and Kannenburg (1978) for each genotype as a stability parameter and the genotypic variances across environments (S_i^2).

Type 2: A genotype is considered to be stable if its response to environments is parallel to the mean response of all genotypes in the trial. Becker and Léon, (1988) called this stability the dynamic or agronomic concept of stability. A stable genotype has no deviations from the general response to environments and thus permits a predictable response to environments. A regression coefficient (b_i) (Finlay and Wilkinson, 1963) and Shukla's (1972) stability variance (σ^2_i) can be used to measure type 2 stability.

Type 3: A genotype is considered to be stable if the residual MS from the regression model on the environmental index is small. The environmental index implicates the mean yield of all the genotypes in each location minus the grand mean of all the genotypes in all locations. Type 3 is also part of the dynamic or agronomic stability concept according Becker and Léon (1988).

Methods to describe type 3 stability are the methods of Eberhart and Russell (1966) and Perkins and Jinks (1968). Becker and Leon (1988) stated that all stability procedures based on quantifying GEI effects belong to the dynamic concept. This includes the procedures for partitioning the GEI of Wricke's (1962) ecovalence and Shukla's (1972) stability of variance, procedures using the regression approach such as proposed by Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Perkins and Jinks (1968), as well as non-parametric stability analyses.

Lin *et al*., (1986) defined four groups of stability statistics; they integrated type 1, type 2 and type 3 stabilities with the four groups. Group A was regarded as type 1, groups B and C as type 2 and group D as type 3 stability.

Group A:	DG (Deviation of average genotype effect)	SS (sum of squares)
Group B:	GE (GE interaction term)	SS
Group C:	DG or GE	Regression coefficient
Group D:	DG or GE	Regression deviation

Lin and Binns (1988a) proposed type 4 stability concepts on the basis of predictable and unpredictable non-genetic variation. The predictable component related to locations and the unpredictable component related to years. They suggested the use of a regression approach for the predictable portion and the mean square for years x locations for each genotype as a measure of the unpredictable variation.

2.3 Statistical methods to measure G x E Interaction

A combined analysis of variance procedure is the most common method used to identify the existence of GEI from replicated multilocation trials. If the GEI variance is found to be significant, one or more of the various methods for measuring the stability of genotypes can be used to identify the stable genotype(s). A wide range of methods is available for the analysis of GEI and can be broadly classified into four groups: the analysis of components of variance, stability analysis, multivariate methods and qualitative methods.

2.3.1 Conventional analysis of variance

Consider a trial in which the yield of G genotypes is measured in E environments each with R replicates. The classic model for analysing the total yield variation contained in GER observations is the analysis of variance (Fisher, 1918, 1925). The within-environment residual mean square measures the error in estimating the genotype means due to differences in soil fertility and other factors, such as shading and competition from one plot to another. After removing the replicate effect when combining the data, the GE observations are partitioned into two sources: (a) additive main effect for genotypes and environments and (b) nonadditive effects due to GEI. The analysis of variance of the combined data expresses the observed (Y_{ij}) mean yield of the i^{th} genotype at the j^{th} environment as

$$Y_{ij} = \mu + G_i + E_j + GE_{ij} + e_{ij} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (1)$$

where μ is the general mean; $G_{i,}E_{j,}$ and GE_{ij} represent the effect of the genotype, environment, and the GEI, respectively; and e_{ij} is the average of the random errors associated with the r^{th} plot that receives the i^{th} genotype in the j^{th} environment. The nonadditivity interaction as defined in (1) implies that the expected value of the i^{th} genotype in the j^{th} environment (Y_{ij}) depends not only on the levels of G and separately but also on the particular combination of levels of G and E (Crossa, 1990).

The major limitation in this analysis is that the error variances over environments should be homogeneous to test for genotypic differences. If error variances are heterogeneous, this analysis is open to criticism as the F-test of the GEI mean squares against the pooled error variances is biased towards significant results. A correct test for significance, by weighting each genotype mean by the inverse of its estimated variance, has been used by Yates and Cochran (1938) and Cochran and Cox (1957). This weighted analysis gives less weight to environments that have a high residual mean square. The disadvantage of weighted analysis is, however, that weights may be correlated to environment yield responses (high yielding environments showing higher error variance and low yielding sites presenting lower error variances) and this could mask the true performance of some genotypes in certain environments (Crossa, 1990).

One of the main deficiencies of the combined analysis of variance of multilocation trials is that it does not explore any underlying structure within the observed nonadditivity (GEI). The analysis of variance fails to determine the pattern of response of genotypes and environments. The valuable information contained in $(G-1)$ $(E-1)$ degrees of freedom is particularly wasted if no further analysis is done. Since the nonadditive structure of the data matrix has a non-random (pattern) and random (noise) component, the advantage of the additive model is lost if the pattern component of the nonadditive structure is not further partitioned into functions of one variable each (Crossa, 1990).

Analysis of variance of multilocation trials is useful for estimating variance components related to different sources of variation, including genotypes and GEI. In general, variance component methodology is important in multilocation trials, since errors in measuring the yield performance of a genotype arise largely from GEI. Therefore, knowledge of the size of this interaction is required to (a) obtain efficient estimates of the genotypic effects and (b) determine optimum resource allocations, that is the number of plots and locations to be included in future trials.

In a breeding program, variance component methodology is used to estimate the heritability and predicted gain of a trait under selection (Crossa, 1990).

2.3.2 Stability analysis or parametric approach

Stability analysis provides a general summary of the response patterns of genotypes to environmental change. Freeman (1973) termed the main type of stability analysis, joint regression analysis or joint linear regression (JLR). It involves the regression of the genotypic means on an environmental index. Joint regression analysis provides a means of testing whether the genotypes have characteristic linear responses to changes in environments. Joint regression analysis was first proposed by Yates and Cochran (1938) and then widely used and reviewed by various authors (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Perkins and Jinks, 1968; Wright, 1971; Freeman and Perkins, 1971; Shukla, 1972; Hardwick and Wood, 1972; Freeman, 1973; Hill, 1975; Lin *et al*., 1986; Westcott, 1986, Becker and Léon, 1988; Baker, 1988; Crossa, 1990; Hohls, 1995).

2.3.2.1 Regression coefficient (b_i) and deviation mean square ($S^2_{d_i}$)

Joint linear regression (JLR) is a model used for analysing and interpreting the nonadditive structure (interaction) of two-way classification data. The GEI is partitioned into a component due to linear regression (b_i) of the i^{th} genotype on the environment mean, and a deviation (d_{ij}):

$$(GE)_{ij} = b_i E_j + d_{ij} \text{.....(2)}$$

and thus

$$Y_{ij} = \mu + G_i + E_j + (b_i E_j + d_{ij}) + e_{ij} \text{.....(3)}$$

This model uses the marginal means of the environments as independent variables in the regression analysis and restricts the interaction to a multiplicative form. The

method divides the (*G-1*) (*E-1*) df for interaction into *G-1* df for heterogeneity among genotype regressions and the remainder (*G-1*) (*E-2*) for deviation. Further details about interaction are obtained by regressing the performance of each genotype on the environmental means. Finlay and Wilkinson (1963) determined the regression coefficient by regressing variety mean on the environmental mean, and plotting the obtained genotype regression coefficients against the genotype mean yields. Figure 2.1 is a generalized interpretation of the genotype pattern obtained when genotype regression coefficients are plotted against genotype mean yields.

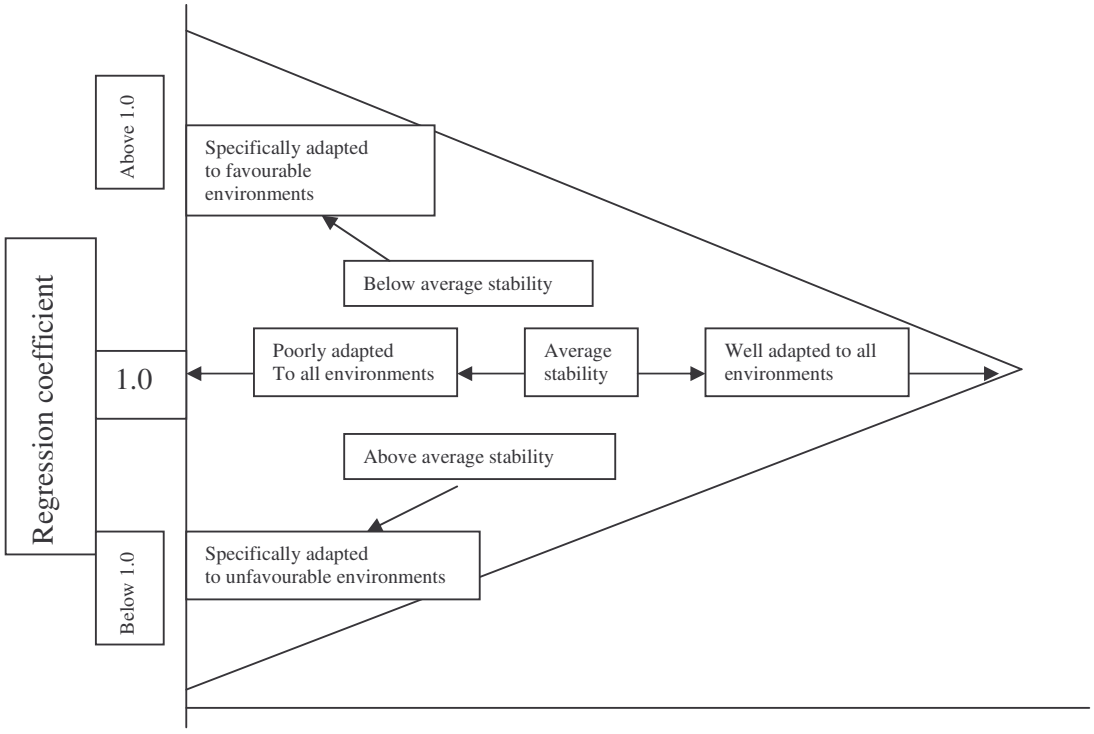

Figure 2.1 A generalized interpretation of the genotypic pattern obtained when, genotypic regression coefficients are plotted against genotypic mean, adapted from Finlay and Wilkinson (1963).

Finlay and Wilkinson (1963) defined a genotype with $b_i = 0$ as stable, while Eberhart and Russell (1966) defined a genotype with $b_i = 1$ to be stable. Perkins and Jinks (1968) proposed an equivalent statistical analysis whereby the observed values are adjusted for environmental effects before the regression.

Eberhart and Russell (1966) proposed pooling the sum of squares for environments and GEI and subdividing it into a linear effect between environments (with 1 df), a linear effect for genotype x environment (with *E-2* df). In effect the residual mean squares from the regression model across environments is used as an index of stability, and a stable genotype is one in which the deviation from regression mean squares ($S^2_{d_i}$) is small.

$$S^2_{d_i} = \frac{1}{E-2} [E_j (X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X}..)^2 - (b_i - 1)^2 E_j (\bar{X}_j - \bar{X}..)^2] \ldots\ldots\ldots (4)$$

The regression approach has been shown to be the most useful for geneticists (Freeman and Perkins, 1971; Freeman, 1973; Hill, 1975; Westcott, 1986), but it should be noted that these authors have pointed out several statistical and biological limitations and criticisms.

The first statistical criticism is that the genotype mean (x-variable) is not independent from the marginal means of the environments (y-variable). Regressing one set of variables on another that is not independent violates one of the assumptions of regression analysis (Freeman and Perkins, 1971; Freeman, 1973). This problem may be overcome if a large number of genotypes are used (15-20).

The second statistical limitation is that errors associated with the slopes of the genotypes are not statistically independent, because sum of squares for deviation with (*G-1*) (*E-2*) df, can not be subdivided orthogonally among the *G* genotypes (Crossa, 1990).

The third statistical problem is that it assumes a linear relationship between interaction and environmental means. When this assumption is violated, the effectiveness of the analysis is reduced, and results may be misleading (Mungomery *et al*., 1974; Westcott, 1986).

A major biological problem pointed out by Westcott (1986) and Crossa (1990) is when only a few low or high yielding sites are included in the analysis. The genotype fit may be determined largely by its performance in a few extreme environments, which in turn generates misleading results and thus regression analysis should be used with caution when the data set includes results from only a few high or low yielding locations.

Becker and Léon (1988) noted when studying the most appropriate biometrical method, that the regression approach is of little use if the regression coefficient (b_i) is included in the definition of "stability". For this reason (b_i) is generally viewed by authors not as a measure of stability but rather as additional information on the average response of a genotype to advantageous environmental conditions. This is schematically presented in Figure 2.2 as cited by Becker and Léon, 1988.

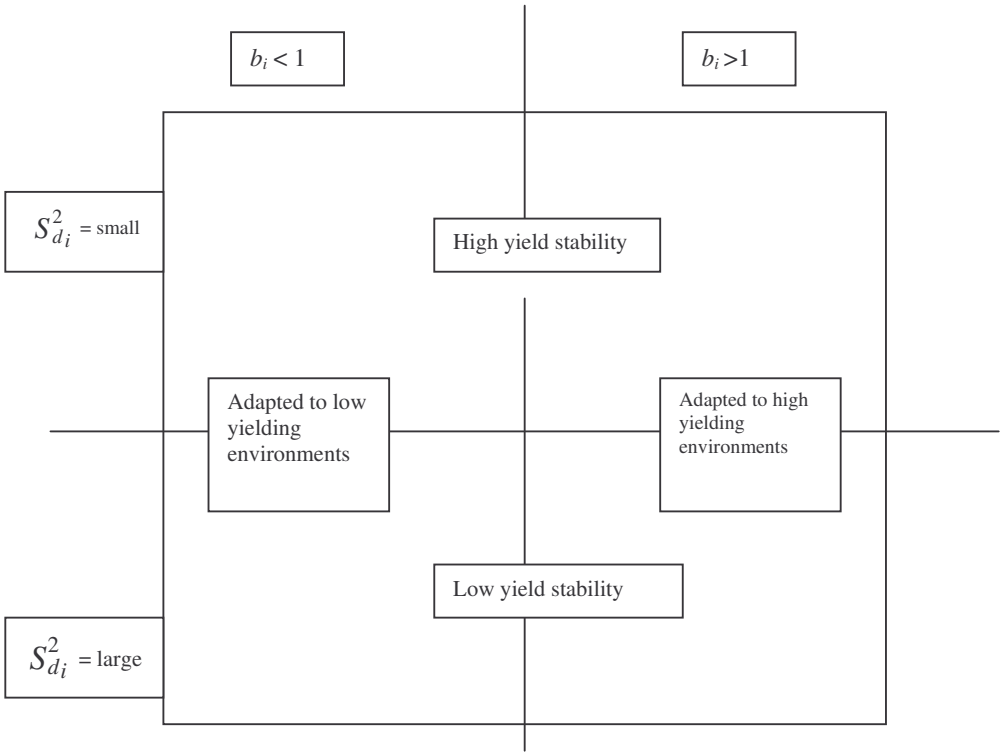

Figure 2.2 Interpretation of parameters b_i and $S^2_{d_i}$ for the regression approach, adapted from Haufe and Geidel (1978) as cited by Becker and Léon (1988)

Crossa (1990) concluded that in trying to determine which genotype is superior with the regression approach, plant breeders have difficulty reaching a compromise between the yield mean, slope and deviation from regression, because the genotype's response to environments is intrinsically multivariate and regression tries to transform it into a univariate problem (Lin *et al*., 1986).

2.3.3 Other measurements of yield stability

Alternative methods of determining genotype stability based on the GEI is also available. The more important and frequently used methodologies are discussed as follow.

2.3.3.1 Coefficient of determination (r_i^2)

Pinthus (1973) proposed to use the coefficient of determination (r_i^2) instead of deviation mean squares to estimate stability of genotypes, because r_i^2 is strongly related to $S_{d_i}^2$ (Becker, 1981).

Coefficient of determination: $r_i^2 = 1 - \frac{S_{d_i}^2}{S^2 x_i}$ …….. (5)

The application of r_i^2 and b_i has the advantage that both statistics are dependent of units of measurement.

2.3.3.2 Ecovalence (W_i)

Wricke (1962, 1964) defined the concept of ecovalence as the contribution of each genotype to the GEI sum of squares. The ecovalence (W_i) or stability of the i^{th} genotype is its interaction with the environments, squared and summed across environments, and express as

$$W_i = [\overline{Y_{ij}} - \overline{Y_{i.}} - \overline{Y_{.j}} - \overline{Y_{..}}]^2 \text{……(6)}$$

Where Y_{ij} is the mean performance of genotype i in the j^{th} environment and $Y_{i.}$ and $Y_{.j}$ are the genotype and environment mean deviations, respectively, and $Y..$ is the overall mean. For this reason, genotypes with a low W_i value have smaller deviations from the mean across environments and are thus more stable.

According to Becker and Léon (1988) ecovalence measures the contribution of a genotype to the GEI, a genotype with zero ecovalence is regarded as stable. Becker and Léon (1988) illustrated ecovalence by using a numerical example of plot yields of genotype *i* in various environments against the respective mean of environments (Figure 2.3).

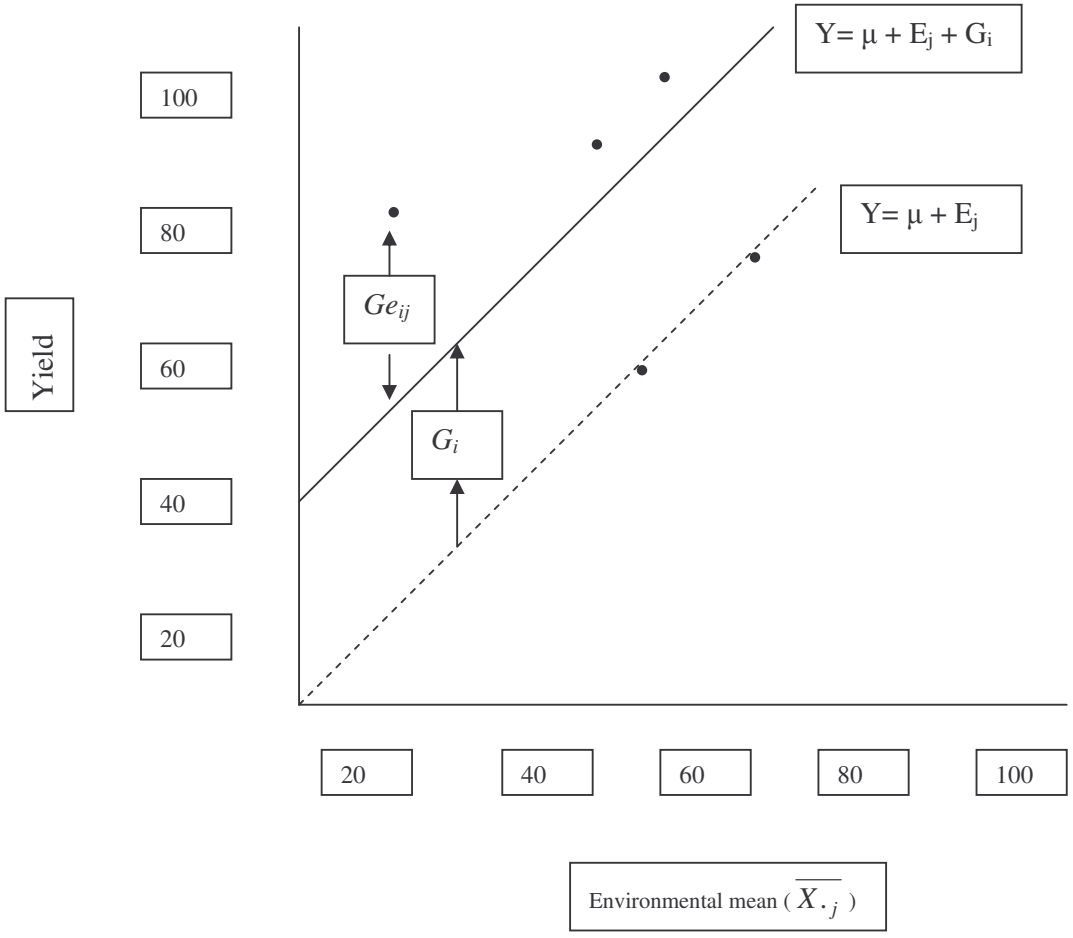

Figure 2.3 Graphical representation of GEI: The stability statistic ecovalence (W_i) is the sum of squares of deviations from the upper unbroken line

The lower broken line estimates the average yield of all genotypes simply using information about the general mean (μ) and the environmental effects (E_j), while the upper unbroken line takes into account the genotypic effect (G_i) and therefore estimates the yield of genotype *i* deviations of yield from the upper unbroken line

are the GEI effects of genotype *i* and are summed and squared across environments and constitutes ecovalence (W_i).

2.3.3.3 Shukla's stability variance parameter (σ_i^2).

Shukla (1972) defined the stability variance of genotype *i* as its variance across environments after the main effects of environmental means have been removed. Since the genotype main effect is constant, the stability variance is thus based on the residual ($GE_{ij} + e_{ij}$) matrix in a two-way classification. The stability statistic is termed "stability variance" (σ_i^2) and is estimated as follows:

$$\hat{\sigma}_i^2 = \frac{1}{(G-1)(G-2)(E-1)}[G(G-1)\sum_j (Y_{ij} - \overline{Y_{i.}} - \overline{Y_{.j}} + \overline{Y_{..}})^2 - \sum_i \sum_j (Y_{ij} - \overline{Y_{i.}} - \overline{Y_{.j}} + \overline{Y_{..}})^2]\text{..} \quad (7)$$

Where Y_{ij} is the mean yield of the i^{th} genotype in the j^{th} environment, $\overline{Y}_{j.}$ is the mean of the genotype *i* in all environments, $\overline{Y}_{.j}$ is the mean of all genotypes in j^{th} environments and $\overline{Y}_{..}$ is the mean of all genotypes in all environments. A genotype is called stable if its stability variance (σ_i^2) is equal to the environmental variance (σ_e^2) which means that σ_i^2=0. A relatively large value of (σ_i^2) will thus indicate greater instability of genotype *i*. As the stability variance is the difference between two sums of squares, it can be negative, but negative estimates of variances are not uncommon in variance component problems. Negative estimates of σ_i^2 may be taken as equal to zero as usual (Shukla, 1972). Homogeneity of estimates can be tested using Shukla's (1972) approximate test (Lin *et al*, 1986).

The stability variance is a linear combination of the ecovalence, and therefore both W_i and σ_i^2 are equivalent for ranking purposes (Wricke and Weber, 1980).

2.3.3.4 Cultivar performance measure (P_i).

Lin and Binns (1988a) defined the superiority measure (P_i) of the i^{th} test cultivar as the MS of distance between the i^{th} test cultivar and the maximum response as

$$P_i = [n(\overline{X}_i - \overline{M}_.)^2 + (\sum_{j=1}^{n}(X_{ij} - \overline{X}_{i.} - M_{j.} + \overline{M}_.)^2]/2n \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (8)$$

Where X_{ij} is the average response of the i^{th} genotype in the j^{th} environment, $\overline{X}_i$ is the mean deviation of genotype i, M_j is the genotype with maximum response among all genotypes in the j^{th} location, and n is the number of locations. The first term of the equation represents the genotype sum of squares and the second part the GE sum of squares. The smaller the value of P_i, the less is the distance to the genotype with maximum yield and the better the genotype. A pair wise GEI mean square between the maximum and each genotype is also calculated. This method is similar to the one used by Plaisted and Peterson (1959), except that, (a) the stability statistics are based on both the average genotypic effects and GEI effects and (b) each genotype is compared only with the one maximum response at each environment (Crossa, 1990).

2.3.4 Crossover interactions and nonparametric analysis.

Crossa (1990), Gregorious and Namkoong (1986) stated that GEI becomes very important in agricultural production, when there are changes in a genotype's rank over environments. These are called crossovers or qualitative interactions, in contrast to non-crossovers or quantitative interactions (Peto, 1982; Gail and Simon, 1985). With a qualitative interaction, genotype differences vary in direction among environments, whereas with quantitative interactions, genotypic differences change in magnitude but not in direction. If significant qualitative

interactions occur, subsets of genotypes are to be recommended only for certain environments, whereas with quantitative interactions the genotypes with superior means can be used in all environments. Therefore, it is important to test for crossover interactions (Baker, 1988).

Some advantages of nonparametric statistics compared to parametric ones are: reduction of the bias caused by outliers, no assumptions are needed about the distribution of the analyzed values, homogeneity of variances, and additivity (linearity) of effects are not necessary requirements (Hühn, 1966).

Further advantages are that nonparametric stability statistics are expected to be less sensitive to errors of measurement than parametric estimates and the addition or deletion of one or a few observations is not likely to cause great variation in the estimate as would be the case for stability statistics (Nassar and Hühn, 1987). Baker (1988), Virk and Mangat (1991) studied two statistical tests to determine crossover interaction in spring wheat and pearl millet respectively. The two tests were that of (a) Azzalini and Cox (1984) who developed a conservative test for changes in rank order among treatments in a two-way design. This test is based upon the null hypothesis that there is no crossover interaction. Thus, rejection of the null hypothesis implies that the treatments show crossover interactions, (b) Gail and Simon (1985) developed a test for crossover interactions between two treatments evaluated in a series of independent trials where error variances may be heterogeneous. Their method seems particularly appropriate to analysis of differences between two genotypes tested in a series of different environments.

2.3.5 Multivariate analysis methods

According to Crossa (1990) multivariate analysis has three main purposes: (a) to eliminate noise from the data pattern (i.e. to distinguish systematic from non-

systematic variation); (b) to summarize the data; and (c) to reveal a structure in the data. In contrast with classic statistical methods, the function of multivariate analysis is to elucidate the internal structure of the data from which hypotheses can be generated and later tested by statistical methods (Gauch, 1982a; Gauch, 1982b).

Multivariate analysis is appropriate for analysing two-way matrices of G genotypes and E environments. The response of any genotype in E environments may be conceived as a pattern in E-dimensional space, with the coordinate of an individual axis being the yield or other metric of the genotype in one environment.

Two groups of multivariate techniques have been used to elucidate the internal structure of genotype x environment interaction:

1. Ordination techniques, such as principal component analysis, principal coordinate's analysis, and factor analysis, assume that the data are continuous. These techniques attempt to represent genotype and environment relationships as faithfully as possible in a low dimensional space. A graphical output displays similar genotypes or environments near each other and dissimilar items are farther apart. Ordination is effective for showing relationships and reducing noise (Gauch, 1982b).
2. Classification techniques such as cluster analysis and discriminant analysis, seek discontinuities in the data. These methods involve grouping similar entities in clusters and are effective for summarizing redundancy in the data (Crossa, 1990).

2.3.5.1 Principal component analysis

Principal component analysis (PCA) is the most frequently used multivariate method (Crossa, 1990; Purchase, 1997). Its aim is to transform the data from one

set of coordinate axes to another, which preserves, as much as possible, the original configuration of the set of points and concentrates most of the data structure in the first principal component axis. Various limitations have been noted for this technique (Perkins, 1972; Williams, 1976; Zobel *et al*., 1988). Crossa (1990) pointed out that the linear regression method uses only one statistic, the regression coefficient, to describe the pattern of response of a genotype across environments, and most of the information is wasted in accounting for deviation. Principal component analysis (PCA) is a generalization of linear regression that overcomes this difficulty by giving more than one statistic, the scores on the principal component axes, to describe the response of a genotype (Eisemann, 1981).

2.3.5.2 Principal coordinates analysis

Principal coordinate analysis is a generalization of the PCA analysis in which any measure of similarity between individuals can be used; this type of analysis was first used by Gower (1966). Its objectives and limitations are similar to those of PCA, and also has the following advantages as pointed out by Crossa (1990): (a) it is trustworthy when used for data that include extremely low or high yielding sites; (b) it does not depend on the set of genotypes included in the analysis; and (c) it is simple to identify stable varieties from the sequence of graphic displays.

2.3.5.3 Factor analysis

Factor analysis is related to PCA, the “factors” of the former being similar to the principal components of the latter. A large number of correlated variables are reduced to a small number of main factors. Variation is explained in terms of general factors common to all variables and in terms of factors unique to each variable (Crossa, 1990).

2.3.5.4 Cluster analysis

Cluster analysis is a numerical classification technique that defines groups of clusters of individuals. The first is non-hierarchical classification, which assigns each item to a class. The second type is hierarchical classification, which groups the individuals into clusters and arranges these into a hierarchy for the purpose of studying relationships in the data (Crossa, 1990). Comprehensive reviews of the applications of cluster analysis to study GEI can be found in Lin *et al*. (1986) and Westcott (1987).

2.3.5.5. Additive main effects and multiplicative interaction (AMMI)

The additive main effect and multiplicative interaction (AMMI) method integrates analysis of variance and principal components analysis into a unified approach (Gauch, 1988). According to Gauch and Zobel (1988); Zobel *et al*. (1988) and Crossa *et al.* (1990), it can be used to analyse multilocation trials.
Zobel *et al*. (1988) pointed out that, considering the three traditional models, analysis of variance (ANOVA) fails to detect a significant interaction component, principal component analysis (PCA) fails to identify and separate the significant genotype and environment main effects, linear regression models account for only a small portion of the interaction sum of squares.

The AMMI method is used for three main purposes. The first is model diagnoses, AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool of diagnosing other models as sub cases when these are better for particular data sets (Gauch, 1988). Secondly, AMMI clarifies the GEI. AMMI summarizes patterns and relationships of genotypes and environments (Zobel *et al*., 1988; Crossa *et al.*, 1990). The third use is to improve the accuracy of yield estimates. Gains have been obtained in the accuracy of yield

estimates that are equivalent to increasing the number of replicates by a factor of two to five (Zobel *et al*., 1988; Crossa, 1990). Such gains may be used to reduce testing cost by reducing the number of replications, to include more treatments in the experiments, or to improve efficiency in selecting the best genotypes.

The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the genotype-environment interaction. It has proven useful for understanding complex GEI. The results can be graphed in a useful biplot that shows both main and interaction effects for both the genotypes and environments.
AMMI combines analysis of variance (ANOVA) into a single model with additive and multiplicative parameters.

The model equation is:

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij} \qquad (9)$$

Where Y_{ij} is the yield of the i^{th} genotype in the j^{th} environment; μ is the grand mean; G_i and E_j are the genotype and environment deviations from the grand mean, respectively; λ_k is the eigenvalue of the PCA analysis axis k; α_{ik} and γ_{jk} are the genotype and environment principal component scores for axis k; n is the number of principal components retained in the model and e_{ij} is the error term.

The combination of analysis of variance and principal components analysis in the AMMI model, along with prediction assessment, is a valuable approach for understanding GEI and obtaining better yield estimates. The interaction is explained in the form of a biplot display where, PCA scores are plotted against each other and it provides visual inspection and interpretation of the GEI

components. Integrating biplot display and genotypic stability statistics enable genotypes to be grouped based on similarity of performance across diverse environments.

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CHAPTER 3

Comparison between different yield stability procedures in maize

3.1 Abstract

Nine late maturing maize hybrids, with 125 to 134 relative maturity RM (days), and fourteen hybrids with ultra short to medium maturity, 111 to 124 RM, were evaluated for genotype x environment interaction (GEI) and yield stability across 42 environments during 2001 to 2003. The objectives were to estimate the components of variance associated with the first and second order interactions and to determine their effects. Several statistical analyses were conducted to determine yield stability: (1) coefficient of variability (CV_i); (2) mean ($\overline{X}$); (3) stability variance ($\sigma^2{}_i$); (4) ecovalence (W_i); (5) regression coefficient (b_i); (6) deviation from regression (S^2_{di}); (7) cultivar superiority measure (P_i); (8) variance of ranks (S1); (9) AMMI stability value (ASV) as described by Purchase (1997).

A standard multi-factor analysis of variance test showed the main effects due to years, locations and the first order interactions (year x location) were highly significant. The main effect for genotype, first order interaction (genotype x locations), (genotype x year) and second order interaction (genotype x locations x year) were highly significant. The highly significant interactions indicate that genotypes need to be tested in several years and locations in order to select stable genotypes.

Spearman's rank correlation coefficient between the stability parameters indicated that Shukla's stability variance (σ^2_i), Wricke's ecovalence (W_i), Eberhart & Russell's deviation from regression (S^2_{di}), the non-parametric stability measure of Nassar & Hühn, (S1) mean absolute difference of ranks and AMMI stability value (ASV) had a highly significant correspondence over the three years of study. The ASV and Nassar & Hühn's (S1) were not significantly correlated.

No significant rank correlation between Lin & Binns's superiority measure (P_i) and Finlay & Wilkinson's procedure (b_i) with the other procedures were found.
The last two procedures are not recommended for use on their own as a measurement of yield stability.

3.2 Introduction

Dry land maize is the most important crop produced in South Africa. This is also the most important crop for breeding purposes. Maize is produced on between 2.5 and 3.2 million hectares annually and the national average yield varies between 2.2 and 2.8 ton per ha^{-1}. The considerable variation in soil and climate has resulted in significant variation in yield performance of maize hybrids annually, thus genotype x environment interaction (GEI) is an important issue facing plant breeders and agronomists in South Africa. In assessing the performance of maize hybrids in South Africa, it is essential that the yield stability of such hybrids, in addition to their yield performance, be determined in order to make specific selections and recommendations to maize producers.

Selection of genotypes is based on the assessment of their phenotypic value in varying environments. Genotype x environment interaction (GEI), which is

associated with the differential performance of genetic materials, tested at different locations and in different years and its influence on the selection of and recommendation of genotypes has long been recognized (Lin *et al*. 1986; Becker and Léon, 1988; Crossa, 1990; Purchase *et al.* 2000). Evaluation of genotypic performance at a number of locations provides useful information to determine their adaptation and stability (Crossa, 1990). Measuring GEI helps to determine an optimum breeding strategy, to breed for specific or general adaptation, which depends on the expression of stability under a limited or wide range. (Crossa, 1990; Ramagosa and Fox, 1993).

Lin *et al*. (1986); Becker and Léon (1988), Crossa (1990) and Hohls (1995) discussed a wide range of methods available for the analysis of GEI and stability and it can be divided into four groups: 1) the analysis of components of variance, 2) stability analysis, 3) qualitative methods and 4) multivariate methods. Plant breeders generally agree on the importance of high yield stability, but there is less accord on the most appropriate definition of "stability" and the methods to measure and to improve yield stability (Becker and Léon, 1988). Different concepts and definitions of stability have been described over the years (Lin *et al*., 1986; Becker and Léon, 1988).

Lin *et al*. (1986) identified three concepts of stability (see page 13): Type 1 is also called a static or a biological concept of stability (Becker and Léon, 1988). It is useful for quality traits, disease resistance, or for stress characters like winter hardiness. Parameters used to describe this type of stability are coefficient of variability (CV_i) used by Francis and Kannenburg (1978) for each genotype as a stability parameter and the genotypic variances across environments (s_i^2).

Type 2 is also called the dynamic or agronomic concept of stability (Becker and Léon, 1988). A stable genotype has no deviations from the general response to

environments and thus permits a predictable response to environments. A regression coefficient (b_i) and $b_i = 0$ is more stable (Finlay and Wilkinson, 1963) and Shukla's (1972) stability variance (σ^2_i) can be used to measure type 2 stability.

Type 3 is also part of the dynamic or agronomic stability concept according to Becker and Léon (1988). Methods to describe type 3 stability are the methods of Eberhart and Russel (1966) and Perkins and Jinks (1968). Eberhart and Russel (1966) use the regression coefficient (b_i) and $b_i = 1$ is more stable and the deviation from regression ($S^2_{d_i}$).

Becker and Léon (1988) stated that all stability procedures based on quantifying GEI effects belong to the dynamic concept. This includes the procedures for partitioning the GEI of Wricke's (1962) ecovalence and Shukla's (1972) stability of variance, procedures using the regression approach such as proposed by Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Perkins and Jinks (1968), as well as non-parametric stability analyses.

Lin & Binns (1988a; 1988b) proposed the cultivar performance measure (P_i) and defined P_i of genotype i as the mean square of distance between genotype i and the genotype with the maximum response. The smaller the estimated value of P_i, the less its distance to the genotype with maximum yield, and thus the better the genotype.

The main problem with stability statistics is that they don't provide an accurate picture of the complete response pattern (Hohls, 1995). The reason is that a genotype's response to varying environments is multivariate (Lin *et al.,* 1986) whereas the stability indices are usually univariate.

Through multivariate analysis, genotypes with similar responses can be clustered, and thus the data can be summarized and analysed more easily (Gauch, 1982; Crossa, 1990). Characterization of the response patterns of genotypes to environmental change enables extrapolation to a much wider range of environments than those tested (Hohls, 1995).

One of the multivariate techniques is the AMMI model, (additive main effects and multiplicative interaction method). It combines the analysis of variance of genotypes and the environment main effects with principal component analysis of the GEI into a unified approach (Gauch, 1988; Zobel *et al*., 1988; Gauch and Zobel, 1996).

The results can be graphically represented in an easily interpretable and informative biplot that shows both main effects and GEI. The AMMI model has been used extensively with great success over the past few years to analyse and understand various crop genotype x environment interaction (Crossa, 1990; Yau, 1995; Yan and Hunt, 1998).

The objectives of this study were to estimate the component of variance associated with the first and second order interactions and to determine their effects, and to compare the various stability statistics to determine the most suitable method for assessing the maize genotype's yield stability in the major maize growing areas of South Africa.

3.3. Materials and methods

3.3.1 Materials

Twenty-three hybrids, listed in Table 3.1, were evaluated over a period of three years from 2001 to 2003 42 environments (14 per year) (Table3.2). These environments were spread throughout the major maize growing areas of South Africa. The relative maturity of these hybrids ranged from very early, 111 RM, to late, 134 RM. Nine hybrids were full season (125-134 RM), eight were early to medium season (120-124 RM) and six were super early season (111-118 RM). The 23 hybrids were evaluated for grain yield, harvest moisture, test weight, lodging and final stand in the 14 rain fed environments from 2001 to 2003 (Table 3.2), evenly spread through the maize growing area of South Africa.

The experimental layout was a randomized complete block design (RCBD) with two replications. Trials were planted according to the practises of the respective farmer (co-operator) at each site. See Table 3.2 for row widths, plot lengths, rows per plot, plot sizes and plant densities.

Management and fertilization at each site were done according to the practises of each farmer (co-operator) for his farm and the specific field. Fertilization rates with planting were inflated with about 10% to insure good and even stands and development.

All the sites with row widths of 0.91m or 0.75m were planted with a vacuum precision planter and no thinning was necessary. The 1.5m and 2.1m row width trials were planted with a cone planter at 20% higher density and then thinned at, V4 to V6 stage (5-7 leaves visible), to the planned density for that area. The plant

population for research trials were planted at 10-15% higher density than farming practises for the area.

Table 3.1 Entry number, hybrid code, relative maturity, brand name and owner company of the 23 hybrids used in the study

ENTRY	CODE	RM	BRAND NAME	COMPANY	COLOUR
1	CRN 3505	128	CARNIA	MONSANTO	WHITE
2	CRN 3549	130	CARNIA	MONSANTO	WHITE
3	PAN 6573	130	PANNAR	PANNAR	WHITE
4	SNK 2551	132	SENSAKO	MONSANTO	WHITE
5	CRN 3760	133	CARNIA	MONSANTO	YELLOW
6	CRN 4760B	133	CARNIA	MONSANTO	YELLOW
7	DKC 80-10	124	DEKALB	MONSANTO	YELLOW
8	PAN 6568	133	PANNAR	PANNAR	YELLOW
9	SNK 8520	134	SENSAKO	MONSANTO	YELLOW
10	SB 7551	125	EXPERIMENTAL	MONSANTO	WHITE
11	PAN 6615	122	PANNAR	PANNAR	WHITE
12	PHB 3203W	120	PIONEER	PHI	WHITE
13	PHB 32A03	117	PIONEER	PHI	WHITE
14	SNK 6025	120	SENSAKO	MONSANTO	WHITE
15	SA 7401	124	EXPERIMENTAL	MONSANTO	YELLOW
16	SNK 6726	117	SENSAKO	MONSANTO	YELLOW
17	SA 7101	121	EXPERIMENTAL	MONSANTO	YELLOW
18	DKC 63-20	113	DEKALB	MONSANTO	YELLOW
19	DKC 61-24	111	DEKALB	MONSANTO	YELLOW
20	EXP 962	112	EXPERIMENTAL	MONSANTO	YELLOW
21	DK 617	111	DEKALB	MONSANTO	YELLOW
22	PAN 6710	118	PANNAR	PANNAR	YELLOW
23	DKC 71-21	121	DEKALB	MONSANTO	WHITE

Table 3.2 Fourteen dryland locations that were used in the study from 2001 to 2003

LOC #	LOC_NAME	LAT*	LONG*	PROVINCE	PLOT M^2	DENSITY
1	DELMAS	-26.15	28.68	MPUMALANGA	12.00	44000
2	PETIT	-26.90	28.37	GAUTENG	12.00	44000
3	FICKSBURG	-28.86	27.90	FREE STATE	14.56	44000
4	MEERLUS	-26.31	29.53	MPUMALANGA	14.56	44000
5	RIETGAT	-26.15	26.17	NORTH WEST	14.56	28000
6	BERGVILLE	-28.73	29.37	KWA ZULU NATAL	14.56	44000
7	ERMELO	-26.51	29.99	MPUMALANGA	14.56	44000
8	BOTHAVILLE	-27.39	26.62	FREE STATE	16.50	22000
9	OGIES	-26.05	29.50	MPUMALANGA	14.56	44000
10	PIET RETIEF	-27.00	30.80	MPUMALANGA	14.56	44000
11	WONDERFONTEIN	-25.85	29.80	MPUMALANGA	14.56	44000
12	KROONSTAD	-27.66	27.23	FREE STATE	16.50	22000
13	KAMEEL	-26.40	25.10	NORTH WEST	23.00	18000
14	VILJOENSKROON	-27.21	26.95	FREE STATE	16.50	22000

3.3.2 Measurements

The trials were harvested with a New Holland TR88 double plot combine specially designed to harvest and record data for two plots at a time. Grain mass kg per plot (SHW), moisture percentage (MST) and test weight (TWT) were recorded. All the plots were counted to get the final stand per plot (FNS), as well as the root lodging (RTLG) and stalk lodging (STLG). The relative maturity were determined with linear regression from the known relative maturities of the commercial hybrids in the experiment, the hybrids PAN 6568 (133 RM), CRN 3549 (130 RM), DKC 80-10 (124 RM), PHB 3203W (120 RM), PAN 6710 (118 RM) and DKC 61-24 (111 RM) were used to determine the RM of other entries. Only the grain yield was used for the stability analysis.

3.3.3 Statistical analysis

An analysis of variance (ANOVA) was done for each location separately as randomized complete block design. A combined analysis of variance was done from the mean data from each location, to create the means data for the different statistical analyses methods. The software package, Agrobase™ 1999 (Agronomix Software Inc.), was used for most statistical analyses. Bartlett's (1974) test was used to determine the homogeneity of variances between environments to determine the validity of the combined analysis of variance on the data.

The following were determined from the ANOVA analysis, the effects of the genotypes, locations and years as well as their first and second order interactions. Genotypes were assumed to be fixed, and year and location effects random. The ANOVA method for estimating variance components consists of equating mean squares to their expectations and solving the resulting set of simultaneous equations as shown in Tables 3.3 and 3.4 and are based on the model provided by Allard (1960), which was developed by Comstock and Moll (1963) for the determination of interaction variance components.

Table 3.3 Form of variance analysis and mean square expectations for GEI

Source	DF	MS	Expected mean square
Years (Y)	(Y-1)		
Locations (L)	(L-1)		
Y x L	(Y-1)(L-1)		
Reps in Loc and Years	LY(R-1)		
Genotypes (G)	(G-1)	MS5	$\sigma^2_e + r\sigma^2_{gly} + rl\sigma^2_{gy} + ry\sigma^2_{gl} + rly\sigma^2_g$
G x L	(G-1)(L-1)	MS4	$\sigma^2_e + r\sigma^2_{gly} + ry\sigma^2_{gl}$
G x Y	(G-1)(Y-1)	MS3	$\sigma^2_e + r\sigma^2_{gly} + rl\sigma^2_{gy}$
G x L x Y	(G-1)(L-1)(Y-1)	MS2	$\sigma^2_e + r\sigma^2_{gly}$
Error	LY(G-1)(R-1)	MS1	σ^2_e

Where, Y, L, G and R are the number of years, locations, genotypes and replications, respectively. The σ^2_e and σ^2_g are components of variance of error and genotypes respectively. Combinations of the subscript identify the components, for the interactions. MS1 to MS5 are the observed values of the various mean squares.

Table 3.4 Estimates of variance components and methods of determining GEI

Variance component	Methods of Determination
Genotypes (σ^2_g)	(MS5+MS2-MS3-MS4) / *rly*
Genotypes x locations (σ^2_{gl})	(MS4-MS2) / *ry*
Genotypes x years (σ^2_{gy})	(MS3-MS2) / *rl*
Genotypes x locations x years (σ^2_{gly})	(MS2-MS1) / *r*
Error (σ^2_e)	MS1

Where, MS1 to MS5 are the values of the appropriate mean squares as indicated in Table 3.3; r, l, and y are the numbers of replicates, locations, and years, respectively, in which the hybrids were evaluated.

The following analyses of the stability models were performed using Agrobase 1999™ (Agrobase, 1999).

The Coefficient of variability (CV_i), (Francis and Kannenburg, 1978).

Lin and Binn's cultivar performance measure (P_i), (Linn and Binns, 1988a).

Shukla's procedure of stability (σ^2_i), (Shukla, 1972).

Finlay and Wilkinson's joint regression analysis (b_i), (Finlay and Wilkinson, 1963).

Eberhart and Russell's joint regression analysis (S^2_{di}), (Eberhart and Russell, 1966).

Wricke's ecovalence (W_i), (Wricke, 1962).

Mean absolute difference (S1) and variance of ranks (S2), (Nassar and Hühn, 1987).

The AMMI stability value (ASV) as described by Purchase (1997).

The AMMI model does not make provision for a quantitative stability measure, such a measure is essential in order to quantify and rank genotypes according their yield stability, the following measure was proposed by Purchase (1997):

$$\text{AMMI Stability Value (ASV)} = \sqrt{\left[\frac{IPCA1SumofSquares}{IPCA2SumofSquares}(IPCA1score)\right]^2 + [IPCA2score]^2}$$

In effect the ASV is the distance from zero in a two dimensional scattergram of IPCA 1 (Interaction Principal Component Analysis axis 1) scores against IPCA 2 scores. Since the IPCA 1 score contributes more to G x E sum of squares, it has to be weighted by the proportional difference between IPCA 1 and IPCA 2 scores to compensate for the relative contribution of IPCA 1 and IPCA 2 total G x E sum of squares. The distance from zero is then determined by using the theorem of Pythagoras.

To statistically compare between the above stability analysis procedures, Spearman's coefficient of rank correlation (r_s) was determined (Steel and Torrie, 1980). Consider n genotypes are arranged in the same following order to two stability parameters X_i indicates the ranking order (or number) of the i^{th} genotype for the first parameter, Y_i, indicates the ranking order of the i^{th} genotype of the second parameter, then $d_i = X_i - Y_i$ (i = 1,2,3…..n) and Spearman's rank correlation coefficient (r_s) (Steel and Torrie, 1980) can be described as:

$$r_s = \frac{6\sum d_i^2}{n(n^2-1)}$$

All the genotypes were ranked according the assigned values from each procedure's analysis and definition. The ranked orders were used to determine Spearman's ranked correlation coefficient between the different procedures. Ranking numbers are whole numbers and when two or more equal numbers occur, the average of the ranking numbers that they otherwise would have received is ascribed to each genotype.

The significance of r_s was tested by means of Student's t test (Steel & Torrie, 1980) where:

$$t = \frac{r_s \sqrt{n-2}}{\sqrt{1-r_s^2}}$$

with n-2 degrees of freedom. If $t \geq t_{(0.01:n-2)}$, the null hypothesis is discarded and r_s is described as highly significant.

3.4 Results and discussion

3.4.1 Analysis of variance and estimation of variance components.

The relative performance of genotypes based on the mean grain yield and other agronomic traits over years and locations are presented in Table 3.5. Yield, moisture and test weight performances are ranked. Grain yield is given in quintals ha^{-1} (ton $ha^{-1} = \frac{\text{quintals ha}^{-1}}{10}$). The first ranked hybrid for grain yield is DKC 80-10 with CRN 4760B ranked second and CRN 3505 ranked third. The first two are yellow hybrids and the third one a white hybrid. The hybrid with the highest moisture content (MST) was CRN 4760B (133 RM) and DK 617 the lowest moisture content (111 RM). The best hybrid for test weight (TWT) was SNK 8520 (orange yellow flint grain) and the worst one was PAN 6710 (soft yellow dent).

The analysis of variance (ANOVA) is shown in Table 3.7 and the partitioning of the sum of squares of the components indicated locations to be 53.8% of the total variation, 22.5% due to year x location, 6.3% due to genotype x year, 9.7% due to genotype x year x location, year, genotype and error were very low with 0.2%, 2.5% and 3.6% respectively. This indicates the big influence of environment on yield performance of maize hybrids in South Africa. The relatively large proportion of genotype x environment variance, more than double, when compared to that of genotypes as main effect is a very important consequence.

Main effects due to year, location, year x location, genotypes, genotypes x year, genotype x location, genotype x year x location and rep in loc x year were all highly significant (P<0.01) for grain yield (Table 3.7)

Table 3.6 indicates the mean yield, ranking and CV of the 23 hybrids evaluated at 42 sites in the main maize growing areas of South Africa from 2001-2003.
The hybrid with the lowest coefficient of variation across the years and locations was SNK 8520, with a CV of 35.3%, followed by CRN 4760B with 38.7% and DKC 80-10 next with a CV of 39.3%.

When individual estimates of variance for grain yield (Table 3.8) were expressed as a percent of the total variation (σ^2_{g+} σ^2_{gy+} σ^2_{gl+} σ^2_{gly+} σ^2_{e}) the σ^2_{g} component accounted for 8% of the total variation. The σ^2_{gy} was 1.7% and σ^2_{gl} was 6.83% of the total variation, indicating that the genotypes were less consistent over locations than over years. This means that location selection needs more effort. All the components were highly significant (P<0.01) and the biggest variation came from σ^2_{gly} and σ^2_{e} with 52.4% and 32% of the total variation respectively. The importance of the σ^2_{gly} component indicates that factors such as rainfall, temperature, and disease incidence can result in conditions unique to each year-location combination and that the genotypes respond differently to these

conditions. The very large σ^2_{gly} component is not uncommon for South African conditions and that is why testing over more years and many environments is very important (Hohls, 1995).

Table 3.5 Mean performance of 23 hybrids, for different traits, over years and locations (Yield, MST and TWT are ranked)

Entry	Code	Yield	Rank	MST	Rank	TWT	Rank	FNS	STLG	RTLG
1	CRN 3505	57.58	3	18.89	7	74.81	6	39.24	1.58	0.37
2	CRN 3549	52.76	12	18.80	9	74.39	10	38.74	1.76	0.44
3	PAN 6573	49.15	20	19.44	5	73.69	15	39.36	1.68	0.79
4	SNK 2551	54.81	7	19.25	6	74.25	12	37.73	2.61	0.82
5	CRN 3760	54.79	8	20.23	2	74.92	5	37.33	1.23	0.42
6	CRN 4760B	57.99	2	20.57	1	74.51	7	38.10	0.64	0.73
7	DKC 80-10	62.27	1	17.22	11	75.25	4	40.67	0.87	0.2
8	PAN 6568	56.01	6	19.99	4	72.79	20	40.76	1.54	0.62
9	SNK 8520	56.15	5	20.21	3	77.17	1	37.69	1.07	0.81
10	SB 7551	53.58	11	18.88	8	73.91	13	39.35	2.83	0.77
11	PAN 6615	47.79	21	16.55	13	73.29	17	39.77	2.19	0.51
12	PHB 3203W	49.89	18	15.59	15	74.45	8	40.85	0.89	0.3
13	PHB 32A03	47.00	22	14.41	18	75.81	3	40.44	0.85	0.35
14	SNK 6025	45.66	23	14.31	19	73.2	18	40.82	1.43	0.2
15	SA 7401	56.24	4	17.76	10	74.39	9	40.75	0.48	0.13
16	SNK 6726	52.52	13	14.95	17	75.95	2	40.36	0.42	0.19
17	SA 7101	54.64	9	16.68	12	73.69	14	40.86	0.5	0.2
18	DKC 63-20	52.46	14	13.42	21	73.52	16	38.57	0.4	0.2
19	DKC 61-24	51.9	15	13.43	20	74.38	11	40.56	0.38	0.32
20	EXP 962	50.33	17	13.36	22	72.48	21	39.15	0.49	0.21
21	DK 617	50.34	16	13.14	23	73.01	19	40.32	0.52	0.13
22	PAN 6710	53.91	10	14.98	16	70.63	23	39.48	1.87	0.48
23	DKC 71-21	49.67	19	15.85	14	71.68	22	39.42	1.56	0.45

Yield=quintals ha, MST=moisture, TWT=test weight, FNS=Final stand count, STLG=stalk lodge count, RTLG=root lodge count.

Table 3.6 Mean yield (quintals ha^{-1}) and CV of the 23 hybrids evaluated at 42 locations in South Africa for the period 2001-2003

Entry	Code	Yield*	Rank	CV
7	DKC 80-10	62.27	1	39.3
6	CRN 4760B	57.99	2	38.7
1	CRN 3505	57.58	3	47.3
15	SA 7401	56.24	4	43.4
9	SNK 8520	56.15	5	35.3
8	PAN 6568	56.01	6	41.8
4	SNK 2551	54.81	7	52.0
5	CRN 3760	54.79	8	45.6
17	SA 7101	54.64	9	42.2
22	PAN 6710	53.91	10	45.3
10	SB 7551	53.58	11	48.8
2	CRN 3549	52.76	12	45.2
16	SNK 6726	52.52	13	43.4
18	DKC 63-20	52.46	14	44.7
19	DKC 61-24	51.90	15	42.2
21	DK 617	50.34	16	43.5
20	EXP 962	50.33	17	43.8
12	PHB 3203W	49.89	18	54.1
23	DKC 71-21	49.67	19	50.5
3	PAN 6573	49.15	20	51.0
11	PAN 6615	47.79	21	54.6
13	PHB 2A03	47.00	22	55.7
14	SNK 6025	45.66	23	51.3

Grand mean = 52.932 R-squared = 0.9641 CV = 12.66%

LSD for ENTRY = 1.7031 S.E.D. = 1.0344

t (1-sided a=0.050, 924 df) = 1.6465 MSE = 44.93788

*Yield=quintals ha^{-1}

Table 3.7 Combined ANOVA for yield and the percentage sum of squares of the 23 hybrids tested at 42 environments over a period of three years 2001-2003

Source	df	SS	SS%	MS	F-value	Pr> F
Total	1931	1158092.4				
YEAR	2	2263.3	**0.2**	1131.633	25.18	0.0000
LOC	13	623229.8	**53.8**	47940.756	1066.82	0.0000
YEAR x LOC	26	260953.7	**22.5**	10036.682	223.35	0.0000
GENOTYPE	22	28581.0	**2.5**	1299.138	28.91	0.0000
GENOTYPE x YEAR	44	11632.7	**1.0**	264.379	5.88	0.0000
GENOTYPE x LOC	286	73219.5	**6.3**	256.012	5.7	0.0000
GENOTYPE x YEAR x LOC	572	112483.6	**9.7**	196.65	4.38	0.0000
REP in YEAR x LOC	42	4206.2	**0.3**	100.147	2.23	0.0000
Residual	924.0	41522.6	**3.6**	44.938		

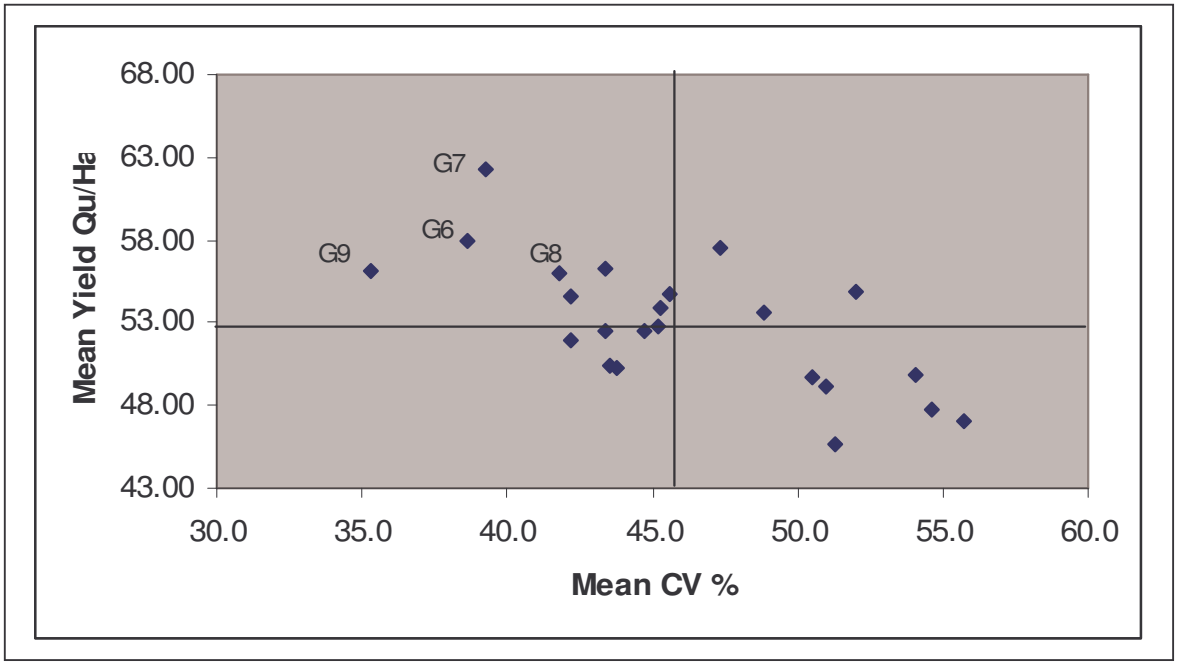
Table 3.8 Estimates of variance components for grain yield, genotypes and their interactions with locations and years.

Variance component	Method of Determination	Yield	
Genotypes (σ^2_g)	(MS5+MS2-MS3-MS4) / *rly*	11.61	8.02%
Genotypes x locations (σ^2_{gl})	(MS3-MS2) / *ry*	9.89	6.83%
Genotypes x years (σ^2_{gy})	(MS4-MS2) / *rl*	2.42	1.70%
Genotypes x locations x years (σ^2_{gly})	(MS2-MS1) / *r*	75.86	52.42%
Error (σ^2_e)	MS1	44.94	31.05%

3.4.2 Francis and Kannenberg's coefficient of variability (CV_i)

The mean CV analysis introduced by Francis (1977) was designed to aid in studies on the physiological basis of yield stability. He introduced a simple graphical approach to assess performance and stability concurrently. It measures the performance and CV for each genotype over all environments and the mean yield plotted against the CV. It was found to characterize genotypes in groups rather than individually (Francis and Kannenberg, 1978). In Figure 3.1 the mean yield is

plotted against the CV. High yield and small variation group of genotypes appear the most desirable using any approach. The stable genotype is the one that provides a high yield performance and consistent low CV. According to this definition the following hybrids fall into the high yield and low variation group and can be considered the most stable SNK 8520 (G9), DKC 80-10 (G7), CRN 4760B (G6) and PAN 6568 (G8).



G7=Entry 7, DKC 80-10; G9=Entry 9, SNK 8520; G6=Entry 6, CRN 4760B and G8=Entry 8, PAN 6568.

Figure 3.1 Mean yield (qu/ha) plotted against CV (%) from data on 23 hybrids and 42 locations over a period of three years.

3.4.3 Lin and Binns's cultivar performance measure (P_i)

As a stability statistic the cultivar performance measure (P_i) of Lin & Binns (1988a) is estimated by the square of differences between a genotype's and the maximum genotype mean at a location, summed and divided by twice the number of locations. The genotypes with the lowest (P_i) values are considered the most

stable. Table 3.9 presents the cultivar performance measure (P_i) for grain yield of the 23 hybrids tested at 14 locations per year for three years, 2001-2003.

Table 3.9 Lin & Binns's (1988a) cultivar performance measure (P_i) for the 23 hybrids tested at 42 locations, for the years 2001-2003

Entry No.	Code	P_i	Rank	Mean Yield	Rank
7	DKC 80-10	43.66	1	62.27	1
1	CRN 3505	77.29	2	57.58	3
9	SNK 8520	91.15	3	56.15	5
8	PAN 6568	93.45	4	56.01	6
6	CRN 4760B	103.26	5	57.99	2
15	SA 7401	103.95	6	56.24	4
4	SNK 2551	110.47	7	54.81	7
17	SA 7101	119.10	8	54.64	9
2	CRN 3549	122.37	9	52.76	12
5	CRN 3760	124.79	10	54.79	8
22	PAN 6710	137.85	11	53.91	10
10	SB 7551	137.86	12	53.58	11
18	DKC 63-20	141.74	13	52.46	14
16	SNK 6726	147.45	14	52.52	13
19	DKC 61-24	157.58	15	51.90	15
21	DK 617	174.59	16	50.34	16
3	PAN 6573	184.48	17	49.15	20
20	EXP 962	186.02	18	50.33	17
23	DKC 71-21	189.80	19	49.67	19
12	PHB 3203W	198.73	20	49.89	18
11	PAN 6615	217.58	21	47.79	21
13	PHB 32A03	258.95	22	47.00	22
14	SNK 6025	262.49	23	45.66	23

From this analysis, the most stable cultivar ranked first for P_i and for mean yield was DKC 80-10 followed by CRN 3505 ranked second for P_i and for mean yield. Others with low P_i values and high ranking for mean yield was SNK 8520, PAN 6568, CRN 4760B and SNK 2551. The ranks of the P_i measure and mean yield are in agreement (Table 3.9) and indicate that the P_i measure is more an indication of

performance and not really an indication of stability. The most unstable hybrids according this analysis were SNK 6025, PHB 32A03, PAN 6615 and PHB 3203W which are also very early maturity hybrids (Table 3.1).

3.4.4 Shukla's stability variance procedure (σ_i^2).

Shukla's (1972) stability variance values and the stability ranking as well as the mean yield with its ranking are given in Table 3.10. The most stable hybrids as indicated by this stability parameter were CRN 3549, PAN 6615, DKC 63-20, PAN 6573 and SA 7401. The hybrids with a poor stability according this procedure were SNK 2551, CRN 4760B, CRN 3505, PHB 3203W and SNK 8520. The hybrids CRN 4760B, CRN 3505 were respectively ranked second and third for mean yield. The hybrid DKC 80-10, ranked first for mean yield, showed intermediate stability and ranked eighth for Shukla's stability variance.

Table 3.10 Stability variance (Shukla, 1972) results for the 23 Hybrids tested over three years 2001-2003 at 42 locations

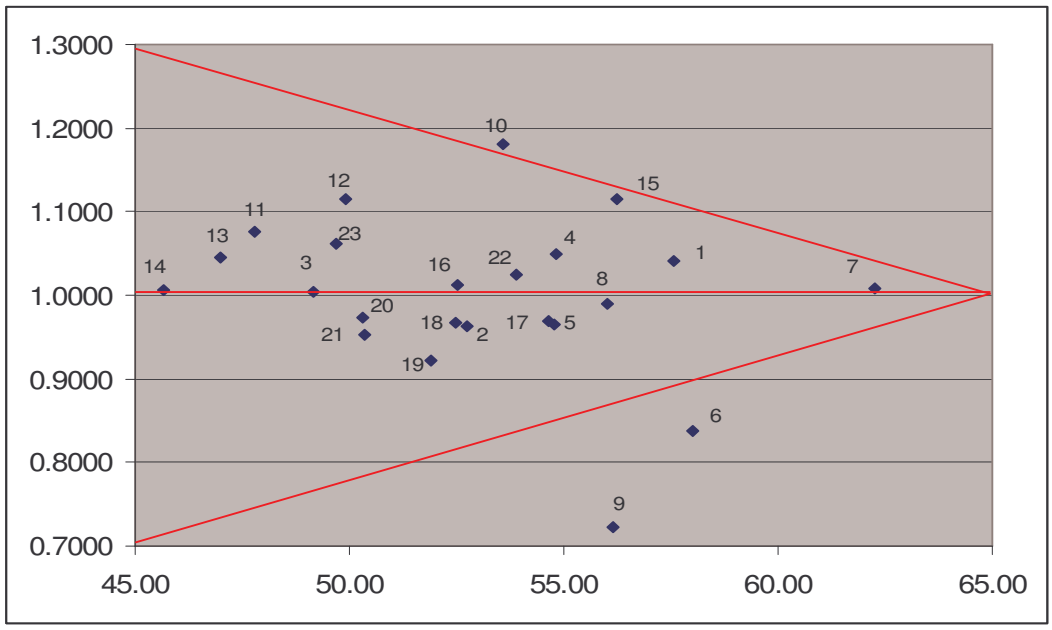
Entry	Code	Stability Variance	Rank	Mean Yield	Rank
2	CRN 3549	83.66	1	52.76	12
11	PAN 6615	97.82	2	47.79	21
18	DKC 63-20	114.25	3	52.46	14
3	PAN 6573	128.01	4	49.15	20
15	SA 7401	141.55	5	56.24	4
21	DK 617	161.53	6	50.34	16
16	SNK 6726	167.96	7	52.52	13
7	DKC 80-10	171.00	8	62.27	1
20	EXP 962	184.04	9	50.33	17
23	DKC 71-21	192.55	10	49.67	19
22	PAN 6710	211.94	11	53.91	10
17	SA 7101	218.77	12	54.64	9
19	DKC 61-24	235.81	13	51.90	15
10	SB 7551	237.15	14	53.58	11
14	SNK 6025	241.52	15	45.66	23
5	CRN 3760	259.53	16	54.79	8
8	PAN 6568	262.07	17	56.01	6
13	PHB 32A03	337.19	18	47.00	22
9	SNK 8520	372.23	19	56.15	5
12	PHB 3203W	384.07	20	49.89	18
1	CRN 3505	446.04	21	57.58	3
6	CRN 4760B	551.02	22	57.99	2
4	SNK 2551	688.84	23	54.81	7

3.4.5 Finlay and Wilkinson's joint regression analysis (b_i).

According to Finlay and Wilkinson (1963), regression coefficients approximating to 1.0 indicate average stability, but must always be associated and interpreted with the genotype mean yield to determine adaptability. When the regression coefficients are approximating to 1.0 and are associated with high yield mean, genotypes are adapted to all environments. When associated with low mean yields, genotypes are poorly adapted to all environments. Regression coefficients above 1.0 indicate genotypes with increasing sensitivity to environmental change, showing below average stability and great specific adaptability to high yielding environments. Regression coefficients decreasing below 1.0 provide a measure of

greater resistance to environmental change, having above average stability but showing more specific adapted to low yielding environments.

Figure 3.2 indicates that DKC 80-10 (entry 7), CRN 3505 (entry 1) and PAN 6568 (entry 8) are the most stable and adapted to most of the environments. SB 7551 (entry 10), PHB 3203W (entry 12), PAN 6615 (entry 11) and SA 7401 (entry 15) are below average stability but specifically adapted to high yielding environments. Entries 21, 19 and 9 which are DK 617, DKC 61-24 and SNK 8520 respectively, have above average stability, but are more specifically adapted to lower yielding environments. Entries 3, 13 and 14, which are PAN 6573, PHB 32A03 and SNK 6025 respectively, are not adapted to any of the environments, and are low yielding. The other hybrids in the centre of the triangle are of average stability according this procedure (see Figure 2.1 for the graphical explanation of Finlay and Wilkinson's model).



Note: 1, 2, 3 ….n = Entry nr. of hybrids see Table 3.1; Regression coefficient plotted on Y-axis and mean yield plotted on X-axis

Figure 3.2 Regression coefficients plotted against the mean yield

3.4.6 Eberhart & Russell's joint regression analysis.

The Eberhart & Russell (1966) procedure involves the use of joint linear regression where the yield of each genotype is regressed on the environmental mean yield. The analysis of variance for the regression model is presented in Table 3.11. The sums of squares due to environments and genotype x environment are partitioned into environments (linear), genotype x environment (linear) and deviations from the regression model. The genotype's performance is generally expressed in terms of three parameters, mean yield ($\bar{x}$), regression coefficient (b) and the deviation ($S^2_{d_i}$) from the regression. According to this model a stable genotype should have a high mean yield, b = 1.0 and $S^2_{d_i}$ = 0. It is however specifically the deviation from the regression ($S^2_{d_i}$) which is used as a measure of a genotype's stability across environments. In Table 3.12 the results of regressing the genotype mean yield on the environmental mean yield over three years are indicated.

Table 3.11 Analysis of variance for linear regressions of hybrid mean yield on environmental mean yield over three years 2001-2003

Source	df	SS	MS	F-value	Pr> F
Total	1931	120839.41			
Genotypes	22	4763.23	216.51	5.27	0.0000
E+ in G x E	299	116076.18	388.22		
E (linear)	1	103872.32			
G x E (linear)	22	871.67	39.62	0.96	0.5094
Pooled deviation	276	11332.19	41.06		
Residual	1610	13158.43	8.17		

Grand mean = 52.934 R-squared = 0.9024 CV = 13.23%

In Table 3.11 the G x E (linear) sum of squares were not as large portion of the G x E interaction when compared with the environment E (linear) sum of squares and the residual sum of squares. Hence, only the deviation mean square was considered important. Genotypes were highly significant different from each other but the G x E (linear) interaction was not significant.

In Table 3.12 the stability parameters according to the model of Eberhart & Russell are given. The most stable hybrids with the lowest S^2_{di} values were CRN 3549 ranked first, PAN 6615 ranked second, SA 7401 ranked third, DKC 63-20 ranked forth and PAN 6573 ranked fifth.

The most unstable hybrids with the highest S^2_{di} values were SNK 2551 ranked last, CRN 4760B ranked second last and CRN 3505 ranked third from last. If the mean yield ($\bar{x}$), regression coefficient value (b) and the deviation from the regression S^2_{di} are considered together, then the most stable hybrid would be DKC 80-10 with a mean yield $\bar{x}$ = 6.2 ton ha^{-1} ranked first, b = 1.0085 close to 1 and the S^2_{di} = 22 ranked ninth.

Table 3.12 The sum of squares, probability, mean yield, regression coefficient (b) and deviation from regression $S^2_{d_i}$ for the 23 genotypes evaluated in 42 environments over three years 2001-2003

Entry	Code	Sum of Squares	F-Ratio	Pr>F	b_i	$S^2_{d_i}$	Rank	Mean Yield	Rank
2	CRN 3549	183.1749	1.8677	0.034	0.9622	7.0916	1	52.76	12
11	PAN 6615	192.1098	1.9588	0.024	1.0752	7.8362	2	47.79	21
15	SA 7401	243.8082	2.4859	0.003	1.1156	12.1444	3	56.24	4
18	DKC 63-20	245.1944	2.5001	0.003	0.9669	12.2599	4	52.46	14
3	PAN 6573	277.2567	2.8270	0.001	1.0046	14.9318	5	49.15	20
21	DK 617	333.4614	3.4001	0.000	0.9524	19.6155	6	50.34	16
10	SB 7551	344.9317	3.5170	0.000	1.1812	20.5714	7	53.58	11
16	SNK 6726	355.8103	3.6279	0.000	1.0114	21.4779	8	52.52	13
7	DKC 80-10	362.0751	3.6918	0.000	1.0085	22.0000	9	62.27	1
20	EXP 962	385.1145	3.9267	0.000	0.9738	23.9199	10	50.33	17
23	DKC 71-21	388.3627	3.9598	0.000	1.0607	24.1906	11	49.67	19
9	SNK 8520	412.2588	4.2035	0.000	0.7223	26.1820	12	56.15	5
22	PAN 6710	440.6374	4.4929	0.000	1.0247	28.5469	13	53.91	10
17	SA 7101	452.4871	4.6137	0.000	0.9687	29.5343	14	54.64	9
19	DKC 61-24	463.6002	4.7270	0.000	0.9226	30.4604	15	51.90	15
14	SNK 6025	501.7909	5.1164	0.000	1.0053	33.6430	16	45.66	23
5	CRN 3760	531.8037	5.4224	0.000	0.9644	36.1440	17	54.79	8
8	PAN 6568	542.1263	5.5277	0.000	0.9902	37.0043	18	56.01	6
13	PHB 32A03	681.9914	6.9538	0.000	1.0451	48.6597	19	47.00	22
12	PHB 3203W	723.8764	7.3808	0.000	1.1153	52.1501	20	49.89	18
1	CRN 3505	898.7940	9.1643	0.000	1.0413	66.7266	21	57.58	3
6	CRN 4760B	995.7311	10.1527	0.000	0.8380	74.8047	22	57.99	2
4	SNK 2551	1375.7897	14.0279	0.000	1.0494	106.4762	23	54.81	7

3.4.7 Wricke's ecovalence analysis (W_i).

Wricke (1962) defined the concept of ecovalence, to describe the stability of a genotype, as the contribution of each genotype to the genotype x environment interaction sum of squares. The ecovalence (W_i) or the stability of the i^{th} genotype is its interaction with environments, squared and summed across environments. Genotypes with low ecovalence have smaller fluctuations across environments and therefore are stable. Wricke's ecovalence was determined for each of the 23 genotypes evaluated at 42 environments for three years 2001-2003 in the main maize growing areas of South Africa (Table 3.13)

Table 3.13 Wricke's ecovalence value for 23 hybrids at 42 environments for three years 2001-2003

Entry	Code	(W_i)	Ranked	Mean Yield	Rank
2	CRN 3549	189.6269	1	52.76	12
11	PAN 6615	217.6336	2	47.79	21
18	DKC 63-20	250.1292	3	52.46	14
3	PAN 6573	277.3527	4	49.15	20
15	SA 7401	304.1437	5	56.24	4
21	DK 617	343.6726	6	50.34	16
16	SNK 6726	356.3944	7	52.52	13
7	DKC 80-10	362.3976	8	62.27	1
20	EXP 962	388.2060	9	50.33	17
23	DKC 71-21	405.0248	10	49.67	19
22	PAN 6710	443.4005	11	53.91	10
17	SA 7101	456.8980	12	54.64	9
19	DKC 61-24	490.6210	13	51.90	15
10	SB 7551	493.2633	14	53.58	11
14	SNK 6025	501.9160	15	45.66	23
5	CRN 3760	537.5415	16	54.79	8
8	PAN 6568	542.5627	17	56.01	6
13	PHB 32A03	691.1687	18	47.00	22
9	SNK 8520	760.4785	19	56.15	5
12	PHB 3203W	783.9181	20	49.89	18
1	CRN 3505	906.4951	21	57.58	3
6	CRN 4760B	1114.1851	22	57.99	2
4	SNK 2551	1386.8258	23	54.81	7

The most stable hybrids according to the ecovalence method of Wricke (1962) were CRN 3549, PAN 6615, DKC 63-20 and PAN 6573. These hybrids were not the best ranked for mean yield, being 12th, 21st, 14th and 20th respectively.

The most unstable hybrids according the ecovalence method were SNK 2551, CRN 4760B, CRN 3505 and PHB 3203W these hybrids were ranked 7th, 2nd, 3rd and 18th for mean yield respectively (Table 3.13).

3.4.8 Nassar and Hühn's mean absolute rank difference (S1).

Nassar and Hühn (1987) described non-parametric measures of stability based on ranks and provide a viable alternative to existing parametric analyses. Table 3.14 presents the non-parametric measure for grain yield of 23 hybrids in 42 environments over three years in South Africa.

This non-parametric test is based on the ranks of the genotypes across locations. This gives equal weight to each location or environment. Genotypes with less change in rank are expected to be more stable. The mean absolute rank difference (S1) estimates are all possible pair wise rank differences across locations for each genotype. The S2 estimates are simply the variances of ranks for each genotype over environments (Nassar and Hühn, 1987; Hühn, 1990). For S1, entries may be tested for significantly less or more stable than the average stability/instability. For the variance of ranks (S2), smaller estimates may indicate relative stability. Often, S2 has less power for detecting stability than S1. The S1 may loose power when genotypes are similar in their interactions with the environments.

Usually S1 is the preferred parameter because of its ease of computation, its clear and relevant interpretation. Furthermore, an efficient test of significance is available (Hühn, 1990).

Table 3.14 Mean absolute rank difference (S1) and variance of ranks (S2) for mean yield of 23 hybrids over three years in South Africa

Entry	Code	S(1)	Ranked	Z(1)	S(2)	Z(2)	Mean Yield	Rank
11	PAN 6615	5.637	1	3.720	22.026	3.678	47.79	21
2	CRN 3549	5.802	2	3.136	22.918	3.386	52.76	12
16	SNK 6726	6.341	3	1.576	29.536	1.594	52.52	13
7	DKC 80-10	6.363	4	1.524	26.964	2.211	62.27	1
3	PAN 6573	6.418	5	1.397	27.980	1.955	49.15	20
18	DKC 63-20	7.022	6	0.364	34.087	0.749	52.46	14
15	SA 7401	7.132	7	0.248	33.597	0.824	56.24	4
21	DK 617	7.198	8	0.189	35.311	0.575	50.34	16
5	CRN 3760	7.495	9	0.023	38.837	0.203	54.79	8
23	DKC 71-21	7.495	10	0.023	39.857	0.131	49.67	19
20	EXP 962	7.857	11	0.038	40.781	0.079	50.33	17
14	SNK 6025	8.033	12	0.133	43.087	0.006	45.66	23
17	SA 7101	8.132	13	0.211	45.265	0.012	54.64	9
9	SNK 8520	8.571	14	0.774	49.122	0.200	56.15	5
8	PAN 6568	8.659	15	0.929	49.633	0.242	56.01	6
12	PHB 3203W	8.725	16	1.055	50.143	0.287	49.89	18
10	SB 7551	8.824	17	1.259	52.801	0.590	53.58	11
22	PAN 6710	8.857	18	1.330	52.245	0.518	53.91	10
13	PHB 32A03	8.912	19	1.455	52.638	0.568	47.00	22
19	DKC 61-24	9.022	20	1.719	54.311	0.810	51.90	15
4	SNK 2551	9.560	21	3.337	64.143	3.091	54.81	7
6	CRN 4760B	9.780	22	4.150*	65.000	3.359	57.99	2
1	CRN 3505	10.187	23	5.887*	72.597	6.230*	57.58	3

Overall Chi-square for stability = 34.4759, 23 df. Individual Z(1) distributed as single df. Chi-squares.

Overall Chi-square for stability = 31.2977, 23 df. Individual Z(2) distributed as single df. Chi-squares.

According to this procedure PAN 6615, CRN 3549, SNK 6726 and DKC 80-10, were the most stable, with CRN 3505, CRN 4760B, SNK 2551 and DKC 61-24

the most unstable. Both CRN 4760B and CRN 3505 were significantly less stable than the average stability.

3.4.9 The AMMI stability value (ASV)

The ASV as described by Purchase (1997) is comparable with the methods of Shukla, Wricke and Eberhart & Russell in South African wheat (Purchase *et al*, 2000). This is also the finding of this study for South African maize hybrids. Table 3.15 indicates the AMMI 2 model IPCA 1 and IPCA 2 scores for each hybrid and also the ASV with its ranking for the 23 hybrids.

Table 3.15 AMMI stability value (ASV) and ranking with the IPCA 1 & 2 scores for the 23 hybrids evaluated at 42 locations over three years 2001 to 2003

Entry	Code	Mean	IPCAScore1	IPCAScore2	ASV	Rank
7	DKC 80-10	62.27	1.231	1.319	2.938	10
6	CRN 4760B	57.99	3.236	1.482	7.060	22
1	CRN 3505	57.58	-0.849	3.678	4.099	14
15	SA 7401	56.24	1.029	-1.149	2.478	8
9	SNK 8520	56.15	1.676	0.945	3.698	13
8	PAN 6568	56.01	1.967	1.878	4.597	17
4	SNK 2551	54.81	-3.382	2.785	7.730	23
5	CRN 3760	54.79	2.415	0.415	5.168	20
17	SA 7101	54.64	2.077	-0.887	4.518	16
22	PAN 6710	53.91	1.299	-0.482	2.812	9
10	SB 7551	53.59	-0.881	-0.619	1.978	4
2	CRN 3549	52.77	-0.988	0.855	2.274	6
16	SNK 6726	52.52	0.661	-1.738	2.238	5
18	DKC 63-20	52.46	0.217	-0.951	1.058	1
19	DKC 61-24	51.90	0.097	-1.949	1.959	3
21	DK 617	50.34	0.666	-0.949	1.709	2
20	EXP 962	50.33	1.257	-1.668	3.158	12
12	PHB 3203W	49.89	-2.870	-0.681	6.160	21
23	DKC 71-21	49.67	-2.028	-0.917	4.422	15
3	PAN 6573	49.16	-0.970	1.183	2.383	7
11	PAN 6615	47.79	-1.432	-0.316	3.071	11
13	PHB 32A03	47.00	-2.226	-1.343	4.934	19
14	SNK 6025	45.66	-2.201	-0.890	4.778	18

According to the ASV ranking, the following hybrids were the most stable, DKC 63-20, DK 617, DKC 61-24, SB 7551 and SNK 6726 and all these hybrids are early maturing. The most unstable were SNK 2551, CRN 4760B, and PHB 3203W and these hybrids all have a medium to long maturity.

3.4.10 Comparison of the stability procedures.

Table 3.16 indicate the values and ranking orders for stability of the 23 maize hybrids, according the different stability parameters.

According to Shukla's (1972) stability variance, Wricke's (1962) ecovalence, Eberhart and Russell's (1966) deviation from regression and Nassar and Hühn's (1987) variance of ranks the most stable hybrids were CRN 3549 and PAN 6615.

Spearman's coefficient of rank correlation (Steel & Torrie, 1980) was then determined for each of the possible pair wise comparisons of the ranks of the different stability statistics (Table 3.18). Mean yield was highly significantly positively correlated ($P<0.01$) with CV and P_i but non-significantly negatively correlated with all other parameters.

High significance ($P<0.01$) for Spearman's rank correlation coefficients were noted between Shukla's stability variance procedure, Eberhart & Russell's deviation parameter, Wricke's ecovalence procedure, Nassar and Hühn's mean absolute rank difference procedure and the ASV procedure from the AMMI model. The procedures of Shukla and Wricke had a total correspondence ($r = 1.000$). This indicates that these two procedures were equivalent for ranking purposes which correspond with previous findings (Wricke & Weber, 1980; Purchase, 1997).

Lin and Binns's (P_i) procedure showed the greatest deviation from all the other procedures, having negative rank correlation coefficients compared to the other procedures. It was significantly correlated to mean yield and CV. Lin and Binns define stability as the deviation of a specific genotype's performance from the performance of the best cultivar in a trial. This implies that a stable cultivar is one that performs in tandem with the environment.

This procedure appears to be considerably more of a genotype performance measure, rather than a stability measure over sites. The genotype mean yield (main effect) could then rather be used to identify a superior yield performing cultivar. DKC 80-10, ranked first on mean yield, was ranked first for this procedure as the most stable cultivar. The most stable hybrids according to the other procedures, CRN 3549 and PAN 6615 were unstable according to Lin and Binn's procedure.

Finlay and Wilkinson's procedure also shows limited correspondence to the procedures of Shukla, Eberhart & Russell, Wricke and ASV. It shows significant positive rank correlations with CV (r = 0.64427*) but non-significant positive rank correlations with mean yield, P_i, σ^2, W_i, S1 and ASV. It shows negative non significant correlation with S^2_{di}. This procedure also showed a big deviation from other procedures in assessing yield stability

The Eberhart and Russell procedure showed highly significant correspondence (P<0.01) with the procedures of σ^2, W_i, S1 and ASV (r = 0.94071**), (r = 0.94071**), (r = 0.83004**) and (r = 0.79545**) respectively. It showed negative correlation with mean yield and P_i, also non-significantly positive correlation with CV and Finlay and Wilkinson's procedures. Their definition of stability is based on a genotype's average sensitivity to environmental fluctuations and is

determined by using joint linear regression analysis in which the average deviation from the regression, or response to environments, is determined. The Eberhart and Russell's definition of a stable genotype is one unit of regression coefficient ($b_i = 1.0$) and the deviations from regression as small as possible ($S^2_{di} = 0$).

The Wricke's procedure of stability statistic showed the highest significant positive correlation (P<0.01) with σ^2 (1.000**), S^2_{di} (0.94071**), S1 (0.86364**), ASV (0.74407**). A rank correlation coefficient of 1.0 was found between Shukla's and Wricke's procedures (Table 3.17). This indicated that the two procedures were equivalent for ranking purposes. Shukla's stability variance is a linear combination of deviation mean squares , in other words the ecovalence of Wricke. This equivalency for ranking was reported by (Wricke & Weber, 1980; Purchase, 1997).

Nassar and Hühn's variance of ranks was highly significantly positively correlated with the procedures σ^2, S^2_{di} and W_i. This showed a similarity to the procedures of Shukla, Eberhart and Russell and Wricke. It was also positively correlated with Finlay and Wilkinson's procedure but not significantly. It was positively but non-significantly correlated with ASV.

Purchase's AMMI stability value was positively significantly correlated with σ^2, S^2_{di} and W_i but it did not correspond with P_i, CV, mean yield, b_i and S1. Although it was corresponding with Shukla, Wricke and Eberhart and Russell the correlation was not as highly significant as was the finding in the wheat study of Purchase *et al*., (2000).

Table 3.16 Mean yield (qu/ha) and various stability measurements and their ranking orders of 23 maize hybrids evaluated across 42 environments over three years 2001-2003 in the main maize growing areas of South Africa

Entry	Code	Mean Yield	Rank	CV	Rank	(P_i)	Rank	σ^2	Rank	W_i	Rank	b_i	*Rank*	S^2_{di}	Rank	S1	Rank	S2	Rank	ASV	Rank
1	CRN3505	57.6	3	47.3	15	77.3	2	446.0	21	906.50	21	1.04	16	66.73	21	10.19	23	72.6	23	4.099	14
2	CRN3549	52.8	12	45.2	12	122.4	9	83.7	1	189.63	1	0.96	5	7.09	1	5.80	2	22.9	2	2.274	6
3	PAN6573	49.2	20	51.0	18	184.5	17	128.0	4	277.35	4	1.00	11	14.93	5	6.42	5	28.0	4	2.383	7
4	SNK2551	54.8	7	52.0	20	110.5	7	688.8	23	1386.83	23	1.05	18	106.48	23	9.56	21	64.1	21	7.730	23
5	CRN3760	54.8	8	45.6	14	124.8	10	259.5	16	537.54	16	0.96	6	36.14	17	7.50	9	38.8	9	5.168	20
6	CRN4760B	58.0	2	38.7	2	103.3	5	551.0	22	1114.19	22	0.84	2	74.80	22	9.78	22	65.0	22	7.060	22
7	DKC80-10	62.3	1	39.3	3	43.7	1	171.0	8	362.40	8	1.01	13	22.00	9	6.36	4	27.0	3	2.938	10
8	PAN6568	56.0	6	41.8	4	93.4	4	262.1	17	542.56	17	0.99	10	37.00	18	8.66	15	49.6	15	4.597	17
9	SNK8520	56.2	5	35.3	1	91.2	3	372.2	19	760.48	19	0.72	1	26.18	12	8.57	14	49.1	14	3.698	13
10	SB7551	53.6	11	48.8	16	137.9	12	237.2	14	493.26	14	1.18	23	20.57	7	8.82	17	52.8	19	1.978	4
11	PAN6615	47.8	21	54.6	22	217.6	21	97.8	2	217.63	2	1.08	20	7.84	2	5.64	1	22.0	1	3.071	11
12	PHB3203	49.9	18	54.1	21	198.7	20	384.1	20	783.92	20	1.12	21	52.15	20	8.73	16	50.1	16	6.160	21
13	PHB32A03	47.0	22	55.7	23	258.9	22	337.2	18	691.17	18	1.05	17	48.66	19	8.91	19	52.6	18	4.934	19
14	SNK6025	45.7	23	51.3	19	262.5	23	241.5	15	501.92	15	1.01	12	33.64	16	8.03	12	43.1	12	4.778	18
15	SA7401	56.2	4	43.4	7	104.0	6	141.6	5	304.14	5	1.12	22	12.14	4	7.13	7	33.6	6	2.478	8
16	SNK6726	52.5	13	43.4	8	147.4	14	168.0	7	356.39	7	1.01	14	21.48	8	6.34	3	29.5	5	2.238	5
17	SA7101	54.6	9	42.2	5	119.1	8	218.8	12	456.90	12	0.97	8	29.53	14	8.13	13	45.3	13	4.518	16
18	DKC63-20	52.5	14	44.7	11	141.7	13	114.2	3	250.13	3	0.97	7	12.26	3	7.02	6	34.1	7	1.058	1
19	DKC61-24	51.9	15	42.2	6	157.6	15	235.8	13	490.62	13	0.92	3	30.46	15	9.02	20	54.3	20	1.959	3
20	EXP962	50.3	17	43.8	10	186.0	18	184.0	9	388.21	9	0.97	9	23.92	10	7.86	11	40.8	11	3.158	12
21	DK617	50.3	16	43.5	9	174.6	16	161.5	6	343.67	6	0.95	4	19.62	6	7.20	8	35.3	8	1.709	2
22	PAN6710	53.9	10	45.3	13	137.8	11	211.9	11	443.40	11	1.02	15	28.55	13	8.86	18	52.2	17	2.812	9
23	DKC71-21	49.7	19	50.5	17	189.8	19	192.5	10	405.02	10	1.06	19	24.19	11	7.50	10	39.9	10	4.422	15

Note: CV% = Francis & Kannenberg's (1978) Coefficient of variability; P_i = Lin & Binns's (1988) cultivar superiority performance; σ^2_i = Shukla's (1972) stability variance; W_i = Wricke's (1962) ecovalence; b_i = Finlay and Wilkinson's (1963) regression coefficient; S^2_{di} = Eberhart & Russell's (1966) deviation from regression parameter; S1 & S2 = Nassar & Hühn's (1987) absolute rank difference and variance of ranks; ASV = AMMI stability value.

Table 3.17 Spearman's rank correlation for all the stability parameters for 2001-2003

	Mean Yield	**CV**	P_i	σ^2	W_i	b_i	S^2_{di}	***S1***
Mean Yield	*							
CV	0.66403**	*						
P_i	0.97332**	0.66996**	*					
σ^2	-0.31324	0.03162	-0.24802	*				
W_i	-0.31324	0.03162	-0.24802	1.0000**	*			
b_i	0.22530	0.64427**	0.28854	0.00494	0.00494	*		
S^2_{di}	-0.23320	0.06917	-0.16403	0.94071**	0.94071**	-0.02273	*	
S1	-0.24605	0.02767	-0.21047	0.87747**	0.86364**	0.01877	0.83004**	*
ASV	-0.11858	0.22925	-0.05534	0.74407**	0.74407**	0.11561	0.79545**	0.47233

* and ** = Significant according to Student's t test at the 0.05 and the 0.01 probability levels respectively.

Note: CV = Francis & Kannenberg's (1978) Coefficient of variability; P_i = Lin & Binns's (1988) cultivar superiority performance; σ^2_i = Shukla's (1972) stability variance; W_i = Wricke's (1962) ecovalence; b_i = Finlay and Wilkinson's (1963) regression coefficient; S^2_{di} = Eberhart & Russell's (1966) deviation from regression parameter; S1 = Nassar & Hühn's (1987) Absolute rank difference; ASV = AMMI stability value.

3.4.11 Conclusion.

According to Spearman's rank correlation coefficients (Steel & Torrie, 1980) the following procedures were in correspondence with the ranking of the genotypes, namely Shukla's stability variance, Wricke's ecovalence, Eberhart and Russell's deviation from regression, Nassar and Hühn's absolute rank difference and to a lesser extent the ASV of Purchase. All these stability parameters had a highly significant correspondence over the three years of study, except for Nassar and Hühn's procedure and Purchase's ASV which did not have a significantly correlation between them.

The procedures of Wricke and Shukla had a total correspondence (r=1.000), these procedures were equivalent for ranking purposes which correspond with previous findings in other crops (Wricke and Weber, 1980; Purchase *et al*., 2000).
The procedures of Lin and Binns and Finlay and Wilkinson showed the greatest deviation from all the other procedures, showing negative or non-significantly correlation with the other procedures (Table 3.17).

The procedure of Lin and Binns appeared to be more of a genotype performance measure, rather than a stability measure. These last two measures are not recommended for use on their own as a measurement of yield stability. The best procedures to select the most stable hybrids appeared to be Wricke's, Shukla's and Eberhart and Russell's procedures, this conclusion is based on their high correlation and ranking of genotypes, which corresponded with the performance of the hybrids in practise.

Nassar and Hühn's procedure and the ASV seemed to be lower correlated to the methods mentioned above, but can be used to validate the selection of genotypes by these three methods. Purchase *et al*. (2000) indicated that the ASV was highly

correlated to these three mentioned procedures and ASV can be useful to rank genotypes. This method also ascribes the sources of instability to different principal components, which in turn can be clearly explained in terms of environmental and/or biological factor(s).

3.5 References

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CHAPTER 4

Assessment of genotype x environment interaction and adaptation of South African maize hybrids using Multivariate Statistical Analysis (AMMI)

4.1 Abstract

Nine late maturing maize hybrids, 125 to 134 relative maturity RM (days), and fourteen hybrids with ultra short to medium maturity, 111 to 124 RM, were evaluated under dry land conditions across 42 environments for genotype x environment interaction (GEI) and yield stability during 2001 to 2003. The Additive Main Effects and Multiplicative Interaction (AMMI) statistical model was used to describe Genotype x Environment Interaction (GEI) and adaptation to certain environments. The AMMI model 2 was used for this data set. The AMMI 2 combined analysis of variance (ANOVA) indicated significant differences between hybrids and environments as main effects. GEI was highly significant. The IPCA 1 axes explained 68% of the total G x E interaction with the IPCA 2 axes explaining 32% of the interaction. They were significant in the ANOVA analysis and that indicated that the AMMI model 2 was the best fit for the data set. DKC 80-10 showed the best adaptation to all environments but a little more so to the higher yielding environments. CRN 4760 was also stable but more adapted to the lower yielding environments. CRN 3505 showed specific adaptation to certain environments but without a fixed pattern.

4.2 Introduction

Maize is produced on between 2.5 and 3.2 million hectares annually and mainly under dry land conditions. The national average yield varies between 2.2 and 2.8 ton ha^{-1}. The rainfall also differs from year to year and area to area, the western area is very dry with a mean annual rainfall of 250-550 mm and has more sandy loam soils. The eastern area has a more reliable and higher rainfall of 600-800 mm annually with soils with higher clay percentage. The rainfall is erratic and not spread evenly, thunder showers with precipitation between 40- 60 mm can fall in a short period of time, which causes water loss through run off.

The considerable variation in soil and climate has resulted in significant variation in annual yield performance of maize hybrids. Genotype x environment interaction (GEI) is an important issue facing plant breeders and agronomists in South Africa. The environmental variation creates problems in a breeding programme as selection of genotypes with improved yield performance, yield stability, grain quality and other agronomic phenotypic traits are based on data generated over a limited, and possibly not always a representative, number of environments and years. GEI which is associated with the differential performance of genetic materials, tested at different locations and in different years and its influence on the selection and recommendation of genotypes has long been recognized (Lin *et al*., 1986; Becker and Léon, 1988; Crossa, 1990; Purchase *et al*., 2000). Evaluation of genotypic performance at a number of locations provides useful information to determine their adaptation and stability (Crossa, 1990).

Lin *et al*. (1986); Becker and Léon (1988), Crossa (1990) and Hohls (1995) discussed a wide range of methods available for the analysis of GEI and stability

and it can be divided into four groups: 1) the analysis of components of variance, 2) stability analysis, 3) qualitative methods and 4) multivariate methods.

The first three methods were described in full detail in Chapter 3, but in this chapter, one of the multivariate methods will be discussed, namely the additive main effects and multiplicative interaction method (AMMI). It combines the analysis of variance of genotypes and the environment main effects with principal component analysis of the GEI into an unified approach (Gauch, 1988; Zobel *et al*., 1988; Gauch and Zobel, 1996).

The three main purposes of multivariate analysis are: (i) to eliminate noise from the data pattern, (ii) to summarize the data and, (iii) to reveal a structure in the data. (Crossa, 1990). Through multivariate analysis, genotypes with similar responses can be clustered, hypotheses generated and later tested, the data can be summarized and analysed more easily (Gauch, 1982; Crossa, 1990; Hohls, 1995).

The results can be graphically represented in an easily interpretable and informative biplot that shows both main effects and GEI. The AMMI model has been used extensively with great success over the past few years to analyse and understand genotype x environment interaction in various crops. (Crossa, 1990; Gauch & Zobel, 1996; Smit & De Beer, 1991; Smith & Smith, 1992; Yau, 1995; Yan and Hunt, 1998,).

The objectives of this study were to analyse and describe GEI and adaptation in maize hybrid yield performance in South Africa during 2001 to 2003 across 42 environments, by means of the AMMI statistical model.

4.3. Materials and methods

4.3.1 Materials

Twenty-three hybrids, listed in Table 4.1, were evaluated over a period of three years from 2001 to 2003 at a total of 42 environments (14 per year) (Table 4.2). These environments were spread throughout the major maize growing areas of South Africa. The relative maturity of these hybrids ranges from very early 111 RM to late 134 RM. Nine hybrids are full season (125-134 RM), eight were early to medium season (120-124 RM) and six were super early season (111-118 RM).

Table 4.1 Entry number, hybrid code, relative maturity (days), brand name and owner-company of the 23 hybrids used in the study

ENTRY	CODE	RM	BRAND NAME	COMPANY	COLOUR
1	CRN 3505	128	CARNIA	MONSANTO	WHITE
2	CRN 3549	130	CARNIA	MONSANTO	WHITE
3	PAN 6573	130	PANNAR	PANNAR	WHITE
4	SNK 2551	132	SENSAKO	MONSANTO	WHITE
5	CRN 3760	133	CARNIA	MONSANTO	YELLOW
6	CRN 4760B	133	CARNIA	MONSANTO	YELLOW
7	DKC 80-10	124	DEKALB	MONSANTO	YELLOW
8	PAN 6568	133	PANNAR	PANNAR	YELLOW
9	SNK 8520	134	SENSAKO	MONSANTO	YELLOW
10	SB 7551	125	EXPERIMENTAL	MONSANTO	WHITE
11	PAN 6615	122	PANNAR	PANNAR	WHITE
12	PHB 3203W	120	PIONEER	PHI	WHITE
13	PHB 32A03	117	PIONEER	PHI	WHITE
14	SNK6025	120	SENSAKO	MONSANTO	WHITE
15	SA 7401	124	EXPERIMENTAL	MONSANTO	YELLOW
16	SNK 6726	117	SENSAKO	MONSANTO	YELLOW
17	SA 7101	121	EXPERIMENTAL	MONSANTO	YELLOW
18	DKC 63-20	113	DEKALB	MONSANTO	YELLOW
19	DKC 61-24	111	DEKALB	MONSANTO	YELLOW
20	EXP 962	112	EXPERIMENTAL	MONSANTO	YELLOW
21	DK 617	111	DEKALB	MONSANTO	YELLOW
22	PAN 6710	118	PANNAR	PANNAR	YELLOW
23	DKC 71-21	121	DEKALB	MONSANTO	WHITE

The 23 hybrids were evaluated for grain yield, harvest moisture, test weight, lodging and final stand in the 14 rain fed environments from 2001 to 2003 (Table 4.3), evenly spread through the maize growing area of South Africa.

Table 4.2 Fourteen dry land locations that were used in the study from 2001 to 2003

LOC #	LOC_NAME	LAT*	LONG*	PROVINCE	PLOT M^2	DENSITY
1	DELMAS	-26.15	28.68	MPUMALANGA	12.00	44000
2	PETIT	-26.90	28.37	GAUTENG	12.00	44000
3	FICKSBURG	-28.86	27.90	FREE STATE	14.56	44000
4	MEERLUS	-26.31	29.53	MPUMALANGA	14.56	44000
5	RIETGAT	-26.15	26.17	NORTH WEST	14.56	28000
6	BERGVILLE	-28.73	29.37	KWA ZULU NATAL	14.56	44000
7	ERMELO	-26.51	29.99	MPUMALANGA	14.56	44000
8	BOTHAVILLE	-27.39	26.62	FREE STATE	16.50	22000
9	OGIES	-26.05	29.50	MPUMALANGA	14.56	44000
10	PIET RETIEF	-27.00	30.80	MPUMALANGA	14.56	44000
11	WONDERFONTEIN	-25.85	29.80	MPUMALANGA	14.56	44000
12	KROONSTAD	-27.66	27.23	FREE STATE	16.50	22000
13	KAMEEL	-26.40	25.10	NORTH WEST	23.00	18000
14	VILJOENSKROON	-27.21	26.95	FREE STATE	16.50	22000

The experimental layout was a randomized complete block design (RCBD) with two replications. Trials were planted according to the practices of the respective farmer (co-operator) at each site. See Table 4.2 for plot sizes and plant densities.

Management and fertilization at each site were done according to the practises of each farmer (co-operator) for his farm and the specific field. Fertilization rates with planting were inflated with about 10% to insure even development.

All the sites with row widths of 0.91m or 0.75m (Eastern areas) were planted with a vacuum precision planter and no thinning was necessary. The 1.5m and 2.1m row width trials (Western areas) were planted with a cone planter at 20% more density and then thinned at V4 to V6 stage to the planned density for that area.

The plant population for research trials were planted at 10-15% higher density than farming practises for that area.

4.3.2 Measurements

The trials were harvested with a New Holland TR88 double plot combine specially designed to harvest and record data for two plots at a time. Grain mass kg per plot (SHW), moisture percentage (MST) and test weight (TWT) for each genotype was recorded. All the plots were counted to get the final stand per plot (FNS), as well as the root lodging (RTLG) and stalk lodging (STLG). The relative maturity were determined with linear regression from the known relative maturities of the commercial hybrids in the experiment, the hybrids PAN 6568 (133 RM), CRN 3549 (130 RM), DKC 80-10 (124 RM), PHB 3203W (120 RM), PAN 6710 (118RM) and DKC 61-24 (111 RM) were used to determine the RM of other entries.

4.3.3 Statistical analysis

An analysis of variance (ANOVA) was done for each location separately as a randomized complete block design. A combined analysis of variance was done on the mean data obtained from each location. Bartlett's (1947) test was done to determine the homogeneity of variances between environments to determine the validity of the combined analysis of variance on the data.

The combined analysis of variance according to the AMMI 2 model was performed using Agrobase 1999^{TM} (Agrobase, 1999) (Table 4.4). To graphically explain the GEI and adaptation of the hybrids to the environments, the AMMI model 2 biplot was used where the IPCA 1 scores were plotted against the mean yield (Figure 4.1). To further explain the GEI and adaptation a biplot between the

IPCA 1 scores and IPCA 2 scores were given, this was done because the IPCA 2 axes was important in explaining 32% of the total GEI (Figure 4.2).
Table 4.7 indicates the environments and the best adapted hybrids selected from the AMMI analysis for each environment.

4.4 Results and discussion

4.4.1 Mean performance for different traits of the 23 hybrids evaluated over three years

The relative performance of genotypes based on the mean grain yield and other agronomic traits over years and locations are presented in Table 4.3. The yield, moisture and test weight performances were ranked. Grain yield is given in quintals ha^{-1} (Ton $ha^{-1} = \frac{\text{quintals ha}^{-1}}{10}$). The highest ranked hybrid for grain yield was DKC 80-10 while CRN 4760B was ranked second and CRN 3505 ranked third. The first two are yellow endosperm hybrids and the third one a white endosperm hybrid. The hybrid with the highest moisture content (MST) was CRN 4760B (20.57%) (133 RM) and DK 617 the lowest moisture content (13.14%) (111 RM). The best hybrid for test weight (TWT) is SNK 8520 (orange yellow flint grain) and the worst one PAN 6710 (soft yellow dent).

4.4.2 Combined analysis of variance (ANOVA) according to the best AMMI model

The combined analysis of variance (ANOVA) of the 23 hybrids over three years and 42 locations according to the AMMI 2 model are presented in Table 4.4. The AMMI 2 model was used as it gave the best fit for this data set. The ANOVA indicated highly significant differences ($P<0.01$) for environments, genotypes and importantly genotype x environment interaction (GEI). The IPCA 1 and IPCA 2

axes were also highly significant (P<0.01). Variance components (%) of the sum of squares, ranged from 3.55% for genotypes, 77.52% for environments and 9.11% for GEI. This indicated the overwhelming influence that environments have on the yield performance of maize hybrids in South Africa. Of greater importance is the fact that the G x E variation is more than double the variation of genotypes as main effect.

Table 4.3 **M**ean performances of 23 hybrids, for different traits, over years and locations (Yield, MST and TWT are ranked)

Entry	Code	Yield	Rank	MST	Rank	TWT	Rank	FNS	STLG	RTLG
1	CRN 3505	57.58	3	18.89	7	74.81	6	39.24	1.58	0.37
2	CRN 3549	52.76	12	18.80	9	74.39	10	38.74	1.76	0.44
3	PAN 6573	49.15	20	19.44	5	73.69	15	39.36	1.68	0.79
4	SNK 2551	54.81	7	19.25	6	74.25	12	37.73	2.61	0.82
5	CRN 3760	54.79	8	20.23	2	74.92	5	37.33	1.23	0.42
6	CRN 4760B	57.99	2	20.57	1	74.51	7	38.10	0.64	0.73
7	DKC 80-10	62.27	1	17.22	11	75.25	4	40.67	0.87	0.2
8	PAN 6568	56.01	6	19.99	4	72.79	20	40.76	1.54	0.62
9	SNK 8520	56.15	5	20.21	3	77.17	1	37.69	1.07	0.81
10	SB 7551	53.58	11	18.88	8	73.91	13	39.35	2.83	0.77
11	PAN 6615	47.79	21	16.55	13	73.29	17	39.77	2.19	0.51
12	PHB 3203W	49.89	18	15.59	15	74.45	8	40.85	0.89	0.3
13	PHB 32A03	47.00	22	14.41	18	75.81	3	40.44	0.85	0.35
14	SNK 6025	45.66	23	14.31	19	73.2	18	40.82	1.43	0.2
15	SA 7401	56.24	4	17.76	10	74.39	9	40.75	0.48	0.13
16	SNK 6726	52.52	13	14.95	17	75.95	2	40.36	0.42	0.19
17	SA 7101	54.64	9	16.68	12	73.69	14	40.86	0.5	0.2
18	DKC 63-20	52.46	14	13.42	21	73.52	16	38.57	0.4	0.2
19	DKC 61-24	51.9	15	13.43	20	74.38	11	40.56	0.38	0.32
20	EXP 962	50.33	17	13.36	22	72.48	21	39.15	0.49	0.21
21	DK 617	50.34	16	13.14	23	73.01	19	40.32	0.52	0.13
22	PAN 6710	53.91	10	14.98	16	70.63	23	39.48	1.87	0.48
23	DKC 71-21	49.67	19	15.85	14	71.68	22	39.42	1.56	0.45

Yield=quintals per ha, MST=moisture, TWT=test weight, FNS=Final stand count, STLG=stalk lodge count, RTLG=root lodge count.

Grand mean yield = 52.932 R-squared = 0.9641 CV = 12.66%

LSD for yield = 1.7031 S.E.D. = 1.0344

t (1-sided a=0.050, 924 df) = 1.6465 MSE = 44.93788

*Yield=quintals per ha^{-1}

Table 4.4 Combined analysis of variance (ANOVA) according to the AMMI 2 model for the three years 2001 to 2003

Source	df	SS	MS	F-value	Pr> F
Total	1931	803987.02			
Environments	13	623233.94	47941.07	455.87	0.000
Reps within Env.	70	7361.45	105.16		
Genotype	22	28579.40	1299.06	5.07	0.000
Genotype x Env.	286	73223.13	256.03	5.51	0.000
IPCA 1	34	32086.77	943.73	20.30	0.000
IPCA 2	32	15041.66	470.05	10.11	0.000
IPCA Residual	220	26094.71	118.61		
Residual	1540	71589.10	46.49		

Grand mean = 52.934 R-squared = 0.9110 CV = 12.88%

Genetic variance for entries = 12.417, with a std. error of 4.472

Genetic variance for entries x env. = 34.923, with a std. error of 3.567

IPCA Axis	Eigenvalue	% GxE Explained	Cumulative %
1	5347.79534	68.08	68.08
2	2506.94248	31.92	100.00

The IPCA 1 and IPCA 2 axes explained 68.08% and 31.92% of the total GEI. They were both significant (P<0.01) (Table 4.4) and this indicate that the AMMI 2 model is the best fit for this data set.

4.4.3 The AMMI model 2-biplot

Tables 4.4 and 4.5 present the AMMI analysis data with the IPCA 1 and IPCA 2 scores for the environments and the hybrids respectively. It indicates the names and graph ID, of the environments and the hybrids, when interpreting the AMMI 2 biplot (Figure 4.1). In Figure 4.1 the IPCA 1 scores for both the hybrids (lower case) and the environments (upper case) were plotted against the mean yield for the hybrids and the environments respectively. By plotting both the hybrids and the environments on the same graph, the associations between the hybrids and the

environments can be seen clearly. The IPCA scores of a genotype in the AMMI analysis are an indication of the stability or adaptation over environments. The greater the IPCA scores, either negative or positive, (as it is a relative value), the more specific adapted is a genotype to certain environments. The more the IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled.

When looking at the environments it is clear that there is a good variation in the different environments sampled, they are spread from the lower yielding environments in quadrants I and IV and the high yielding environments in quadrants II and III. Most of the higher yielding environments are in quadrant IV. The high yielding environments are Delmas (A), Petit (B), Meerlus (D), Piet Retief (J), Bergville (F) and Ermelo (G) which are all eastern locations, except Bergville that is a site in Kwazulu-Natal, but also clusters with the eastern sites. Wonderfontein (K), Ficksburg (C) and Ogies (I) are lower yielding eastern sites clustering together. The western sites Kroonstad (L), Kameel (M), Bothaville (H), Viljoenskroon (N) and Rietgat (Lichtenburg) (E), to a lesser extent, are clustering in quadrant I and are the lower yielding sites. This is expected, with the western areas historically prone to drought, erratic rain fall, and very high temperatures, thus representing lower yielding environments.

The hybrids have considerably less variation around the mean yield of 52.93 quintals ha^{-1} than the environments. The hybrids DKC 80-10 (g), CRN 4760B (f), CRN 3505 (a) and SNK 2551 (d) are specifically adapted to the higher yielding environments. Considering only the IPCA 1 scores CRN 4760B (f), SNK 2551 (d), CRN 3760 (e), PAN 6568 (h), and SNK 8520 (i) were the more unstable hybrids, and also adapted to the higher yielding or more favourable environments. The hybrids mentioned above are also the longer maturity hybrids (see Table 4.3 for moisture readings).

Hybrids adapted to the lower yielding environments are DKC 61-24 (s), EXP 962 (t) and DK 617 (u). These hybrids seem stable just considering IPCA 1 scores. Other hybrids adapted to lower yielding locations, but that are not very stable were PAN 6573 (c), PAN 6615 (k), PHB 32A03 (m), SNK 6025 (n), DKC 71-21 (w) and PHB 3203W (l). The most stable hybrids just considering IPCA 1 scores, were SNK 6726 (p), DKC 63-20 (r), DKC 61-24 (s), SB 7551 (j) and CRN 3549 (b).

Since IPCA 2 scores also play a significant role (32%) in explaining the GEI, the IPCA 1 scores were plotted against the IPCA 2 scores to further explore adaptation (Figure 4.2). CRN 3505 (a) is now an outlier (unstable) with SNK 2551 (d), PAN 6558 (h), CRN 4760 (f), PHB 3203W (l) and PHB 32A03 (m) unstable but to a lesser extent.

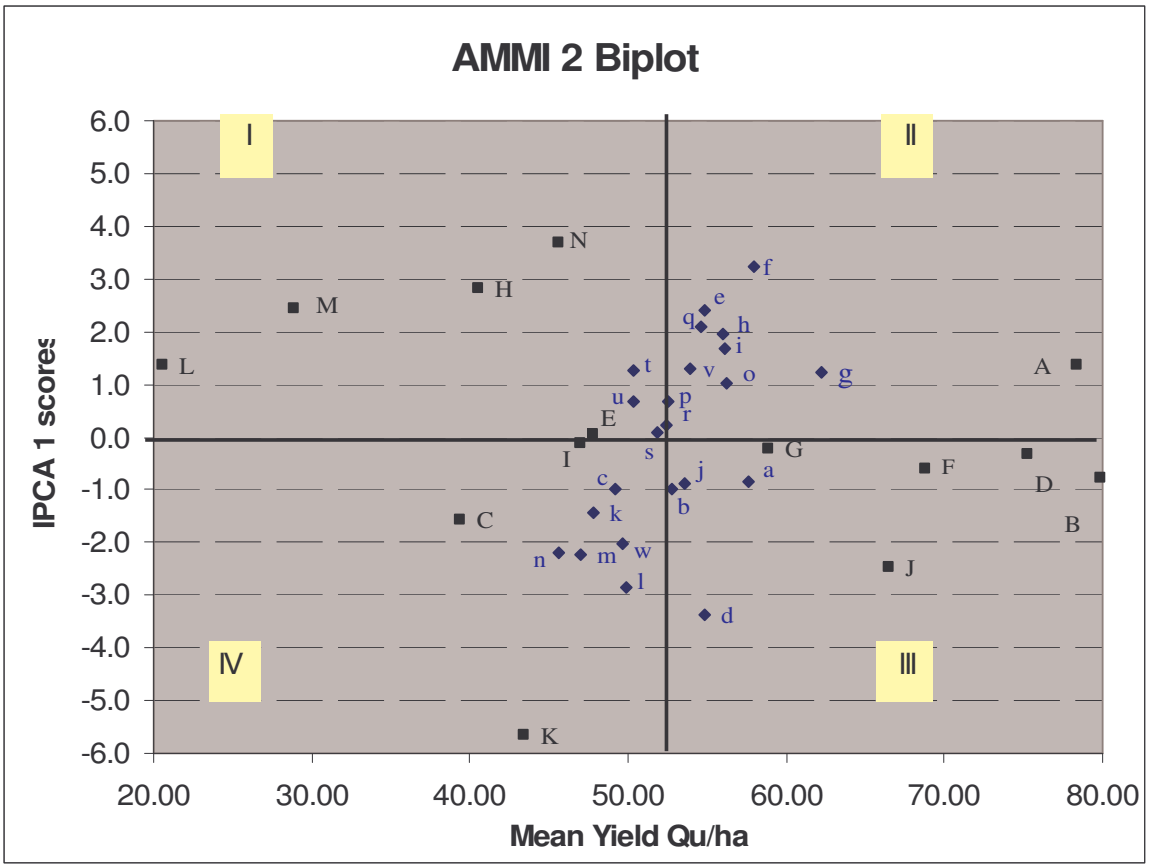
PAN 6573 (c), CRN 3549 (b), SNK 2551 (j), PAN 6615 (k), DKC 80-10 (g), DKC 63-20 (r), PAN 6710 (v) and DK 617 (u) are showing to be more stable, when plotting the IPCA 1 and IPCA 2 scores.

Table 4.5 The IPCA 1 and IPCA 2 scores for the 14 sites, sorted on environmental mean yield, used in the study

Env. nr	Locations	Graph ID	Env. mean	Score 1	Score 2
2	Petit	B	79.93	-0.7772	1.4105
1	Delmas	A	78.43	1.3737	1.2131
4	Meerlus	D	75.26	-0.3435	-2.3839
6	Bergville	F	68.82	-0.593	-0.93
10	Piet Retief	J	66.49	-2.4795	0.1488
7	Ermelo	G	58.89	-0.2144	-0.9659
5	Rietgat	E	47.86	0.0411	0.4572
9	Ogies	I	46.95	-0.1112	1.9448
14	Viljoenskroon	N	45.6	3.6754	-1.2644
11	Wonderfontein	K	43.44	-5.6643	1.1917
8	Bothaville	H	40.59	2.8246	-1.649
3	Ficksburg	C	39.37	-1.5676	-2.8773
13	Kameel	M	28.86	2.4536	4.5201
12	Kroonstad	L	20.59	1.3825	-0.8157

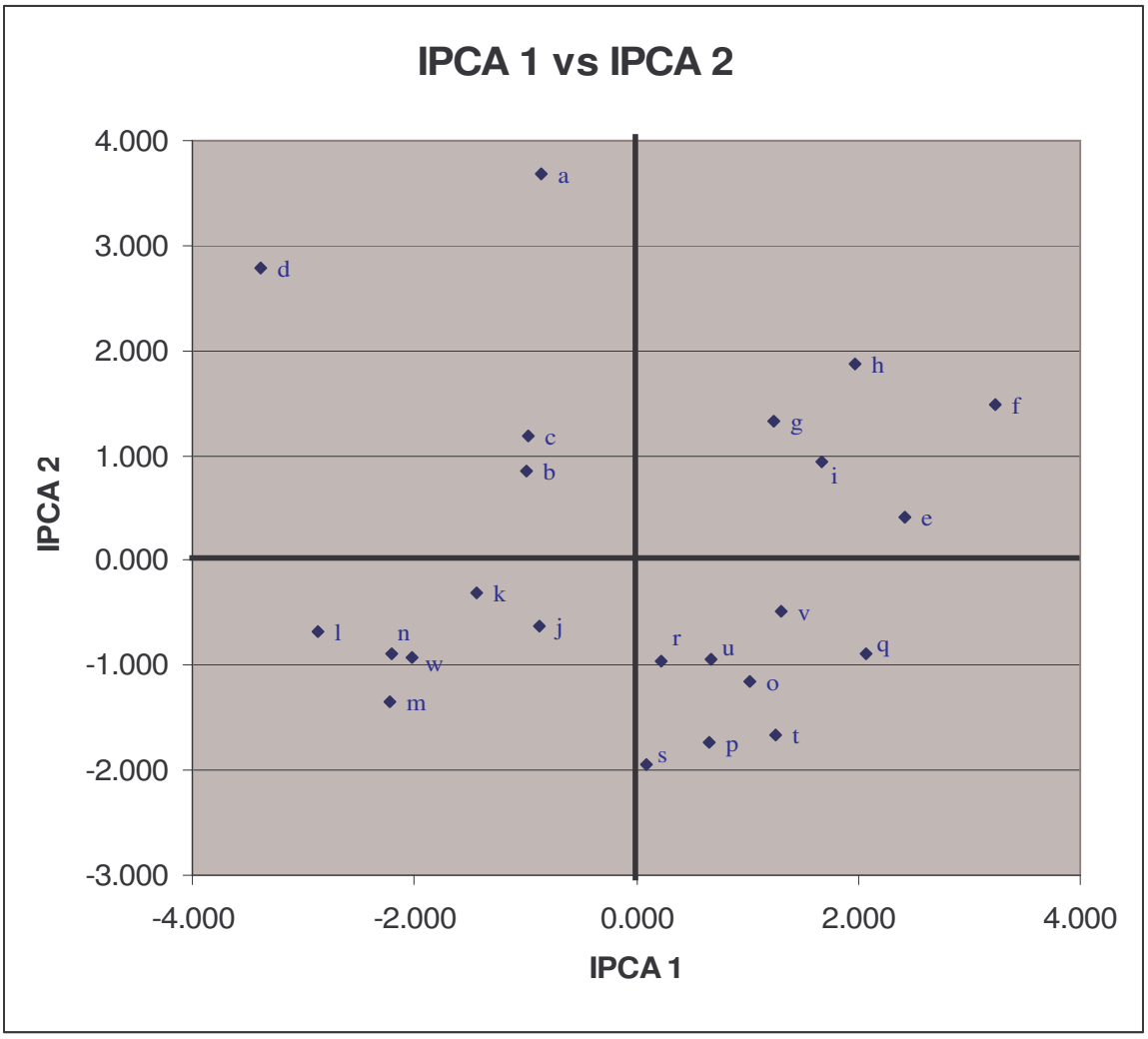
Table 4.6 IPCA 1 and IPCA 2 scores for the 23 hybrids sorted on mean yield and evaluated at 42 locations over three years 2001 to 2003

Entry	Code	Graph ID	Mean Yield	IPCAScore1	IPCAScore2
7	DKC 80-10	g	62.27	1.231	1.319
6	CRN 4760B	f	57.99	3.236	1.482
1	CRN 3505	a	57.58	-0.849	3.678
15	SA 7401	o	56.24	1.029	-1.149
9	SNK 8520	i	56.15	1.676	0.945
8	PAN 6568	h	56.01	1.967	1.878
4	SNK 2551	d	54.81	-3.382	2.785
5	CRN 3760	e	54.79	2.415	0.415
17	SA 7101	q	54.64	2.077	-0.887
22	PAN 6710	v	53.91	1.299	-0.482
10	SB 7551	j	53.59	-0.881	-0.619
2	CRN 3549	b	52.77	-0.988	0.855
16	SNK 6726	p	52.52	0.661	-1.738
18	DKC 63-20	r	52.46	0.217	-0.951
19	DKC 61-24	s	51.90	0.097	-1.949
21	DK 617	u	50.34	0.666	-0.949
20	EXP 962	t	50.33	1.257	-1.668
12	PHB 3203W	l	49.89	-2.870	-0.681
23	DKC 71-21	w	49.67	-2.028	-0.917
3	PAN 6573	c	49.16	-0.970	1.183
11	PAN 6615	k	47.79	-1.432	-0.316
13	PHB 32A03	m	47.00	-2.226	-1.343
14	SNK 6025	n	45.66	-2.201	-0.890



Note that the upper case letters are for the environments and the lower case for the hybrids, see Tables 4.4 and 4.5 for the identity of the environments and hybrids respectively.

Figure 4.1 AMMI model 2 biplot for 23 maize hybrids and 14 environments evaluated during 2001 to 2003 in South Africa



The lower case letters indicate the hybrids, see Table 4.5 to identify hybrids.

Figure 4.2 Plotted IPCA 1 and IPCA 2 scores of maize hybrids evaluated during 2001 to 2003 in South Africa

4.4.4 Adaptation of the hybrids according to the AMMI 2 model

The AMMI model summarise patterns and relationships of genotypes and environments successfully. In Table 4.7 the best AMMI selections for the hybrids per environment are shown. This is an indication of the best adapted hybrids in relation to the different environments. The hybrid best adapted to most environments was DKC 80-10 but was better adapted to the higher yielding,

favourable environments. CRN 4760B was better performing in the lower to medium yielding environments, but also stable over all environments. CRN 3505 was showing adaptation to specific environments rather than favourable or unfavourable environments. The other hybrids that were selected do not show a distinct pattern of adaptation and are more specific adapted either to lower or higher yielding environments. It is clear that the AMMI model can be used to analyse the GEI and can be used to identify the superior genotypes. It can also be used in the selection of the best environments for genotype evaluation.

Table 4.7 The AMMI model's best five hybrid selections for mean yield in relation to the environments evaluated during 2001-2003

Env. nr	Sites	Env. mean	Score 1	Hybrid 1	Hybrid 2	Hybrid 3	Hybrid 4	Hybrid 5
2	Petit	79.93	-0.7772	DKC80-10	CRN3505	SNK2551	SB7551	SA7401
1	Delmas	78.43	1.3737	DKC80-10	CRN4760B	PAN6568	CRN3505	CRN3760
4	Meerlus	75.26	-0.3435	SA7401	DKC80-10	SB7551	SNK6726	SA7101
6	Bergville	68.82	-0.593	DKC80-10	SNK8520	DKC61-24	CRN4760B	SA7401
10	Piet Retief	66.49	-2.4795	SNK2551	CRN3505	DKC80-10	PION3203	CRN3549
7	Ermelo	58.89	-0.2144	DKC80-10	SA7401	SB7551	PAN6710	SA7101
5	Rietgat	47.86	0.0411	DKC80-10	CRN3505	CRN4760B	PAN6568	SA7401
9	Ogies	46.95	-0.1112	CRN3505	DKC80-10	CRN4760B	SNK8520	SNK2551
14	Viljoenskroon	45.6	3.6754	DKC80-10	CRN4760B	SA7401	SA7101	CRN3760
11	Wonderfontein	43.44	-5.6643	SNK2551	CRN3505	PION3203	DKC71-21	CRN3549
8	Bothaville	40.59	2.8246	CRN4760B	SNK8520	DKC80-10	SA7101	CRN3760
3	Ficksburg	39.37	-1.5676	SA7401	DKC61-24	SB7551	DKC80-10	SNK6726
13	Kameel	28.86	2.4536	CRN4760B	CRN3505	DKC80-10	PAN6568	SNK8520
12	Kroonstad	20.59	1.3825	SNK8520	CRN4760B	DKC80-10	DKC61-24	DKC63-20

4.4.5 Conclusion

The study has clearly shown that the AMMI model can summarize patterns and relationships of genotypes and environments successfully, as well as provide a valuable prediction assessment although Becker & Léon (1988) stated that multivariate methods are too sophisticated to provide a simple measure of yield stability which allows a ranking of genotypes. It is clearly showing the adaptation of hybrids to environments and can be used to identify the superior genotypes in relation with the environments and years.

4.5 References

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CHAPTER 5

Summary

5.1 Summary

The objectives of the study were to evaluate different statistical methods to describe genotype x environment interaction over three years, with maize hybrids across several environments. The environment and soil variables have a major effect on the performance of maize hybrids in South Africa. The second objective was to evaluate and compare the different statistical stability models and procedures, to identify the best stability model to accurately assess and rank maize hybrids according to their stability over environments and years. The third objective was to describe genotype x environment interaction and the adaptation of maize hybrids to different environments over years.

Twenty three maize hybrids were evaluated at 42 environments between 2001 and 2003 in the major maize producing areas in South Africa. Grain yield and other agronomic traits were determined but mean grain yield was used to determine stability with the following stability procedures: CV (coefficient of variation), Linn and Binns, Shukla, Wricke, Finlay and Wilkinson, Eberhart and Russell, and the ASV (AMMI stability value). The comparison of the procedures were done with Spearman's rank correlation coefficient and the significance determined with student's *t*-test.

Linn and Binns cultivar performance measure ranked the hybrids, with high (P_i) values as the most stable. CRN 80-10 was ranked first, CRN 3505 ranked second and SNK 8520 ranked third. The unstable hybrids with low (P_i) values were SNK 6025, PHB 32A03 and PAN 6615. Linn and Binns procedure was not

significantly correlated, with any of the other procedures. It was only significantly correlated with mean yield (r = 0.97332**), thus confirmed that it is more a measure of performance and not really a stability parameter.

Finlay and Wilkinson's regression coefficient indicated that DKC 80-10, CRN 3505 and PAN 6568 showed average stability and were adapted to most of the environments. SB 7551, PHB 3203W and SA 7401 have below average stability and adapted to the higher yielding environments. DK 617, DKC 61-24 and SNK 8520 were of average stability but were specifically adapted to low yielding environments. This method was also not comparable to the other methods and was only positive and significantly correlated with CV.

Shukla's stability variance indicated that CRN 3549, PAN 6615, DKC 63-20, PAN 6573 and SA 7401 were stable and SNK 2551, CRN 4760B, CRN 3505, PHB 3203W and SNK 8520 were unstable hybrids. DKC 80-10 was the highest yielding hybrid but only average on stability. This method compared well with the procedures of Eberhart and Russell, Nassar and Hühn, Wricke and the ASV (AMMI). The comparison of the rank correlations were all significant and positive. Shukla's and Wricke's methods had total correspondence (r = 1.000**). These methods will rank hybrids equivalently according to their stability.

Wricke's ecovalence ranked CRN 3549, PAN 6615, DKC 63-20 and PAN 6573 as the most stable hybrids with SNK 2551, CRN 4760B, CRN 3505, and PHB 3203W as the most unstable hybrids. Wricke's ecovalence was positively and significantly correlated with Shukla, Eberhart and Russell, Nassar and Hühn and ASV.

Eberhart and Russell's deviation from regression indicated that CRN 3549, PAN 6615, SA 7401, DKC 63-20 and PAN 6573 were the stable hybrids. SNK 2551,

CRN 4760B and CRN 3505 were the unstable hybrids. It corresponded with the methods of Shukla, Wricke, Nassar and Hühn and the ASV.

Nassar and Hühn's mean absolute rank method indicated PAN 6615, CRN 3549, SNK 6726 and DKC 80-10 as the stable hybrids. CRN 3505, CRN 760B, SNK 2551 and DKC63-20 were the most unstable hybrids. This method was significantly and positively correlated with Shukla, Wricke and Eberhart and Russell. It was not correlated with ASV, Linn and Binns and Finlay and Wilkinson.

The AMMI stability value (ASV) ranked DKC 63-20, DK 617, DKC 61-24 en SB 7551 as stable. SNK 2551, CRN 4760B, PHB 3203W en CRN 3760 was unstable. ASV was significantly correlated with the methods of Shukla, Wricke and Eberhart and Russell.

Die AMMI model 2 indicated Delmas (quadrant II), Petit, Meerlus, Bergville, Piet Retief and Ermelo (quadrant III) as the high yielding environments. DKC 80-10, CRN 4760B, PAN 6568, SNK 8520 and SA 7401 were adapted to the high yielding environments but specific to Delmas. CRN 3505, SB 7551, SNK 2551 and CRN 3549 are also adapted to high yielding environments but more specific to Petit, Meerlus, Bergville and Ermelo.

Kroonstad, Kameel, Bothaville, Viljoenskroon and Rietgat are the average to low yielding environments and are clustered in quadrant I. DK 617, SNK 6726, DKC 63-20 and DKC 61-24 were adapted to these environments. Ficksburg, Wonderfontein and Ogies were clustered in quadrant IV and shown to be average to low yielding environments, hybrids that were specific adapted to these environments were PHB 3203W, PHB 32A03, DKC 71-21, PAN 6615 and PAN 6573. Die AMMI method successfully summarized patterns and relationship of the

hybrids with the environments. AMMI indicated the genotype x environment interactions and clustered the hybrids according their adaptability to certain environments. The graphical AMMI biplot explained and described the hybrid's adaptation and interaction with the environments.

5.2 Opsomming

Die studie is onderneem om die verskillende metodes van genotipe x omgewingsinteraksie-analise met mielie-basters te vergelyk in verskeie lokaliteite oor drie jaar. Die omgewings- en grondveranderlikes het 'n groot effek op die prestasie van mielie-basters in Suid-Afrika, daarom was 'n tweede doelwit gewees om die verskillende stabiliteitsmodelle en statistiese prosedures te ondersoek en vergelyk, om sodoende die beste modelle te identifiseer wat die stabiliteit van mielie-basters in die wisselende toestande die akkuraatste kan beskryf. Die derde doelwit was om deur die AMMI model die interaksie van die genotipes met die omgewing te bepaal en ook om die aanpasbaarheid van die mielie-basters ten opsigte van die verskillende toetslokaliteite te verduidelik.

Drie en twintig mielie-basters is oor 42 lokaliteite gedurende die periode van 2001 tot 2003 in die mielie-produseerende areas van Suid-Afrika getoets. Graanopbrengs en ander karaktertrekke is bepaal, maar die basters is vir gemiddelde graanopbrengs en opbrengsstabiliteit volgens die volgende statistiese modelle en prosedures geëvalueer naamlik, die KV (variansie koëffisiënt), Linn & Binns, Shukla, Wricke, Finlay & Wilkinson, Eberhart & Russell, en die ASV (AMMI stabiliteits-waarde). Om die metodes te vergelyk is Spearman se rangorde-korrelasiekoëffisiënt gebruik, en die betekenisvolheid is deur middel van Student se *t*-toets bepaal.

Lin & Binns se cultivarprestasie-maatstaf het die volgende basters as stabiel aangetoon, en dus met ´n hoë (P_i) waarde, CRN 80-10 was eerste in die rangorde, tweede was CRN 3505 en derde SNK 8520. Die basters wat as die mees onstabielste, en dus met ´n lae (P_i) waarde uitgewys was, is SNK 6025, PHB 32A03 en PAN 6615. Lin & Binns se rangorde was hoogs betekenisvol (r=0.97332**) met die gemiddelde opbrengs gekorreleerd, ´n aanduiding dat die metode eerder ´n prestasie-maatstaf is as wat dit stabiliteit aandui. Die metode se rangorde het die meeste afgewyk van die ander metodes se rangordes, en was onbetekenisvol positief of negatief gekorreleerd met die ander metodes.

Finlay & Wilkinson se regressie-koëffisiënt het aangedui dat DKC 80-10, CRN 3505 en PAN 6568 gemiddelde stabiliteit het en aangepas is by die meeste lokaliteite. SB 7551, PHB 3203W en SA 7401 het onder gemiddelde stabiliteit, maar is spesifiek aangepas by hoër opbrengs lokaliteite. DK 617, DKC 61-24 en SNK 8520 het gemiddelde stabiliteit maar is spesifiek aangepas by laer opbrengs lokaliteite. Die metode was saam met Lin & Binns se metode die verste verwyderd was van die ander metodes as die rangorde korrelasies vergelyk word. Die metode was positief en betekenisvol gekorreleerd met KV.

Shukla se stabiliteits variansie-metode het CRN 3549, PAN 6615, DKC 63-20, PAN 6573 en SA 7401 as die mees stabielste basters aangewys. Die basters met die swakste stabiliteit was SNK 2551, CRN 4760B, CRN 3505, PHB 3203W en SNK 8520. Die baster DKC 80-10 met die hoogste gemiddelde opbrengs het slegs gemiddelde stabiliteit getoon. Die metode het baie goed vergelyk met Eberhart & Russell, Nassar & Hühn, Wricke asook die ASV (AMMI) as die korrelasies in rangorde vergelyk word. Shukla en Wricke se stabiliteits metodes was presies dieselfde gekorreleerd (r=1.000**) en bewys dus dat die twee metodes basters se stabiliteits rangordes identies klassifiseer.

Wricke se ekovalensie-konsep het CRN 3549, PAN 6615, DKC 63-20 en PAN 6573 as die stabielste basters geklassifiseer. SNK 2551, CRN 4760B, CRN 3505, en PHB 3203W was as onstabiel geidentifiseer. Wricke se metode was betekenisvol positief gekorreleerd met die metodes van Shukla, Eberhart & Russel, Nassar & Hühn en ASV.

Eberhart & Russell se regressie analise-metode wat die afwyking van die regressie as maatstaf gebruik, het CRN 3549, PAN 6615, SA 7401, DKC 63-20 en PAN 6573 as die stabielste basters aangetoon. SNK 2551, CRN 4760B en CRN 3505 het die swakste stabiliteit getoon. Die metode het ook ooreengestem met die metodes van Shukla, Wricke, Nassar & Hühn en die ASV en was betekenisvol positief gekorreleerd met die metodes.

Nassar en Hühn se gemiddelde absolute rangorde metode, wat ´n nie-parametriese metode is, het PAN 6615, CRN 3549, SNK 6726 en DKC 80-10 as die stabiele basters aangetoon. CRN 3505, CRN 4760B, SNK 2551 en DKC 63-20 was onstabiel volgens die metode. Die metode was ook betekenisvol positief gekorreleerd met Shukla, Wricke, en Eberhart & Russel. Dit was nie betekenisvol gekorreleerd met ASV, Finlay & Wilkinson en Linn & Binns se metodes nie.

Die AMMI se stabiliteits waarde (ASV) het DKC 63-20, DK 617, DKC 61-24 en SB 7551 as stabiel geklassifiseer. SNK 2551, CRN 4760B, PHB 3203W en CRN 3760 was as onstabiel aangetoon. ASV was slegs betekenisvol gekorreleerd met Shukla, Wricke en Eberhart & Russell se metodes.

Die AMMI model het Delmas (kwadrant II), Petit, Meerlus, Bergville, Piet Retief en Ermelo (kwadrant III) as die hoë potensiaal lokaliteite geklassifiseer. DKC 80-10, CRN 4760B, PAN 6568, SNK 8520, SA 7401 is aangepas vir die hoër potensiaal lokaliteite en meer spesifiek vir Delmas. CRN 3505, SB 7551, SNK

2551 en CRN 3549 is ook aangepas vir die hoër potensiaal lokaliteite maar meer spesifiek tot Petit, Meerlus, Bergville en Ermelo.

Kroonstad, Kameel, Bothaville, Viljoenskroon en Rietgat was meer gemiddeld tot lae potensiaal lokaliteite en val in kwadrant I. DK 617, SNK 6726, DKC 63-20 en DKC 61-24 was meer aangepas tot hierdie lokaliteite. Ficksburg, Wonderfontein en Ogies val in kwadrant IV en groepeer in die medium lae potensiaal lokaliteite. Basters wat meer spesifiek tot hierdie lokaliteite aangepas is, was PHB 3203W, PHB 32A03, DKC 71-21, PAN 6615 en PAN 6573.

Die AMMI metode was suksesvol om die aanpassing ten opsigte van die opbrengs patrone, en die potensiaal van die lokaliteite aan te toon. Die grafiese voorstelling van die AMMI-as se tellings en die gemiddelde opbrengs in ‘n twee-dimensionele grafiek, help om die aanpassing en die genotipe x omgewings interaksie te verduidelik.