GENOTYPE X ENVIRONMENT INTERACTION EFFECTS ON DEVELOPMENTAL TIME, KERNEL MODIFICATION AND YIELD OF EXPERIMENTAL QUALITY PROTEIN MAIZE (*Zea mays* L) HYBRID VARIETIES

By

Justify Gotami Shava

A thesis submitted in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE IN CROP SCIENCE** (Plant Breeding)

Department of Crop Science
Faculty of Agriculture
University of Zimbabwe
P O Box MP 167
Mt Pleasant
Harare

October 2007

Genotype × Environment Interaction Effects on Developmental Time, Kernel Modification and Yield of Experimental Quality Protein Maize (Zea mays L) Hybrid Varieties

By

Justify Gotami Shava

A thesis submitted in partial fulfilment of the requirements for the degree of MASTER OF SCIENCE IN CROP SCIENCE (Plant Breeding)

Department of Crop Science
Faculty of Agriculture
University of Zimbabwe
P O Box MP 167
Mt Pleasant
Harare

October 2007

The undersigned certify that they have read and recommend to the department of Crop Science the thesis entitled, 'Genotype × Environment Interaction Effects on the Developmental Time, Kernel Modification and Yield of Experimental Quality Protein Maize (*Zea mays* L.) hybrid Varieties.'

Submitted by

Justify Gotami Shava

In partial fulfillment of the requirements for the degree of MASTER OF SCIENCE IN CROP SCIENCE (Plant Breeding)

Department of Crop science
Faculty of Agriculture
University of Zimbabwe
P O Box MP 167
Mt Pleasant
Harare

October 2007

APPROVED BY:

A/CHAIRPERSON: Dr Chris Nyakanda……...Date...……

SUPERVISOR: Mr Cousin Musvosvi…….Date……...

CO-SUPERVISORS: Dr Charles Mutengwa……Date……

Dr John MacRobert…….....Date……..

ABSTRACT

Genotype × environment interactions occur in crops grown in more than one environment such that it is unusual for a single genotype to perform better than other genotypes at all the locations in which they are grown posing a challenge to breeders who must either develop genotypes with broad or specific adaptation. An investigation into the effects of genotype × environment interactions on grain yield, kernel modification, plant height, ear height, ear position, number of ears per plant, grain texture, days to 50 % anthesis and 50 % silking, and the anthesis–silking interval for 24 Quality Protein Maize (QPM) hybrids plus one normal check grown at five locations, ART Farm, CIMMYT Low N, Kadoma Research Station, Rattray Arnold Research Station and Shamva was carried out in 2006/7. The experiment was a 5 × 5 alpha Lattice design with two replicates at each location. The mean location grain yield ranged from 1.6 t/ha at Kadoma Reasearch Station to 11.104 t/ha at Art Farm. Genotype × environment interactions were significant ($P<0.05$) for plant height, but not for grain yield, kernel modification, days to 50 % athesis and 50 % silking, number of ears per plant and anthesis–silking interval ($P = 0.05$). The "which-won-where" GGE biplot showed that genotypes 1150 (A7/A), 1172 (A8/A), 1361 (A11/A), 791 (A10/B) and 1345 (A10/A) outperformed other genotypes in terms of yield at Art Farm; 791 (A10/B), 1361 (A11/A), 1003 (A1/A), 1345 (A10/A) and 389 (A4/B) outperformed others at CIMMYT Low N; O6t 359 (A3/B), 865 (A9/B), 1345 (A10/A), 1141 (A6/A) and 507 (A6/B) won at Kadoma Research Station, O6t 1361 (A11/A), 359 (A3/B), 1479 (A12/A) and 955 (A12/B) won at Rattray Arnold Research Station while O6t 359 (A3/B), 1003 (A1/A), 1361 (A11/A) and 466 (A5/B) won at Shamva. O6t 389 (A4/B), 865 (A9/B), 307 (A1/B), 1479 (A12/A) showed broad adaptation across the five locations tested. There were no significant relationship between grain yield and number of ears per plant ($R^2 = 0.1041$), plant height ($R^2 = 0.341$) and anthesis-silking interval ($R^2 = 0.0059$). An index of selection that incorporated kernel modification and grain texture indicated that the environments, genotypes and the genotype × environment interaction were all significant ($P<0.05$) suggesting that this index may be used in future QPM breeding for selecting simultaneously for kernel modification and grain texture. The testers were not significantly different from each other on their effect on grain yield when crossed to each of the lines A1 – A12 used to form those hybrids. However, lines and the locations were significantly different ($P < 0.05$).

DEDICATION

To my parents and my beloved ones Valodia and Nicole.

ACKNOWLEDGEMENTS

I am highly indebted to the following: Dr John MacRobert for supporting this project and make it a reality; Dr Ian Alexander Robertson who assisted me financially in order to enroll for the program, Dr Charles Mutengwa and Mr Cousin Musvosvi who supervised me to the end. I also thank CIMMYT as an organization for allowing me access and use of their valuable resources. Special thanks go to the CIMMYT guys, Morris Masukume, Evelot Nyamutowa and Joseph Makamba who were always willing to technically assist all the times. Thank you uncle Tino and brother Saul Wande for encouraging and supporting me financially throughout this program even if things were tough. I also thank Lewis Machida for teaching me the many computer skills that have made this document a reality.

CONTENTS

LIST OF TABLES

FIGURES

APPEND1CES

ABBREVIATIONS

ART – Agricultural Research Trust Farm

ASI – anthesis-silking interval

CLN – CIMMYT Low Nitrogen Plot (Harare)

CM - centimeters

DA – number of days to 50 % anthesis

EH – ear height

EPO – ear position

EPP – number of ears per plant

GYF – grain yield (field)

GYG – grain yield

INDEX – index of kernel modification and grain texture

KAD – Kadoma Research Centre

M - meters

MD 1 – kernel modification score 1

MD 2 – kernel modification score 2

MD 4 – kernel modification score 4

MD 5 – kernel modification score 5

MD 3 – kernel modification score 3

PH – plant height

QPM – Quality Protein Maize

RARS – Rattray Arnold Research Station

RL – lodging

SD – number of days to 50 % silking

SHM – Chakonda (Shamva)

TEXT- grain texture

CHAPTER ONE

INTRODUCTION

It has long been established that the poor quality of normal endosperm maize *(Zea mays* L*)* protein is due to deficiencies of two main amino acids lysine and tryptophan, as well as smaller ones such as isoleucine (Bressain, 1972). This is attributable to the presence, to the tune of 50 %, of prolamin (zein) in the normal maize endosperm, which is an unbalanced protein with deficiencies in lysine and tryptophan and excesses of leucine (Prasanna, Vasal, Kassahun, and Singh, 2001; Villegas, Eggum, Vasal, and Kohli, 2006). Excessive amounts of leusine reduce protein quality to an unknown extent. This significantly reduces the nutritional benefit for people whose diets are mainly composed of maize products, especially those residing in Sub-Saharan Africa. Since the 1960s extensive work has been done in selecting for mutants among the existing varieties of maize, which had the same beneficial agronomic properties as normal maize but differed only in their lysine and tryptophan content.

Various approaches to improve the protein quality of normal maize based diets have been attempted but one that gained marked interest in plant breeding was that by genetic modifications (Bressain, 1972; Manner, 1972). An *opaque-2* mutant gene, which is located on chromosome number 7, was identified in the early 1960s (Bjarnason and Vasal, 1992). This gave birth to the term Quality Protein Maize (QPM). The *opaque-2* mutant has low prolamin (zein) protein and hence has high levels of lysine and tryptophan amino acids as well as low levels of leucine (Bjarnason and Vasal, 1992). Quality Protein Maize has been shown to offer better quality protein than normal maize in the diets of adults, infants and children and various farm animals. Unfortunately, the QPM had some defects associated with it, which included relatively low yields compared to normal maize. It also succumbed to biological stresses, unacceptable kernel appearance and slower drying rates following physiological maturity (Villegas *et al.*, 2006).

Since the advent of QPM, many breeders worldwide ventured into its breeding in a bid either to increase the quality of protein content or improve the various agronomic properties as well as yield. In line with this effort various *opaque-2* mutant lines, open pollinated varieties (OPVs), and pure lines were produced which were later used to

produce *opaque -2* hybrids (Pixley and Bjarnason, 2002). In Africa, similar projects aimed at producing maize genotypes with improved protein quality were also initiated. Breeders at CIMMYT - Zimbabwe, and other breeders have produced some QPM hybrids. However no genotype × environment interaction tests have been carried out on performance of these newly and locally bred hybrid varieties.

The existence of genotype x environment interactions in plant breeding has long since been observed as seen by Sprague and Federer (1951) who attributed the small advances in genetic improvement to the existence of interactions. Genotype x environment interactions present the breeder with, basically, two problems that are:
a) The need, in spite of the interaction to try to produce a single variety with good general adaptation to the whole range of environmental and agronomic conditions of importance or to breed varieties adapted to specific subsets of these environments.
b) After choosing the range of environments within which a selection is to be targeted, breeders have to decide how best to evaluate their material with respect to its adaptability to this defined spectrum (Wright, 1975).

It is very important to quantify the genotype x environment interaction effect on yield, and on each physiological component, caused by each genotype and the different environment in which each yield trial is conducted. The breeder has to determine whether interaction of genotype and the environment is of a magnitude and type that favours the production of a single well adapted variety or production of separate varieties for specific single environments or defined subgroups of environments (Wallace, Bandoin, Beaver, Coyne, Halseth, Masaya, Munger, Myers, Silbernagel, Yourstone, and Zobel, 1993). Environments do differ such that even in subregions, microenvironments do occur that have conditions peculiar to themselves only, such as day lenghth, nutrition, temperature, moisture, pests and disease incidence.

Because genotype × environment interaction is the norm rather than the exception for most quantitative traits in plants, it is therefore important that breeders select for genotypes that are specifically adapted to certain sites. This translates to selecting hybrids that have the highest rates of yield accumulation in that environment. Subsequently, this can accelerate advance towards the highest potential yield at each geographical site. Higher yield for many sites will raise average regional yield and

higher yield for multiple regions in turn will raise average national yield and consequently the yield on worldwide bases increases (Wallace *et al.*, 1993).

Location and the duration of the growing season are physical factors that determine yield because they modulate and sometimes terminate gene activities. Since there is variation in the environment and duration of the growing season, recommendations are sometimes made that each microenvironment within each ecological zone be planted to hybrids or open pollinated varieties developed specifically for that microenvironment (Eberhart, 1989). In this regard many inroads have been made in Zimbabwe and regionally in normal maize but in as far as QPM is concerned no such efforts have been documented. In Zimbabwe, the environmental factor that has an effect on the final yield is mainly water (Caulfield and Havazvidi, 1989). Other factors include temperature, nitrogen nutrition and biotic stresses that include diseases like Maize Streak Virus (MSV) and insect pest attack, for example, maize stalk borer (*Busseola fusca*) (Caulfield and Havazvidi, 1989). These factors affect the yield of the final crop at various stages of development and their impact depends on locations. This research aims to determine the genotype x environment interactions on developmental time and yield of QPM hybrids grown in different localities. An assessment of genotype x environment interactions of these locally bred QPM hybrids is thus the subject of this research.

1.1 Objectives

1.1.1 Broad objective

To determine the genotype x environment interaction effects on developmental time, kernel modification and yield of experimental QPM hybrid varieties.

1.1.2 Specific objectives

1. To determine genotype x environment interaction effects on yield and yield variables, and anthesis-silking interval of each of 24 Seedco QPM experimental hybrids.

2. To determine genotype x environment interaction effects on Quality Protein Maize (QPM) modification of each of the 24 Seedco QPM experimental hybrids in different environments.

1.2 Hypothesis

1. Significant genotype x environment interaction effects exist on the yield and yield variables, and anthesis-silking interval of each of the twenty-four Seedco experimental QPM hybrids.
2. Significant genotype x environment interaction effects exist on kernel modification (QPM modification) in each of the twenty-four Seedco experimental QPM hybrids such that there is variation in the extent of modification in each of the twenty-four Seedco experimental QPM hybrids across the set environments.

CHAPTER TWO

LITERATURE REVIEW

2.1 The Importance of Maize (*Zea mays* L.)

Maize (*Zea mays* L.) is a staple food in 22 countries of the world and is a primary provider of calories, supplying almost 20 % of the world's food calories (Pixley, 2002). It is also used as a feed in livestock production. Overall maize consumption is expected to increase by 50 % globally, and by 93 % in sub-Saharan Africa from 1995 to 2020 (Pixley, 2002). Human consumption accounts for 70 % of all maize consumption in sub-Saharan Africa but much of the global use of maize is for animal feed. Maize provides about 15 % of all food crop protein although maize protein is of poor quality.

2.2 The History of Quality Protein Maize

The poor protein content of normal maize results from having almost half of its endosperm protein being constituted by zein fraction, which lacks lysine in its amino acid constitution. There are mutant genes that affect the quality of protein in maize by reducing the synthesis of zein (prolamin) in their endosperm protein resulting in increased proportions of other protein factors that have good levels of lysine and tryptophan. These mutants were discovered during the period 1963 - 1964 (Villegas, Eggum, and Kohli, 2006; Pixley and Bjarnason, 2002). These high lysine mutants include *Opaque -2* (o_2), *Floury - 2* (fl_2), *Opaque - 7* (o_7), *Opaque - 6* (o_6), and *Floury - 3* (fl_3). Adequate proof exists that *Opaque-2* varieties have better amino acid balance and 60 % to 130 % more lysine and tryptophan than normal maize, plus 12 % to 40 % reduction in isoleucine and leucine contents (Singh and Asnani, 1972). For example, in comparisons between normal and *Opaque - 2* versions of Tuxpeno maize on a whole grain analysis, tryptophan levels improved from 0.4 % of total protein present in grain to 1 %. Lysine content also increased from 2 % to 3.8 %. A concomitant decline in the levels of leucine from 18.8 % to 11.2 % was also noted. Isoleucine content also declined from 4.5 % of total grain protein present to 3.7 %. Although several genes were found to almost double the lysine and tryptophan content of maize endosperm, the *Opaque-2* gene has been used extensively to convert normal maize genotypes to quality protein maize.

Straight *Opaque - 2* versions of normal open pollinated varieties and the parental inbred lines involved in hybrid formation were obtained in the first six to seven years of intensive research (Villegas *et al.*, 2006). In the 1970s some *Opaque-2* varieties came into production but they failed to perform well compared to the normal varieties. Some of the weaknesses of the early QPM varieties included reduced kernel weight, unacceptable kernel appearance, greater susceptibility to ear rot pathogens, more infestation by weevils during storage and slower drying of kernel following physiological maturity (Pixley and Bjarnarson, 2002; Villegas *et al.*, 2006). The period from 1972 to date, saw breeders putting considerable efforts in breeding programmes that aimed to alleviate the inherent weaknesses of QPM. These weaknesses have now been overcome and many plant breeders, especially those operating under CIMMYT, are testing many promising QPM hybrids across the world.

2.3 Genetics of Quality Protein Maize

The *Opaque-2* mutant gene is located on chromosome number 7 and this gene behaves as a simple recessive (Bjarnason and Vasal, 1992). The *Opaque-2* gene does not show dosage effects and as a result it is expressed in the triploid endorsperm only when three dosages of the recessive allele are present and this is so for both kernel and biological characteristics. Several characteristics of *Opaque-2* mutants have been documented that include low zein (prolamin) protein factor, soft chalky endorsperm and deficiency in the amount of dry matter produced (Bjarnason and Vasal, 1992; Villegas *et al.*, 2006). Numerous research results have shown that mutants with high lysine had the capacity to inhibit the production of many components or subunits of the zein fraction (Bjarnason and Vasal, 1992; Prasanna *et al.*, 2001). Zeins have been divided into four clear groups, which are alpha zeins (encoded for by a multigene famiy), beta, delta, and gamma zeins encoded by oligogenes. It was shown that the *Opaque-2* differentially regulates and reduces the transcription of alpha zein component of the zein fraction. The remaining (non zein) protein fractions experience a concomitant increase. Two of the protein types, albumins and glutelin have much higher lysine and tryptophan content than the others by virtue of their increased fraction among endosperm proteins and better leucine/isoleucine ratio results. Since these non zein fractions have increased levels of albumins and glutelin as a result of the opaque - 2 gene, the lysine and tryptophan content of the endosperm is greatly increased in *Opaque - 2* maize.

However, *opaque-2* mutants have been shown to have some pleiotropic effects (Prasanna, Vasal, and Singh, 2001). There is a reduction in protein content from 9.2 % in normal maize to 8.2 % in soft *opaque - 2* maize (Pixley, 2002). This reduction however is compensated by increased grain size. Several secondary undesirable effects have been documented which include higher ribonuclease activity than normal maize, premature cessation of dry matter accumulation, increased potash and zinc content, reduced glutamate dehydrogenase, changes in several soluble proteins and an increase in trypsin inhibitor compared to that of normal maize (Bjarnason and Vasal, 1992). High lysine mutants adversely affect several important agronomic traits and storage ability. Fortunately, the use of modifying genes in QPM breeding has proved to be very important as their use has helped to overcome serious problems in the agronomic performance of these materials.

2.4. Modifying Genes

According to Vasal (2001), modifying genes or genetic modifiers are a series of genes that do not have any effect on their own but do interact and modify the expression of quality protein maize mutant genes. The effect of modifying genes could be on any trait but marked changes have been noticed in regards to kernel phenotype, of more importance being the chalky characteristic of *opaque-2* mutants. Genetic modifiers overcome the problems associated with the *opaque - 2* gene maintaining improved quality of protein in maize. They are quantitative in nature and have complex inheritance. Mostly, modifier genes have additive gene action making them easily heritable. However, maternal effects (gene dosage in endosperm) can influence F1 and F2 modification even in the presence of these modifier genes (Pixley, 2002). The expression of these modifier genes has been shown to vary immensely in different genotypes. Though there are conflicting reports on the issue, modified/vitreous endosperm has been shown to have more protein levels than the opaque endosperm. However, according to Bernado (2002), modifier genes have often been found to reduce protein quality. There are great variations existing for protein quality of modified versus opaque fractions. This observation, therefore, emphasizes the need for careful monitoring of the protein quality and quantity during the selection process. Modifiers may also affect kernel weight although they are that beneficial.

2.5 Multisite Testing and its Significance in Plant Breeding

Multisite testing refers to a situation where the same genotypes are grown in many different locations of different climatic or soil properties to evaluate their performances in each of these environments. Growing regions have to be subdivided into several relatively homogeneous mega-environments and genotypes be bred and targeted for adaptation to each of the mega-environments (Gauch and Zobel, 1997). The aim of this would be to maximize the potential of genotypes throughout a crop's variegated growing environments, despite differences in cultivar rankings from place to place which are brought about by genotype × environment interactions. Genotype - environment interactions cause no genotype to win everywhere always. Instead, they cause different genotypes to be superior in different locations.

"Mega-environment" is a term coined by researchers at CIMMYT and they defined it as, " a portion of a crop species' growing region with a fairly homogeneous environment that causes genotypes to perform best." Mega-environments can be international or transcontinental defined by similar biotic and abiotic stresses, cropping system requirements, consumer preferences and for convenience, by a volume of production of the relevant crop enough to warrant its attention (Gauch and Zobel, 1997). According to Freeman (1973), the main reason for growing genotypes in a wide range of environments is to estimate their stability.

Multisite trials play an important role in selecting the best cultivars for use in the future years at different locations and in assessing a cultivar's stability across environments before its commercial release (Vargas, Crossa, van Eeuwijk, Ramirez, and Sayre, 1999). A cultivar grown in different environments will frequently show significant fluctuations in yield and other traits' performance relative to other cultivars. Multienvironment or multisite trials are important in plant breeding for testing general and specific cultivar adaptation (dos S. Dias and Krzanowski, 2003). Environments or locations differ in such climatic factors as temperature, rainfall, humidity and incident radiation; and soil factors such as fertility, acidity/alkalinity and soil texture and structure. Cultivars grown in multi-environment trials react differently to these environmental changes resulting in differences in growth rates and partitioning of nutrients. When comparisons on performance are made, several cultivar attributes are considered of which grain yield is one of the most important. Testing of varieties across environments should be carried

out at a number of places to increase the chances of identifying genotypes adapted to several environments (Allard and Bradshaw, 1964). These will be well-buffered varieties that are able to adjust their life processes in ways such as to maintain productivity at a high level despite unpredictable fluctuation of the environment. Selecting these well-buffered genotypes, however, is a difficult task. Some breeders suggest the use of multi-site trials to breed many varieties, each of which will be adapted to a specific environment. This approach will result in high yield levels for specific microenvironments and the aggregate yield of the different environments result in high regional yields. So, if the environment is the one with adverse effects, it means that the approach aims to cure the genotype not the environment, for example it is easier to breed for varieties tolerant to salinity than remedy salinity itself.

2.6 Genotype x Environment Interactions and their Implications in Plant Breeding

Genotype x environment interactions have resulted in some reductions in breeding progress for such traits as grain yield in such a way that breeders have invested their time and efforts in investigating the nature and implications of these genotype x environment interactions in plant breeding.

2.6.1 Sources of genotype x environment interactions

Environmental factors have a greater effect on quantitative characteristics than on qualitative characteristics resulting in genotype - environment interactions. According to Sprague and Federer (1951) the interactions between genotypes and environments in plant breeding were discovered during the turn of the twentieth century (Allard and Bradshaw, 1964). The existence of interactions is the cause of the small increase in genetic advance. As such, it was generally agreed among breeders that interactions between genotypes and environments have an impact on the breeding of better varieties. Since then various researches in plant breeding were directed towards a better understanding of these genotype x environment interactions. Many definitions of genotype x environment interactions exist. According to Hakizimana, Haley, and Turnipseed (2000), genotype x environment interactions may be defined as the failure of genotypes to have the same relative performance from one environment to another. On the other hand, Simmonds (1981) and Yan and Hunt (2001) reported that genotype x environment interactions commonly refer to yield variation that cannot be explained by genotype main effects and the environment main effect. Falconer (1989) reported that,

the existence of interactions between genotypes and the environments changes the phenotypic value of an individual from being, simply, the relation; P = G + E, where P = phenotype, G = genotypic effects, and E = environmental effects. The other component, the interaction component, changes the relationship to $P = G + E + I_{GE,}$ where I_{GE} is the interaction component, and the interaction component gives rise to another source of variation. Interactions come in several forms. It can be envisaged as whether genotype A does better than B in each environment, or, whether A is superior to B in one environment and inferior to B in the other, or, whether a change in environment affects the genotypes in opposite directions (Allard and Bradshaw, 1964; Falconer, 1989).

These inconsistent differences in performance among genotypes from one environment to another arise because of two main reasons according to Yang and Baker (1991):
1. The differences in response of the same set of genes to different environments, and
2. The expression of different sets of genes in different environments.

Specifically, some studies on genotype x environment interactions have suggested that they are due to inconsistent genotype responses to factors like temperature, soil moisture, soil type, fertility level, or pests and diseases from location to location and year to year. In studies of genotype × environment interactions, an environment refers to a set of non-genetic factors that affect the phenotypic value associated with a genotype. These environmental variables include physical and chemical attributes of the soil; climatic factors such as precipitation and temperature; the amount, distribution of sunlight; and the number and kind of biological organisms to which plants are exposed (Bernado, 2002). These variations in environmental factors can therefore cause yield and its components, for example, kernel number and kernel weight, to vary from one environment to another (Hakizimana *et al.*, 2000).

Interactions are a significant challenge to plant breeders because they complicate breeding procedures and limit the usefulness of selection in any individual environment. According to Wright (1975) the occurrence of genotype - environment interactions presents the breeder with basically two sets of problems. The first one is that the breeder has to decide, in spite of the interaction, to attempt to produce a single variety with good general adaptation to the whole range of environmental and agronomic

conditions of importance without subdivision or to breed varieties adapted to specific subsets of these environments. Broad adaptation is exploited if regions/environments are not subdivided, whereas subdivision also allows for narrow adaptation to be exploited. The second problem is that of deciding how best to evaluate his materials with respect to its adaptability to that defined environment after selecting the range of environments within which a selection is to be grown.

2.6.2 Types of genotype x environment interactions

Yang and Baker (1991) reported that, genotype x environment interactions in crop and animal breeding are important in selection only when genotype ranks in terms of performance changes from one environment to another. They went on to distinguish between two types of interactions that are prevalent in crop and animal breeding. There are qualitative or crossover interactions and quantitative or non-crossover interactions.

2.6.2.1 Qualitative/ Crossover Interactions

This type of interaction involves changes in genotype ranks from one environment to another and this reflects the lack of perfect correlation between the environments (Bernado, 2002). The sign (i.e., + or -) of the difference between the performances of the genotypes changes but their absolute difference remain constant. In certain cases of genotype × environment interactions there is crossover interactions but the absolute difference between the performances of the two genotypes changes between the environments. In other words in the absence of crossover interactions it means the performance of varieties vary in terms of various traits which include, yield, disease resistance, response to nutrition, soil properties etc, as the varieties are planted in different environments (Vasal, 2001). Put in another way, in the absence of crossovers, the genotype that is the best in one environment will be the best in all environments. What it means therefore is that in the presence of crossovers the breeders must select one genotype for one set of environments and different genotypes for other environments (Yang and Baker, 1991).

2.6.2.2 Quantitative/Non-crossover Interactions

In this type of genotype performance in a set of environments, one genotype is superior to the other genotypes in all environments but the difference between their performances is not constant (Bernado, 2002). The rankings of the genotypes at each environment do not change in this type of genotype × environment interaction.

However, if the target population of environments changes, non-crossover interaction may not hold true (Bernado, 2002). Non-crossover interactions are regarded as heterogeneity or error variances. Since heterogeneity of variance can also arise from linkage or epistasis, confirmation tests have to be carried out to see if the variations of genotype differences across the environments are due to non-crossover interactions. The tests for the presence or absence of epistasis or linkage are based on the expectation of heterogeneity among various genetic variances and covariances estimated from the same or different environments (Falconer, 1989).

2.6.2.3 Importance of genotype x environment Interactions in plant breeding

A knowledge of the presence and type of genotype x environment interaction can help breeders make informed decisions to optimise breeding methods, selection intensity and testing procedures (Baker, 1969; Hakizimana *et al.*, 2000; Yan and Hunt, 2001). In addition, knowledge of the existence of interaction helps the breeder to know whether the best genotype in one environment will be the best in all the other environments, and the appropriate approach if there is no interaction. If interactions exist then it may mean that particular genotypes must be sought for particular environments (Briggs and Knowles, 1967; Falconer, 1989). The later approach would be justified because environmental difference has more effect on some genotypes than it has on others. As has been pointed out before, these regional or locational optimisation of the components of yield, hence yield itself, go a long way in the optimisation of the average national, regional, continental and global yields. The breeder must aim to produce varieties that minimize unfavorable genotype x environment interactions, that is, varieties that are able to control their developmental processes in such away as to give high and consistent performance. This can be possible if a breeder has a thorough understanding of the genotype × environmental interactions, which will aid him or her in the formulation of breeding objectives, the identification of the ideal, test conditions, and formulation of recommendations of areas of optimal cultivar adaptation.

2.7 Genotypic Responses to Environmental Factors

Genotypes respond differently when planted in different environments. Some have certain traits enhanced while other traits are depressed. The opposite may be true for other genotypes.

2.7.1 Response to a single environmental factor

At times it is advisable to apply genotype x environment interaction tests to situations where the environmental factors are known and thereby to interpret some of its aspects. The simplest possible situation occurs when only one factor of the environment is varied and where that one factor is precisely controlled (Gauch, 1988). An optimum is obtained normally if cultivars are grown in a wide range of the environment factor, for example, temperature or irrigation. By maintaining the other environmental factors constant and varying only one environmental factor, one is able to determine the genotype x environment interactions of genotypes to various levels of the environmental condition. This is true when a number of genotypes are grown on this wide range of levels of this single environment. However, when this type of experiment is used and the method of cultivar yield regression on the environmental mean is used to estimate cultivar performance, similar cultivars have been shown to largely determine the values of environmental mean and these cultivars normally show little deviation from the linear regression (Eberhart and Russell, 1966). This approach is not appropriate for evaluations under field conditions as, in such cases, many factors affect the overall crop yields.

2.7.2 Genotypic responses to several environmental factors

When several factors are involved, results change as the optimum level of an environmental factor is not a constant but varies with levels of other environmental factors (Singh and Asnani, 1972). What is required to interpret genotype x environmental interactions is therefore the response of the genotypes to various combinations of several factors. Such comprehensive data can only be obtained from very large experiments. In this case multiple regressions would be appropriate. In field situations, many environmental factors influence growth and yield. These include temperature, radiation and moisture, which are uncontrollable. They fluctuate rapidly and their levels are relatively difficult to record. It is for this reason that the average response of genotypes is used to measure the environment. According to Yan and Kang (2003), this approach is valuable where an assessment is being made of many varieties but ultimately it will be necessary to determine the major limiting factors influencing yield.

2.7.3 Dealing with genotype × environment interaction

Genotype × environment interactions cause fluctuations in the performance of many different cultivars in many regions. If genotype × environment interactions are successfully identified, Bernado (2002) suggests three alternative approaches to coping up with them. The first approach is to ignore them. However, ignoring these interactions does not assume that they are absent. Rather, their presence is visualized and potential cultivars are tested in wide range of environments. On the basis of their average performances across all the environments, cultivars are recommended for growing. However, the cultivars chosen in this way should not probably be the best ones available for each specific environment. The second approach is to reduce the genotype × environment interaction by partioning the target group of environments into smaller more homogeneous subgroups using cluster analysis and principal component analysis. Cultivar recommendations are then made separately for each subgroup of environments. This approach looks better than just ignoring the genotype- environment interactions. The third and probably the best approach to deal with genotype × environment interactions is to exploit them. Identifying cultivars best suited to specific environments so that the productivity in that environment is maximized does this. Here, the information on the performance of genotypes as a linear function of the level of productivity in each environment is provided by stability analysis.

2.8 A Review of the Methods used for Analysing Genotype x Eenvironment Interactions

2.8.1 Introduction

Genotype x environment interactions and phenotypic stability have been studied, described and interpreted using many statistical methods. The usual statistical analyses applied to yield trials include analysis of variance (ANOVA), principal component analysis (PCA), and linear regression (LR). These have been shown to be inadequate in analysing a complex data structure (Zobel, Wright and Gauch, Jr, 1998). These methods can be divided into two major groups, univariate and multivariate stability statistics. Methods such as analysis of variance, regression on the environmental mean models; the Additive Main effects and Multiplicative Interactions (AMMI) models as well as Partial Least Squares (PLS) regression models are some of them. All of these use only the phenotype response variable of interest.

There has been, however, a movement from less direct and less informative methods of interpreting genotype x environment interactions (GEI) to the more direct and more informative models. AMMI models are more informative than the conventional analysis of variance model in describing GEI and provide greater scope for modeling and interpreting GEI than the simple regression on the site mean because GEI can be modeled in more than one dimension. The latest development, the PLS regression model is even better in directness and informativeness. Below is a review of these conventional and current methods of GEI study.

2.8.2 The Analysis of Variance (ANOVA) model

This is the basic model for the analysis of the two-way table of cultivar yield by environment data. It regards the interaction as a single composite source with its (G-1)(E-1) degrees of freedom. The ANOVA is an additive model. Since it is an additive model, it has the problem that it describes only the main effects effectively without handling the GE interaction satisfactorily (Zobel *et al.*, 1988). It gives no insight into the particular patterns of genotypes or environments that give rise to the interaction. Though ANOVA can test significance of the interaction, the test might be misleading.

2.8.3 Simple regression of cultivar performance on the environmental mean

This is the most commonly used procedure for modeling GEI. It is depicted as a set of regressions for each cultivar in which the heterogeneity of slopes accounts for the GEI (Bernado, 2002). Since the differences of slopes in this model generally explain only a small proportion of the usually complex GEI, a more elaborate model is often necessary for an adequate description of GEI. There are several differences in the fitting procedure of the most commonly used model because staged fitting of the interaction component is known not to give a least squares fit. In general, this model confounds the interaction with the main effects, reducing its power for general significance testing (Zobel *et al.*, 1988).

2.8.4 The Factorial Regression models (FR)

These models have also been shown to have multiplicative structure for interaction like the Additive Main effects and Multiplicative Interaction (AMMI) (Crossa *et al*., 1990) The main difference between the FR and AMMI models is that in FR, the GEI (residual matrix consisting of the two way table of means corrected for cultivar and site main

effects) is modelled directly as a function of the cultivar and environmental variables. The FR is effective in identifying the environmental and cultivar covariables that explains a relatively large proportion of the total GEI variability in two complex data sets (Vargas, Reynolds, Ramirez, Sayre, and Talbot, 1998). It directly incorporates the external variables into the model. According to Vargas *et al.,* (1998), the main advantage of the FR is that parameters are estimated and hypotheses are tested in relation to the available external variables. When environmental and cultivar variables are considered simultaneously, multiple FR with a stepwise variable selection procedure provides a useful tool for selecting the most relevant covariables and their cross products for explaining GEI (Vargas *et al.*, 1998).

2.8.5 The Joint Regression Analysis

This method is popular among the univariate methods. This is because it is very simple in calculation and application (Goncalves, Bortoletto, Martins, da Costa, Gallo, 2003). It can be used even where environmental parameters like rainfall, temperature, humidity and others are not measurable. It provides a conceptual model for genotypic stability. However, there are some objections to the joint regression model. The first one is that the estimated main effects, that is, the additive main effect of years represent only an estimate of the true year effect and hence is subject to error (Eberhart and Russell, 1966). This problem will cause the estimated regression coefficient to be biased although their ranking will not be disturbed. The second bias results from the presence, in the year effect, of the genotypic effects that are to be regressed on it. The coefficient of regression, $\beta_{i,}$ will be biased. The bias arises because the assumption has to be made in regression analysis that the independent variable in this case, the environmental mean, is measured without error (Bernado, 2002). The bias depends on the number of genotypes and the ratio of the between environments variation to the error mean square. In well-designed experiments, this ratio will be large and the bias will be small, but not necessarily negligible (Hardwick and Wood, 1972). The bias will also tend to be small for a large number of genotypes.

2.8.6 Principal Component Analysis (PCA)

The PCA is a data reduction method useful for explaining genotype × environment interaction with only a few variables. PCA transforms data into linear combinations of the original variables (Vargas et al., 1999). These linear combinations are called

principal components and are uncorrelated with each other. The first principal component accounts for the largest percentage of the variation in the data, the second principal component accounts for the second largest percentage of the variation, and so on. Environments are grouped on the basis of scores for the first few principal components axes instead of grouping them on the basis of their interaction values (Yang and Baker, 1991). Principal components are extracted by rotating the axes corresponding to the original variables in such a way that the explained variance by the principal component is maximised. PCA is useful if the first few principal components accounts for a large percentage of the variation (Vargas *et al*., 1999). Unfortunately, empirical evidence indicates that the first few principal components do not always explain a large percentage of variance due to genotype × environment interactions (Bernado, 2002). In this case, PCA loses much of its usefulness in partitioning environments into homogeneous subgroups.

2.8.7 The Additive Main effects and Multiplicative Interaction (AMMI) Model

The objective of AMMI analysis is to obtain an improved estimate of the performance of a genotype in a particular environment (Bernardo, 2002). The rationale behind the AMMI approach is that the observed performance of a genotype in a particular environment is not the best estimate of the true performance of the genotype in that environment. This rationale is based on a subdivision of the interaction into two components. The first component is due to repeatable patterns of genotype × environment interaction and the second component that is called 'noise' is due to non-repeatable genotype × environment interactions. The concept behind AMMI model is that the first principal component axes tend to capture most of the variance due to genotype × environment interactions as a result of repeatable patterns (Bernado, 2002).

The AMMI model first applies the additive analysis of variance (ANOVA) model to two way data, and then applies the principal component analysis (PCA) model to the residual from the additive model that is, to the interaction (Gauch, 1988). According to Gauch and Zobel (1997), statistical strategies for identifying mega-environments should meet the following four criteria: it should show flexibility in handling yield trials with various designs; it should focus on that fraction of variation that is relevant for identifying mega-environments; it should show duality in giving interpreted information on both genotypes and environments and finally it should be relevant for the primary

objective of showing which genotype wins where. These criteria are fully met when the AMMI model with the usual bi-plots are supplemented with many new types of graphs. A biplot is helpful for visually interpreting the performance of genotypes in different environments. AMMI model postulates additive components for the main effects of genotypes and environments and multiplicative components for the effect of the interaction (dos S. Dias and Krzanowski, 2003). As such, AMMI analysis of yield trials is a useful extension of the more familiar ANOVA, PCA and linear regression procedures, especially when given a large genotype-environment interaction. This method provides more opportunity for modelling and interpreting GEI than the simple regression on the site mean model because it allows modelling the GEI in more than one dimension (Vargas *et al.*, 1998).

When information on environmental variables is available (precipitation, temperature, etc), it can be correlated to, or regressed on the AMMI environmental scores so that an interpretation of the causes of grain yield GEI can be attempted. However, Zobel *et al.* (1988) have found some limitations associated with this method. AMMI analysis is sensitive to multicollinearity and is non-parsimonious. One inherent difficulty with AMMI approach is that much of variation in environmental factors is unpredictable across different years. Also, AMMI does not distinguish between non-crossover and crossover interactions (Bernado, 2002). When using this method, it is not easy to relate many environmental variables to several principal component factors simultaneously. Another problem is that of difficulties in retaining the optimal number of principal components for interpretations. To try and reduce these problems, the Partial Least Squares (PLS) was developed (2.8.9).

2.8.8 Stability Analysis

The main reason for growing genotypes in a wide range of environments is to estimate their stability. It is an encouraged practice in plant breeding to select stable genotypes that interact less with the environments in which they are to be grown (Eberhart and Russel, 1966). The concept of stability has been defined in various ways. Some researchers have called it ecovalence and defined it as the contribution of a genotype to the genotype - environmental interaction sum of squares (Eberhart and Russel, 1966). The aim of stability analysis is to examine the reaction of a genotype relative to other genotypes in different environments. It allows the identification of genotypes that are

stable or unstable. In applying stability analysis, the breeder would be aiming at selecting genotypes that are consistently high yielding, over the range of environments that occur in different locations or seasons. The concept of stability implies that some measure that distinguishes one environment from another is required. This environmental index should be based on environment factors that affect the performance of genotypes like soil properties, climatic factors or biotic and abiotic stresses (Bernado, 2002). These indices are not yet developed and until they are developed the belief is that the effect of the j^{th} environment can serve as a useful environmental index. Basing selection on stability analysis is often inefficient due to genotype x environment interactions and as such, selection for stability is not possible until a suitable model with suitable parameters is available to provide the criteria for ranking varieties for stability. According to Eberhart and Russell (1966), the model for stability analysis involves a simple multiplicative model: the b_i value for genotype, i, is multiplied by the t_j value for environment. It gives a means of estimating the stability of varieties in a specific environment and season, which provides a way for ranking them.

2.8.9 The Partial Least Squares Regression Model (PLS)

Prediction ability was the main goal of PLS development. The method is more appropriately used when the number of variables is much larger than the number of observations and there is high collinearity among variables. This sophisticated statistical model incorporates external environmental and/or cultivar variables for studying and interpreting genotype x environmental interaction (GEI) (Bernado, 2002). It relates GEI effects as independent variables (Y) to external environmental or cultivar variables as the explanatory variables (X) in a single estimation procedure (Vargas *et al.*, 1998). The PLS method is a more direct and parsimonious model. While the AMMI method has problems in situations where there is multicollinearity, PLS regression models are appropriate in these situations. The PLS model describes GEI in terms of differential sensitivity of cultivars to environmental variables like the factorial regression model (Wallace *et al*., 1993)

2.9 Numbers of Replicates and Environments to use in Genotype x Environment Interactions Trials.

One of the questions posed in GEI trials is the number of replicates to use in trials per site in order to obtain correct and dependable inferences. Another matter is the number

of environments to use at a time. Many suggestions pertaining to these questions have been put across. Experiments were also carried out with the aim of determining the minimum number of replicates and environments to incorporate in such multisite trials (Bernado, 2002). Formulas have been generated that give the number of replicates per location. Generally, it is agreeable that increasing the value of r (replicates) will reduce the variance of a genotype mean because the contribution of V_E (environmental variance) is reduced. At the same time increasing the value of e (environments) will lead to larger decrease in variance of genotype mean because the contribution of V_E and V_{GE} (interaction variance) are both reduced.

It is argued that a single observation does not contribute much to the multivariate structure; so, neither does its deletion remove such. Use of one replicate in each environment causes V_E and V_{GE} to be confounded (Bernado, 2002). Also, increasing the number of replicates to more than two per site was seen to be of no significant benefit in trials of this nature (i.e. GE interaction trials). Considering that resources are expensive and the shortage of planting seed, which normally happens, two replicates are good for each multisite trial. To cut costs of running trials, breeders at CIMMYT use an alpha lattice design with only two replicates and also, it is the reason why in this trial only two replicates were used.

If only one environment is used for testing genotypes, the V_G and V_{GE} become confounded. Actually, the estimate of V_G is biased upward by V_{GE} (Bernado, 2002). Increasing the number of environments is also expensive, so, if the vast environment could be divided into fairly large sub-environments called mega-environments the better. If the environments could be grouped into large sets this cuts on the expenses involved. Also, the advantage of increasing e (environments) is maintained only if V_{GE} is kept constant.

CHAPTER THREE

MATERIALS AND METHODS

3.1 Planting Material and Experimental design

Twenty-four Seed Co Ltd experimental QPM hybrids from Line x Tester crosses plus one standard check hybrid, SC 2785 (Table 3.1) were planted at five locations, *viz*; Kadoma Research Centre, CIMMYT-Zimbabwe (Low N conditions), ART Farm, Rattray Arnold Research Station, and Shamva.

Table 3.1 QPM genotypes used in the trial

Entry #	Name	Line	Tester	HETEROTIC GROUP	HETEROTIC GROUP	QPM
		Code	code	Female	Male	Donor
1	06t545	A8	B	S	A/B	CML181
2	06t1006	A2	A	N	A	CML144
3	06t1150	A7	A	S	A	HYBRID
4	06t359	A3	B	S	A/B	CML181
5	06t1395	A9	A	O	A	CML159'
6	06t865	A9	B	B	A/B	CML159'
7	06t313	A2	B	N	A/B	CML144
8	06t498	A6	B	S	A/B	CML144
9	06t507	A7	B	S	A/B	HYBRID
10	06t791	A10	B	N	A/B	HYBRID
11	06t1361	A11	A	S	A	CML144
12	06t1141	A6	A	S	A	CML144
13	06t1172	A8	A	S	A	CML181
14	06t955	A12	B	N	A/B	CML141
15	06t389	A4	B	S	A/B	CML141
16	06t1076	A4	A	S	A	CML141
17	06t307	A1	B	S	A/B	CML144
18	06t811	A11	B	S	A/B	CML144
19	06t1479	A12	A	N	A	CML141
20	06t1054	A3	A	S	A	CML181
21	06t1003	A1	A	S	A	CML144
22	06t1345	A10	A	N	A	HYBRID
23	06t466	A5	B	H	A/B	HG
24	06t117	A5	A	K	A	HG
25	SC2785					

The experimental QPM hybrids were developed from lines bred for endosperm modification (QPM modification). For example, Seed Co line of heterotic group S was crossed to QPM donor CML 144 to produce a line coded A1. The line A1 was crossed to a single cross tester A to give the hybrid O6t 1003. In short, O6t 1003 = A1/A and

O6t 307 = A1/B where A1 (Inbred line) came from the cross (S/CML 144). The material was planted in a 5 x 5 alpha lattice design with two replicates per location. Each hybrid was randomly allocated to a plot consisting of two rows with each row having 17 stations, making 34 stations per plot. The inter-row spacing was 0.75 m and the intra-row spacing was 0.25 m.

3.2 Field Management

Field management basically consisted of land preparation, fertilizer and water management as well as weed and pest management.

3.2.1 Land preparation and planting

Ploughing was done using a tractor drawn disc plough at four of the five locations. At Chakonda (Shamva), an ox-drawn mouldboard plough was used for land preparation. A pre-marked wire was used to mark planting stations at spacing of 0.75 m between rows and 0.25 m within rows, which were 4 m long. Seed were sown by hand to achieve a final plant density of 53 000 plants per hectare at all of the five locations. Planting was done within a time frame of a week in mid - December 2006 at all the locations except for Shamva, which was planted in mid January 2007.

3.2.2 Fertilizer application and water management

A basal application of 300 kg/ha Compound D fertiliser (8 % N: 14 % P_2O_5: 7 % K_2O) was applied at each planting station at all the other locations except CIMMYT-Zimbabwe, which was under low N conditions. Topdressing was also done using Ammonium Nitrate (34.5 % N) at five weeks after emergence at all the other locations except for CIMMYT-Zimbabwe where the field grown was depleted of N over a long period of time and is inherently low in N or there is no N at all. As for water management all the locations were managed under natural rainfall conditions.

3.2.3 Pest and weed management

Trials was kept weed free throughout the season. Weeds were controlled initially using a mixture of Atrazine (Atrazine WP), Dual (Metolachlor) and Gramoxone (Paraquat) at 4.5, 1.8, and 1.0 L/ha respectively, as a pre-emergence control. These herbicides were applied using a knapsack sprayer with a flat fan nozzle. From four weeks onwards, weeds were controlled solely by hand weeding using hoes. Karate (Lambda

cyhalothrin) was also mixed with the herbicides at a rate of 100ml/ha in 200 L of water to control soil-borne pests.

3.3 Description of the Locations

Five locations occurring in different Agro-ecological regions (Natural Farming Regions) of Zimbabwe were chosen for testing the experimental hybrids.

3.3.1 Kadoma

The trial was situated at Kadoma Research Station. Kadoma is a medium potential area with an annual average rainfall of 727 mm. It has an altitude of 1155 m. The site is at latitude of 18.32^{o}S and a longitude of 31.50^{o} E. The soils at this site are red clays.

3.3.2 CIMMYT-Zimbabwe (Harare)

It is a high potential area situated at the University of Zimbabwe Farm about 12 km North of the City of Harare. It has an altitude of 1468 m and has red clay soils. Block O, which was used for setting this trial, is inherently low in Nitrogen and is used for screening material for low N tolerance. Harare has a mean annual rainfall of 820 mm and latitude of 17.80^{o} S and a longitude of 18.32^{o}E.

3.3.3 ART Farm

This location is also near Harare. It has a mean annual rainfall of 820 mm and latitude of 17.80^{o} S and a longitude of 18.32^{o}E. The soils are red clays and the difference between this location and CIMMYT-Zimbabwe lies in it having optimum/ normal N fertiliser conditions. The altitude is 1468 m.

3.3.4 Rattray Arnold Research Station

The station is 40 km from Harare along Shamva road. It has red clay soils and is 1450 m, latitude of 17.90^{o} S and a longitude of 16.32^{o}E. It is a medium potential area with mean annual rainfall of 800 mm. The trial was managed under optimum conditions at this site.

3.3.5 Chakonda (Shamva)

This is a medium potential area with a mean annual rainfall of 700 mm. The soils are sandy and its altitude is 1368 m. The latitude is 15.25^{o}S and the longitude is 14.90^{o}E. The location is in a smallholder farming area.

3.3 Measurements

The following traits were measured and other related parameters like anthesis-silking interval calculated from the directly measurable parameters.

3.3.1 Grain yield

Shelled grain weight per plot adjusted to 12.5 % grain moisture and converted to tons per hectare for each experimental hybrid for every location.

3.3.2 Anthesis and silking dates (ASI)

Measured as number of days after planting when 50 % of the plants per hybrid at every location were shedding pollen and silking respectively.

3.3.3 Plant height (PH)

Measured as the height between the base of the plant to the insertion of the first tassel branch of the same plant. A representative plant was selected in each plot among all the plants and its height measured to the nearest centimeter.

3.3.4 Grain Texture

Scored using a scale from 1 (= flint) to 5 (= dent) for every hybrid at each of the five locations. Grain texture scores were used in the formulation of the index of selection for kernel modification and grain texture.

3.3.5 Number of ears per plant (EPP)

Counted as number of ears with at least one fully developed grain divided by the number of harvested plants. EPP values of below 1 indicates partial barrenness, an EPP value above 1 indicates partial prolificacy. If taken under drought or N stress, values of greater or equal to 1 indicate stress tolerance.

3.3.6 Endosperm modification

Score for the extent of modification (extent of opaqueness) of kernels rated on a scale from 1 (fully modified/normal looking kernels) to 5 (unmodified/opaque kernels) as evaluated on a light table. A sample of 100 kernels from the shelled grain was grouped into each of the five classes and the number of kernels in each class recorded and modification evaluated per plot basis.

3.3.7 Index of Selection

An index of selection that incorporated all the kernel modification scores and grain texture was used. The index was of the form S = (6 – TEXT) + (3* MD 1)/5 + (2 * MD 2)/5 + (MD 3)/5 where S is the resultant score, TEXT is the grain texture and MD stands for modifications. Score 1 had the highest weight and score 5 the least. The maximum score with this model was 30 and any score above 16.5 was acceptable.

3.4 Statistical Analysis

The data was analysed using the AMMI analysis, which was performed using AGROBASE 2000. AMMI analysis first fits additive effects for genotypes (G) and environments (E) by the usual additive analysis of variance procedure, and then fits multiplicative effects for genotype - environment (GE) interaction by principal component analysis (PCA).

The Model is

$$\mathbf{Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{r} \lambda_k \alpha_{ik} \gamma_{jk} + R_{ij}} \quad \text{where,}$$

$\mathbf{Y_{ij}}$ is the yield of the i^{th} genotype in the j^{th} environment.

$\boldsymbol{\mu}$ is the grand mean

$\mathbf{g_i}$ is the mean of the i^{th} genotype minus the grand mean.

$\mathbf{e_j}$ is the mean of the j^{th} environment minus the grand mean.

$\boldsymbol{\lambda_k}$ is the square root of the eigenvalue of the PCA axis k.

$\boldsymbol{\alpha_{ik}}$ and $\boldsymbol{\gamma_{jk}}$ are the principal component scores for PCA axis k of the i^{th} genotype and the j^{th} environment respectively.

$\mathbf{R_{ij}}$ is the residual.

The 'which–won–where' biplot was generated based on the SREG model as generated by the GGE biplot software GGE version 5.2 2006 developed by Yan (2001) and Yan and Kang (2003). A Genotype-Genotype × Environment Interaction (GGE) biplot from the Site Regression (SREG) model is originated when the environment centered G + (G × E) data is subjected to singular value decomposition. The first principal component (PC1) scores of the genotypes and the environments were plotted against their respective PC2 scores. The Line × Tester analysis was done in Minitab 12 for Windows (2001).

CHAPTER FOUR

RESULTS

4.1Grain Yield

The mean genotype and mean location grain yields are presented (Table 4.1). For grain yield, the genotypes and the environments were highly significant ($P<0.01$) (Appendix A and Table 4.2). The genotype × environment interaction was not significant ($P>0.05$). ART Farm (11.1 t/ha) had the highest location and genotype mean yields while Kadoma (1.597 t/ha) had the lowest location mean yields. The highest yielding genotype at ART Farm (ART), CIMMYT Low N (CLN), Kadoma (KAD), Rattray Arnold Reseacrch Station (RAR) and Shamva (SHM) were O6t 1150 (A7/A) (13.4 t/ha), O6t 791 (A10/B) (4.8 t/ha), O6t 359 (A3/B) (2.4 t/ha), O6t 1361 (A11/A) (7.1 t/ha), and O6t 359 (A3/B) (4.0 t/ha), respectively, while the least yielding genotypes were O6t 1141 (A6/A) (8.5 t/ha), O6t 507 (A6/B) (1.6 t/ha), O6t 1479 (A12/A) (0.3 t/ha), O6t 1395 (A9/A) (3.7 t/ha) and O6t 389 (A4/B) (0.9 t/ha), respectively. At each location tested, some hybrids yielded more than the standard check hybrid, SC 2785. These include the following hybrids, O6t 545 (A8/B), O6t 359 (A3/B), O6t 791 (A10/B), O6t 1361 (A11/A), O6t 1172 (A8/A), O6t 955 (A12/B), and O6t 1345 (A10/A) (Table 4.1).

Figure 4.1 Representative cobs of O6t 1003 (A1/A) harvested at sites 1-6 (ART Farm, CIMMYT Low N, Kadoma, Rattray Arnold, Shamva and Muzarabani, respectively.)

.

Table 4.1 Mean grain yield (t/ha) of hybrids at the five locations in 2006/7

Entry	Name	Line/Tester	Art Farm	CIMMYT Low N	Kadoma	Rattray Arnold	Shamva	Mean
1	06t1003	A1/A	10.7	3.8	0.6	5.3	3.6	4.8[ab]
2	06t1006	A2/A	10.6	2.9	1.7	5.6	3	4.8[ab]
3	06t1054	A3/A	12.2	2.3	1.2	6.6	1.7	4.8[ab]
4	06t1076	A4/A	12.2	2.6	1.7	5.9	2.3	4.9[ab]
5	06t117	A5/A	8.9	2.6	1.6	4.6	2	3.9[ab]
6	06t1141	A6/A	8.5	2.7	2	6.6	1.9	4.3[ab]
7	06t1150	A7/A	13.4	3.1	1.3	4.6	1.5	4.8[ab]
8	06t1172	A8/A	13.4	2.9	1.6	5.3	2	5.0[ab]
9	06t1395	A9/A	9.5	2.7	1.8	3.7	1.5	3.9[ab]
10	06t1345	A10/A	12.7	3.1	2.4	5.7	2.4	5.3[ab]
11	06t1361	A11/A	13.1	4	1.8	7.1	3.3	5.9[ab]
12	06t1479	A12/A	10.3	3	0.3	6.8	1.6	4.4[ab]
13	06t307	A1/B	10.7	2.7	1.3	6	2.2	4.6[ab]
14	06t313	A2/B	9.4	2.7	2	5.1	2.4	4.3[ab]
15	06t359	A3/B	10.7	3	2.5	6.9	4	5.4[ab]
16	06t389	A4/B	11.3	3.2	1.4	6	0.9	4.6[ab]
17	06t466	A5/B	9.7	2.7	1.1	5.7	3	4.4[ab]
18	06t507	A6/B	12.5	1.6	1.9	5.8	1.2	4.6[ab]
19	06t498	A7/B	9.1	2.1	1.6	5	1.5	3.8[ab]
20	06t545	A8/B	12.8	2.2	1.8	5.5	2.9	5.0[a]
21	06t865	A9/B	10.7	2.6	2.1	5.7	1.8	4.6[ab]
22	06t791	A10/A	12.2	4.9	1.8	5.3	1.5	5.2[ab]
23	06t811	A11/B	8.5	2.3	1.4	4	1.8	3.6[ab]
24	06t955	A12/B	12.3	2.9	1.3	6.7	2.1	5.0[ab]
25	SC2785	SC2785	12	2.9	1.5	6.1	2	4.9[b]
	MEAN		11.1[a]	2.9[b]	1.6[c]	5.7[c]	2.2[c]	4.7
	LSD(0.05)		5.6	2.6	2.4	3.4	2.7	3.4
	CV(%)		17.3	31.4	52.5	20.5	43.4	33
	SED		1.9	0.9	0.8	1.2	0.9	1.1

NB: Means followed by the same letter in a column and row are significantly different at $P<0.05$. Row means were separated using Turkey's Test (0.05) and column means were separated using the LSD (0.05).

Table 4.2 Analysis of variance summaries for grain yield, plant height, anthesis silking interval, days to 50% anthesis, days to 50% silking, number of ears per plant and the index of selection for kernel modification and grain texture

	Grain Yield		Plant Height		Anthesis-Silking Interval		Days to silking		Days to anthesis		Ears per plant		Index	
Source	Df	MS	Df	MS	df	MS	df	MS	df	MS	df	MS	df	MS
Total	249		249		249		249		249		249		249	
Environments	4	767.655**	4	71755.5**	4	32.6*	4	467**	4	275.5**	4	0.7**	4	71755.5**
Reps within Env.	5	1.793	5	567.9	5	3.3	5	78	5	7.1	5	0.04	5	568
Genotypes	24	2.719*	24	1461.6**	24	5*	24	16**	24	15.1*	24	0.1**	24	1461.6**
Genotype-Env.	96	1.562	96	443.5**	96	2.7	96	6	96	4.8	96	0.04	96	443.5
IPCA 1	27	3.297	27	777.5	27	3.8	27	12	27	8.5	27	0.1	27	777.5
IPCA 2	25	1.051	25	526.4	25	2.9	25	5	25	4.1	25	0.02	25	526.4
IPCA 3	23	0.772	23	257.6	23	1.1	23	3.3	23	3.4	23	0.02	23	257.6
IPCA 4	21	0.805	21	119	21	0.5	21	2.5	21	2.2	21	0.01	21	119
Residual	120	1.489	120	149.9	120	2.182	120	4.9	120	3.9	120	0.06	120	149.9

* indicates significance at P<0.05.** indicates significance at P<0.01.

4.1.1 Regression of variety mean yield on location mean yield

Figure 4.2 shows the differences in the gradients (β_1) values between each hybrid whose variety mean yields were plotted against mean location yield. A cluster of points on the figure corresponds to mean location yields at each location. From left to right a cluster represents a location with the least overall grain yield (Kadoma) to the one with the highest location mean yield (ART Farm). Criss-crossing of regression lines show changes in ranks for grain yield for the respective hybrids from one location to another. Differences in $\beta 1$ values between the hybrids show differences in their interactions with each of the five locations ART Farm, CIMMYT Low N, Kadoma, Rattray Arnold Resaerch Station and Shamva. Hybrid O6t 1479 (A11/A) is relatively high yielding across all tested locations. So it shows high adaptation to the tested locations. Hybrid O6t 307 (A1/B) has moderate adaptation all of the locations tested while O6t 1150 (A7/A) is a poor performer at CIMMYT Low N, Kadoma and Shamva but yields high at ART Farm and Rattray Arnold Research Station.

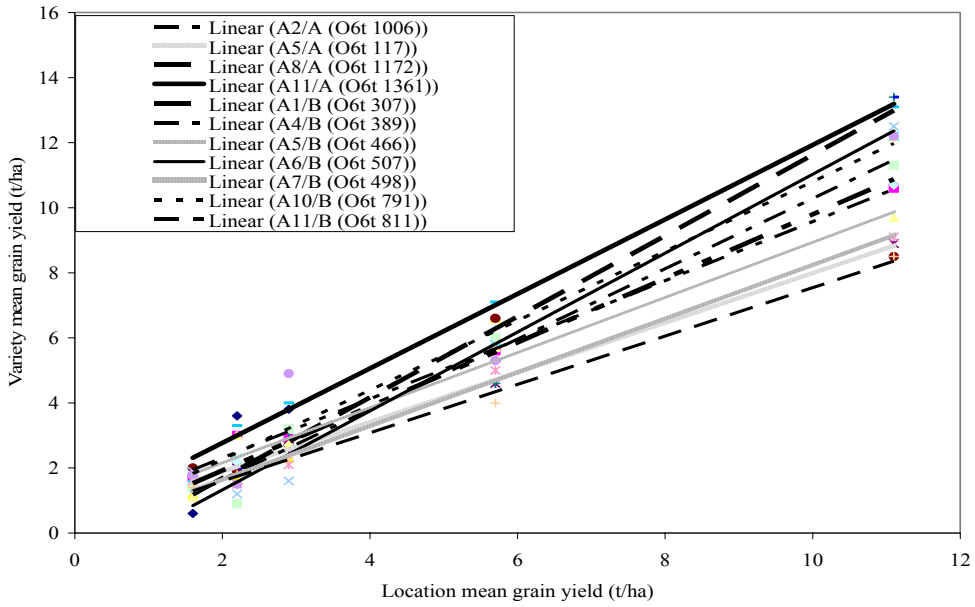

Figure 4.2 Regression of the yields of 11 varieties/hybrids/genotypes against location mean yield (t/ha). Only 11 hybrids were chosen to illustrate particular hybrid responces.

4.1.2 Plot of regression coefficients (β_1) against variety mean yield (t/ha)

The regression coefficients (β1) of each hybrid plotted against hybrid mean yield is presented (Figure 4.3). Hybrids with $\beta_1 \geq 1$ line (e.g. A7/B, A8/A and A4/B) and with high mean yields are adapted to high potential locations like ART Farm and Rattray Arnold Research Station. Hybrids A3/B had an above average yield but $\beta 1 < 1$, indicating that it is adapted to unfavourable conditions like CIMMYT Low N, Kadoma and Shamva. Hybrids A7/B, A8/A, A4/B, A12/A and A4/A are sensitive to environmental changes since they have β_1 values above 1.

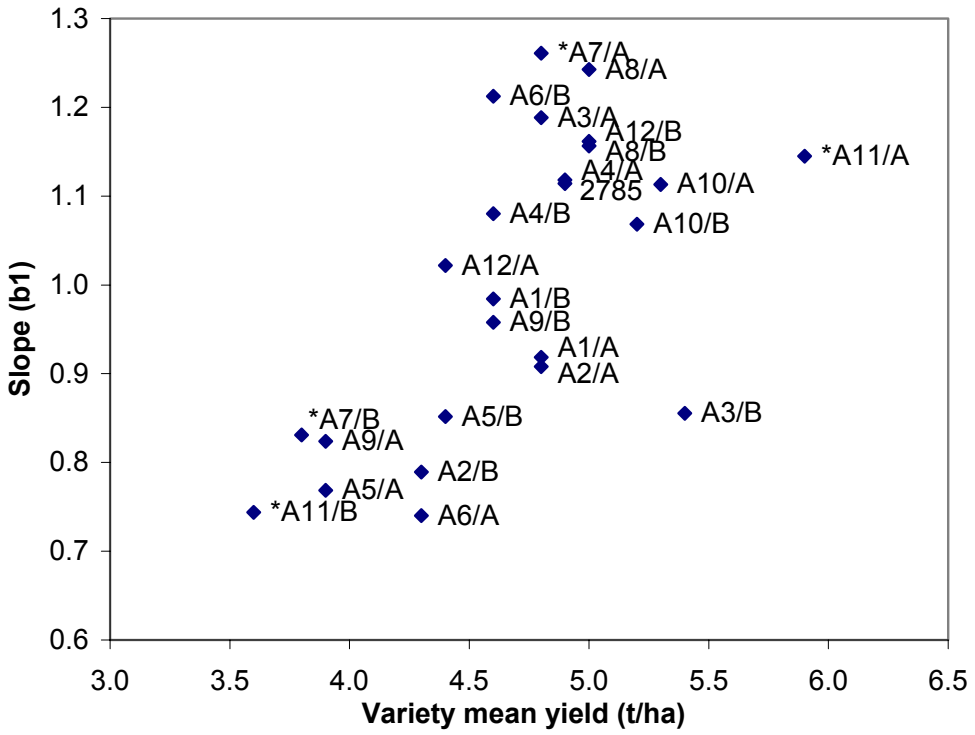

Figure 4.3 Scatter plot of regression coefficients (β_1) against variety mean yield (t/ha) for the 25 hybrids.

4.1.3 Correlations between grain yield and some traits

At ART Farm, CIMMYT Low N, and Rattray Arnold Research Station, grain yield was positively correlated with plant height (Table 4. 3). At Kadoma and Shamva, no significant correlation was noted. Significant negative correlations between grain yield and anthesis-silking interval, days to silking and days to anthesis were found at three other locations except at Rattray Arnold and Shamva. Mean across location correlation between grain yield and plant height was positive (0.581) and there were small non-significant negative correlations between mean across location grain yield and mean across location anthesis-silking interval, days to silking and days to anthesis.

Table 4.3 Correlation coefficients between grain yield and plant height, days to 50 silking, days to 50 % anthesis and the anthesis-silking interval for each location and across locations in 2006/7

	Plant Height	Days to Silking	Days to anthesis	Anthesi-Silking interval
ART Farm	0.596	-0.301**	-0.306**	-0.11*
Cimmyt Low N	0.477	-0.287	-0.096	-0.429**
Kadoma	0.177	-0.07*	-0.049*	-0.023**
Rattray Arnold	0.444	-0.315	-0.203	-0.155
Shamva	0.012	-0.4	-0.366*	-0.126
Site mean	0.581**	-0.146	-0.04	-0.154

* indicates significance at P<0.05, ** indicates significance at P<0.01.

4.1.4 Relationship between means across site mean grain yield (t/ha) and plant height

A positive correlation between mean across site grain yield (t/ha) and plant height (cm) was shown (R^2 = 0.341) (Figure 4.4) show the relationship between grain yield and plant height. A positive relationship was displayed. As plant height increased, the yield of the hybrid increased on average across the locations. This trend in mean acrossite yield is similar to what is observable at each of the individual site where tall hybrids yield relatively higher than short hybrids.

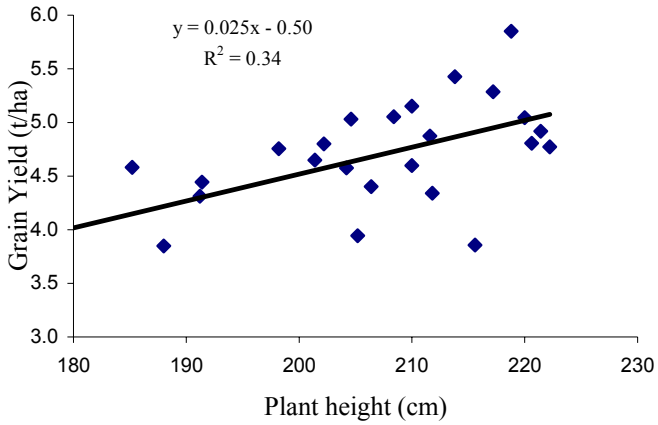

Figure 4.4 Relationship between site mean grain yield (t/ha) and plant height

4.1.5 Relationship between mean across site grain yield (t/ha) and mean across site anthesis-silking interval

There was a slightly negative relationship (R^2 = 0.0059) between mean across site grain yield (t/ha) and mean across site anthesis silking interval (Figure 4.6).

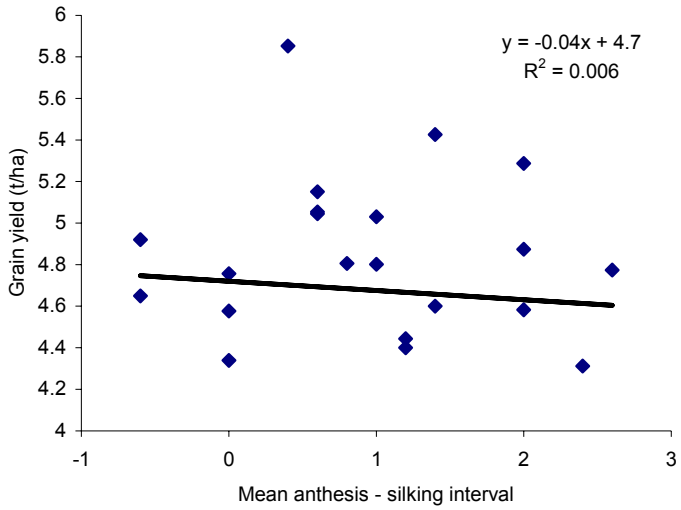

Figure 4.5 Relationship between mean across site grain yield (t/ha) and anthesis-silking interval

4.1.6 Relationship between mean across site grain yield (t/ha) and mean across site number of ears per plant (EPP)

There was a slightly positive relationship ($R^2 = 0.10$) between mean across site grain yield (t/ha) and mean across site number of ears per plant (EPP) (Figure 4.5).

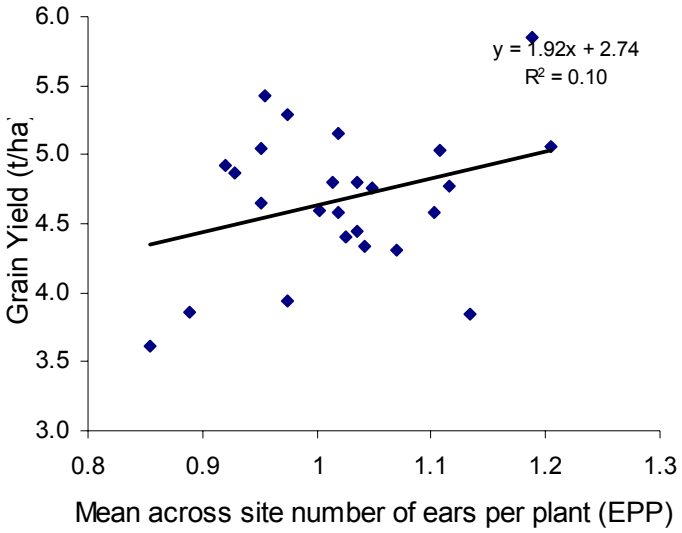

Figure 4.6 Relationship between mean across site (t/ha) and mean across site number of ears per plant (EPP) in 2006/7

4.1.7 AMMI Biplot for grain yield (t/ha)

The AMMI biplot (Figure 4.7) indicated that O6t 1361 (A11/A) (5.9 t/ha) was the highest yielding across the locations as it is located furthest along the 0.0 IPCA 1 axis. Conversely, the lowest yielding genotype, across sites, was O6t 811 (A11/B) (3.6 t/ha). Genotypes close to the origin of the axis like O6t 389 (A4/B), O6t 865 (A9/B) and O6t 1150 (A7/A) have stable grain yield across the locations in the sense that they are among the highest yielding at each location while genotypes furthest from the origin have the most variable grain yield across the locations. Genotypes and locations occurring on opposite sides of the 0.0 IPCA 1 axis have negative interactions while those occurring on the same side have positive interactions. Genotypes occurring in diametrically opposite quadrats differ in both interaction scores and main effects e.g., O6t 1361 (A11/A) and O6t 811 (A9/A).

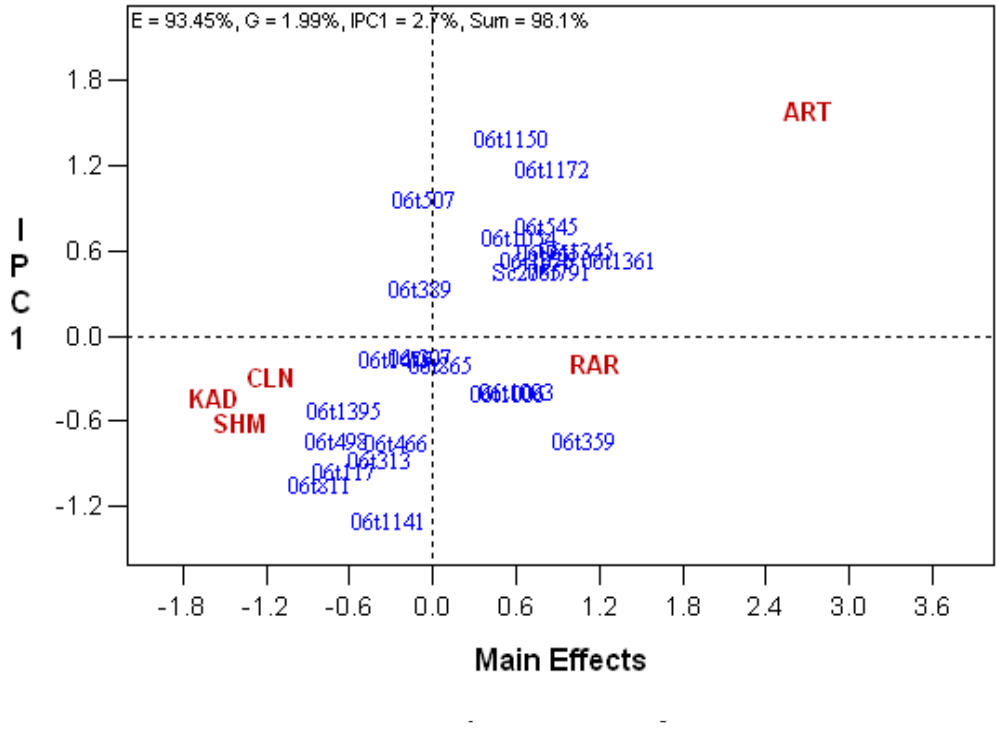

Figure 4.7 AMMI Biplot of the standardized mean grain yield (t/ha) and the first principal component axis scores of the 25 QPM experimental hybrids and five envoronments in which they were tested. The 0.0 Main Effects axis represents the Grand Mean across all the locations.

4.1.8 Which-won-where in terms of grain yield (t/ha)

GGE biplot analysis clearly shows the relative performance of genotypes at any given location. Such information can be used to rank genotypes in terms of the highest yielders at any given location. A GGE biplot (Figure 4.8) was therefore used to clearly illustrate those genotypes that were best yielding at any given location. Genotypes and the locations are plotted on a graph in such a way that those genotypes that outperform other genotypes in terms of yield at any particular location are clustered around that location on the graph (Figure 4.8). The markers of the outermost genotypes were joined together to produce a polygon and this polygon was dissected into six sectors by lines originating from the origin and approaching the sides of the polygon perpendicularly. Locations are found in only three sectors. The genotypes whose markers are found in the same sector as a location performed best in that location. For example O6t 1150 (A7/A)(13.4 t/ha) yielded highest at Art Farm (ART) while O6t 1361 (A11/A) (7.1 t/ha) yielded highest at Rattray Arnold Research Station. Genotypes (e.g., O6t 811 (A11/A)

and O6t117 (A5/A)) not associated with any location were not among the best at any of the tested locations but they could have done well or poorly in any of the locations.

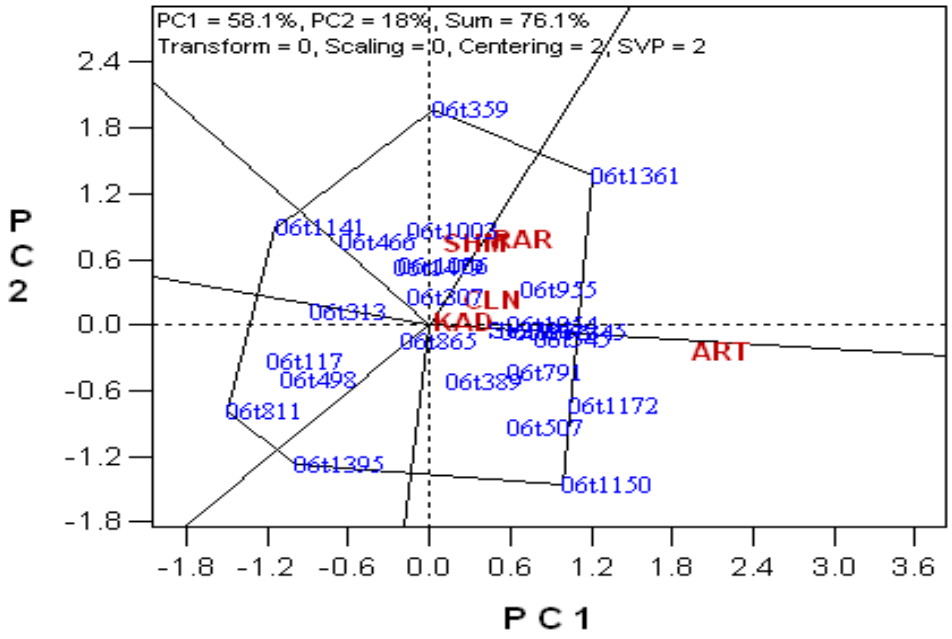

Figure 4.8 The polygon view of GGE biplot showing which QPM experimental hybrid won at which location in terms of Grain Yield (t/ha)

4.1.9 Yield Rankings

Genotypes changed ranks from one location to the next (Table 4.4) suggesting crossover interactions or unstable yields for some genotypes though the interactions were not significant. Genotypes like O6t 1345 (A10/A), O6t 1361 (A11/A) and O6t 359 (A3/B) with relatively high yield rankings can be said to have wide adaptation to the selected test locations.

Table 4.4 Hybrid (genotype) rankings for grain yield at the five locations in 2006/7

Entry	Name	Line/Tester	Art Farm	CIMMYT Low N	Kadoma	Rattray Arnold	Shamva	Mean Rank
1	06T1003	A1/A	16	3	24	17	2	12
2	06T1006	A2/A	17	11	11	15	5	12
3	06T1054	A3/A	8	22	22	5	18	15
4	06T1076	A4/A	9	20	12	10	9	12
5	06T117	A5/A	23	18	14	23	12	18
6	06T1141	A6/A	24	17	4	6	15	13
7	06T1150	A7/A	1	6	21	22	23	15
8	06T1172	A8/A	2	9	13	19	13	11
9	06T1395	A9/A	20	13	9	25	21	18
10	06T1345	A10/A	5	4	3	13	7	6
11	06T1361	A11/A	3	2	10	1	3	4
12	06T1479	A12/A	18	8	25	3	19	15
13	06T307	A1/B	14	14	20	9	10	13
14	06T313	A2/B	21	16	5	20	8	14
15	06T359	A3/B	13	7	1	2	1	5
16	06T389	A4/B	12	5	18	8	25	14
17	06T466	A5/B	19	15	23	14	4	15
18	06T507	A6/B	6	25	6	11	24	14
19	06T498	A7/B	22	24	15	21	22	21
20	06T545	A8/B	4	23	8	16	6	11
21	06T865	A9/B	15	19	2	12	17	13
22	06T791	A10/B	10	1	7	18	20	11
23	06T811	A11/B	25	21	17	24	16	21
24	06T955	A12/B	7	12	19	4	11	11
25	SC2785	SC2785	11	10	16	7	14	12

4.1.10 Line × Tester analysis

The line by tester interaction was significant ($p<0.05$) (Appendix B). However, the lines, testers, location by line interaction, location by line by tester interaction and the location by line interaction were not significant. Ranks of hybrids formed by crossing all the lines to either of the testers A or B showed that line A11/A ranked first in its group but when line A11 is crossed to tester B it ranks very low in this B group of hybrids (Table 4.5).

Table 4.5 Hybrids, their across location mean yield, coefficients of determination (R^2) and their regression coefficients (β_1)

Tester A					Tester B				
Name	**Line/Tester**	**Mean Yield**	**R^2**	**β_1**	**Name**	**Line/Tester**	**Mean Yield**	**R^2**	**B_1**
O6t1003	A1/A	4.8	0.934	0.92	O6t307	A1/B	4.6	0.995	0.9841
O6t1006	A2/A	4.8	0.993	0.91	O6t313	A2/B	4.3	0.998	0.7894
O6t1054	A3/A	4.8	0.993	1.19	O6t359	A3/B	5.4	0.962	0.8554
O6t1076	A4/A	4.9	0.997	1.12	O6t389	A4/B	4.6	0.980	1.0804
O6t117	A5/A	3.9	1.000	0.77	O6t466	A5/B	4.4	0.973	0.8518
O6t1141	A6/A	4.3	0.916	0.74	O6t507	A6/B	4.6	0.979	1.2124
O6t1150	A7/A	4.8	0.971	1.26	O6t498	A7/B	3.8	0.992	0.8311
O6t1172	A8/A	5.0	0.986	1.24	O6t545	A8/B	5.0	0.978	1.1567
O6t1395	A9/A	3.9	0.964	0.82	O6t865	A9/B	4.6	0.992	0.9579
O6t1345	A10/A	5.3	0.988	1.11	O6t791	A10/B	5.2	0.938	1.0683
O6t1361	A11/A	5.9	0.995	1.14	O6t811	A11/B	3.6	0.996	0.7439
O6t1479	A12/A	4.4	0.949	1.02	O6t955	A12/B	5.0	0.996	1.1615
	Mean	4.73	0.974	1.02		Mean	4.59	0.981	0.9744

4.2 Plant Height

For plant height, genotypes (G), environments (E) and the genotype × environment interaction (GEI) was highly significant ($P<0.01$) (Table 4.2 and Appendix C). The variety and environmental means for plant height is shown (Table 4.6). Plants were generally taller at ART Farm (average = 252 cm) than anywhere else other than at RAR. Shortest plants were at Shamva (average = 170 cm).

Table 4.6 Mean plant height (cm) for the hybrids at five locations in 2006/7

Entry	Name	Line/Tester	ART Farm.	CIMMYT Low N.	Rattray Kadoma	Rattray Arnold	Rattray Shamva	Mean
1	06t1003	A1/A	247	190	183	238	153	202^{ab}
2	06t1006	A2/A	251	190	171	225	154	198^{ab}
3	06t1054	A3/A	262	193	184	265	199	220^{a}
4	06t1076	A4/A	282	200	221	245	159	221^{a}
5	06t117	A5/A	246	195	187	228	170	205^{ab}
6	06t1141	A6/A	256	185	174	255	189	212^{b}
7	06t1150	A7/A	266	213	204	250	178	222^{a}
8	06t1172	A8/A	262	198	195	243	202	220^{a}
9	06t1395	A9/A	269	205	154	240	210	216^{a}
10	06t1345	A10/A	269	200	184	260	173	217^{a}
11	06t1361	A11/A	265	200	199	235	195	219^{a}
12	06t1479	A12/A	252	203	165	265	147	206^{ab}
13	06t307	A1/B	247	193	122	248	116	185^{c}
14	06t313	A2/B	235	173	160	220	168	191^{c}
15	06t359	A3/B	250	190	190	255	184	214^{a}
16	06t389	A4/B	264	190	186	240	141	204^{ab}
17	06t466	A5/B	236	178	143	225	175	191^{c}
18	06t507	A6/B	255	175	198	255	167	210^{ab}
19	06t498	A7/B	218	160	157	238	167	188^{c}
20	06t545	A8/B	254	190	175	255	149	205^{ab}
21	06t865	A9/B	238	195	172	243	159	201^{ab}
22	06t791	A10/B	260	200	179	225	186	210^{ab}
23	06t811	A11/B	220	160	164	205	141	178^{c}
24	06t955	A12/B	234	200	188	218	202	208^{ab}
25	SC2785	SC2785	280	198	166	253	161	211^{ab}
	MEAN		252^{a}	190^{b}	176^{ab}	241^{a}	170^{ab}	206
	$LSD_{0.05}$		38.8	34.9	30.4	41.5	9.6	31
	CV(%)		5.2	6.3	8.1	5.9	2.7	5.6
	SED		13.3	12	14.4	14.2	4.6	11.7

NB: Means followed by the same letter in a column and row is significantly different at P<0.05. Row means were separated using Turkey's Test (0.05) and column means were separated using the LSD (0.05).

4.3 Days to 50 % anthesis (DA)

Genotype and environment effects on number of days to 50 % anthesis were highly significant (P<0.01), but genotype × environment interaction was not significant

(P>0.05) (Table 4.7 and Appendix D). Mean location number of days to anthesis differed among genotypes as can be noted from Turkey's mean separations (Table 4.7). Kadoma and Rattray Arnold Research had mean days to anthesis of 71 days. At all the locations the experimental genotypes had intermediate (between 70 and 80 days) duration from planting to anthesis. Hybrids O6t 359 (A4/B), SC 2785 and O6t 1054 (A3/A) were the earliest while O6t 1395 (A9/A) was the latest.

Table 4.7 Mean number of days from planting to 50 % anthesis for the hybrids in 2006/7

Entry	Name	Line/Tester	ART Farm	CIMMYT Low N	Rattray Kadoma	Rattray Arnold	Rattray Shamva	Mean
1	06t1003	A1/A	72	75	76	71	70	73^{ab}
2	06t1006	A2/A	74	76	71	71	69	72^{ab}
3	06t1054	A3/A	69	75	68	67	70	70^{b}
4	06t1076	A4/A	72	75	70	71	71	72^{ab}
5	06t117	A5/A	72	72	71	71	70	71^{ab}
6	06t1141	A6/A	74	75	70	71	70	72^{ab}
7	06t1150	A7/A	73	76	75	73	70	73^{ab}
8	06t1172	A8/A	71	76	75	74	68	73^{ab}
9	06t1395	A9/A	74	78	76	70	72	74^{a}
10	06t1345	A10/A	72	78	73	70	70	73^{ab}
11	06t1361	A11/A	75	78	73	73	70	74^{a}
12	06t1479	A12/A	72	77	70	72	72	73^{ab}
13	06t307	A1/B	73	75	72	72	73	73^{ab}
14	06t313	A2/B	73	76	68	70	68	71^{a}
15	06t359	A3/B	71	74	67	68	69	70^{a}
16	06t389	A4/B	72	75	68	71	71	71^{ab}
17	06t466	A5/B	75	75	67	70	69	71^{ab}
18	06t507	A6/B	72	78	69	70	69	72^{ab}
19	06t498	A7/B	74	76	73	72	72	73^{ab}
20	06t545	A8/B	72	76	71	71	68	72^{ab}
21	06t865	A9/B	74	79	73	73	71	74^{a}
22	06t791	A10/B	73	77	71	72	71	73^{ab}
23	06t811	A11/B	72	76	70	72	68	72^{ab}
24	06t955	A12/B	73	77	68	72	70	72^{ab}
25	SC2785	SC2785	70	74	68	67	70	70^{ab}
	MEAN		72^{b}	76^{a}	71^{b}	71^{b}	70^{b}	72
	LSD		5.1	5.4	8.2	3.9	5.3	5.58
	CV		2.4	2.5	4.0	1.9	2.6	2.7
	SED		1.8	1.9	2.8	1.3	1.8	1.9

NB: Means followed by the same letter in a column or row are not significantly different at P<0.05. Row means were separated using Turkey's Test (0.05) and column means were separated using the LSD (0.05).

4.4 Days to 50 % silking (SD)

Like the days to anthesis, genotypes and the environments were highly significant (P<0.01) but the genotype × environment interaction was not significant (P>0.05)

(Appendix E). Location mean days to flowering show that the earliest silking was at Rattray Arnold (after 70 days) while CIMMYT Low N was the latest (78 days) (Table 4.8). At ART Farm (73 days) mean flowering was later than at Rattray Arnold. The earliest to silk at ART Farm (ART), CIMMYT Low N, Kadoma (KAD), Rattray Arnold Research Station (RAR) and Shamva (SHM) were O6t 1054 (A3/A), O6t 389 (A4/B), O6t 1006 (A2/A), and O6t 1141 (A6/A) respectively while the latest were O6t 498 (A7/B), O6t 507 (A6/B), O6t 1150 (A7/A) and O6t 307 (A1/B) respectively.

Table 4.8 Mean number of days from planting to 50 % silking at the five locations in 2006/7

Entry	Name	Line/Tester	ART Farm	CIMMYT Low N	Rattray Kadoma	Rattray Arnold	Rattray Shamva	Mean
1	06t1003	A1/A	74	77	73	71	70	71[b]
2	06t1006	A2/A	75	77	72	66	70	72[ab]
3	06t1054	A3/A	70	77	68	67	71	73[ab]
4	06t1076	A4/A	71	76	70	69	70	71[b]
5	06t117	A5/A	73	77	72	70	72	72[ab]
6	06t1141	A6/A	75	76	71	69	69	74[ab]
7	06t1150	A7/A	74	80	77	73	74	72[ab]
8	06t1172	A8/A	73	76	75	71	71	72[ab]
9	06t1395	A9/A	74	80	77	71	70	72[ab]
10	06t1345	A10/A	74	79	75	72	73	73[ab]
11	06t1361	A11/A	75	78	72	72	72	74[ab]
12	06t1479	A12/A	74	80	70	71	74	74[ab]
13	06t307	A1/B	75	78	73	72	75	72[ab]
14	06t313	A2/B	74	79	69	72	71	73[ab]
15	06t359	A3/B	71	77	67	69	71	75a
16	06t389	A4/B	71	77	66	69	74	72[ab]
17	06t466	A5/B	75	78	67	70	71	75[a]
18	06t507	A6/B	73	83	68	69	72	74[ab]
19	06t498	A7/B	75	78	72	72	73	73[ab]
20	O6t545	A8/B	71	78	71	72	71	73[ab]
21	06t865	A9/B	75	79	73	71	70	75[a]
22	06t791	A10/B	74	78	70	71	74	73[ab]
23	06t811	A11/B	74	80	70	71	73	74[ab]
24	06t955	A12/B	73	80	69	71	70	73[ab]
25	SC2785	SC2785	71	76	70	68	74	72[ab]
	MEAN		73[b]	78[a]	71[bc]	70[c]	72[bc]	72.8
	LSD(0.05)		5.4	5.9	8.7	4.8	6.5	6.26
	CV(%)		2.6	2.6	4.2	2.3	3.1	2.96
	SED		1.9	2	3	1.6	2.2	2.14

NB: Means followed by the same letter in a column and row is significantly different at P<0.05. Row means were separated using Turkey's Test (0.05) and column means were separated using the LSD (0.05).

4.5 Anthesis-silking interval (ASI)

Anthesis–silking interval (ASI) followed the trends of days to anthesis and days to silking with genotypes (P = 0.017) and the environment (P = 0.023) being highly significant at P < 0.05 (Appendix F) but the genotype × environment interaction effects

were not significant (Table 4.9). Genotypes O6t 1076 (A4/A) and O6t 865 (A9/B) had negative mean ASI and O6t 1150 had the highest positive ASI of 3. Mean across site ASI for all the five locations was within acceptable limits of ± 3 but at some locations, certain genotypes had unacceptably high values than any other location, especially under low nitrogen.

Table 4.9 Mean anthesis-silking interval (ASI) for the hybrids at the five locations in 2006/7

Entry	Name	Line/ Tester	ART Farm	CIMMYT Low N	Kadoma	Rattray Arnold	Shamva	Mean
1	06t1003	A1/A	2	3	1	0	-1	1^{abc}
2	06t1006	A2/A	2	1	1	-5	1	0^{bc}
3	06t1054	A3/A	1	2	-1	1	1	1^{abc}
4	06t1076	A4/A	-1	1	0	-2	-1	-1^{c}
5	06t117	A5/A	1	5	1	-1	2	2^{ab}
6	06t1141	A6/A	1	1	1	-2	-1	0^{bc}
7	06t1150	A7/A	2	4	2	1	4	3^{a}
8	06t1172	A8/A	2	0	0	-3	4	1^{abc}
9	06t1395	A9/A	-2	2	1	1	-2	0^{bc}
10	06t1345	A10/A	2	1	2	2	3	2^{ab}
11	06t1361	A11/A	1	0	0	-1	2	0^{bc}
12	06t1479	A12/A	2	3	0	-1	2	1^{abc}
13	06t307	A1/B	2	3	2	0	3	2^{ab}
14	06t313	A2/B	2	3	2	2	3	2^{ab}
15	06t359	A3/B	1	3	0	1	2	1^{abc}
16	06t389	A4/B	-1	3	-2	-3	3	0^{bc}
17	06t466	A5/B	0	3	0	1	2	1^{abc}
18	06t507	A6/B	1	5	-1	-1	3	1^{abc}
19	06t498	A7/B	2	2	-2	-1	1	0^{bc}
20	06t545	A8/B	-1	3	-1	1	3	1^{abc}
21	06t865	A9/B	1	-1	0	-2	-1	-1^{c}
22	06t791	A10/B	1	1	-1	-1	3	1^{abc}
23	06t811	A11/B	1	4	1	-1	5	2^{ab}
24	06t955	A12/B	0	3	1	-1	0	1^{abc}
25	SC2785	SC2785	1	2	2	1	4	2^{ab}
	MEAN		1^{ab}	2^{a}	0^{bc}	-1^{c}	2^{a}	1
	LSD(0.05)		3.6	4.0	3.1	3.3	6.0	4
	CV(%)		152.4	65.7	332.2	-281.6	123.5	78.4
	SED		1.2	1.4	1.1	1.6	2.0	1

NB: Means followed by the same letter in a column and row are significantly different at $P<0.05$. Row means were separated using Turkey's Test (0.05) and column means were separated using the LSD (0.05).

4.6 Number of ears per plant (EPP)

Genotypes and the environments were highly significant for EPP ($P<0.01$) (Appendix G). The genotype × environment interaction was not significant ($P>0.05$). ART Farm (1.1) and Kadoma (1.1) had high location means for EPP (Table 4.10). CIMMYT Low N (0.9) had the lowest value. At ART Farm and Kadoma, most genotypes showed partial prolificacy while at Shamva, Rattray Arnold Research Station and CIMMYT Low N some genotypes showed partial barrenness.

Table 4.10 Mean number of ears per plant (EPP) for the hybrids at each of the five locations in 2006/7

Entry	Name	Line/Tester	ART Farm	CIMMYT Low N	Kadoma	Rattray Arnold	Shamva	Mean
1	06t1003	A1/A	1.2	1.0	1.1	1.0	1.0	1.0[a]
2	06t1006	A2/A	1.2	1.0	1.1	1.0	1.0	1.0[a]
3	06t1054	A3/A	1.2	0.7	1.3	1.0	1.0	1.0[a]
4	06t1076	A4/A	0.9	0.8	0.9	1.0	1.0	0.9[a]
5	06t117	A5/A	1.1	0.9	1.1	0.9	1.0	1.0[a]
6	06t1141	A6/A	1.3	0.8	1.1	1.0	1.0	1.0[a]
7	06t1150	A7/A	1.3	0.8	1.7	0.8	1.0	1.1[a]
8	06t1172	A8/A	1.1	1.0	0.8	0.9	1.0	1.0[a]
9	06t1395	A9/A	0.9	0.7	1.2	0.8	1.0	0.9[a]
10	06t1345	A10/A	1.1	1.0	1.0	0.8	1.0	1.0[a]
11	06t1361	A11/A	1.6	1.0	1.3	1.2	1.0	1.2[a]
12	06t1479	A12/A	1.2	0.8	1.0	1.2	1.0	1.0[a]
13	06t307	A1/B	1.2	1.0	1.3	1.1	1.0	1.1[a]
14	06t313	A2/B	1.2	0.9	1.2	1.0	1.0	1.1[a]
15	06t359	A3/B	1.1	1.0	0.9	0.9	1.0	1.0[a]
16	06t389	A4/B	1.1	1.1	1.0	0.9	1.0	1.0[a]
17	06t466	A5/B	1.2	0.9	1.1	1.0	1.0	1.0[a]
18	06t507	A6/B	1.1	0.7	1.3	1.0	1.0	1.0[a]
19	06t498	A7/B	1.2	1.0	1.5	1.0	1.0	1.1[a]
20	06t545	A8/B	1.1	0.9	1.5	1.1	1.0	1.2[a]
21	06t865	A9/B	1.1	0.8	1.1	0.8	1.0	1.0[a]
22	06t791	A10/A	1.1	1.0	1.1	0.9	1.0	1.0[a]
23	06t811	A11/B	0.9	0.8	0.9	0.7	1.0	0.9[a]
24	06t955	A12/B	1.3	0.9	1.8	1.1	1.0	1.2[a]
25	SC2785	SC2785	0.9	1.0	0.7	1.0	1.0	1.0[a]
	MEAN		1.1[a]	0.9[a]	1.1[a]	1.0[a]	1.0[a]	1.0
	LSD(0.05)		0.4	0.4	1.5	0.4	0.03	0.5
	CV(%)		13.1	13.7	44.6	14.1	1.4	17.4
	SED		0.1	0.1	0.5	0.1	0.01	0.2

NB: Means followed by the same letter in a column and row is significantly different at $P<0.05$. Row means were separated using Turkey's Test (0.05) and column means were separated using the LSD (0.05).

4.7 Kernel Modification score 3

Analysis on the light table has revealed that a greater proportion of the experimental hybrids' kernels had modification scores of 3 (Figure 4.9 and 4.10). Even the check hybrid, SC 2785, was scored three for kernel modification on the light table. It

therefore means that a score of 3 in this instance is the best score we can achieve. As a result a score of 3 has been chosen in this trial as the best modification that was attainable. For kernel modification score 3 genotypes were not significant across the locations ($P>0.05$) (Appendix H). Environments and the genotype × environment interaction were highly significant ($P<0.01$). Highest mean percentage modification occurred at ART Farm (64 %) and the lowest occurred at Shamva (24 %). At each of the locations ART Farm (ART), CIMMYT Low N, Kadoma (KAD), Rattray Arnold Research Station (RAR) and Shamva (SHM) the genotypes that showed the highest level of percent kernel modification were O6t 865 (A9/B), O6t 117 (A5/A), O6t 466 (A5/B), O6t 1076 (A4/A) and O6t 865 (A9/B) respectively and the least modified were O6t 466 (A5/B), O6t 1172 (A8/A), O6t 545 (A8/B), O6T 359 (A3/B) and O6t 1141 (A6/A), respectively.

Figure 4.9 Kernels in modification score 3

The picture shows the average modification in opaque 2 maize genotype. The picture shows regular pattern of modification. Some kernels however may be modified irregularly.

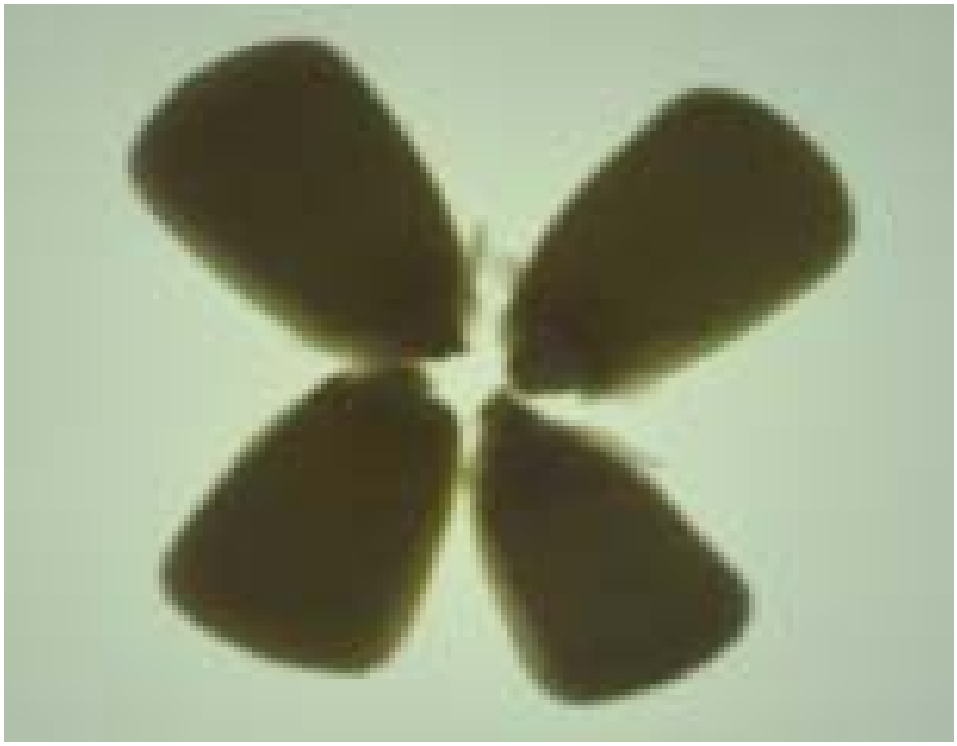

Figure 4.10 Kernels in modification score 5

The kernels are completely opaque. Farmers who prefer the normal kernels do not desire these chalky kernels. Kernel modification score 5 is selected against by breeders who try as much as possible to attain a score of 1 (normal kernel modification).

4.8 Index of kernel modification and grain texture

For the index, genotypes and the genotype × environment interaction effects were highly significant ($P<0.01$) (Appendix I). The environments were non-significant ($P>0.05$). Location means ranged from 16.8 (ART) to 19.2 (RAR). Highest values at ART, CLN, KAD, RAR, and SHM were 23.6 (O6t 389 (A4/B)), 20.8 (O6t 1150 (A7/A)), 22.9 (O6t 1395 (A9/A)), 22.8 (O6t 1361 (A11/A)) and 22.7 (O6t 1003 (A1/A)) respectively while the lowest were 7.0 (O6t 1054 (A3/A)), 12.8 (O6t 1003 (A1/A)), 13.1 (O6t 359 (A3/B)), 12.5 (O6t 1172 (A8/A)) and 13.6 (O6t 545 (A8/B)) respectively. Table 4.11 shows summarized data for the index.

Table 4.11 Scores of the indexed grain texture and kernel modification at the five locations in 2006/7

Entry	Name	Line/Tester	ART Farm	CIMMYT Low N	Kadoma	Rattray Arnold	Shamva	Mean
1	06t1003	A1/A	12	13	22	14	23	17^{abc}
2	06t1006	A2/A	19	16	15	23	22	19^{abc}
3	06t1054	A3/A	7	16	17	14	14	14^{c}
4	06t1076	A4/A	17	18	19	19	20	19^{abc}
5	06t117	A5/A	17	18	14	18	17	17^{abc}
6	06t1141	A6/A	23	22	15	19	18	19^{ab}
7	06t1150	A7/A	13	21	21	17	18	18^{abc}
8	06t1172	A8/A	13	18	16	13	21	16^{abc}
9	06t1395	A9/A	19	18	23	23	21	21^{a}
10	06t1345	A10/A	9	17	19	15	18	16^{abc}
11	06t1361	A11/A	23	20	20	23	18	21^{a}
12	06t1479	A12/A	13	15	21	16	21	17^{abc}
13	06t307	A1/B	16	20	21	21	18	19^{abc}
14	06t313	A2/B	21	20	19	22	18	20^{a}
15	06t359	A3/B	20	19	13	20	20	18^{abc}
16	06t389	A4/B	24	20	20	22	19	21^{a}
17	06t466	A5/B	20	18	17	23	18	19^{abc}
18	06t507	A6/B	24	18	20	22	18	20^{a}
19	06t498	A7/B	20	21	19	24	21	21^{a}
20	O6t545	A8/B	13	18	19	22	14	17^{abc}
21	06t865	A9/B	19	19	21	22	17	20^{ab}
22	06t791	A10/A	12	16	17	15	20	16^{abc}
23	06t811	A11/B	16	19	19	23	21	19^{ab}
24	06t955	A12/B	21	20	18	19	16	19^{abc}
25	SC2785	SC2785	10	14	15	12	20	14^{bc}
	MEAN		17^{a}	18^{b}	18^{b}	19^{c}	19^{c}	18
	LSD(0.05)		14	6	5	8	12	9
	CV (%)		28	12	10	14	22	17
	SED		5	2	2	3	4	3

NB: Means followed by the same letter in a column and row is significantly different at P<0.05. Row means were separated using Turkey's Test (0.05) and column means were separated using the LSD (0.05).

CHAPTER FIVE

DISCUSSION

5.1 Grain Yield (GYG)

For genotypes and the environments, the p-values for grain yield were significant ($P< 0.05$ and $p<0.01$ respectively). Unlike the results of Setimela (1996) and Gauch and Zobel (1997), there was no significant genotype × environment interaction for yield ($P>0.05$) (Appendix A). Though the interaction was not significant, genotypes exhibited differences in grain yield across the locations. Environments also had different mean yields showing that these environments had some influence on the differences in the performances of these hybrids across the environments. Unlike the observations of Atlin, McRae and Lu (2000), the genotype × environment interaction was not significant (Appendix A). This could have partly been due to differences in the selected locations in edaphic, climatic and agronomic management approaches employed (Vargas *et al.*, 1999). The occurrences of these differences are further supported by the fact that these locations are found in different agro-ecological regions of Zimbabwe. Yield is a multiple of plant stand, ears per plant, ear size, plant height and grain number. Variations in plant stand, plant height, number of ears per plant and grain number across the locations results in variations in overall grain yield amongst the tested hybrids. However, genotype ranks changed from one location to the other unlike the findings of Yang and Baker (1991) suggesting crossover interactions even though these interactions are not significant as shown by non parallel regression lines on Figure 4.2.

At ART Farm, under optimum conditions of high N, high rainfall, good weed and pest management with red fertile clay soils, extremely high yields (average =11.1 t/ha) were observed. Low nitrogen conditions at UZ Farm (CIMMYT Low N) resulted in low yields (2.6 t/ha), which can be attributed to lack of N nutrition and less than optimal agronomic management conditions. This observation is in line with Banziger, Edmeades, Beck and Bellon (2000) who reported that nitrogen deficiency reduces grain yield and the reduction could be as much as over 50 % in extreme cases. Shamva, which is in Natural Region IV with sandy soils of poor fertility and below average rainfall yielded, on average for all the genotypes, greater than Kadoma, which is in Natural Region III. This could be due to a severe dry spell that followed planting which

resulted in poor germination and hence poor plant stands. Drought reduces photosynthesis per plant and if drought occurs at flowering it may also cause kernel and ear abortion (Edmeades *et al.*, 2000). This in turn results in yield reductions. Rattray Arnold Research Station (RAR), which is in Region IIa, produced relatively low yields (5.7 t/ha) compared to those at ART Farm (11.1 t/ha) although they are in the same natural region. Differences could be a result of differences in crop management patterns as in fertilizer regimes, pest and weed management as well as irrigation management coupled with relatively late planting as Shamva was planted relatively late in December. Stress, i.e., low nitrogen fertility and drought prolong developmental time and this had a bearing on yield because genotypes that flowered late yielded more than those that flowered early. Hybrids that were tall tended to yield more. Also, plants with high EPP values had more yield at all the locations. Banziger *et al.* (2000) found a highly positive correlation between grain yield and EPP and grain yield and ASI. However, these results only showed very low correlations between grain yield and the two parameters except under low nitrogen (CIMMYT Low N) where there was a moderate correlation between grain yield and ASI (Table 4.3). Under drought conditions at Kadoma, there was no correlation between grain yield and DA and SD. Grain yield and plant height (PH) were highly and positively correlated at ART Farm, CIMMYT Low N and at Rattray Arnold Research Station while at Kadoma a relatively low correlation was recorded. This shows that tall genotypes give relatively high yields though this contradicts the suggestions of Banziger *et al.* (2000) who suggest that tall plants yield relatively less than their genetic potential as the large stems result in increased competition for assimilates between the stems and ears.

5.2 Grain Yield Biplot Analysis

The AMMI biplot (Figure 4.6) showed which genotypes were stable and which ones do well in which environments. Positions on the biplot closer to the origin mean that genotypes here are stable across the locations. As such, experimental hybrids, O6t 389 (A4/B), O6t 865 (A9/B), O6t 307 (A1/B) and O6t 1479 (A12/A) were stable across all the five locations at which they were tested. The experimental hybrids near a particular location are associated with that particular location (Zobel *et al.*, 2003). Association with that area means that the hybrids interact positively with the location. Again in Figure 4.7 experimental hybrids O6t 1150 (A7/A), O6t 1172 (A8/A), O6t 955 (A12/B), O6t 1054 (A3/A), O6t 1361 (A11/A), O6t 1345 (A10/A), O6t 791 (A10/B) and O6t 359

(A3/B) are associated with ART Farm. These experimental hybrids did well at ART Farm and are the highest yielding here. At Rattray Arnold Research Station (RAR), O6t 359 (A3/B), O6t 1361 (A11/A) and O6t 1479 (A12/A) among others are the best grain yielding varieties and this is further confirmed by Table 4.1 and Table 4.4 where they are among the top yielding here. Kadoma (KAD), CIMMYT Low N (CLN) and Shamva (SHM) had almost the same location means as can be seen by them being situated together at the lower left corner of the biplot. Experimental hybrids like O6t 1361 (A11/A), O6t 791 (A10/B), O6t 1003 (A1/A), O6t 1345 (A10/A), O6t 1003 (A1/A), O6t 1150 (A7/A) and O6t 466 (A5/B) perform well or were associated with one or more of these three locations. These experimental hybrids perform well in unfavorable environments as their yields are below the across site grand mean. Associations between hybrids and locations obtained in this trial are similar to the results of Gauch, Jr and Zobel (1997) in a multisite trial with 32 genotypes across fifteen locations. It should also be pointed out that the nominal yields obtained in this trial are not indicative of the maximum potential yields of the experimental hybrids involved as 2007 was generally a drought. Instead, the yields give an insight into the performance of the hybrids in each of the locations in which the trials were carried out.

On the biplot (Figure 4.6), genotypes or environments that appear almost on a perpendicular line to the y-axis have similar mean yields for example O6t 507 (A6/B) and O6t 389 (A4/B) have similar means. Also, O6t 1395 (A9/A), O6t 498 (A7/B) and O6t 117 (A5/A) have similar means. The same is true for O6t 313 (A2/B) and O6t 1141 (A6/A). Hybrids and environments that fall almost on a horizontal line have similar interaction patterns. Hybrids O6t 1006 and O6t 1003 (A1/A) have similar interactions; O6T 498 (A7/B) and O6T 466 (A5/B) have similar interactions (Zobel *et al.*, 1988). Likewise, O6t 1361 (A11/A) and O6t 1076 (A4/A) have similar interactions. Experimental hybrids at the 0.0 Main Effects line have their grain yield means equal to the Grand Mean Yield. Hybrids on the left of the grand mean line have lower yields than the grand mean and those on the right side have means greater.

As can be noticed on Figure 4.5 lower location means are associated with Kadoma (KAD), CIMMYT Low N (CLN) and Shamva (SHM) with Kadoma recording the lowest mean yields. (Movement along the 0.0 IPC1 line from left to right imply increase in mean across site yields). ART Farm (ART) had the highest value for site

mean yield followed by Rattray Arnold Research Station (RAR), then CIMMYT Low N (CLN), Shamva (SHM) coming fourth. ART Farm yield is expected to surpass all the yields at the other locations because it is situated in a high potential area (Agroecological Region IIa) and crop management here is intense with optimum levels of inputs being applied. Rattray Arnold Research Station, which occurs in the same region but at slightly lower altitude, is a high potential area but differs from ART Farm in the extent of intense crop management employed. ART Farm can be regarded as an ideal environment for crop testing in Zimbabwe that results in the highest possible performance of the crop in Zimbabwe hence very high yields unattainable anywhere else are always associated with it. As can be observed on the various figures and tables given, all the other parameters of the plants were relatively lower at RARS than at ART Farm.

CIMMYT Low N is situated at the UZ Farm, which is located near ART Farm. Agronomic management is not as optimal as at ART Farm and N fertility was deliberately lacking at this location for the experimental hybrids were planted in a field that is inherently lacking in nitrogen fertility. As was suggested by Crossa, Gauch, Jr and Zobel (1990) in a similar trial, low yields here can be attributed to low N levels typical of this field as the other agronomic management levels were similar to those employed at Rattray Arnold Research Station (RAR) and Kadoma. Yield here was supposed to be very close or equal to that at RARS if enough N levels were made available. A somewhat surprising result was obtained at Kadoma (KAD) whose mean yield was below that at Shamva. Kadoma is in Natural Region III while Shamva (Chakonda) is in Natural Region IV. Kadoma (1.6 tons/ha) was supposed to produce a mean location yield greater than that at Shamva (2.1 tons/ha) given that the edaphic, climatic and agronomic management employed at Shamva (Chakonda) are unfavorable compared to those at Kadoma. The soils at Chakonda (Shamva) are granite sands having relatively low levels in major nutrients like N, P and K. Rains experienced in this area are often erratic and below an annual average of 400 mm. On the other hand, at Kadoma, soils are red clays and mean annual rainfall is above 700 mm. However, this pattern of results can be explained in terms of the poor crop stand experienced at Kadoma due to the fact that there were no rains for a long period after planting resulting in poor germination hence poor crop stands.

5.3 Which-Won-Where in Terms of Grain Yield

The GGE biplot (Figure 4.7) may be used to show which genotype wins where in terms of grain yield. Markers of the experimental hybrids furthest from the biplot origin formed the corners of a polygon and lines starting from the center of the biplot dividing it into six sectors were drawn. Out of the six sectors only three have locations in them and hybrids in those sectors performed best and won in those locations. The three groups of locations represented by each sector are different in some way. Experimental hybrids O6t 1150 (A7/A), O6t 1172 (A8/A), O6t 1361 (A11/A), O6t 791 (A10/B), and O6t 1345 (A10/A) won at ART Farm. At CIMMYT Low N, O6t 791 (A10/B), O6t 1361 (A11/A), O6t 1003 (A1/A), O6t 1345 (A10/A) and O6t 389 (A4/B) are the top five winning experimental hybrids or outperforming other hybrids under low N conditions (CIMMYT Low N). O6t 359 (A3/B), O6t 865 (A9/B), O6t 1345 (A10/A), O6t 1141 (A6/A) and O6t 507 (A6/B) won at Kadoma Research Station (KAD). At Rattray Anorld Research Station (RAR), O6t 1361 (A11/A), O6t 359 (A3/B), O6t 1479 (A12/A), O6t 955 (A12/B) and O6t 1054 (A3/A) were the five winning experimental hybrids while at Shamva (SHM), O6t 359 (A3/B), O6t 1003 (A1/A), O6t 1361 (A11/A), O6t 466 (A5/B) and O6t 1006 (A2/A) were the highest grain yielding. Since the genotypes change ranks from one location to the next, crossover interactions exist for grain yield.

The failure to pick up the interactions can be attributed to the fact that the locations used in this trial are too few. If more locations had been used, probably, significant interactions would have been obtained. What it means is that, to obtain maximum possible yields at each of these particular environments, farmers must plant these hybrids in those locations where they win (Setimela *et al.*, 2007). By doing so they will be exploiting what is termed specific adaptation. Though at other locations the other experimental hybrids still do better it would be advantageous to associate each hybrid with a location where it performs the best compared to other hybrids. Some hybrids may however not be associated with any location suggesting that they may be the best or the worst based on the distance from the biplot origin relative to grain yield.

5.4 Plant Height (PH)

The plant heights (PH) for the twenty-five experimental QPM hybrids at the five locations differed significantly ($p<0.01$) (Appendix B). Locations were also

significantly different ($p < 0.01$). This conclusion is in line with what Setimela (1996) discovered in a similar research in Botswana. The plants were tallest at ART Farm, followed by those at Rattray Anorld Research Station (RAR). Plant heights at Kadoma came third and at the fourth position were those at Chakonda (Shamva) (SHM). Plants at CIMMYT (Low N) were the shortest (Tables 4.7 and 4.8). Experimental hybrid O6t 1076 (A4/A) was the tallest at ART Farm. Under low N at CIMMYT (CLN), experimental hybrid O6t 1479 (A12/A) was the tallest. There was a significant and highly positive correlation (0.6) between plant height and grain yield at ART Farm just like the results of Setimela (1996). At all the other locations, there were moderate correlations between grain yield and plant height. The tallest hybrids at each of the five locations could accumulate biomass more than the other hybrids for they were the highest yielders.

According to Gauch and Zobel (1997), differences in microenvironments can be defined in terms of different biotic and abiotic stresses and cropping system requirement. As such, the differences in plant heights were expected since the chosen locations are different as shown by their being in different Agro-ecological zones in Zimbabwe and/or the fact that the different sites employ different agronomic management regimes. Zimbabwe is divided into five Agro-ecological regions based on the agricultural potential of the area (Rukuni, Taonezvi, Eicher, Munyuki-Hungwe and Matondi, 2006), which is a function of many factors, rainfall being the major one. Because of the variations in edaphic, agronomic practices and climatic conditions, changes in rankings from one location to the next were observed suggesting that crossover interactions exist for plant height (PH) in the tested genotypes (Zobel *et al.,* 1988). This observation suggests that breeders must select for genotypes adapted specifically to certain environments for plant height and ear height, a plant height of less than 200 cm and an ear height of around 100 cm being acceptable (Wallace *et al.*, 1993).

ART Farm is in Agro-ecological Region IIa and crop management is intensive with optimum rainfall, fertilization and weed and pest management. CIMMYT-Low N is also in Natural Region IIa and the climatic and edaphic conditions are almost like at ART Farm. The difference lies in the management employed. The soils at these locations including Rattray Arnold Research Station are heavy, fertile red clays. In this

case, low nitrogen levels could have been the limiting factor and all the other agronomic management conditions are generally lower than at ART Farm. Tall plants tended to yield high. This observation was also noted by Setimela (1996) who found that yield of genotypes were positively correlated with plant height. Plants that had high plant height and ear height values had higher yields than those with lower values. What it means is that these hybrids had relatively higher capacity to accumulate biomass than other hybrids. Such hybrids are good especially for use as forage, fodder and/or silage crops since such attributes as high biomass accumulation are required in this area.

The disadvantage of tall plants when it comes to grain yield harvesting lies in their being susceptible to lodging (Vivek, Banziger and Pixley, 2002). Very tall plants have relatively high values of ear height and ear position and they tend to suffer grain yield losses due to lodging, especially when they are to be combine harvested. At Chakonda (Shamva) (SHM), which is in Natural Region IV, and has sandy soils with low nitrogen fertility, plants tended to be short. Another reason for poor performance at Shamva could be late planting as the site was planted in early January when other locations were planted in December, in line with Caulfield and Havazvidi (1989) who observed that location and duration of the growing season are physical factors that determine yield since they modulate and at times terminate gene activity. Areas in Natural region IV tend to receive low rainfall which results in reduced biomass accumulation and hence short plants with relatively low yields.

Since the experimental hybrids used in this trial were related in the sense that one set of parents (A_1 to A_{12}) information on plant heights can be used to evaluate the performances of the testers when combined with each of the lines they are crossed to. Tester A combines well with each of the lines A_1 to A_{12} to give tall plants at all the locations whilst tester B produced relatively short plants. For example, at ART Farm, O6t 1006 (A2/A) (251 cm), a product of A2 and tester A, is taller than O6t 313 (A2/B) (235 cm) derived from A_2 and tester B. The outcome also shows that the lines belonging to heterotic group S are tall regardless of which tester has been used because most genotypes from this group were above 250 cm in height.

5.5 Regression of variety mean yields against location mean yields

According to Eberhart and Russell (1966), a plot of variety mean yield against location mean yields with the corresponding regression lines illustrates the differential reactions of the hybrids to changing environments. Such a plot has the advantage that it clearly depicts the presence of crossover or non-crossover interactions. Crossover interactions are seen by regression lines that cut across (crossover) each other in the plot showing, that the hybrids will be changing ranks from one location to the next. If there are no crossover interactions the plot will be composed of a series of lines that do not cut across each other with equal gradients. According to Eberhart and Russell (1966) stated that the presence of interactions in this case would be envisaged as differences in the slopes of the regression lines and such interactions will be non-crossover interactions. From Figure 4.1 it can be seen that O6t 359 (A3/B) gives relatively high yield at Kadoma, CIMMYT Low N and Shamva (low potential environments) but is a relatively low yielder at Rattray Research Station and ART Farm. Genotype O6t 1361 (A11/A) yields high across all the locations for it is second in ranking at CIMMYT Low N, Kadoma and Shamva and is the first in ranking at Rattray Arnold Research Station and Art Farm (Figure 4.1) while variety O6t 811 (A11/B) ranks low at all locations.

Although the AMMI analysis of this trial did not sense the interactions as significant, Figure 4.1 shows that interactions of a crossover nature are present but rather are not significant. Maybe it is because the locations are too few for the interactions to be significant. Eberhart and Russell (1966) also suggested the need to consider the linear component of the genotype × environment interactions in which they utilised relative β_1 values to estimate the adaptability of a given hybrid to a particular location. A widely adapted genotype was defined as one with $\beta_1 = 1$ in this trial, values for the regression coefficients ranged from 0.7401 (A6/A) to 1.2611 (A7/A) (Figure 4.2 and Table 4.5). Genotypes like O6t 1003 (A1/A), O6t 1006 (A2/A), O6t 1479 (A12/A), O6t 1395 (A9/B), O6t 811 (A11/B), O6t 117 (A5/B), O6t 1395 (A9/A) and O6t 359 (A3/B) had wide adaptability since they had regression coefficients (β_1) that were not significantly different from unity (1). Eberhart and Russell (1966) state that genotypes with high mean yield and regression coefficients equal to unity have wide adaptation. In this regard, O6t 1003 (A1/A) and O6t 1006 (A2/A) show wide adaptability as they had β_1 values close to 1 and yields above average. Their coefficient of determination (R^2) values were also high, 0.9184 and 0.9081 respectively confirming that adaptability. In

this plot, (Figure 4.2), hybrids with β_1 values greater than 1 are regarded as responsive to environmental changes. So genotypes at the top right hand corner with β_1 values greater than 1 and mean variety yields above average, such as O6t 1150 (A7/B) and O6t 811 (A11/B) are adapted to favourable locations like ART Farm and Rattray Arnold Research Station. Those genotypes with regression coefficients of less than 1 and below average grain yields indicate that they offer greater resistance to environmental stresses and are adapted to poor environments (Goncalves de S *et al.*, 2003). Examples of these genotypes are O6t 1150 (A7/B), O6t 811 (A11/B) and O6t 117 (A5/A).

The gradient (of variety mean yield against location mean yield) versus variety mean yield plot (Figure 4.2) can also be used to evaluate the relative performance of experimental hybrids relative to the tester SC 2785. All hybrids that are to the right of 2785 on the plot like O6t 1076 (A4/A), O6t 955 (A12/B), O6t 1150 (A7/A) and O6t 1361 (A11/A) yield above the tester hybrids in high potential areas like ART Farm and Rattray Arnold Research Station. These hybrids are good hybrids that may be considered for release on the commercial market. Similarly in the low potential areas O6t 1054 (A3/B) out yielded the tester hybrid SC 2785. This hybrid may also be considered for release for commercial production under unfavourable conditions of poor soil fertility and low rainfall conditions like CIMMYT Low N, Kadoma and Shamva.

5.6 Line × Tester Analysis for Grain Yield

The across site analysis showed that the locations and the line by tester interaction were significant ($p< 0.05$) (Appendix B). However, the lines, testers, location by line and location by tester and locations by line interactions were not significant. The line by tester crosses were also evaluated and it was discovered that only crosses O6t 1003 (A11/A) and a standard check hybrid SC 2785 significantly differed from each other and the rest of the hybrids. Hybrids formed by crossing line A11 and tester A and A11 and tester B changed rank quite notably. O6t 1361 (A1/A) ranked first among all the lines crossed to tester A. O6t 811 (A1/B) ranked the least (Table 4.5) with tester B. This finding can be explained in terms of general combining ability (GCA) of line A11. Line A11 can be said to have poor general combining ability compared to the rest of the lines used in the formation of these hybrids that did not change ranks significantly when crossed to either of the testers A or B. So line A10, A8, A4 and A11 have relatively

high GCA. It is therefore discouraged to use line A1 in hybrid formations rather lines A2 to A12 may be used as they have relatively high specific combining ability (SCA) values.

5.7 A discussion of the methods used to explore the genotype × environment interactions on grain yield.

More than one method can be used to explore genotype × environment interactions ranging from the simple regression methods to the more complex AMMI biplot and the GGE biplot analysis. Each method has its own strength and weaknesses but generally each show useful information that the other method may not show clearly. For example, the regression of cultivar mean on the location mean yield in Figure 4.1 shows clearly the nature of the interactions present. That is, whether the interactions are crossover or non-crossover. This information is not readily available when the AMMI and the GGE biplots are utilised. On the other hand the GGE "which-won-where" biplot (Figure 4.7) clearly shows the hybrids clustered around the locations where they performed best. This is not clearly shown by the regression method and the AMMI biplot. The regression method only tends to distinguish only the favourable locations from the unfavourable locations using the β_1 values. Although these methods show the relative performance with respect to a trait, in this case grain yield, for each variety and the relative interactions of the genotypes to locations, they do not show exactly the causes of these interactions. Regression of cultivar performance on location mean yield show interactions as relative differences in the coefficient of regression (β_1) values, and the AMMI and the GGE biplots as the PC1 and the PC2 scores respectively. Because of the weaknesses and the strengths associated with each of the approaches an integration of them like what has been displayed in this trial can provide quite an informative and useful discussion and conclusion from the results.

5.8 Ears per Plant (EPP)

Across the sites there were highly significant differences between the genotypes and environments on the number of ears per plant (EPP). The environment played a part on the number of ears occurring on each plant. Number of ears per plant is a measure of prolificacy or barrenness of plants. EPP values of less than 1 suggest that the hybrid has partial barrenness while values greater than 1 indicate partial prolificacy. If EPP is taken under low N or drought stress, values of greater or equal to 1 indicate stress

tolerance (Vivek *et al.*, 2002). Genotypes like O6t 498 (A7/B), O6t 389 (A4/B), O6t 791 (A10/B) and O6t 1345 (A10/A) were relatively tolerant to low N because they were the best yielding under low N and had EPP > 1, while O6t 955 (A12/B), O6t 545 (A8/B), O6t 1361 (A11/A) that yielded least under low nitrogen conditions and others which had EPP values greater than 1 at Kadoma and Shamva exhibited drought tolerance.

Genotypes with EPP values above 0.5 have relatively higher grain yields compared to their counterparts at the respective locations. EPP values at ART Farm were greater than 1 and may have contributed to increased mean genotype and location yields compared to other locations. Lines A3, A6, and A11 showed increased EPP values when crossed to tester A relative to tester B suggesting that tester B is more prolific than tester A. The remaining nine lines increased their EPP values when crossed to tester B. This trait can be exploited and genotypes that show prolificacy at any location be planted where they yield most to maximize location yields (Freeman, 1973). Location yields result in high aggregate regional yields and in the end high average national and continental yields.

5.9 Days to Anthesis (DA) and Silking (SD)

For days to silking, genotypes and the environments were highly significant but the genotype × environment interaction was not significant (Appendix D and Appendix E). CIMMYT Low N had the longest periods from planting to both anthesis (76 days) (Table 4.7) and silking (78 days) (Table 4.8) compared to other locations. This observation supports what Uhart and Andrade (1995) obtained that nitrogen deficiency delays reproductive and vegetative phenology. There were small negative correlations between grain yield and number of days to silking at all the locations except Kadoma where there was no correlation at all in contradiction to a highly positive correlation obtained by Uhart and Andrade (1995) between the two parameters. Edmeades, Balanos, Elings, Ribaut and Banziger (2000) noted that anthesis was delayed by 0.6 days if there is a deficiency in nitrogen in the soil.

The differences in days to silking for the hybrids can be attributed to climatic, edaphic and agronomic management factors and to a smaller extent to genotypes since the genotypes were related. According to Uhart and Andlande (1995), nitrogen reduces ear

growth rate at flowering resulting in increased duration from planting to flowering. Edmeades, Balanos, Elings, Ribaut and Banziger (2000) found that silking was delayed when maize is exposed to drought. This observation helps to explain the later silking at Kadoma where drought conditions were experienced during the season. According to Edmeades *et al.* (2000), when drought occurs at flowering, silking is delayed but anthesis and anther dehiscence is accelerated. At ART Farm, CIMMYT Low N, Rattray Arnold Research Station and Shamva, there were highly significant and negative correlations between grain yield and number of days to 50 % silking (SD) (Figure 4.8). Dwyer, Ma, Evenson and Hamilton (1994) also found a significant correlation between grain yield and the number of days to 50 % silking (SD). However, at Kadoma no correlation between the two parameters was shown. Yield has already been shown to increase with increase in days to reproductive maturity (Dwyer *et al.*, 1994).

CIMMYT Low N and ART Farm received similar amounts of rainfall and are located at almost the same latitude, longitude and altitude and have similar soil types. Differences between CIMMYT Low N and ART Farm lie in nitrogen management and general agronomy as such plants growing at each of these locations differ in developmental time. High nitrogen fertility increases the rate of vegetative growth of plants and thorough pest and weed management increase the crops' competitiveness in exploiting the available soil resources. So, locations that received relatively high nitrogen fertility, rainfall and thorough weed and pest management flowered relatively earlier than those that did not have high levels of these management factors. Rattray Arnold Research Station is slightly lower in altitude (1450 masl) and rainfall (800 mm) though soil types are similar. Together with differences in crop management regimes these factors can contribute significantly to differences in developmental time and yields (Bernado, 2002). As nutrition and moisture affects plant vigour and the rate of plant growth, time to flowering and anthesis–silking interval is also affected. This observation support the results observed here as there was delayed silking and tasselling under low nitrogen conditions at CIMMYT Low N and in drought affected areas like Kadoma and Shamva.

Uhart and Andrande (1995) found that nitrogen deficiency reduced radiation interception resulting in reduced leaf appearance rate and reduced individual leaf area. Edmeades *et al.* (2000), reported that under more than optimal nitrogen fertilisation

coupled with high moisture levels, there is delayed anthesis and silking because there will be luxurious vegetative growth at the expense of reproductive growth resulting in delayed anthesis and silking. Contrary to Edmeades *et al.* (2000) findings, when there is poor nitrogen fertility and drought, compensatory flowering occurs before the usual athesis and silking time. In these situations yield is compromised.

At ART Farm, the relatively late flowering could be due to luxurious nutrient consumption and favorable ambient and air temperatures as there was heavy nutrient input at this location. The remaining two (Kadoma and Shamva) locations could represent the true smallholder performance of these genotypes as they are not much different and can be equated to conditions marginal as are in rural Zimbabwe. This is because rural Zimbabwe soils are typically sandy and rocky receiving little rainfall. The areas frequently experience mid season droughts like what happened this season (Caulfield and Havazvidi, 1989). Mean annual rainfall, altitude and mean annual temperatures differ across the selected five sites. Just like Gauch and Zobel (1997) discovered, these factors can affect developmental time of plants and eventually the yield potential (Uhart and Andrade, 1995). Crop management as in fertilizer management, pest management and weed management also influence developmental time of plants as has been mentioned earlier. A combination of these factors could have led to variations in developmental time for the same hybrid from one location to the next in a season.

5.10 Anthesis–Silking Interval (ASI)

There were significant differences across the locations for anthesis-silking interval (ASI) for locations, genotypes and the environments (Appendix F). ASI is related to developmental time of days to anthesis and days to silking. ASI is one of the major determinants of yield in maize. The ASI has to be short enough to allow synchrony between male flowering and female flowering. If there is no synchrony, fertilization is likely to be compromised and seed filling will not occur or will be poor leading to complete or partial barrenness (Edmeades *et al.*, 2000). Usually varieties that have a short ASI tend to achieve high grain yields while the opposite is true for those that have asynchrony between male and female flowering (Uhart and Andrade, 1995).

ASI values of +/- 3 days are acceptable. Again, differences in ASI across the environments can be attributed to difference in edaphic, climatic and agronomic

management factors occurring at each of the different locations and their contributions to the developmental time and patterns of each of the varieties. As Edmeades *et al* (2000) found, the anthesis–silking interval was large under low nitrogen conditions at CIMMYT Low N. However, unlike Edmeades *et al.* (2000), who found a significant and highly positive correlation, there was a moderate, negative correlation (-0.429) between ASI and grain yield under low nitrogen conditions. Banziger *et al.* (2006) reported that drought delays silking resulting in increased ASI. The same was reported by Edmeades *et al.* (2000) under low nitrogen conditions and drought.

ASI values at ART Farm tended to be very small which can partly account for the highest yield achieved here. ASI values at ART Farm were small because optimal management employed at this location. Tester A generally tends to result in improved ASI on the lines with which it is crossed compared to Tester B. The increase, however, falls within the acceptable limits of +/-3. This tester can be used to decrease the ASI in breeding programmes especially of those lines that have too high ASI values that do not allow synchrony between the male and female flowering. ASI is affected by factors that affect silking and anthesis development as nutrition and rainfall together with air temperature. For instance, Sito, Gaspar and Nginamau (2004) reported that increased ASI result in barrenness and lower yields. Temperature increases the rate at which plants grow provided other factors are held optimal. Crops that grow in environments that have high temperatures tend to grow fast reaching flowering early and lowering the ASI. Edmeades *et al.* (2000) found that anthesis and anther dehiscence may be accelerated by high air temperature and low relative humidity. In the same way as nutrition and moisture increase the rates of plant growth ASI is also affected.

5.11 Kernel Modification

Kernel modification measures the extent to which the kernels of the *opaque – 2* maize have been modified from being opaque to being normal. Kernel modification is assessed on a light table using scores ranging from 1 to 5, where 1 is normal (completely modified) and 5 being opaque (unmodified) (Figure 4.10). Scores below 3 for kernel modification were difficult to attain because of the inherent subjectivity. In scoring in this experiment most varieties reach a score of 3. As a result, for this trial, a score of three is considered the best score attainable and has been chosen for modification success ratings.

Genotypes were significantly different for kernel modification scores 1, 2, 3 and 5 across the sites ($p<0.05$) but not significant for kernel modification score 4 ($P<0.05$) (Appendices J, K, L, M, and N). However, at each location, genotypes tended to show differences in kernel modification. Environments were also significant for scores 2 to 5 but not for score 1. Genotype × environment interaction was only significant for scores 3 and 5 and not significant for scores 1, 2 and 4. There was more modification at ART Farm than other locations. Genotypes like O6T 1345 (A10/A) and O6t 865 (A9/B) can be taken as being completely modified at ART Farm. Modifier genes act as a group to rectify the deleterious effects associated with the *opaque - 2* gene, some of which being the chalky and opaque appearance of the kernels (Wallace *et al.*, 2002). Since the environments and the genotype × environment interaction was significant across the sites, this suggests that the environment has some influence on the action of these modifier genes on kernel modification because of their differences already mentioned earlier. Vasal (2001) suggested that different genotypes in different ecological niches could be modified to different extents. Crossing the lines with tester A resulted in a considerable improvement in kernel modification relative to tester B. Therefore tester A could be a better donor for modifier genes than B.

5.12 Index of Kernel Modification and Grain Texture (INDEX)

In plant breeding, selection indices are used to select genotypes for more than one trait (Falconer, 1989) (Appendix I). For the index of modification and texture, genotypes and the genotype × environment interaction were significantly different ($P<0.01$). In this index, which incorporates grain texture and kernel modification, the highest score possible is 30. This score is obtained by assuming that all the kernels sampled (100 %) have a modification score of three and below and the grain texture of that hybrid is one. To get the minimum acceptable score, we assume that 50 % of the kernels are score 3 and below in terms of modification and a score of 3 at most in terms of grain texture (TEXT) to get a minimum acceptable score of 16.5. So, any genotype using this index with a score of 16.5 and above will be considered as having, simultaneously, the acceptable levels of kernel modification and grain texture.

CHAPTER 6

CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

- There were no significant genotype × environment interactions for grain yield, anthesis-silking interval, ear position, number of ears per plant, number of days from planting to silking, and number of days from planting to anthesis.
- There were significant genotype × environment interactions for kernel modification score 3.
- Hybrids formed using tester A had better kernel modification than those made using tester B.
- The following genotypes showed broad/wide adaptation for grain yield; A1/B (O6t 307), A9/B (O6t 865), A12/A (O6t1479), A1/A (O6t 1003) and A2/A (O6t 1006).
- Hybrids A12/B (O6t 955), A8/B (O6t 545), A4/A (O6t 1076), A10/B (O6t 791), A10/A (O6t 1345), A11/A (O6t 1361) and A8/A (O6t 1172) yield above the standard check hybrid SC 2785.
- Genotypes A10/B (O6t 791), A8/B (O6t 545), A7/A (O6t 1150), A2/A (O6t 1172), A11/A (O6t 1361), A10/A (O6t 1345) and A3/A (O6t 1054) are associated with ART Farm and outperform other genotypes in terms of grain yield at this location.
- Genotypes A3/A (O6t 1054), A12/B (O6t 955), and A11/A (O6t 1361) are associated with low nitrogen conditions and outperform other genotypes in terms of grain yield under these conditions
- Genotypes A9/A (O6t 865) and A1/B (O6t 307) are associated with drought conditions (Kadoma and Shamva) and outperform other genotypes in terms of grain yield under these conditions.
- Under low nitrogen conditions anthesis-silking interval was negatively correlated with grain yield.
- Grain yield was positively correlated with plant height.
- An index of the form (6-Text) + (3 * MD 1)/5 + (2 * MD 2)/5 + (MD 3)/5 can be used to simultaneously select for kernel modification and grain texture in QPM breeding programmes.

- High potential areas exhibited better kernel modification than marginal areas. So, rainfall, soil type, altitude, nutrient management and temperatures influence the action of modifier genes in QPM genotypes.
- Line A1 has poor general combining ability (GCA) while lines A2 – A12 have good GCA.
- There are no significant differences on the effect of tester A or B on grain yield.

6.2 Recommendations

- Since there were no significant genotype × environment interactions, the tested genotypes could be grown in any of the tested locations without major reduction in yield expected. However, further trials have to be conducted with more replicates than two to truly ascertain the observation that genotype × environment interactions do not exist on grain yield.
- When selecting for kernel modification in QPM hybrids, optimal environmental and management conditions should be maintained because environmental conditions affect kernel modification in QPM genotypes.
- Number of ears per plant (EPP), plant height and anthesis-silking interval are good indicaters of yield potential as there is a correlation between grain yield and these parameters. Hence they may be used in estimating yield potential.
- Genotypes that perform best in a certain location during multisite trials should always be grown in those locations they perform best during normal production to maximize the yields of the genotypes in those locations and hence increase aggregate regional yields.
- The index of kernel modification and grain texture developed here can be effectively used to select simultaneously for kernel modification and grain texture.
- Line A1 may not be used in formulation of hybrids because it has poor general combining ability instead, lines A2 – A12 can be used because they have good general combining ability.
- Either of the testers A or B may be used in crosses interchangeably since they are not significantly different.

- Hybrids A11/A (O6t 1361) and A10/B (O6t 791) should be tested further and released on the market to be grown in any of the tested locations because they have broad adaptation.
- Hybrid A9/B can be multiplied and commercially recommended for growing in low potential areas.

REFERENCES

Aastvelt, H. and Martens, H. (1986) ANOVA Interactions Interpreted by Partial Least Squares Regression. *Biometrics*, **42**, 829-844.

Agromix Software, Inc (2007) *Agrobase GII Statistical Package*.

Atlin, G. N., McRae, K. B. and Lu, X (2000) Genotype × Region Interaction for Two-Row Barley Yield in Canada. *Crop Science* **40**, 992-998.

Allard, R. W. and Bradshaw, A. D. (1964) Implications of Genotype – Environmental Interactions in Applied Plant Breeding. *Crop Science*, **4**, 503-508.

Baker, R. D. (1969) Genotype - Environment Interactions in Yield of Wheat. *Canadian Journal of Plant Science*, **49**, 743 - 751.

Banziger, M., Edmeades, G. O., Beck, D. and Bellon, M. (2000) *Breeding for Drought and Nitrogen Stress Tolerance in Maize: From Theory to Practice*. Mexico, D F. CIMMYT.

Bernado, R. (2002) *Breeding for Quantitative Traits in Plants*. Woodbury, Minnesota. Stemma Press, 122-146.

Bjarnason, M. and Vasal, S. K. (1992) Breeding of Quality Protein Maize: *Plant Breeding Reviews*, **9**. John Wiley and Sons. Inc. 452-461.

Briggs, F. N. and Knowles, P.F. (1967) *Introduction to Plant Breeding*. New York. Reinhold Publishing Corporation. 168 –170.

Bressain, R. (1972) Improving Maize Diets with Amino Acid Protein Supplements. In: *Proceeding of the CIMMYT - Purdue International Symposium on Protein Quality in Maize*. Straudsberg. Dowden, Hutchinson and Ross Inc. 365-381.

Caulfield, M. and Havazvidi, E. K. (1989) Zimbabwe hybrid maize seed industry: Emphasis in cob rots and isolation. In: *Maize Improvement Production and Protection in Eastern and Southern Africa.* Proceedings of the Third Eastern and Southern Africa Regional Maize Workshop. September 18-22, 1989. 372-384.

Crossa, J, Gauch, Jr H. G. and Zobel, R. W. (1990). Additive Main Effects and Multiplicative Interaction Analysis of Two Maize Cultivar Trials. *Crop Science* **30**, 493-500.

dos S. Dias, C. T. and Krzanowski, W. J. (2003) Model Selection and Cross Validation in Additive Main Effects and Multiplicative Interaction Models. *Crop Science*, **43**, 865 – 873.

Dwyer, L. M., Ma, B. L., Evenson, L. and Hamilton, R. I. (1994) Maize Physiological Traits Related to Grain Yield and Harvest Moisture in Mid to Short Season Environments. *Crop Science*, **34**, 985-992.

Eberhart, S.A. (1989) Comprehensive Breeding Systems for Developing Improved Maize Hybrids. In: *Maize Improvement Production and Protection in Eastern and Southern Africa.* Proceedings of the Third Eastern and Southern Africa Regional Maize Workshop. September 18-22, 1989. 155-167.

Eberhart, S.A. and Russell, W. A. (1966) Stability Parameters for Comparing Varieties. *Crop Science*, **6**,455 – 462.

Edmeades, G. O., Balanos, J., Elings, A., Ribaut, J. M. and Banziger, M. (2000) The Role and Regulation of Anthesis-Silking Interval in Maize. In: *Physiology and Modeling Kernel Set in Maize*. CSSA Special Publication. Number 29. 86-96.

Falconer, D.S. (1989) *Introduction to Quantitative Genetics (3rd edition*) New York. Longman Scientific and Technical. 188.

Freeman, G.H. (1973) Statistical Methods for the Analysis of Genotype - Environment Interactions. *Heredity*, **31**, 339-354.

Gauch, H. G. (1988) Model Selection and Validation for Yield Trials with Interactions. *Biometrics*, **44**, 705-715.

Gauch, H. G., Jr, and Zobel, R. W. (1997) Identifying Mega-Environments and Targeting Genotypes . *Crop Science*, **37**, 311 – 326.

Goncalves de, S., Bortoletto, G., Martins S., da Costa, Z., and Gallo, M. (2003) Genotype-environment Interaction and Phenotypic Stability for Girth growth and Rubber Yield of *Havea* clones in Sao Paulo State, Brazil. *Genetics and Molecular* Biology, **26.4**, 441-448.

Hakizimana, F., Haley, S. D. and Turnipseed, E. B. (2000) Repeatability and Genotype - Environmental Interactions of Coleoptile Length Measurements in Winter Wheat. *Crop Science*, **40,** 233 – 241.

Hardwick, R. C. and Wood, J.T. (1972) Regression Methods for Studying Genotype-Environment interactions. *Heredity*, **28**, 209-222.

Manner, J. H. (1972) Quality Protein Maize in Swine Nutrition. In: *Maize Improvement Production and Protection in Eastern and Southern Africa*. Proceedings of the Third Eastern and Southern Africa Regional Maize Workshop. September 18-22, 1989

Minitab Software, Inc (2001) *Minitab 12 For Windows*.

Pixley, K. (2002) *Quality Protein Maize: Overview and breeding strategies*. CIMMYT Harare. 466-472.

Pixley, K. V. and Bjarnason, M. S. (2002) Stability of Grain Yield, Endorsperm Modification and Protein Quality of Hybrid and Open-Pollinated Quality Protein Maize (QPM) Cultivars. *Crop Science*, **42**, 1882-1890.

Prasanna, B. M., Vasal, S. K., Kassahun, B. and Singh, N. N. (2001) Quality Protein Maize. *Current Science*, **81**, 499 –516.

Rukuni, M., Tawonezvi, P., Eicher, C., Munyuki-Hungwe, M. and Matondi, P. (2006) (Eds) *Zimbabwe's Agricultural Revolution Revisited*. UZ Publications, Harare. 466.

Setimela, P. S. (1996) Evaluation of Maize Hybrids for Yield and Stability in Kenya. In: *Maize Productivity Gains Through Research and Technology Dissemination: Proceedings of the Fifth Eastern and Southern Africa Regional Maize Conference*, Held in Arusha, Tanzania, 82-86.

Setimela, P. S., Vivek, B., Banziger, M., Crossa, J. and Maiden, F. (2007) Evaluation of Early to Medium Maturing Open Pollinated Maize Varieties in SADC Region using GGE Biplot Based on the SREG Model. *Field Crop Research*, 10-15.

Simmonds, N. W. (1981) *Principles of Crop Improvement*. New York. Longman Group Limited.

Singh, J. and Asnani, V. L. (1972) Present Status and Future Prospects of Breeding for Better Protein Quality in Maize through Opaque -2. In: *High Quality Protein Maize . Proceedings of the CIMMYT- Purdue International Symposium of Protein Quality of Maize*. Straudsburg. Dowden Hutchinson and Ross Inc. 4-6 December 1972. 345-352.

Sito, E. P., Gaspar, E. and Nginamau, D. (2004) Role of Stress Tolerant Germplasm in Increasing Maize Productivity in Drought-Prone Areas of Angola. In: *Resilient Crops for Water Limited Environments: Proceedings of a Workshop Held at Cuernavaca Mexico*, 24-28 May 2004. 222-231.

Sprague, G. F. and Federer, W. T. (1951) Variance Components in Corn Yield Trials: II. Error, Year × Variety, Location × Variety, and Variety Components. *Agronomy Journal 43*, **1**, 535-541.

Uhart, S. A. and Andrade, F. H. (1995) Nitrogen Deficiency in Maize: Effects on Crop Growth, Development, Dry matter Partitioning and Kernel Set. *Crop Science*, **34**, 1306-1311.

Vargas, M., Reynolds, M., Ramirez, M. E., Sayre, K., and Talbot, M (1998) Interpreting Genotype-Environment Interaction in Wheat by Partial Least Squares Regression. *Crop Science*, **38**, 679-689.

Vargas, M., Crossa, J., van Eeuwijk, F. A., Ramirez, M. E., Sayre, K. (1999) Using Partial Least Squares, Regression , Factorial regression and AMMI Models for Interpreting Genotype - Environment Interactions. *Crop Science*, **39**, 955-967.

Vasal, S. K. (2001) High Quality Protein Corn. In: Hallauer A. R. (Ed) *Specialty Corns* (2nd Ed), CRC Press LLC, 85-129.

Villegas, E. M., Eggum, W., and Kohli, M. (2006) Progress in Nutritional Improvement of Maize and Triticale. *http://www.unu. edu/ unupress /food / 8.F.O21e /8Fo2/E06. htm. 7/5/2006.*

Vivek, B., Banziger, and Pixley, K. V. (2002) *Characterisation of Maize Germplasm Grown in Eastern and Southern Africa: Results of the 2001 Regional Trials Coordinated by CIMMYT*. Harare, Zimbabwe. CIMMYT, 125-131.

Wallace, D. H., Bandoin, K., Beaver, M., Coyne, C., Hailseth, D.,Masaya, B., Munger, C., Silbernagel, H., Yourstone, K. and Zobel, R. W. (1993) Improving Efficiency for Breeding of Higher Crop Yield. *Theoretical and Applied Genetics*, **86**, 27-40.

Wright, A. J. (1975) The Significance of Breeding of Linear Regression Analysis of Genotype - Environment Interactions. *Heredity* **50**, 611 – 623.

Yan, W. (2001) GGE-Biplot – a Windows application for graphical analysis of multienvironment trial data and other types of two way data. *Agronomy Journal*, **93**. 1111-1118.

Yan, W. and Hunt, L.A. (2001) Interpretation of GE interaction for Winter Wheat Yield in Ontario. *Crop Science*, **41**,19-25.

Yan, W. and Kang M. S. (2003) *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists and Agronomists*. CRC Press, Boca Raton, FL. 345-351.

Yang, R.C. and Baker R. J. (1991) Genotype × Environment Interactions in Two Wheat Crosses. *Crop Science*, **31**, 81-87.

Zobel, R. W., Wright, M. J. and Gauch, H. G., Jr, (1988) Statistical Analysis of a Yield Trial. *Agronomy Journal*, **80**, 388 – 393.

APPENDICES

Appendix A: Grain Yield

Source	df	SS	MS	Fvalue	Pr> F
Total	249	3473.445			
Environments	4	3070.622	767.655	428.11	0.000
Reps within Env.	5	8.966	1.793		
Genotype	24	65.261	2.719	1.74	0.023
Genotype x Env.	96	149.937	1.562	1.05	0.397
IPCA 1	27	89.011	3.297	2.21	0.008
IPCA 2	25	26.263	1.051	0.71	0.848
IPCA 3	23	17.757	0.772	0.52	0.969
IPCA 4	21	16.906	0.805	0.54	0.946
Residual	120	178.660	1.489		

Appendix B: Line × Tester Analysis

Source of Variation	**d.f.**	**S.S.**	**M.S.**	**F.**	**P**
Location	4	239.7105	59.9276	109.85	0.001
Residual	5	2.7277	0.5455	2.98	
Line	11	3.3870	0.3079	1.68	0.087
Tester	1	0.1279	0.1279	0.70	0.405
Location.Line	44	9.6153	0.2185	1.19	0.229
Location.Tester	4	0.1169	0.0292	0.16	0.958
Line.Tester	11	4.3968	0.3997	2.18	0.020
Location.Line.Tester	44	10.1855	0.2315	1.26	0.164
Residual	115	21.0876	0.1834		
Total	239	291.3553			

Appendix C: Plant Height

Source	df	SS	MS	Fvalue	PrF
Total	249	385508.195			
Environments	4	287022.089	71755.522	126.35	0.000
Reps within Env.	5	2839.537	567.907		
Genotype	24	35078.140	1461.589	3.30	0.000
Genotype x Env.	96	42579.647	443.538	2.96	0.000
IPCA 1	27	20993.093	777.522	5.19	0.000
IPCA 2	25	13161.152	526.446	3.51	0.000
IPCA 3	23	5925.550	257.633	1.72	0.032
IPCA 4	21	2499.852	119.041	0.79	0.720
Residual	120	17988.783	149.907		

Appendix D: Days to 50 % anthesis

Source	df	SS	MS	Fvalue	Pr> F
Total	249	2429.972			
Environments	4	1102.304	275.576	38.94	0.006
Reps within Env.	5	35.388	7.078		
Genotype	24	363.264	15.136	3.17	0.000
Genotype x Env.	96	458.496	4.776	1.22	0.154
IPCA 1	27	230.428	8.534	2.18	0.003
IPCA 2	25	102.940	4.118	1.05	0.418
IPCA 3	23	79.124	3.440	0.88	0.626
IPCA 4	21	46.004	2.191	0.56	0.930
Residual	120	470.520	3.921		

Appendix E: Number of days to 50 % silking

Source	df	SS	MS	Fvalue	PrF
Total	249	3446.939			
Environments	4	1867.799	466.950	58.40	0.002
Reps within Env.	5	39.976	7.995		
Genotype	24	383.538	15.981	2.66	0.003
Genotype x Env.	96	575.897	5.999	1.24	0.131
IPCA 1	27	322.272	11.936	2.47	0.004
IPCA 2	25	126.199	5.048	1.04	0.411
IPCA 3	23	75.036	3.262	0.68	0.866
IPCA 4	21	52.390	2.495	0.52	0.950
Residual	120	579.728	4.831		

Appendix F: Anthesis – silking interval

Source	df	SS	MS	Fvalue	Pr> F
Total	249	199635.920			
Environments	4	97.720	32.573	9.91	0.023
Reps within Env.	5	13.150	3.288		
Genotype	24	120.570	5.024	1.85	0.017
Genotype x Env.	96	195.030	2.709	1.24	0.164
IPCA 1	26	99.963	3.845	1.76	0.022
IPCA 2	24	70.464	2.936	1.35	0.150
IPCA 3	22	24.603	1.118	0.51	0.965
Residual	96	209.450	2.182		

Appendix G: Number of ears per plant

Source	df	SS	MS	Fvalue	Pr> F
Total	249	16.038			
Environments	4	2.613	0.653	14.13	0.002
Reps within Env.	5	0.231	0.046		
Genotype	24	1.843	0.077	1.99	0.001
Genotype x Env.	96	3.702	0.039	0.60	0.995
IPCA 1	27	2.532	0.094	1.47	0.080
IPCA 2	25	0.583	0.023	0.37	0.995
IPCA 3	23	0.391	0.017	0.27	0.997
IPCA 4	21	0.195	0.009	0.15	1.000
Residual	120	7.649	0.064		

Appendix H: Kernel Modification 3

Source	df	SS	MS	Fvalue	PrF
Total	249	167948.144			
Environments	4	106780.999	26695.250	99.34	0.001
Reps within Env.	5	1343.583	268.717		
Genotype	24	8454.762	352.282	1.08	0.072
Genotype x Env.	96	31179.433	324.786	1.93	0.003
IPCA 1	27	12931.194	478.933	2.85	0.001
IPCA 2	25	10443.058	417.722	2.48	0.006
IPCA 3	23	5355.1312	32.832	1.38	0.036
IPCA 4	21	2450.049	116.669	0.69	0.036
Residual	120	20189.366	168.245		

Appendix I: Index of Texture and Modification

Source	df	SS	MS	Fvalue	PrF
Total	249	4162.868			
Environments	4	170.593	42.648	1.97	0.232
Reps within Env.	5	108.500	21.700		
Genotype	24	1025.449	42.727	2.60	0.004
Genotype x Env.	96	1578.177	16.439	1.54	0.014
IPCA 1	27	916.095	33.929	3.18	0.000
IPCA 2	25	352.196	14.088	1.32	0.162
IPCA 3	23	172.245	7.489	0.70	0.839
IPCA 4	21	137.641	6.554	0.61	0.904
Residual	120	1280.150	10.668		

Appendix J: Kernel Modification 5

Source	df	SS	MS	Fvalue	PrF
Total	249	2974.395			
Environments	4	165.343	41.336	3.37	0.006
Reps within Env.	5	61.363	12.273		
Genotype	24	457.554	19.065	1.55	0.006
Genotype x Env.	96	1183.185	12.325	1.34	0.006
IPCA 1	27	568.622	21.060	2.28	0.003
IPCA 2	25	345.493	13.820	1.50	0.070
IPCA 3	23	182.961	7.955	0.86	0.040
IPCA 4	21	86.109	4.100	0.44	0.008
Residual	120	1106.950	9.225		

Appendix K: Kernel Modification 4

Source	df	SS	MS	Fvalue	PrF
Total	249	10592.163			
Environments	4	2386.960	596.740	17.44	0.009
Reps within Env.	5	171.043	34.209		
Genotype	24	786.800	32.783	0.95	0.039
Genotype x Env.	96	3318.240	34.565	1.06	0.083
IPCA 1	27	1495.295	55.381	1.69	0.020
IPCA 2	25	828.739	33.150	1.01	0.051
IPCA 3	23	538.937	23.432	0.72	0.029
IPCA 4	21	455.269	21.679	0.66	0.621
Residual	120	3929.120	32.743		

Appendix L: Kernel Modification 2

Source	df	SS	MS	Fvalue	PrF
Total	249	174429.363			
Environments	4	114306.696	28576.674	101.33	0.000
Reps within Env.	5	1410.027	282.005		
Genotype	24	7546.536	314.439	1.15	0.005
Genotype x Env.	96	26294.104	273.897	1.32	0.078
IPCA 1	27	9871.442	365.609	1.76	0.022
IPCA 2	25	8038.180	321.527	1.55	0.067
IPCA 3	23	5316.299	231.143	1.12	0.033
IPCA 4	21	3068.182	146.104	0.70	0.021
Residual	120	24872.000	207.267		

Appendix M: Kernel Modification 1

Source	df	SS	MS	F-value	PrF
Total	249	28876.983			
Environments	4	3576.160	894.040	10.53	0.019
Reps within Env.	5	424.343	84.869		
Genotype	24	2179.200	90.800	1.09	0.065
Genotype x Env.	96	8005.040	83.386	0.68	0.075
IPCA 1	27	7057.786	261.399	2.14	0.009
IPCA 2	25	789.500	31.580	0.26	0.099
IPCA 3	23	103.388	4.495	0.04	0.100
IPCA 4	21	54.366	2.589	0.02	0.100
Residual	120	1469	2.24012	2.435	

Appendix N: Grain Texture

Source	df	SS	MS	Fvalue	PrF
Total	24	9340.032			
Environments	4	27.520	6.880	3.86	0.000
Reps within Env.	5	8.912	1.782		
Genotype	24	93.800	3.908	3.12	0.000
Genotype x Env.	96	120.080	1.251	1.67	0.008
IPCA 1	27	76.948	2.850	3.81	0.000
IPCA 2	25	21.043	0.842	1.13	0.250
IPCA 3	23	12.834	0.558	0.75	0.870
IPCA 4	21	9.256	0.441	0.59	0.910
Residual	120	89.720	0.748		

Appendix O: Ear Position

Source	df	SS	MS	Fvalue	Pr> F
Total	249	0.731			
Environments	4	0.134	0.033	10.84	0.011
Reps within Env.	5	0.015	0.003		
Genotype	24	0.097	0.004	1.40	0.113
Genotype x Env.	96	0.276	0.003	1.65	0.005
IPCA 1	27	0.128	0.005	2.72	0.001
IPCA 2	25	0.062	0.002	1.44	0.108
IPCA 3	23	0.056	0.002	1.41	0.128
IPCA 4	21	0.030	0.001	0.82	0.694
Residual	120	0.209	0.002		

Appendix P: Ear height

Source	df	SS	MS	Fvalue	Pr> F
Total	249	159616.401			
Environments	4	113414.318	28353.579	125.76	0.000
Reps within Env.	5	1127.328	225.466		
Genotype	24	11751.547	489.648	2.27	0.000
Genotype x Env.	96	20710.354	215.733	2.05	0.001
IPCA 1	27	7791.053	288.558	2.75	0.001
IPCA 2	25	6325.020	253.001	2.41	0.008
IPCA 3	23	4783.304	207.970	1.98	0.005
IPCA 4	21	1810.976	86.237	0.82	0.692
Residual	120	12612.854	105.107		

Appendix Q: Summary of the raw obtained at Art Farm

Name	gyg	gyf	tex	moi	np	asi	ph	eh	epo	rl	epp	sd	ne	da	Md1	md2	md3	md4	md5	mix
06T545	12.8	20.7	4	13.3	18	-1	254	140	0.5	0.1	1.1	71	20	72	6	11	70.6	17	2.5	13.0
06T1006	10.6	17.5	2	13.2	18	1.5	251	119	0.4	0.1	1.2	75	22	74	0	15	65	12	3.4	18.6
06T1150	13.4	21.9	3	10.9	17	1.5	266	138	0.5	0.1	1.3	74	22	73	0	11	56.2	11	6.6	12.8
06T359	10.7	16.1	3	12.1	18	0.5	250	117	0.5	0.1	1.1	71	19	71	27	49.5	42.2	4.5	-1	20.3
06T1395	9.5	15.0	3	15.3	17	-1	269	157	0.6	0.1	0.9	74	14	74	35.5	18	58.9	12	4.7	19.5
06T865	10.7	17.2	2	16.0	17	1	238	124	0.5	0.1	1.1	75	19	74	2	22	91.9	2	-1	18.6
06T313	9.4	14.4	1	11.9	18	1.5	235	123	0.5	0.1	1.2	74	22	73	2.5	33	51.5	11	6.4	21.3
06T498	9.1	14.9	1	13.1	18	1.5	218	107	0.5	0.1	1.2	75	22	74	0	8	84	12	3.7	19.6
06T507	12.5	16.2	1	13.0	18	1	255	159	0.6	0.1	1.1	73	20	72	25	16	64.2	9.5	4.8	23.9
06T791	12.2	18.7	4	13.9	18	0.5	260	141	0.5	0.1	1.1	74	20	73	5	19	76.2	13	3.3	11.9
06T1361	13.1	21.9	2	12.1	18	0.5	265	124	0.5	0.1	1.6	75	29	75	26	13.5	77.2	4.5	3.8	22.7
06T1141	8.5	17.5	2	11.2	18	1	256	139	0.5	0.1	1.3	75	23	74	40	14	58.8	10	5.1	23.1
06T1172	13.4	21.8	5	12.4	18	2	262	124	0.5	0.1	1.1	73	20	71	13.5	36.5	41.2	6	0.4	13.0
06T955	12.3	18.9	2	11.7	18	0	234	113	0.5	0.1	1.3	73	23	73	25	14.5	69.1	10	1.5	20.6
06T389	11.3	18.4	2	13.6	18	-1	264	154	0.6	0.1	1.1	71	20	72	33	12.5	66.2	7.5	6.2	23.6
06T1076	12.2	20.9	4	11.6	18	-1	282	133	0.5	0.1	0.9	71	17	72	23	31.5	69	7.5	-4	17.2
06T307	10.7	17.4	3	11.4	18	1.5	247	120	0.5	0.1	1.2	75	21	73	1.5	23	71.4	11	2.6	16.2
06T811	8.5	14.2	3	12.7	18	1	220	101	0.5	0.1	0.9	73	17	72	0.5	8.5	101	6	-2	15.6
06T1479	10.3	16.2	4	12.9	18	2	252	114	0.5	0.1	1.2	74	21	72	0	20	56.3	8	3	12.9
06T1054	12.2	18.0	5	13.9	18	1	262	127	0.5	0.1	1.2	70	21	69	0	6.5	66.4	15	9.8	7.0
06T1003	10.7	16.9	4	11.6	17	2	247	132	0.5	0.1	1.2	74	20	72	11.5	6.5	84.3	10	4.1	12.4
06T1345	12.7	21.0	5	12.7	18	1.5	269	130	0.5	0.1	1.1	74	19	72	0	12	89.8	9.5	0.8	9.3
06T466	9.7	16.2	1	13.9	18	0	236	120	0.5	0.1	1.2	75	22	75	0	18.5	33.6	22	4.8	19.7
06T117	8.9	14.2	2	14.6	18	1	246	127	0.5	0.1	1.1	73	19	72	0.5	12.5	69	12	-0	17.1
SC2785	12.0	12.9	5	13.4	18	0.5	270	128	0.5	0.1	0.9	71	17	70	0	32	72.6	9	2.9	10.3
MEAN	11.1	17.6	2.7	12.9	18	0.8	252	128	0.5	0.1	1.1	73	20.2	72	11.1	18.6	67.5	10	2.9	16.8
LSD	5.6	9.3	2	5.6	2	3.6	39	23	0.1	0.1	0.4	5	8.2	5	67.4	50.7	34.3	19	8.9	13.7
Prob. Entry	0.2	0.2	0	0.6	1	0.4	0	0	0	0.7	0.1	0	0.1	0	0.8	0.8	0.1	0.7	0.4	0.04
CV	17.3	18.2	29	14.8	4	152	5.3	8	6.9	42.6	13.1	3	14	2	208	93.6	24	65	144	27.9
Min. Mean	8.5	12.9	1	10.9	16.5	-1	217.5	101	0.4	0.1	0.9	70	14	69	0	6.5	33.6	2	-4	7.0
Max. Mean	13.4	21.9	5	16.0	18	2	282	159	0.6	0.1	1.6	75	28.5	74.5	40	49.5	101	22	9.8	23.9
SED	1.9	3.2	1	1.9	1	1.2	13	11	0	0.1	0.1	2	2.8	2	23.1	17.4	16.2	6.5	4.2	4.0
Rep-Msqr	4.9	14.1	3	3.2	0.38	1.5	496	341	0	0.0	0.0	5	14	4	370	224	205	34	12	45.6
Residual	3.7	10.3	1	3.6	0	1.5	177	116	0	0.0	0.0	4	7.8	3	534	302	262	43	18	22.0
No. of Reps	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Error d.f.	24	24	24	24	24	24	24	16	24	24	24	24	24	24	24	24	16	24	16	24

Gyg = mean grain yield, gyf = mean field grain yield, tex = mean grain texture, moi = mean grain moisture after drying, np = mean number of plants per plot, asi = mean anthesis-silking interval, ph = mean plant height, eh = mean ear height, epo = mean ear position, rl = mean lodging score, epp = mean number of ears per plant, sd = mean number of days to 50 % silking, ne = number of ears harvested per plot, da = mean number of days to 50 % anthesis, md1 = mean percentage kernel modification falling in score 1, md2 = mean percentage kernel modification falling in score 2, md3 = mean percentage kernel modification falling in score 3, md4 = mean percentage kernel modification falling in score 4, md5 = mean percentage kernel modification falling in score 5, index = score obtained after the index of modification has been used.

Appendix R: Summary of the raw data obtained at Cimmyt Low N

Name	gyg	gyf	tex	moi	np	asi	ph	Eh	epo	rl	epp	sd	ne	da	Md1	md2	md3	md4	md5	mix
06T545	2.2	3.7	2	13.1	12	3	190	95	0.5	0.0	0.9	78	11	76	0.5	12.0	69.0	13.5	4.5	18.2
06T1006	2.9	4.6	2	11.9	9	1	190	103	0.5	0.0	1.0	77	10	76	0	1.0	85.0	12.0	1.5	16.4
06T1150	3.1	4.3	1	12.7	15	4	213	95	0.5	0.1	0.8	80	12	76	6.5	7.0	81.5	6.5	5.0	20.8
06T359	3.0	4.5	2	13.3	12	3	190	90	0.5	0.0	1.0	77	12	74	0	15.0	79.5	5.0	0.5	19.0
06T1395	2.7	4.5	2	13.7	14	2	205	98	0.5	0.1	0.7	80	9	78	1	29.5	61.5	6.0	3.0	18.2
06T865	2.6	4.3	2	13.7	13	-1	195	88	0.5	0.2	0.8	79	10	79	0	27.5	57.5	10.5	2.0	19.1
06T313	2.7	4.4	1	12.6	16	3	173	88	0.5	0.0	0.9	79	15	76	0	26.0	54.5	11.5	7.0	20.3
06T498	2.1	3.5	1	13.2	14	2	160	65	0.4	0.0	1.0	78	15	76	0	21.5	68.0	9.5	1.0	20.6
06T507	1.6	2.5	1	12.5	15	5	175	83	0.5	0.1	0.7	83	10	78	0	8.5	38.0	18.5	17.0	17.8
06T791	4.9	8.1	3	12.3	15	1	200	108	0.5	0.0	1.0	78	15	77	1.5	17.5	73.5	11.5	0.0	16.2
06T1361	4.0	6.0	1	12.8	14	0	200	105	0.5	0.0	1.0	78	14	78	0	7.5	82.0	8.5	2.0	19.9
06T1141	2.7	4.2	1	12.6	15	1	185	83	0.5	0.1	0.8	76	13	75	0	43.5	50.5	5.0	1.0	21.9
06T1172	2.9	4.7	3	13.0	11	0	198	98	0.5	0.1	1.0	76	11	76	0	53.0	37.0	8.5	1.5	17.7
06T955	2.9	4.4	2	12.8	14	3	200	98	0.5	0.0	0.9	80	12	77	0	40.0	47.0	10.5	2.5	19.9
06T389	3.2	4.9	1	12.6	15	3	190	88	0.5	0.1	1.1	77	16	75	0.5	21.5	59.5	21.0	3.0	20.2
06T1076	2.6	4.2	2	12.8	15	1	200	93	0.5	0.1	0.8	76	12	75	0	10.0	77.5	12.0	0.5	18.4
06T307	2.7	4.5	2	13.2	12	3	193	95	0.5	0.0	1.0	78	12	75	0.5	25.5	68.0	7.0	0.5	19.5
06T811	2.3	4.0	2	13.0	15	4	160	75	0.5	0.2	0.8	80	12	76	0	16.5	74.5	7.5	1.5	18.9
06T1479	3.0	4.4	3	12.9	15	3	203	83	0.4	0.1	0.8	80	11	77	0	15.0	65.0	9.0	1.0	15.3
06T1054	2.3	3.5	3	12.6	15	2	193	88	0.5	0.0	0.7	77	11	75	2	15.5	68.0	9.5	2.0	15.8
06T1003	3.8	5.9	4	12.5	17	3	190	83	0.4	0.1	1.0	77	16	75	0	18.0	69.0	13.0	0.0	12.8
06T1345	3.3	5.8	2	12.7	13	1	200	98	0.5	0.0	1.0	79	13	78	0	14.5	74.5	6.5	4.0	17.2
06T466	2.7	4.2	2	12.6	16	3	178	90	0.5	0.1	0.9	78	14	75	0	9.5	67.0	14.5	8.5	17.8
06T117	2.6	4.3	2	13.1	15	5	195	88	0.5	0.0	0.9	77	14	72	0	2.5	90.0	6.5	1.0	18.3
SC2785	2.9	4.1	3	12.7	11	2	198	108	0.6	0.2	1.0	76	11	74	0	6.5	84.5	6.5	2.0	13.9
MEAN	2.9	4.5	2	12.8	13.7	2	190.8	91.1	0.5	0.0	0.9	78	12.2	76	0.5	18.6	67.3	10	2.9	18.1
LSD	2.6	4.1	2	1.5	6	4	35	35	0.1	0.3	0.3	6	8	5	5.8	41.3	35.0	19.5	6.4	6.1
Prob. Entry	0.4	0.4	0	0.3	0	0	0	0.2	0.3	0.8	0.1	0	0	0	0.6	0.1	0.0	0.8	0.0	0.0
CV	31.4	31.2	38	4.1	15	66	6.3	13	9.7	172.1	13.7	3	22	3	397	76.1	17.8	66.9	75.8	11.5
Min. Mean	1.6	2.5	1	11.9	9	-0.5	160	65	0.4	0	0.7	75.5	9	71.5	0	1	37	5	0	12.8
Max. Mean	4.9	8.1	3.5	13.7	16.5	5	212.5	107.5	0.5	0.2	1.1	82.5	16	79	6.5	53	90	21	17	21.9
SED	0.9	1.4	1	0.5	2	1	12	12	0.0	0.1	0.1	2	3	2	2	14.1	12.0	6.7	2.2	2.1
Rep-Msqr	0.9	2.2	1	0.3	6	4	338	198	0.0	0.0	0.0	6	8	6	3.7	326.0	397.9	32	26.1	9.6
Residual	0.8	2.0	0	0.3	4	2	143	146	0.0	0.0	0.0	4	7	4	3.9	200.0	143.9	44.8	4.8	4.3
No. of Reps	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Error d.f.	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24

Gyg = mean grain yield, gyf = mean field grain yield, tex = mean grain texture, moi = mean grain moisture after drying, np = mean number of plants per plot, asi = mean anthesis-silking interval, ph = mean plant height, eh = mean ear height, epo = mean ear position, rl = mean lodging score, epp = mean number of ears per plant, sd = mean number of days to 50 % silking, ne = number of ears harvested per plot, da = mean number of days to 50 % anthesis, md1 = mean percentage kernel modification falling in score 1, md2 = mean percentage kernel modification falling in score 2, md3 = mean percentage kernel modification falling in score 3, md4 = mean percentage kernel modification falling in score 4, md5 = mean percentage kernel modification falling in score 5, index = score obtained after the index of modification has been used.

Appendix S: Summary of the data obtained at Kadoma Research Station

Name	gyg	gyf	tex	moi	np	asi	ph	eh	epo	rl	epp	sd	ne	da	md1	md2	md3	md4	md5	mix
06T545	1.8	3.3	3	11.3	6.5	-1	175	89	0.5	0.1	1.5	71	6	71	2.5	78.5	11.5	7	1	19.3
06T1006	1.7	3.0	4	10.0	9.5	1	171	85	0.5	0	1.1	72	8	71	3.5	68.5	11.5	6	4	15.5
06T1150	1.3	1.9	2	11.2	3.5	1.5	204	98	0.5	0	1.7	77	10	75	1.5	64	21	12	2.5	21.2
06T359	2.5	3.7	4	11.3	9.5	0	190	105	0.5	0.1	0.9	67	1	67	4	50.5	28	8.5	1.5	13.1
06T1395	1.8	3.3	2	6.0	5.5	0.5	154	83	0.5	0.1	1.2	77	10	76	1.5	85.5	12	1.5	0	22.9
06T865	2.5	3.5	2	11.3	9	0	172	89	0.5	0	1.1	73	10	73	2	83.5	11.5	3.5	0	21.2
06T313	2.0	3.2	3	11.0	8	1.5	160	80	0.5	0	1.2	69	8	68	2.5	61.5	31	5	2.5	18.6
06T498	1.6	2.6	2	12.8	5.5	-2	157	70	0.5	0	1.5	72	10	73	2	55	29	9.5	1.5	19.3
06T507	1.9	2.9	3	10.9	7	-1	198	114	0.6	0	1.3	68	10	69	2.5	83.5	11.5	2	2.5	19.8
06T791	1.8	3.1	3	11.9	8	-1	179	95	0.5	0	1.1	70	9	71	3	68.5	18.5	2.5	7	17.2
06T1361	1.8	2.8	2	11.9	7	0	199	108	0.6	0.1	1.3	73	8	73	2	65	19.5	9	3.5	19.8
06T1141	2.0	3.1	4	11.8	8.5	1	174	86	0.5	0	1.1	71	9	70	3.5	50.5	34.5	8.5	6.5	14.8
06T1172	1.6	2.5	3	10.8	7.5	0	195	97	0.5	0	0.8	75	3	75	3	59.5	15.5	14	7.5	16.2
06T955	1.3	2.4	3	11.8	6.5	1	188	79	0.4	0	1.8	69	9	68	2.5	52.5	39	3	0	18.1
06T389	1.4	2.1	2	11.3	7	-2	186	83	0.5	0.1	1.0	66	6	68	2	54	36.5	8.5	1	19.5
06T1076	1.7	2.7	2	12.0	8.5	0	221	100	0.5	0.1	0.9	70	7	70	2	54	35.5	6	0	19.5
06T307	1.3	2.5	2	10.9	6	1.5	122	58	0.5	0	1.3	73	7	72	2	77.5	13.5	9	0	20.7
06T811	1.4	2.4	3	11.1	6.5	0.5	164	74	0.5	0	0.9	70	5	70	2.5	70	25.5	4	0.5	19.2
06T1479	0.3	0.8	2	12.0	2.5	0	165	70	0.5	0	1.0	70	3	70	2	76	18	3	1.5	20.8
06T1054	1.2	2.3	3	11.8	5.5	-1	184	83	0.5	0	1.3	68	3	68	3	62.5	25.5	6.5	0	17.0
06T1003	0.6	1.2	2	11.9	3	1	183	92	0.5	0	1.1	73	8	76	1.5	69	20	7.5	2.5	21.6
06T1345	2.4	2.1	3	11.5	12	2	184	79	0.5	0	1.0	75	13	73	2.5	77.5	15.5	1	0.5	19.4
06T466	1.1	1.8	3	11.7	37	0	143	70	0.5	0	1.1	67	4	67	2.5	39.5	46.5	12	2	17.2
06T117	1.6	2.5	3	11.2	8	0.5	187	107	0.6	0.1	1.1	72	13	71	3	26.5	45.5	20	8.5	14.4
SC2785	1.5	2.3	4	11.4	9	1.5	166	82	0.5	0	0.7	70	7	68	3.5	49	33.5	16	0	14.6
MEAN	1.6	2.6	2.5	11.2	8.2	0.32	176.7	86.9	0.5	0	1.1	71	8	70.7	2.5	63.3	24.4	7.4	2.3	18.4
LSD	2.4	4.4	2	5.5	31	3.1	30	22	0.1	0.2	1.5	9	8	8	1.7	37.8	33	15	9.4	5.3
Prob. Entry	0.8	1.0	0	0.7	0.8	0.1	0	0	0.3	0.8	0.9	0	0	0	0	0	0.1	0.1	0.3	0.0
CV	52.5	58.4	23	16.7	130	332	8.1	12	9.7	264	44.6	4	53	4	23	20.5	46.4	70	143	9.9
Min. Mean	0.3	0.8	1.5	6	2.5	-1.5	122	58	0.4	0	0.7	66	1	66.5	1.5	26.5	11.5	1	0	13.1
Max. Mean	2.5	3.7	4	12.8	36.5	2	221	114	0.6	0.1	1.8	76.5	13	76	4	85.5	46.5	19.5	8.5	22.9
SED	0.8	1.5	1	1.9	11	1.1	14	11	0.0	0.1	0.5	3	4	3	0.6	13	11.3	5.2	3.2	1.8
Rep-Msqr	0.5	1.0	1	2.9	78	1.8	544	225	0.0	0	0.1	17	9	16	0.9	422	242	43	13	13.1
Residual	0.7	2.2	0	3.5	115	1.1	206	111	0.0	0	0.2	9	15	8	0.3	168	128	27	10	3.3
No. of Reps	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Error d.f.	24	24	24	24	24	23	16	16	24	24	24	23	16	24	24	24	24	24	24	24

Gyg = mean grain yield, gyf = mean field grain yield, tex = mean grain texture, moi = mean grain moisture after drying, np = mean number of plants per plot, asi = mean anthesis-silking interval, ph = mean plant height, eh = mean ear height, epo = mean ear position, rl = mean lodging score, epp = mean number of ears per plant, sd = mean number of days to 50 % silking, ne = number of ears harvested per plot, da = mean number of days to 50 % anthesis, md1 = mean percentage kernel modification falling in score 1, md2 = mean percentage kernel modification falling in score 2, md3 = mean percentage kernel modification falling in score 3, md4 = mean percentage kernel modification falling in score 4, md5 = mean percentage kernel modification falling in score 5, index = score obtained after the index of modification has been used.

Appendix T: Summary of the raw data obtained at Rattray Arnold Research Station

Name	gyg	gyf	tex	moi	np	ph	eh	epo	rl	epp	sd	ne	da	asi	Md1	md2	md3	md4	md5	mix
06T545	5.5	13.7	2	25.4	16	255	138	0.5	0.1	1.1	72	17	71	1	4	73.5	20.5	1.5	0	22.5
06T1006	5.6	12.0	2	22.7	18	225	130	0.6	0.1	1.0	66	19	71	-5	2	76.5	22	5	2	22.6
06T1150	4.6	10.2	3	19.0	17	250	138	0.6	0.0	0.8	73	14	73	0	4.5	58.5	29	7	1	17.0
06T359	6.9	12.7	3	23.7	19	255	133	0.5	0.0	0.9	69	17	68	1	5.5	71.5	21	1	0	19.5
06T1395	3.7	10.8	1	24.8	19	240	140	0.6	0.1	0.8	71	15	70	1	1.5	61	38	5	0	23.2
06T865	5.7	12.7	2	24.9	18	243	135	0.6	0.0	0.8	71	15	73	-2	2	74.5	22	4	1.5	22.4
06T313	5.1	10.8	2	26.1	17	220	130	0.6	0.1	1.0	72	17	70	2	4.5	73	19.5	2.5	0.5	22.5
06T498	5.0	10.1	1	22.8	17	238	133	0.6	0.0	1.0	72	17	72	-1	5.5	78	16.5	0	0	24.5
06T507	5.8	11.9	2	15.4	17	255	138	0.5	0.1	1.0	69	17	70	-1	1	61	36	2	0	21.6
06T791	5.3	11.2	4	25.2	17	225	110	0.5	0.2	0.9	71	16	72	-1	6	69.5	23	1.5	0	15.0
06T1361	7.1	14.4	1	21.5	18	235	125	0.5	0.1	1.2	72	21	73	-1	3	54	38	5	0	22.8
06T1141	6.6	14.3	3	17.1	18	255	140	0.6	0.1	1.0	69	18	71	-2	4.5	65.5	28.5	1	0.5	19.2
06T1172	5.3	13.2	5	21.4	16	243	135	0.6	0.1	0.9	71	15	74	-3	2	66.5	21	9	1.5	12.5
06T955	6.7	13.5	3	19.2	17	218	110	0.5	0.2	1.1	71	19	72	-1	3	61	30.5	5.5	0	18.6
06T389	6.0	12.1	2	21.9	19	240	125	0.5	0.1	0.9	69	17	71	-3	3.5	63.5	33.5	0.5	0	22.1
06T1076	5.9	11.4	2	20.3	17	245	135	0.6	0.0	1.0	69	16	71	-2	0.5	45	45.5	9	0	18.9
06T307	6.0	12.9	2	25.0	17	248	125	0.5	0.1	1.1	72	18	72	0	2.5	79	22.5	3	0	21.4
06T811	4.0	9.2	2	23.7	17	205	123	0.6	0.0	0.7	71	13	72	-1	6	70.5	22	1.5	0	22.6
06T1479	6.8	13.0	4	22.8	17	265	145	0.6	0.1	1.2	71	20	72	-1	1.5	66.5	22.5	6	3.5	15.5
06T1054	6.6	13.0	4	19.5	18	265	145	0.6	0.1	1.0	67	18	67	0	1	69	26	4	0	14.4
06T1003	5.3	11.7	4	23.9	16	238	110	0.5	0.2	0.9	71	15	71	0	0.5	67	18.5	9.5	4.5	13.7
06T1345	5.7	12.4	4	27.2	16	260	140	0.5	0.1	0.8	72	13	70	2	0.5	81	16.5	0.5	2	15.0
06T466	5.7	10.8	1	24.6	18	225	130	0.6	0.1	1.0	70	18	70	0	2.5	59	37.5	1	0	23.2
06T117	4.6	9.9	3	19.9	18	228	125	0.6	0.0	0.9	70	15	71	-1	0.5	59	38	2.5	0	18.4
SC2785	6.1	12.5	5	20.6	17	253	138	0.6	0.1	1.0	68	17	67	1	0.5	65.5	39	0	0	11.6
MEAN	5.7	12.0	2	22.3	17	241	130.9	0.5	0.0	1.0	70	16.4	71		2.7	66.8	27.5	3.5	0.7	19.2
LSD	3.4	5.2	3	6.8	4	42	32	0.1	0.3	0.4	4.8	7.2	3.9		9.1	33.6	32.3	6.9	3.4	7.8
Prob. Entry	0.4	0.3	0	0.0	1	0	0.1	0.2	0.9	0.2	0	0.7	0		0.8	0.4	0.4	0	0	0.0
CV	20.5	14.9	36	10.5	9	5.9	8.3	7.2	140.1	14.1	2.3	15	1.9		113	17.2	40.3	68	172	13.9
Min. Mean	3.7	9.2	1	15.4	16	205	110	0.5	0	0.7	66	12.5	66.5		0.5	45	16.5	0	0	11.6
Max. Mean	7.1	14.4	5	27.2	19	265	145	0.6	0.2	1.2	73	20.5	73.5		6	81	45.5	9.5	4.5	24.5
SED	1.2	1.8	1	2.3	2	14	11	0.0	0.1	0.1	1.6	2.5	1.3		3.1	11.5	11.1	2.7	1.2	2.7
Rep-Msqr	1.5	3.9	3	17.1	2	490	200	0.0	0.0	0.0	6	8	6		7	142	141	17	2.9	29.7
Residual	1.4	3.2	1	5.5	2	202	118	0.0	0.0	0.0	2.7	6.1	1.8		9.6	133	123	5.6	1.4	7.7
No. of Reps	2	2	2	2	2	2	2	2	2	2	2	2	2		2	2	2	2	2	2
Error d.f.	24	24	24	24	24	24	24	24	24	24	24	24	24		24	24	24	24	24	24

Gyg = mean grain yield, gyf = mean field grain yield, tex = mean grain texture, moi = mean grain moisture after drying, np = mean number of plants per plot, asi = mean anthesis-silking interval, ph = mean plant height, eh = mean ear height, epo = mean ear position, rl = mean lodging score, epp = mean number of ears per plant, sd = mean number of days to 50 % silking, ne = number of ears harvested per plot, da = mean number of days to 50 % anthesis, md1 = mean percentage kernel modification falling in score 1, md2 = mean percentage kernel modification falling in score 2, md3 = mean percentage kernel modification falling in score 3, md4 = mean percentage kernel

modification falling in score 4, md5 = mean percentage kernel modification falling in score 5, index = score obtained after the index of modification has been used.

Appendix U: Summary of the raw data obtained at Chakonda (Shamva)

Name	gyg	gyf	tex	moi	np	asi	ph	eh	epo	rl	epp	sd	ne	da	md1	md2	md3	md4	md5	mix
06T545	2.9	5.5	3.5	12.8	25	2.5	149	86	0.6	0.0	1.0	71	24	68	1.5	25	68	9	2	13.6
06T1006	3.0	4.6	1.5	12.6	29	1	154	78	0.5	0.0	1.0	70	28	69	15	55	15.5	14	1	22.0
06T1150	1.5	3.0	2.5	11.9	24	4	178	72	0.4	0.1	1.0	74	23	70	1.5	68	17.5	11	2	18.4
06T359	4.0	6.0	2	13.2	32	1.5	184	84	0.5	0.1	1.0	71	31	69	13.5	49	17.5	18	2.5	19.8
06T1395	1.5	3.1	1.5	11.5	31	-2	210	97	0.5	0.1	1.0	70	30	72	0	69	18.5	8	5	21.3
06T865	1.8	3.8	2.5	12.9	27	-1	159	76	0.5	0.0	1.0	70	27	71	5	40	43.5	12	0	17.4
06T313	2.4	5.6	2.5	12.0	21	3	168	80	0.5	0.1	1.0	71	20	68	6	49	25	14	6.5	17.6
06T498	1.5	3.1	2	12.4	19	1	167	70	0.4	0.1	1.0	73	19	72	5.5	71	14	6	4	20.6
06T507	1.2	2.4	2.5	11.8	29	3	167	79	0.5	0.0	1.0	72	28	69	3	58	26	7	6	18.1
06T791	1.5	3.2	2.5	13.4	29	3	186	79	0.4	0.0	1.0	74	28	71	14	66	12.5	7	0.5	19.8
06T1361	3.3	5.1	2.5	13.7	24	2	195	100	0.5	0.1	1.0	72	24	70	7	60	13	20	1	18.2
06T1141	1.9	3.9	2.5	12.0	26	-1	189	86	0.5	0.1	1.0	69	25	70	9	60	11	7	4	18.4
06T1172	2.0	2.9	1.5	10.6	28	3.5	202	99	0.5	0.1	1.0	71	27	68	8	57	20	14	1.5	21.4
06T955	2.1	4.2	3	12.5	22	0	203	93	0.5	0.1	1.0	70	22	70	8.5	33	39.5	17	2.5	15.6
06T389	0.9	1.9	2.5	11.1	23	2.5	141	77	0.5	0.1	1.0	74	22	71	9	63	19	9	0.5	19.1
06T1076	2.3	3.7	2	11.9	28	-1	159	86	0.6	0.0	1.0	70	27	71	10.5	59	12.5	17	1.5	20.1
06T307	2.2	4.2	2.5	11.0	28	2.5	116	65	0.6	0.1	1.0	75	27	73	10.5	52	19.5	16	2	18.3
06T811	1.8	3.5	1.5	13.3	27	4.5	142	78	0.6	0.0	0.9	73	25	68	1	60	19	19	2	20.6
06T1479	1.6	3.2	2	12.7	22	2	147	74	0.5	0.1	1.0	74	21	72	13	58	26	3	0	21.1
06T1054	1.7	4.0	3.5	12.8	23	0.5	199	82	0.4	0.1	1.0	71	23	70	2	40	42.5	16	0	13.9
06T1003	3.6	5.6	1	12.9	25	-1	153	78	0.5	0.0	1.0	70	24	70	9.5	50	27	11	2.5	22.8
06T1345	2.4	3.7	2.5	11.6	26	2.5	173	88	0.5	0.1	1.0	73	26	70	1	71	9.5	14	5	18.2
06T466	3.0	4.5	2.5	11.7	25	2	175	81	0.5	0.1	1.0	71	25	69	8	55	17.5	15	4.5	18.1
06T117	2.0	3.6	2.5	11.5	27	2	170	72	0.4	0.0	1.0	72	26	70	0	57	26.5	17	1	17.5
SC2785	2.0	4.1	1.5	12.3	29	3.5	161	92	0.6	0.1	1.0	74	28	70	7	35	37.5	20	1	19.9
MEAN	2.2	3.9	2.3	12.2	26	1.7	170	81.8	0.5	0.1	1.0	72	25	69.9	6.8	54	23.9	13	2.3	18.9
LSD	2.7	4.4	3.7	1.6	10	6	9.6	17	0.1	0.1	0.0	7	9	5	23.4	45	39.7	19	10	11.9
Prob. Entry	0.2	0.5	1	0.0	0	0.2	0	0	0.0	0.5	0.0	0	0	1	0.8	0.3	0	1	0.9	0.9
CV	43.4	38.4	55.6	6.0	13	124	2.7	7.2	8.0	45.0	1.4	3	13	3	119	28	56.9	53	148	21.6
Min. Mean	0.9	1.9	1	10.6	19	-2	116	65	0.4	0.0	0.9	69	18.5	67.5	0	24.5	9.5	3	0	13.6
Max. Mean	4.0	6.0	3.5	13.7	32	4.5	210	99.5	0.6	0.1	1	75	31	72.5	15	71	68	19.5	6.5	22.8
SED	4.0	1.5	1.3	0.7	3	2.1	4.6	5.9	0.0	0.0	0.0	2	3	2	8	15	13.6	7	3.5	4.1
Rep-Msqr	1.2	2.2	0.8	0.9	19	5.9	973	164	0.0	0.0	0.0	6	19	4	42.6	296	357	45	7.3	10.5
Residual	0.9	2.2	1.6	0.5	11	4.2	21	35	0.0	0.0	0.0	5	10	3	64.5	234	185	44	12	16.5
No. of Reps	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Error d.f.	24	24	24	16	24	24	16	24	24	24	24	24	24	24	24	24	24	24	24	24

Gyg = mean grain yield, gyf = mean field grain yield, tex = mean grain texture, moi = mean grain moisture after drying, np = mean number of plants per plot, asi = mean anthesis-silking interval, ph = mean plant height, eh = mean ear height, epo = mean ear position, rl = mean lodging score, epp = mean number of ears per plant, sd = mean number of days to 50 % silking, ne = number of ears harvested per plot, da = mean number of days to 50 % anthesis, md1 = mean percentage kernel modification falling in score 1, md2 = mean percentage kernel modification falling in score 2, md3 = mean

percentage kernel modification falling in score 3, md4 = mean percentage kernel modification falling in score 4, md5 = mean percentage kernel modification falling in score 5, index = score obtained after the index of modification has been used.