

**COMBINING ABILITY AMONG EARLY QUALITY PROTEIN MAIZE  
INBRED LINES UNDER STRESS AND NON-STRESS ENVIRONMENTS**

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**B.Sc. Agric. (Hons)**

**A thesis submitted in partial fulfillment of the requirements for the award of the  
degree of Master of Science in Genetics and Plant Breeding, Department of Plant  
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## **DEDICATION**

This thesis is dedicated to Dr. Alpha Diallo for his contribution to reduction of poverty, hunger and malnutrition in Africa.

## DECLARATION

I hereby declare that this thesis, prepared for the degree of Master of Science in Genetics and Plant Breeding, is my own original work and has not previously in its entirety or in part been submitted to any other university.

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## **ACKNOWLEDGEMENTS**

I express my heartfelt thanks and gratitude to my supervisors Dr. Stephen Githiri, Dr. Alpha Diallo, Dr. George Chemining'wa and Dr. Dan Makumbi for their time, invaluable advice and assistance in the course of my study. Special thanks are due to Dr. Marianne Bänziger (Director of African Livelihood Programme) for allowing me into the research programme. I also thank CIMMYT staff for their support throughout my graduate study. Special thanks goes to Mr. Joseph Kasango for his assistance in preparation of field books, labels and data analysis; Mr. Mailu Muthoka and Vincent Eget for fieldwork support and Mr. Haroun Karaya for his technical assistance and guidance during data collection and thesis writing. With great pleasure and gratitude, I acknowledge Dr. Alpha Diallo for his guidance, wealth of skills and support through the duration of my graduate study.

I am greatly indebted to the University of Nairobi for offering me a scholarship for the graduate study. I deeply appreciate and thank Kenya Agricultural Research Institute (KARI) for offering me land to carry out research and I extend my appreciation to KARI staff for their technical assistance.

I am proud to express my heartfelt appreciation to my mother, brothers, sisters and my fiancée Anne for their love and assistance during my study. Finally but above all, I honour and praise the Almighty God through Jesus for He is the way, and the truth, and the life (John Chapter 14, verse 6)

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## LIST OF ABBREVIATIONS

- AD - Anthesis date
- ASI - Anthesis Silking Interval
- CIMMYT - International Maize and Wheat Improvement Center
- CML-CIMMYT Maize Line
- EA -Ear aspect
- EPP - Ears per plant
- ER - Ear rots
- ET-*Exserohilum turcicum* (turcicum blight)
- GCA-General Combining Ability
- GLS-Gray Leaf Spot
- GY - Grain yield
- HC-Husk cover
- MSV- Maize Streak Virus
- NARs - National Agricultural Research systems
- OPVs-Open Pollinated Varieties
- PA-Plant aspect
- PS-*Puccinia sorghi* (Rust)
- QPM- Quality Protein Maize
- QTLs-Quantitative Trait Loci
- RL - Root lodging
- SCA-Specific Combining Ability
- SD-Silking date
- SL - Stalk lodging

## ABSTRACT

The general combining ability (GCA) and specific combining ability (SCA) are the main criteria for rapid genetic assaying of test genotypes under the line by tester analysis. Information on GCA and SCA has been well documented both in temperate and tropical germplasm. However, little information is known on combining ability of early Quality Protein Maize (QPM) inbred lines under stress and non-stress conditions especially in the tropics. Therefore the objectives of this study were: i) To determine performance of early QPM inbred lines under stress and non-stress conditions ii) To determine performance of early QPM top cross and three way hybrids under stress and non-stress condition iii) Estimate the GCA and SCA of early QPM inbred lines under stress and non-stress conditions.

A total of 50 early QPM inbred lines selected based on performance of the top cross hybrids were advanced to S<sub>4</sub> and crossed to three testers (Susuma, ECA-QPOPE and CML144 x 159). A total of 150 early QPM hybrids plus six experimental checks were evaluated across drought and non drought environment. All experiments were planted in alpha lattice design. Three sites (Kiboko, Embu and Namulonge) were under well watered environments while one site (Kiboko) was under managed drought environment. Data was collected on grain yield and secondary traits. Individual and combined analyses of variance (ANOVA) were performed using proc GLM of SAS. All sites were significant for grain yield. The average grain yield across sites was 6.5 t/ha with a range of 4.7 t/ha to 8.8 t/ha. The average grain yield under managed drought stress was 2.1 t/ha with a range of 0.3 t/ha to 5.0 t/ha. The best four hybrids under drought involved inbred lines with tester 3 (Susuma) and the best hybrid under drought (inbred line15 x tester 3) was also the best hybrid across non drought conditions. Mean grain

yield across non drought conditions was 8.0 t/ha with a range of 5.6 t/ha to 10.7 t/ha. Grain yield for checks under managed drought stress ranged from 0.7 t/ha to 2.0 t/ha whereas under non drought conditions the range was 7.1 t/ha to 10.7 t/ha. The average grain yield for inbred lines under drought was 1.7 t/ha with a range of 0.0 t/ha to 3.2 t/ha. Under non drought condition the average grain yield was 3.9 t/ha with a range of 1.8 t/ha to 6.5 t/ha.

Among the 50 early QPM inbred lines used in this study, 24 inbred lines recorded positive GCA for grain yield under drought. Several hybrids under drought were identified based on per se performance of the inbred line, its GCA and performance in hybrid combination. The hybrids included genotype 11, 12, 29, 126 and 135. Inbred line 44 had the highest positive GCA for grain yield (1.09 t/ha) under non drought conditions. This inbred line had a high grain yield with all the three testers under non drought condition. Among 50 early QPM inbred lines used in this study, 21 lines exhibited positive GCA for grain yield under non drought conditions. Across sites, inbred line 13 had the highest positive and significant GCA for grain yield (0.99 t/ha) with positive GCA for EPP and negative GCA for ASI. Other inbred lines with positive and significant GCA for grain yield across sites include inbred line 15, 28, 38 and 44.

Good specific combiners under non drought conditions include genotype 8, 12, 54, 71 and genotype 93. These hybrids recorded high significant SCA effects for grain yield under non drought conditions. Good specific combiners under drought stress include genotype 5, 11, 12, 15, 35, 52, 105, 109, 112 and genotype 121. Thus these genotypes are potential hybrids for advanced yield testing and consequent release. The best inbred lines may be used as a future breeding stock of drought tolerant early QPM hybrids.

# CHAPTER ONE

## 1.0 Introduction

### 1.1 Background Information

Maize (*Zea mays* L.) is one of the three most popular cereal crops in the world. It is grown on approximately 142 million hectares annually with a production of 638 million metric tonnes (FAOSTAT, 2006). It occupies an important position in the world economy and trade as a food, feed and an industrial grain crop. The United States of America (USA) is still the largest producer of maize with an average production of 282.31 million tonnes in 2005 (FAOSTAT, 2006). In Africa, South Africa had the highest production of 11.74 million tonnes in the year 2005 while in East Africa, Tanzania had a production of 3.34 millions tonnes. Kenya and Uganda produced 2.91 million and 1.17 million tonnes respectively (FAOSTAT, 2006). Globally, maize contributes 15% (representing more than 50 million tons) of the protein and 20% of the calories derived from food crops in the world's diet (National Research Council, 1988). In many developing countries in Latin America, Africa and Asia, maize is the staple food and sometimes the only source of protein in diet, especially as weaning food for babies.

In East and Central Africa (ECA), 38 % of cultivated area is under maize mainly on small scale farm holdings with a high proportion of women performing much of the farm labor (Pingali, 2000). In this region maize provides more than half of the daily calories and protein intakes of most of the population which now numbers more than 270 million and is growing at an annual rate of more than 2.5 per cent (World Bank report, 2006). It is largely used as human food but is increasingly being used as animal feed. The average per capita consumption in Sub Saharan Africa (SSA) is 60 kg per year and ranges from 12 kg per year to 103 kg per year (CGIAR report, 2005). Despite its

importance, normal maize is deficient in amino acids lysine and tryptophan that are essential for the nutrition of monogastric animals and humans (Bressani, 1992). The main reason for the poor protein quality of normal maize is the relatively high concentrations of prolamines or zein storage proteins (50-60%). These proteins are almost devoid of lysine and tryptophan thus causing maize to be nutritionally inferior to rice, wheat and other major cereals in protein quality.

Quality protein maize (QPM) development started as early as 1920s when a natural spontaneous mutation of maize with soft, opaque grains was discovered and delivered to the Connecticut Experiment Station in the United States of America (USA) (Vietmeyer, 2000). This maize mutant was eventually named opaque-2 (o2) by a Connecticut researcher (Singleton, 1939). In the 1960's at Purdue University, USA, geneticist Dr. Oliver Nelson, who began his career as a graduate student at the Connecticut Experiment Station (Crow *et al.*, 2002), provided to Dr. Edwin Mertz seeds of opaque-2 maize to be included in his group's systematic effort to identify maize accessions with improved protein quality (Paes and Bicudo, 1994). In 1961 the Purdue researchers discovered that maize homozygous for the recessive o2 allele (with two copies of the mutation) had substantially higher lysine (69%) in grain endosperm compared to normal maize (Mertz *et al.*, 1964). It was further determined that this genotype also showed a corresponding increase in tryptophan content, and that the increased concentration of these two essential amino-acids (normally deficient in the maize grain endosperm) effectively doubles the biological value of maize protein (Bressani, 1992) with the considerably advantageous result that only half the amount of o2 maize (relative to normal maize) needs to be consumed to obtain the same biologically usable protein (FAO, 1992).



High lysine maize with homozygous embryo and endosperm for mutant alleles opaque-2 at the  $\alpha$ -zeins regulatory gene shows about 60 to 100% increase in lysine and tryptophan and a higher biological value (80%) - a value that measures how well the body can absorb and utilize a protein. Substituting normal maize with high lysine maize on an equal weight basis for growing pigs and sows can reduce the use of synthetic lysine in animal feeds required to maintain proper amino acid balance (Burgoon *et al.*, 1992; Knabe *et al.*, 1992; Asche *et al.*, 1985).

Farmers initially showed little interest in opaque-2 maize because of its low grain yields, chalky-looking grain, and susceptibility to pests and diseases. Starting in 1970s, CIMMYT in collaboration with National Agricultural Research Systems (NARs) converted opaque-2 maize into QPM, which is effectively indistinguishable from normal maize. The development of QPM donor stocks with well modified kernel phenotype and good protein quality was indeed quite important in accelerating rapid development of QPM germplasm. Selection for kernel modification had to be practiced at all stages while simultaneously maintaining protein quality. Intrapopulation selection was enforced for the accumulation of modifier genes. In addition, selection for improved kernel phenotype continued independently in selected modified opaque-2 families. Using these materials several promising materials from CIMMYT and from the national maize programs were converted to QPM. Quality Protein Maize donor stocks thus set a stage for the development of QPM germplasm in a wide array of genetic backgrounds (Vasal, 1994).

In Sub-Saharan Africa, commercial QPM seed is currently available in 17 countries (Table 1) and based on average 2003 - 2005 seed production figures, approximately 200,000 hectares of land are being planted to QPM cultivars. Breeding efforts have led to the release of one or more open pollinated varieties (OPV's) and/or

hybrids in these countries although the total number of different materials is more limited since many releases share the same pedigree. Ghana has a long history of breeding for improved maize cultivars (Morris *et al.*, 1999) and it is the dominant country for QPM production in Africa with approximately 70,000 hectares planted (Table 1).

**Table 1 Quality protein maize cultivars released in Sub-Saharan Africa.**

Country	Area(ha) <sup>a</sup>	Type	Background	Traits <sup>d</sup>	Seed Production (tons)		
					2003	2004	2005
Nigeria <sup>b</sup>	4,500	OPV	Across 8363SR	W, E,I, F	80	100	-
Senegal <sup>b</sup>	500	OPV	Across 8363SR	W, E,I, F	0	20	-
South Africa <sup>b</sup>	12,500	OPV	Across 8363SR	W, E,I, F	250	250	-
Tanzania <sup>d</sup>	4,300	OPV	Across 8363SR	W, E, F	50	83	125
		3WC	CML 144/159//176	W, E,I, F			
		Top C	Obatanpa// CML144/ CML159	W, EI, F			
Togo <sup>b</sup>	750	OPV	Across 8363SR	W, E,I, F	10	20	-
Uganda <sup>d</sup>	46,717	OPV	Across 8363SR	W,E,I, F	770	611	1,422

Table 1 continued: Quality protein maize cultivars released in Sub-Saharan Africa.

Country	Area(ha) <sup>a</sup>	Type	Background	Traits <sup>d</sup>	Seed Production (tons)		
					2003	2004	2005
Benin <sup>b</sup>	4,325	OPV	Across 8363SR	W,E,I, F	73	100	-
Burkina Faso <sup>b</sup>	20,600	OPV		Y	513	311	-
Cameroon <sup>c</sup>	305	OPV	Across 8363SR	W, E,I, F	-	6.1	-
Cote d'Ivoire <sup>c</sup>	565	OPV	Across 8363SR	W, EI, F	-	11.3	-
Ethiopia <sup>d</sup>	7,283	3WC	CML144/159//176	W, I, F	166	186	85
Ghana <sup>b</sup>	71,250	OPV	Across 8363SR		1,350	1,500	-
Guinea <sup>b</sup>	3,875	OPV	Across 8363SR	W, EI, F	30	125	-
Kenya <sup>d</sup>	12				0	0.1	0.6
		OPV	Pool 15	W,EE, F			
		3WC	CML 144/159//181	W, EI, F			
		3WC	CML 144/159//182	W, EI, F			
Malawi <sup>b</sup>	1,125	OPV	Across 8363SR	W, EI, F	8	37	-
Mali <sup>b</sup>	9,000	OPV	Across 8363SR	W, EI, F	160	200	-
Mozambique <sup>b</sup>	11,250	OPV	Across 8363SR	W, EI, F	300	150	-

<sup>a</sup> Hectareage based on average commercial seed production 2003-2005 at a conversion of 50 hectares/ton of seed.

<sup>b</sup> Source: Sasakawa Africa Association Annual Report 2003-2004; [www.saa-tokyo.org/english/lastestinfo/index.html](http://www.saa-tokyo.org/english/lastestinfo/index.html).

<sup>c</sup> Source: CIMMYT Progress Report to Nippon Foundation 2005.

<sup>d</sup> Source: Alpha Diallo personal communication

OPV = open pollinated variety; Top C = top cross non-conventional hybrid; 3WC = three-way cross hybrid; DC = double-cross hybrid; hybrid =undefined hybrid; W = white grain; Y = yellow grain; F = flint; D = dent; S = semi-dent; EE = extra early; E = early; I = intermediate; L = late dash (-) indicate that the information was not available by the time the data was collected.

The vast majority of QPM seed produced is 'Obatanpa' (or improved versions there of) which was developed in collaboration with the International Institute for Tropical Agriculture (IITA). 'Obatanpa' was released in Ghana in 1992 and has since been released officially or is grown in 15 other African nations (Table 1) promoted largely by Sasakawa Global, 2000. Prompted by the success of 'Obatanpa' there was a renewed interest in development and dissemination of QPM in sub-Saharan Africa, supported by three complementary projects funded by the Nippon Foundation (support for QPM germplasm development, dissemination, and training), the Canadian International Development Agency (support for QPM development and QPM dissemination activities in Eastern Africa including socioeconomic and animal and human nutrition studies), and the Rockefeller Foundation (support for Eastern and Southern African scientists to initiate conversion of 19 widely-grown elite maize OPV's and hybrids to QPM) (CIMMYT, 2005).

Activities are led in West Africa by IITA and in Eastern and Southern Africa by CIMMYT, in collaboration with the Africa Maize Network, ECAMAW (East and Central Africa Maize Network) and the SADC (Southern African Development Community) maize breeding network (coordinated by the Southern Africa Drought and Low Soil Fertility Project, SADLF). In each sub-region, activities are highly integrated and coordinated enabling joint development, exchange and broad testing of promising materials for all agro-ecological niches. QPM development in West and Central Africa currently is centered on an IITA initiated QPM breeding program which started in 2002 - 2003 in collaboration with all member countries of WECAMAN (West and Central Africa Maize Network) (CIMMYT, 2005). The program involves optimizing the research strength of strong National Agricultural Research Systems (NARS) (lead Centers) by

assigning them specific research problems. Lead Centers share germplasm and other technologies with the technology adapting NARS. The program involves conversion of elite late, intermediate, early and extra-early maturing populations and OPV's and late maturing inbred lines (including *Striga* sp. tolerant germplasm) to QPM as well as QPM hybrid development. In addition, Ghana is converting the popular 'Obatanpa' to a yellow grain version and is converting the high yielding normal endosperm yellow variety 'Sotubaka' to QPM. Nigeria is converting 8 locally adapted inbred lines as well as the 'Acr Sakatifu' population to QPM.

The QPM breeding program for East Africa led by CIMMYT, in collaboration with NARS and small seed companies currently uses two broad approaches: Testing inbred lines, (both early generation and elite lines such as CIMMYT maize lines (CMLs), hybrids, and OPV's developed primarily from CIMMYT-Mexico headquarters, as well as other breeding programs in Ghana and South Africa, to identify the most adapted cultivars for direct release or use as breeding materials. (ii) Converting existing popular adapted cultivars to QPM.

Test for adaptation in sub-Saharan Africa focuses on biotic and abiotic stresses (Bänziger *et al.*, 1999c). The most important abiotic stresses limiting maize production in eastern and southern Africa are drought and low soil fertility (Bänziger and Diallo, 2004). CIMMYT approached breeding for stress tolerance by simulating abiotic stress factors that are important in the target environment and exposing breeding germplasm to a clearly defined abiotic factor in environments termed 'managed stress environments' (Bänziger and Cooper, 2001). Managed stress environments were established under experimental conditions by growing maize in the dry season and managing drought through controlled irrigation to assess drought tolerance at the seedling, flowering, and

grain filling stages (Bolaños and Edmeades, 1996), and by using fields that were depleted of mineral nitrogen for assessing nitrogen stress tolerance (Bänziger et al., 1997). Through these efforts CIMMYT has developed early QPM inbred lines adapted to drought and/or low nitrogen conditions under managed stress hence the gap remaining is to test their combining ability.

This study focuses on determining combining ability for grain yield in early QPM inbred lines under stressed (drought and low nitrogen) and non-stressed environments, and comprises two experiments which are presented in chapters three and chapter four. In chapter three, data is presented on 128 early QPM top cross hybrids that were evaluated for heterosis and per se performance in three environments (drought stress, low nitrogen and optimal environments). In chapter four, data is presented on General Combining Ability (GCA) and Specific Combining Ability (SCA) for grain yield among superior early QPM inbred lines crossed with three testers and evaluated in four environments (one drought stress environment and three non drought environments)

## **1.2 Problem statement and justification**

Maize is the staple food of millions of people across Sub-Saharan Africa (SSA). The region has an estimated 26 percent prevalence of child malnutrition, and in some countries such as Burkina Faso and Zambia the trends are worsening (Global Monitoring Report, 2007). Maize-based diets in extremely poor areas are low in proteins, vitamins, and important minerals, often leaving people disease prone and unable to work, care for the children or take part in normal activities. Weaned infants are particularly affected by protein deficiencies which impede their physical and mental development. The vast majorities of tropical maize farmers continue to grow maize to meet their subsistence requirements and are resource constrained (Pingali and Pandey, 2000). The rainfall in

most drought stressed zones is unpredictable in both quantity and distribution hence genotypes targeted for these areas should yield well in both the presence and absence of drought (Edmeades and Bänziger, 1997; Byrne *et al.*, 1995). Drought at any stage of crop development affects production, but maximum damage is inflicted when it occurs during the period bracketing flowering.

Edmeades *et al.* (1992) estimated that in the developing world, annual yield losses due to drought may approach 24 million tons, equivalent to 17% of a normal year's production. Since drought is an unpredictable environmental factor, good performance under non-drought conditions is also expected (Vasal *et al.*, 1997). Many investigators have also shown that General Combining Ability (GCA) and Specific Combining Ability (SCA) can interact with environments (Betran *et al.*, 2003a; Han *et al.*, 1991; Beck *et al.*, 1990; Matzinger *et al.*, 1959; Sprague and Tatum, 1942). The importance of multi-environment testing for selecting inbred lines and for screening widely adapted hybrids have been reported (Troyer, 1996). However, most reports about drought tolerant lines focused on moisture deficit environments and the gap of information about their performance under adequate rainfall conditions should be investigated. Thus drought tolerant lines and their hybrids that are expected to perform well in moisture deficit areas should be tested for performance under adequate rainfall conditions.

Tropical soils also vary greatly, giving rise to differences in moisture and nitrogen at a single site within a single year (Beck *et al.*, 1996). The incidence of stress may increase, due partly to global climate changes, displacement of maize to marginal environments by high value crops, and to declines in soil organic matter, reducing soil fertility and water holding capacity (Bänziger *et al.*, 2000). Tropical soils are renowned for their low soil fertility, particularly low nitrogen, and this ranks as the second most

important abiotic constraint to maize production in tropical ecologies (Bellon, 2001). Intensified land use and the rapid decline in fallow periods, coupled with the extension of agriculture into marginal lands, have contributed to a rapid decline in soil fertility, particularly in sub-Saharan Africa (Bellon, 2001). Lost productivity due to the low-N status of soils in Sub-Saharan Africa (SSA) is estimated at around US\$ 500 million annually. Fertilizer use is less than 10 kg/ha with increased usage constrained by high prices, poor infrastructure, risk associated with climatic uncertainty, and lack of credit for small holders (Heisey and Mwangi, 1996). While nitrogen derived from legumes in various systems with maize is possible, land pressure for subsistence food (maize) production limits the adoption of systems that compete for space on the farm (Heisey and Mwangi, 1996).

The discovery of the opaque-2 gene (Mertz *et al.*, 1964) and subsequent efforts by CIMMYT and collaborators, to develop maize inbred lines having the opaque-2 gene along with modifier genes that confer hard vitreous kernel texture and simultaneously selecting for superior agronomic characteristics have led to the development of Quality Protein Maize (QPM). (Vasal, 2000 and Vasal, 1994). Maize conversion programs by CIMMYT have been underway for several decades. The collaboration between CIMMYT and National Agricultural Research systems (NARs), Eastern and Central Africa Maize and Wheat (ECAMAW) research network in conjunction with the Canadian International Development Agency (CIDA) and other development agencies have been fruitful in the development of QPM inbred lines tolerant to drought and/or low Nitrogen. However, the performance and combining ability and relationship between hybrid and inbred line performance in different environments is not well known. In an attempt to tackle these challenges, this study is geared towards developing nutritionally superior



early Quality Protein Maize (QPM) hybrids that yield more than the currently available cultivars under suboptimal conditions of limiting moisture and low soil nitrogen status while yielding as well or better under optimal conditions.

### **1.3 Objectives**

1. To identify superior early Quality Protein Maize (QPM) inbred lines adapted to drought and/or low N ecologies of East Africa.
2. To determine the General Combining Ability (GCA) of the inbred lines and Specific Combining Ability (SCA) of early Quality Protein Maize (QPM) inbred lines by tester under drought and/or low N conditions
3. To identify superior top cross and three way cross early QPM hybrids tolerant to drought and/or low nitrogen conditions

### **1.4 Hypotheses:**

1. There exist superior early QPM inbred lines adapted to drought and/or low N ecologies of East Africa.
2. High GCA and SCA for grain yield exist among early QPM inbred lines under drought and/or low N ecologies of East Africa.
3. Superior top cross and three way early QPM hybrids tolerant to drought and/or low N can be identified.

## CHAPTER TWO

### 2.0 Literature Review

#### 2.1 Maize endosperm protein characteristics

A typical maize kernel averages about 9.5% protein in the endosperm and 18% protein in the embryo on a 15.5 % moisture content basis. Maize endosperm proteins are categorized into two major types; storage proteins and non-storage proteins. Prolamines or zeins are the most abundant storage proteins representing about 50% of the total proteins in mature seed (Soave *et al.*, 1981) and 62-74% of the endosperm proteins (Landry *et al.*, 2000). The other storage proteins comprise glutelins (30-45%), albumins (3%), and globulins (3%). Zeins are specifically expressed during seed development being synthesized by membrane-bound polyribosomes and transported into the lumen of the endoplasmic reticulum where they are packaged in protein bodies during endosperm development (Larkins and Hurkman, 1978). Zein structural genes are represented by six “multigene families” that have been classified on the basis of their molecular weights into 4 distinct types, namely alpha (19 and 22-kDa), beta (14-kDa), gamma (16 and 27-kDa) and delta (18 and 10-kDa) constituting 50-60%, 10-15%, 20-30% and 1-5%, respectively, of the total zein fraction in the maize endosperm (Larkins *et al.*, 1984). All the four types of zeins aggregate to form protein bodies that are stably retained within membrane vesicles. The main function of zeins is to store nitrogen in the developing seed.

#### 2.2 Nutritional superiority and biological value of quality protein maize

The nutritional benefits of Quality Protein Maize (QPM) for people who depend on maize for their energy and protein intake, and for other nutrients, are indeed significant. Mertz *et al.*, (1964) first reported that the lysine content in opaque-2 maize

was 3.3 to 4.0 g per 100 g of endosperm protein, which was more than twice that of normal maize endosperm protein (1.3 g lysine per 100 g endosperm protein). Several researchers later demonstrated the superior protein quality and protein digestibility of QPM over normal maize (Bressani, 1995; Paes and Bicudo, 1994; Graham *et al.*, 1980). The studies indicated that the QPM protein contains, in general, 55% more tryptophan, 30% more lysine and 38% less leucine than that of normal maize.

Besides protein quality, another important factor is biological value (BV) of QPM, which refers to the amount of absorbed nitrogen needed to provide the necessary amino acids for different metabolic functions. The biological value of normal maize protein is 45%, while that of opaque-2 maize is 80%. Only 37% of common maize protein intake is utilized compared to 74% of the same amount of opaque-2 maize protein. A minimum daily intake of approximately 125 g of opaque-2 maize might guarantee nitrogen equilibrium. This cannot be obtained by using even twice the amount of normal maize.

The nitrogen balance index for skim milk and opaque-2 maize protein is 0.80 and 0.72, respectively, which indicates that the protein quality of QPM is 90% that of milk. Besides, around 24 g of normal maize per kg of body weight is required for nitrogen equilibrium, compared to only around 8 g for QPM (Bressani, 1995 and Graham *et al.*, 1980). Further, QPM can be transformed into edible products without deterioration of its quality or acceptability, and can be used in conventional and new food products.

The nutritional and biological superiority of QPM has also been amply demonstrated in model systems such as rats (Mertz *et al.*, 1965), pigs (Maner, 1975; Lodha, 1974), infants and small children as well as adults (Graham *et al.*, 1990; 1980). In Guatemala, it was demonstrated that opaque-2 maize has 90% of the nutritive value of

milk protein in young children. Children in Colombia suffering from Kwashiorkor, a severe protein deficiency disease, were brought back to normalcy on a diet containing only opaque-2 maize as the source of protein.

QPM could play an increasingly important role in reducing the protein supplement in animal feed, if used as an ingredient. Gevers, (1989) indicated the potential utility of high-lysine maize in feeds for monogastric animals, and how QPM could bring in significant immediate rewards through direct industrial exploitation. QPM can also be used as an ingredient in the preparation of composite flours to supplement wheat flour for bread and biscuit preparation. Composite flours (10% maize flour) are used commercially in Sub-Saharan countries such as Zambia, Zimbabwe and Ghana. Brazil also uses composite wheat flours utilizing cassava and maize flours (Prasanna *et al.*; 2001).

### **2.3 Effects of drought stress on maize**

Stress is defined as a factor that causes, through its presence or absence, a reduction in plant grain yield (Tollenaar and Wu, 1999). According to Ashley (1993) meteorological drought occurs when precipitation is significantly below expectation for the time of year and location. Drought is a multi-dimensional stress affecting plants at various levels of their organization (Yordanov *et al.*, 2000). Drought environments are characterized by wide fluctuations in precipitation, in quantity and distribution within and across seasons (Swindale and Bidinger, 1981). No other environmental factor limits global crop productivity more severely than water deficit (Boyer, 1982). The average maize grain yield in the industrialized countries is more than 8 t ha<sup>-1</sup> while in the developing world it is slightly less than 3 t ha<sup>-1</sup>. The major factors contributing to this wide gap in maize grain yields are unrelated climatic conditions (tropical versus

temperate) and differences in farming technologies between the developed and the developing world (Pingali and Pandey, 2000).

In the developing world maize is produced under rain fed conditions, in areas where drought is widely considered to be the most important abiotic constraint to production (Reeder, 1997). Maize grain losses due to drought in the tropics may reach 24 million tons year<sup>-1</sup> (Edmeades *et al.*, 1992). In sub-Saharan Africa, 40% of the maize area experiences occasional drought, whereas 25% of the area is frequently affected (CIMMYT, 1990). Severe drought occurs each year in at least one country within eastern and southern Africa, resulting in frequent crop failures (Waddington *et al.*, 1995). Consequently, the variability of rainfed crop grain yields in this region is of greater socio-economic importance than in any other part of the world (Heisey & Edmeades, 1999).

Moisture deficiency at any growth stage of maize development affects production (Saini and Westgate, 2000; Vasal *et al.*, 1997; Denmead and Shaw, 1960). However, the magnitude of the grain yield reduction depends on the developmental stage of the crop, the severity and duration of the stress, and susceptibility of the genotype to stress (Lorens *et al.*, 1987). Accordingly, maximum reduction in productivity is inflicted when it occurs at or around flowering, more so than at any other time in the crop cycle, particularly during the two weeks bracketing flowering (Edmeades and Bänziger, 1997; Zinselmeier, 1995; Bolanos and Edmeades, 1993b; 1996; Grant *et al.*, 1989; Claassen and Shaw, 1970; Denmead and Shaw, 1960;).

When drought stress is imposed at establishment, it reduces the crop stand while during the vegetative period it reduces the size of the assimilatory structure (Rhoads & Bennet, 1990; Denmead & Shaw, 1960). During vegetative development, drought stress reduces expansion of leaves, stems, and roots and ultimately affects the development of

reproductive organs and potential grain yield (Denmead & Shaw, 1960). The reduced plant size results in a lower assimilation at the time of ear development since production of dry matter is dependent on the size of the assimilatory surface. Herrero and Johnson (1981) reported visible symptoms of midday wilting and of lower leaf senescence due to moisture deficit. Sobrado (1987) also indicated that leaf rolling, which is associated with low leaf water status, reduces the area exposed to radiation.

Denmead and Shaw (1960), indicated that grain yield reduction due to moisture stress during the vegetative, silking and ear stages were 25%, 50%, and 21%, respectively. On the other hand, Grant *et al.* (1989) reported a reduction of two to three times more when drought coincided with flowering, compared with other growth stages. During this period the maize crop responds by abortion of ovaries, kernels and entire ears (Schussler and Westgate, 1991; Rhoads and Bennet, 1990; Kiniry and Ritchie, 1985). In an earlier study, Robins and Domingo (1953) reported that if drought conditions during flowering continue for a week, losses in grain yield might exceed 50%. Drought lasting even one to two days at pollination can reduce grain yield by up to 22% (Fischer *et al.*, 1983). It can even be reduced nearly to zero when severe stress occurs during this period (Edmeades *et al.*, 1994). The stress just prior to anthesis inhibits ear and silk growth more than tassel growth (Westgate, 1997; Edmeades *et al.*, 1993; 1999; Bolaños and Edmeades, 1993b; 1996; Herrero and Johnson, 1981; DuPlessis and Dijkhuis, 1967). The authors indicated that this difference causes increased anthesis-silking interval (ASI) that results in barren or poorly developed ears. DuPlessis and Dijkhuis (1967) found an 82% decline in grain yield as ASI increased from 0 to 28 days. Bolaños and Edmeades (1993b) also reported an almost similar observation on 'Tuxpeño Sequía' that declined in grain yield by 90 % as ASI increased from 0 to 10 days. A long ASI is generally equated with

drought susceptibility, low harvest index, slow ear growth and barrenness (Edmeades *et al.*, 1997d).

In a study involving 270 full-sib families derived from drought-tolerant-population Pool 16DT, Badu-Apraku *et al.* (2004) estimated heritability for drought adaptive traits and genetic correlations among them. Narrow sense heritability for ASI was 23% in non-stress and ranged between 22 to 51% in stress environments, respectively, while heritability for days to anthesis (AD) was 30% in nonstress environments and ranged between 34 to 52% in stress environments. Genetic correlation between grain yield and anthesis date was negative at each of the two sites and across sites while that between grain yield and ASI was positive across sites. Dow *et al.* (1984) reported that the date of mid anthesis and anthesis silking interval were highly correlated to drought resistance (-0.61 and -0.71 respectively).

Water deficit occurring during anthesis does not affect pollen viability (Westgate and Boyer, 1986; Herrero and Johnson, 1981), but it can cause a decline in silk receptivity if pollination is delayed (Bassetti and Westgate, 1993). Even when gamete and floral development proceed normally, and pollen is not limiting, grain number can be reduced by only a few days of dehydration at flowering (Westgate, 1997; Schoper *et al.*, 1986; Westgate and Boyer, 1986). Drought at or immediately after flowering is known to accelerate leaf senescence (Bolaños and Edmeades, 1993a), with reduced leaf area, reduced intercepted radiation and photosynthesis that result in a reduction in photo-assimilate flux to the spikelets (Zinselmeier *et al.*, 1995). Generally, most maize germplasm show increased leaf senescence at flowering, increased ASI, silk delay, reduced number of ears plant<sup>-1</sup>, number of kernels ear<sup>-1</sup> and grain yield. On the contrary, improved maize genotypes obtained through screening under moisture stress at flowering

were found to be tolerant to the effect of the stress. Thus to initiate selection for improvement, it is a priority to assess the available variability in elite adapted populations for these traits. (Zinselmeier *et al.*, 1995)

## **2.4 Effect of low nitrogen stress on maize**

Most farmers in developing countries produce maize under low soil fertility conditions (Oikeh and Horst, 2001; McCown *et al.*, 1992) because of the low N status of tropical soils, low N use efficiency in drought-prone environments, high price ratios between fertilizer and grain, limited availability of fertilizer, and low purchasing power of farmers (Bänziger *et al.*, 1997). Variation in nitrogen supply affects both growth and development of maize plants (McCullough *et al.*, 1994). Uhart and Andrade (1995a) reported that nitrogen deprivation results in reduction of leaf area index, leaf area duration, radiation interception, and radiation use efficiency. Low nitrogen also increases the anthesis-silking interval (Jacobs and Pearson, 1991). Lack of nitrogen enhances kernel abortion (Pearson and Jacob, 1987) and reduces final grain number (Uhart and Andrade, 1995b; Lemcoff and Loomis, 1986).

Delayed senescence (or stay-green) was proposed as indirect selection criteria for low nitrogen tolerance (Moll *et al.*, 1994). Anthesis-silking interval and senescence related traits have been proposed by Bänziger and Lafitte (1997) and Bänziger *et al.* (2000) as secondary traits for improving maize for low nitrogen target environments. Bänziger *et al.* (1997) evaluated maize germplasm adapted to lowland tropics under high and low nitrogen conditions. They found that genotypic variance for grain yield under low nitrogen was about one third of the average genotypic variance for grain yield under high nitrogen, but the average error variance was similar at both low and high nitrogen levels. They found that among low nitrogen experiments, genotypic variance and error



variance for grain yield tended to decrease with increasing relative yield reduction under low nitrogen while heritability did not change. Bänziger *et al.* (1997) further reported that broad sense heritabilities of grain yield under low nitrogen were smaller than under high nitrogen. They reported positive genetic correlation between grain yield under low and high nitrogen. Ceccarelli *et al.* (1992) reported variable genetic correlations between grain yield in low-yielding sites and grain yield in high yielding sites.

Presterl *et al.* (2003) reported a reduction of 37% in grain yield at low N compared to high N conditions. Genotypic correlation for grain yield between performance at high N and low N was 0.74. Genotypic correlation between grain yield at high N and low N decreased significantly with increasing levels of N deficiency stress. Heritability for grain yield averaged 65% both under high N and low N environments (Presterl *et al.*, 2003). In a study to evaluate hybrid progenies of drought-tolerant populations and high-yielding lowland tropical single-cross hybrids in stress and nonstress environments, Zaidi *et al.* (2004) reported that ASI in the drought tolerant top crosses averaged 2.0 and 4.5 days under low N and drought, respectively. Anthesis silking interval averaged 17 and 4 days for single-cross hybrids under drought and low N stress environments, respectively. Ears per plant averaged 0.94 under drought and 1.08 under low N environments for the drought tolerant top cross hybrids.

Lafitte and Edmeades (1994a) evaluated different cycles of full-sib recurrent selection under low and high N conditions. They reported that realized heritability was generally larger for yield under low N than for yield under high N, and that all traits evaluated had larger values of heritability when measured in cycle 2 than in cycle 0 of recurrent selection. Lafitte and Edmeades (1994b) evaluated four cycles of full-sib (FS) recurrent selection under low and high N levels for four seasons. They observed

significant differences among FS families at both N levels for days to anthesis and silking, plant height, grain yield, ear-leaf area at low N, green leaf area below the ear for low N, and ear-leaf chlorophyll concentration for low N. Lafitte and Edmeades (1994b) noted that the observed variance among FS families was adequate to identify significantly different best and worst fractions of the population for most traits studied. Bänziger and Lafitte (1997) evaluated the relative value of secondary traits for improving the identification of high yielding maize genotypes in low N selection environments. They reported genetic correlations between grain yield and secondary traits which indicated that high grain yields were associated with a short anthesis-silking interval, increased number of ears per plant, larger leaf chlorophyll concentrations, and delayed leaf senescence. Pollmer *et al.* (1979) in a study of nitrogen (N) uptake and N translocation among hybrids involving inbred lines highly diverse for percent grain protein found that additive and non-additive gene actions were important in the inheritance of N uptake and translocation. They observed that G x E interactions influenced the inheritances of N uptake and translocation. Similar results were reported by Beauchamp *et al.* (1976).

Four advanced populations selected for drought tolerance and their original cycles were evaluated in low and high N environments (Bänziger *et al.*, 2002). Original and drought-tolerant cycles did not differ consistently in plant and ear biomass, N accumulation, ear N content or ear N concentration at silking. Anthesis-silking interval was reduced in drought-tolerant selection cycles in comparison to the original cycles. Bänziger *et al.* (2002) reported that selection for tolerance to mid-season drought stress reduced ASI in severe N stress and changes in ASI explained changes in ears per plant that occurred with selection for tolerance to drought.

## 2.5 Use of secondary traits in breeding for stress tolerance

Grain yield under stress is the primary and most important trait during selection (Edmeades and Bänziger, 1997). However, heritability for grain yield typically reduces under drought conditions because the genetic variance for grain yield decreases more rapidly than the environmental variance among plots with increasing stress. Under these conditions, secondary traits whose genetic variance increases under stress can increase selection efficiency, provided they have a clear adaptive value under stress, relatively high heritability and are easy to measure (Edmeades *et al.*, 1997d). For drought at flowering, Edmeades *et al.* (1997d) indicated that emphasis should be placed on traits, which affect ear formation or barrenness. Consequently, traits related to tolerance to drought in combination with grain yield can be used as selection index for identifying superior genotypes (Edmeades and Bänziger, 1997). Edmeades *et al.* (1999) pointed out that an ideal secondary trait should' (a) be genetically variable and genetically associated with grain yield under drought; (b) carry no grain yield penalty under favorable conditions; (c) have moderate to high heritability; (d) be cheaper and/or faster to measure than grain yield; (e) stable over the measurement period; (f) be able to be observed at or before flowering so that undesirable parents are not crossed; and (g) be able to provide an estimate of grain yield potential before final harvest.

Many studies on maize have shown the importance of ASI as an indicator of barrenness under stress and to identify stress tolerant genotypes at flowering (Chapman and Edmeades, 1999; Bolaños and Edmeades, 1996; 1993b). DuPlessis and Dijkhuis (1967) recorded a correlation coefficient of  $-0.98$  between ASI and the logarithm of the grain yield per plant. Others found moderately strong associations ( $r_G = -0.58$ ) under severe drought stress (Bolaños & Edmeades, 1996). This indicated that selection for a

reduced ASI under drought stress results in higher and more stable grain yield (Bolaños and Edmeades, 1993a; Edmeades *et al.*, 1993). Westgate (1997) suggested selecting against protandry and for high grain yield across environments. Selecting for silk emergence prior to pollen shed (protogyny) would effectively shift ASI to negative values. A large negative ASI could be advantageous under drought conditions because any delay in emergence would only improve the synchrony between maximum pollen shed and silk emergence and lead to more stable kernel production. Unfortunately, selecting plants for a negative ASI alone will not guarantee high kernel set if drought occurs during the critical pollination period. However, both approaches of selection for a minimum ASI and selection for protogyny and high grain yield across environments assume that development and fecundity of staminate and pistillate flower types must be synchronized for optimum kernel set (Westgate, 1997).

Chapman and Edmeades (1999) pointed out that grain yield, ears per plant, and number of kernels per ear were strongly correlated with ASI under drought conditions, but not when water was plentiful. In general, the reduction in florets ear<sup>-1</sup> with selection for tolerance to drought or low N appears to be an important general mechanism for increasing and stabilizing grain yields under abiotic stress (Lafitte and Edmeades, 1995a). Bänziger *et al.* (1999b) reported that all drought tolerant selection cycles showed delayed leaf senescence during grain filling, and increased N harvest index, harvest index as well as biomass accumulation at maturity. In contrast, Edmeades *et al.* (1999) indicated that tolerance is also associated with an increased partitioning of biomass to the developing ear under drought conditions, so that harvest index and grain yield are increased but not total biomass. Fischer *et al.* (1983) indicated that short maize plants were more tolerant to drought at flowering than taller plants. Similarly, selection for reduced tassel size has

been shown to increase ear size near flowering (Fischer *et al.*, 1987). These studies suggested that competition for assimilate between competing organs at flowering affects ear growth and grain number in maize (Chapman and Edmeades, 1999). However, Bolaños and Edmeades (1996) reported that genetic correlation between grain yield and leaf rolling; senescence (stay green), leaf angle, canopy temperature, tassel branch number, leaf chlorophyll concentration, and plant height were generally less than 0.20. Edmeades *et al.* (1997d) rated ears per plant (EPP), number of kernels per ear (NKE) and ASI as the most valuable of those factors associated with grain yield under drought conditions. Evidence suggests that focusing on traits which are indicative of partitioning in the plant at flowering i.e. EPP and ASI will result in increases in harvest index and grain yield in all moisture regimes (Bolaños and Edmeades, 1996).

## **2.6 Combining ability**

Sprague and Tatum (1942) introduced the concepts of general combining ability (GCA) and specific combining ability (SCA). The authors defined GCA as the average performance of a line in hybrid combinations, while SCA as performance of a hybrid compared to average performance of the parent inbred lines of the hybrid. For random individuals, GCA is associated with additive effects of the genes, while SCA is related to dominance and epistatic effects (non-additive effects) of the genes. However, Rojas and Sprague (1952) verified that the variance of SCA also contains deviations due to the interaction between genotypes and environments, in addition to those that come from dominance and epistasis. Sprague and Tatum (1942) found that GCA was relatively more important than SCA for unselected inbred lines, whereas SCA was more important than GCA for previously selected lines for influencing grain yield and stalk lodging. However, studies have indicated that inbred grain yields predicted GCA more accurately than SCA

(Duvick, 1999). General combining ability (GCA) effects quantitatively measure the comparative performance of parents and cross combinations in relation to one another.

Currently there is good evidence suggesting that hybrids maintain their advantage over open pollinated varieties (OPVs) in both stress and non-stress environments (Tsaftaris, 1999; Dass *et al.*, 1997; Vasal *et al.*, 1997). Duvick (1999) has stressed that hybrids facilitate combination of multiple traits into one cultivar. For convenience when incorporating drought and low N tolerant traits, a hybrid breeding methodology will be the simplest approach, since heterosis is associated with stress tolerance (Srinivasan *et al.*, 1997). The importance of genetic diversity of inbred lines used in crosses is generally acknowledged, and line information indicative of hybrid performance is desirable to reduce hybrid evaluation (Falconer, 1989; Hallauer and Miranda, 1988). Since the final evaluation of inbred lines can be best determined by hybrid performance, evaluation plays an important role in selecting superior parents for hybrid combinations and in studying the nature of genetic variation (Duvick, 1999; Koutsika-Sotiriou, 1999; Hallauer and Miranda, 1988).

Diallel mating is a commonly used experimental design for crossing inbred lines, in which each line is crossed with every other line (Sughroue and Hallauer, 1997; Falconer, 1989; Singh and Paroda, 1984). Griffings (1956) has developed a range of analytical procedures. In general, diallel analyses have been used primarily to estimate genetic variances (Model II) when parents are either random individuals or inbred lines from a random mating population in linkage equilibrium, and to estimate general and specific combining ability effects from crosses of fixed lines (Sughroue and Hallauer, 1997; Hallauer and Miranda, 1988; Singh and Paroda, 1984; Gardner and Eberhart, 1966). If the parents of a diallel are selected on performance, then a fixed effects model

(Model I) should be used in the analysis. Since a reference population does not exist under these circumstances, GCA and SCA are valid with Model 1 (Sughroue and Hallauer, 1997; Hallauer and Miranda, 1988; Wright, 1985).

Sughroue and Hallauer (1997) indicated that estimates of variance components from populations can be used to calculate heritabilities, genetic correlations, and predicted gains from selection. In addition, they reported that estimates of additive and dominance variance from a random sample diallel were significantly different from estimates of additive and dominance variance in a fixed sample diallel in their study. They also indicated over estimation of dominance levels for grain yield in a fixed sample compared to a random sample. Thus genetic estimations made in diallel analysis from fixed lines represent only the lines included in that diallel. Furthermore, the number of parents to be included in a diallel restricts the use of diallel to estimate genetic components. Investigators reported more proportional and significant GCA effects for grain yield, days to silk and plant height in different groups of broad based CIMMYT maize populations and pools across locations (Vasal *et al.*, 1992; Beck *et al.*, 1990; Crossa *et al.*, 1990b;). Mungoma and Pollack (1988) reported similar results of a high proportion of GCA for these traits in a study made between ten corn belt and exotic maize populations. On the other hand, Singh and Asnani (1979) found significant mean squares for GCA and SCA for grain yield and 100- grain weight, number of kernel rows ear<sup>-1</sup>, number of kernels row<sup>-1</sup>, ear length and ear diameter in an 8 x 8 diallel cross of maize inbred lines. These authors concluded that both GCA (additive) and SCA (non additive) effects play an important role in the inheritance of grain yield and its components. Shewangizaw *et al.* (1985) also reported significant GCA and SCA for most traits, but predominance of non additive genetic variance (SCA) in the case of grain yield.

Furthermore, studies for nitrogen use indicated the greater importance of additive gene action (GCA) as compared to non additive (SCA) gene action (Below *et al.*, 1997; Lafitte and Edmeades, 1995b). Dass *et al.* (1997) reported that the Indian varieties Harsha and Navjot had good GCA for a number of characters, and this likely explains their stable performance across a large number of locations.

Estimates of combining abilities across environments have indicated that both GCA and SCA for most characters interacted with environmental change, but GCA was found to be more sensitive to environmental change than SCA. Sprague and Tatum (1942) emphasized that estimates of GCA and SCA are relative to and dependent on the particular set of inbred lines included in the hybrids under testing. Line traits under severe stress were more strongly correlated with top-cross performance under severe drought stress than line traits under normal conditions (Betran *et al.*, 1996). According to this report, selection for a reduction in ASI, senescence and barrenness in the lines, together with line *per se* grain yield performance under drought, could be used to select stress tolerant hybrids. In general, the presence of a number of grain yield limiting constraints on farmers' fields in the tropics (Bänziger *et al.*, 1999b) demand the assessment of drought tolerant lines and their hybrid performance under diverse environments including well watered environments. Besides, knowledge about the combining ability of drought tolerant lines in diverse environments is essential for national research programs that use this germplasm.

## 2.7 Heterosis

Heterosis is the genetic expression of the superiority of a hybrid in relation to its parents (Miranda Filho, 1999). This phenomenon is the opposite of inbreeding depression in that 'hybrid vigor' manifests in increased size, or other parameters resulting from the



increase in heterozygosity in the  $F_1$  generation of crosses between inbred lines (Duvick, 1999; Miranda Filho, 1999; Sprague, 1983). In general, based on parents used, two major types of estimation of heterosis are reported in literature: 1) Mid-parent or average heterosis (MPH), which is the increased vigor of the  $F_1$  over the mean of two parents; 2) High-parent or better parent heterosis (HPH), which is the increased vigor of the  $F_1$  over the better parent (Jinks, 1983). For HPH, the term heterobeltiosis has been suggested to describe the increased performance of the hybrid over the better parent (Fonseca and Patterson, 1968). When dealing with populations, inbreeding depression is an intra-population effect, while heterosis is expressed at the inter-population level. Many authors also pointed out that genetic divergence between parents and non-additive genetic effects are required for heterosis expression (Duvick, 1999; Miranda Filho, 1999; Sprague, 1983; Moll *et al.*, 1965). Although two major theories (dominance and over-dominance) of heterosis have been proposed, mechanisms underlying the phenomena are largely unknown (Coors, 1999; Tsaftaris *et al.*, 1999; Hallauer & Miranda, 1988).

Maize hybrids typically yield two to three times as much as their parental lines. However, since a cross of two extremely low grain yielding lines can give a hybrid with high heterosis, a superior hybrid is not necessarily associated with high heterosis (Duvick, 1999). This author suggested that a cross of two high yielding inbred lines might exhibit less heterosis but nevertheless produce a high yielding hybrid. Besides, a hybrid is superior not only due to heterosis but also due to other heritable factors that are not influenced by heterosis. Heterosis is also modified by the interaction between genotypes and environment (Chapman *et al.*, 2000; Duvick, 1999). Since inbred lines are more sensitive to environmental differences, some traits have been found to be more variable among inbreds than among crossbreds (Falconer, 1989). Similarly, Jinks (1983)

indicated that if homozygous and heterozygous genotypes respond differently to environmental change, the magnitude of heterosis would vary with the environment.

Heterosis is dependent not only on the parent combinations but also on the effect of environmental conditions and species as well as the trait under consideration (Chapman *et al.*, 2000; Young and Virmani, 1990; Jinks, 1983; Knight, 1973). Young & Virmani (1990), for their particular study, reported that the extent of heterosis in rice was higher in a stress environment than in a favorable environment. For temperate maize, Duvick (1999) pointed out that grain yield gains in hybrids always were accompanied by improvement in tolerance to biotic and abiotic stresses, and that improvement occurred in parental inbred lines as well as in their hybrid progeny. Similarly for tropical maize, Betran *et al.* (2003b) reported extremely high expression of heterosis under stress, especially under severe drought stress because of the poor performance of inbred lines under these conditions. It is generally considered that inbred lines with superior grain yields under drought and low N will result in superior hybrids under these stresses, even though their correlations are relatively weak (Vasal *et al.*, 1997).

## **2.8 Genotype by environment interaction**

Plant breeders aim at improving crop production either within a given macro environment or in a wide range of growing conditions. These two approaches have important implications on breeding methodologies and strategies (Ceccarelli, 1989). However, a successful cultivar needs to possess high and stable grain yield potential over a wide range of environmental conditions (Fasoula and Fasoula, 2002; Becker and Leon, 1988; Eberhart and Russel, 1969). The change in rank and the relative differences over a range of locations is defined statistically as genotype by environment interactions (GEI), which is a differential genotypic expression across environments (Janick, 1999; Kang, 1998).

Genotype-by environment interactions are common under drought and makes breeding progress difficult. The GEI may originate from environmental variation in the timing and severity of water deficits, genetic variation in flowering time, and nutrient deficiencies and toxicities whose occurrence and severity interact with water deficits (Bänziger and Cooper 2001; Cooper *et al.* 1999). Also, high error variances such as induced by variable plant stand or variable soil water holding capacity are intrinsic to many field trials grown under drought and impede selection decisions, particularly when trials are conducted far from breeding stations which tend to be placed at more favorable locations.

The presence of GEI in any genetic study simply leads to overestimation of genetical and statistical parameters (Sharma, 1995). However, the knowledge of GEI can help to reduce the cost of extensive genotype evaluation by eliminating unnecessary testing sites and by fine-tuning breeding programs. Various biotic and abiotic stresses have been implicated as causes of GEI. It is an inherited trait that can be incorporated into heterotic combinations (Eberhart and Russel, 1969). Consequently, improving genotype resistance/tolerance to different stresses to which they would likely be exposed might minimize GEI (Kang, 1998). Duvick (1999) and Janick (1999) indicated that maize grain yield increases in the United State of America (USA) have come about principally because of increased stress resistance. Earlier, Eberhart and Russel (1966) demonstrated that heterogeneous populations (varietal crosses or single crosses) tended to have better grain yield stability than homogeneous ones (inbreds). Fehr (1987) also indicated that stability of heterozygous individuals seems to be related to their ability to perform better under stress conditions than homozygous plants. These phenomena demand the assessment of drought tolerant lines and their  $F_1$  performance under diverse environments which is an indicator of general stress tolerance.

A number of statistical methods are now known for estimation of phenotypic stability. Finlay and Wilkinson (1963) developed regression coefficients to study the

adaptation of barley varieties. Eberhart and Russel (1966) improved this model by including non-linear responses (deviation from regression,  $S^2d_i$ ) and the environmental index ( $I_j$ ) instead of site means. According to these authors a stable genotype is one that shows (i) a high mean grain yield, (ii) a regression coefficient ( $b_i$ ) approximating unity, and (iii) a mean square deviation from regression ( $S^2d_i$ ) near zero. However, Jatasra and Paroda (1980) emphasized the use of deviation from regression alone as a measure of stability whereas linear regression could be treated as a genotype response. On the other hand, Crossa (1990) and Sharma (1995) noted a number of limitations of the joint regression method. The authors indicated that: (1) the genotype mean is not independent of the marginal means of the environments; (2) errors associated with slopes of genotypes are not statistically independent, because the sum of squares for deviation, with  $(G-1)(E-1)$  degrees of freedom, cannot be subdivided orthogonally among the  $G$  genotypes; and (3) the assumption of linear relationship between interaction and environmental means can be violated. Many statistical methods have been developed for genotype by environment data (GED) analysis, including additive main effect and multiplicative interactions (AMMI) analysis (Gauch 1992) and GGE biplot analysis (Yan and Kang, 2003; Yan and Tinker, 2006). The biplot (Gabriel, 1971) has become a popular data visualization tool in many scientific research areas, including psychology, medicine, business, sociology, ecology, and agricultural sciences. Earlier uses of biplots in GED analyses include Bradu and Gabriel (1978), Kempton (1984), and Cooper and DeLacy (1994). The biplot tool has become increasingly popular among plant breeders and agricultural researchers since its use in cultivar evaluation and mega-environment investigation (Yan et al., 2000).

## CHAPTER THREE

### 3.0 Evaluation of Early Quality Protein Maize Top Cross Hybrids under Stress and Non-Stress Environments

#### 3.1 Introduction

The QPM breeding program for East Africa led by CIMMYT, in collaboration with National Agricultural Research system (NARs) and seed companies currently uses two broad approaches: (i) Testing inbred lines, (both early generation and elite lines such as CMLs), hybrids, and OPV's developed primarily from CIMMYT-Mexico headquarters, as well as other breeding programs in, Ghana and South Africa, to identify the most adapted cultivars for direct release or use as breeding materials. (ii) Converting existing popular adapted cultivars to QPM. Top cross design has been widely used in early generation testing of inbred lines and in the development of new hybrid combinations (Miranda Filho and Gorgulho, 2001). In this design, new inbred lines are usually crossed with one or several testers to evaluate their general combining ability (GCA), (Hallauer *et al.*; 1988). The use of testers in a maize recurrent selection program has been well documented (Menz *et al.*, 1999; Russell *et al.*, 1992; Hallauer and Miranda, 1988; Hallauer, 1975; Allison and Curnow, 1966; Rawlings and Thompson, 1962; Matzinger, 1953; Jenkins and Brunson, 1932). These authors concluded that choice of a suitable tester should be based on simplicity in its use; its ability to classify the relative merit of lines, maximize genetic gain, and enhance the expected mean grain yield of a population generated using selected cultivars. However, it is difficult to identify a tester having all these characteristics. The use of the parental variety as a tester results in some improvement of the mean performance of the population (Rawlings and Thompson, 1962). Allison and Curnow (1966) suggested use of low-grain yielding varieties as testers.

The use of a single-cross as a tester has been reported by Horner *et al.* (1976). The use of an inbred as tester in a recurrent selection program was suggested by Russell and Eberhart (1975) and it has been widely used by breeders (Walejko and Russell, 1977; Darrah, 1985; Horner *et al.*, 1989). The objective of this study was to:

- i. To determine performance *per se* of early QPM top cross hybrids under stress and non-stress conditions.
- ii. To identify superior, early QPM inbred lines under stress and non-stress conditions.

## **3.2 Materials and methods**

### **3.2.1 Germplasm**

One hundred and twenty eight early Quality Protein Maize (QPM) inbred lines from pool 15 QPM at S<sub>2</sub> obtained from International Maize and Wheat Improvement Center (CIMMYT) were crossed to a genetically broad based tester (Susuma) to generate 128 top cross hybrids. The 128 top cross hybrids and two checks, Susuma and pool 15 QPM-SR, were used in this study. Pool 15 QPM is tropical, early maturing, white flint kernel with selection emphasized on improved kernel modification (hard endosperm) and agronomic characteristics. It has a genetic background of Tuxpeño-1 QPM, Mezcla Tropical Blanca QPM, Blanco Cristalino QPM, Mix. 1-Col. Gpo. 1 x ETO QPM, Tuxpeño Caribe and Mezcla Tropical Blanca, Blanco Cristalino-2 QPM, Pool 16 QPM, and Pool 20 QPM.

### **3.2.2 Experimental sites and treatments**

A total of 130 treatments (128 early QPM top cross hybrids plus 2 standard checks namely Susuma and pool 15 QPM SR) were evaluated across eight experimental sites located in six locations. Kiboko (37.75<sup>0</sup> E, 2.15<sup>0</sup> S, 975 m asl) in Kenya had 3

experimental sites which included low nitrogen (Low N), managed drought and well watered sites. Selian (36.37<sup>0</sup> E, 3.18<sup>0</sup> S 1287 m asl) in Tanzania had one experimental site under managed drought conditions. Embu (37.41<sup>0</sup> E, 0.45<sup>0</sup> S, 1510 m asl), Kakamega (34.45<sup>0</sup> E, 0.16<sup>0</sup> N, 1585 m asl) and Bungoma (34.43<sup>0</sup> E, 0.34<sup>0</sup> N, 1600 m asl) both in Kenya had one site each under well-watered conditions. Alupe (34.30<sup>0</sup> E, 0.50<sup>0</sup> N, 1180 m asl) located in Kenya was considered as random drought and similar traits were recorded as those recorded in the managed drought experiments. The characteristics of these experimental sites are given in Table 2.

**Table 2 Location, climatic and soils characteristics of Experimental sites in this study**

COUNTRY	LOCATION	LONG.	LATIT.	ELEV. (metres asl)	RAIN (mm)	Temperature °c		SOIL TEXTURE
						MAX.	MIN.	
Tanzania	Selian	36.37 <sup>0</sup> E	3.18 <sup>0</sup> S	1287	888	29.8	15.5	volcanic ash
Kenya	Kiboko	37.75 <sup>0</sup> E	2.15 <sup>0</sup> S	975	530	35.1	14.3	sandy clay
Kenya	Alupe	34.30 <sup>0</sup> E	0.50 <sup>0</sup> N	1180	1688	28.6	15.8	sandy loam
Kenya	Embu	37.41 <sup>0</sup> E	0.45 <sup>0</sup> S	1510	1200	25	14.1	clay loam
Kenya	Kakamega	34.45 <sup>0</sup> E	0.16 <sup>0</sup> N	1585	1916	28.6	12.8	sandy loam
Kenya	Bungoma	34.34 <sup>0</sup> E	0.34 <sup>0</sup> N	1600	800	24.0	14	loam

LONG.-longitude LATIT.-latitude ELEV.-elevation MAX-maximum MIN-minimum

### 3.2.3 Experimental design, cultural practices and stress management

All experiments were planted using Alpha (0,1) lattice design (Patterson and Williams, 1976) with two replicates for each environment and 10 plots per incomplete block giving 13 blocks in each replication. The experimental unit was one 4-metre row plot and the spacing was 80 cm by 20 cm. Two seeds were planted per hill and later thinned to one plant per hill two weeks after emergence to achieve a population density of 63,000 plants per hectare.

Managed drought stress experiments were carried out during the dry season when rain was not expected to fall and irrigation was applied as recommended by Bänziger *et*

*al.* (2000). Water stress was achieved by withholding water from 2 weeks before 50% male flowering to the end of flowering period. After flowering, the need for additional water was determined based on the average anthesis silking interval (ASI) as recommended by Bänziger *et al.* (2000).

The low-N experiment was planted in a field with depleted soil nitrogen. The field was prepared by continuously growing sorghum, two cycles per year, without application of any organic or nitrogen fertilizer and removing all crop biomass at harvest to avoid any incorporation of crop residue into the soil. This was continued until yield of normal genotypes, not improved for either drought or low-N stress, averaged between 25 and 30% of the well-fertilized field. In the low-N trials no N fertilizer was applied.

Experiments under well watered conditions were carried out during normal short rain season of 2006 except in the optimal site at Kiboko where irrigation was applied to avoid moisture stress. Under well watered and managed drought experiments, 27 kg N ha<sup>-1</sup> and 60 kg P ha<sup>-1</sup> as di-ammonium phosphate (DAP) were applied prior to planting, with a second dose of 60 kg N ha<sup>-1</sup> side-dressed as calcium ammonium nitrate (CAN) four weeks after emergence. All experiments were kept relatively free from weeds and insect pests using recommended control measures.

### **3.2.4 Data collection**

During crop growth and maturity measurements were recorded on the following agronomic traits: grain weight was measured at harvest and used to calculate grain yield (expressed in tonnes per hectare (t/ha) and adjusted to 12.5% moisture content). Grain moisture (percentage) of grain at harvest was measured using a moisture meter. Silking date (days from planting to 50% silking) and anthesis date (days from planting to 50% pollen shed) were recorded during flowering. Anthesis silking interval was calculated as



the difference between silking and anthesis dates ( $ASI = SD - AD$ ). Plant height (distance in centimeters (cm) from the ground to the tip of tassel) and Ear height (distance in cm from the ground level to the node bearing the main ear) were recorded before harvest from representative plants within a plot. Ear aspect scores were recorded at harvest for each plot on a scale of one to five where 1 was scored for clean, uniform, large, and well-filled ears and 5 for rotten, variable, small, and partially filled ears. Before harvesting, root lodging defined as the percentage of the plants that are inclining by more than 45 degrees, stalk lodging (SL) defined as percentage of plants with stem that are broken below the ear and husk cover defined as percentage of ears with bare tips were recorded for each plot. Ear rot (ER) scores were recorded at harvest as the percentage of ears that were rotten and ears per plant (EPP) were recorded at harvest as the ratio of number of ears to number of plants harvested. An ear means a cob with at least one fully developed grain. Diseases (maize streak virus disease, gray leaf spot (*Cercospora zea-maydis*), rust (*Puccinia sorghi*) and turcicum blight (*Exserohilum turcicum*) were scored on a scale of 1-5 where 1 = no visible infection, 2 = a few scattered infection on leaves below the ear, 3 = many infection on leaves below the ear, with a few spreading above the ear, 4 = severe infection on all but uppermost leaves, and 5 = severe infection on all leaves with most of the leaf tissue being necrotic.

### **3.2.5 Data analyses**

Individual experiments were subjected to analysis of variance (ANOVA) using the process GLM of SAS (SAS ,1997) considering entries as fixed and replicates, plots and blocks within replicates as random factors. Analysis of variance across each management condition and across environments was carried out using process GLM to examine the partitioning of total sum of squares to genotypes, environment and genotype

x environment interaction, and to assess the average performance of genotypes under each management conditions and across environments. The best hybrids were identified by mean separation using least significant difference (LSD). Means across each environment were standardized based on the model  $P_i = (x_{ij} - m_i)/s_i$  where  $P_i$  is the phenotypic values for the trait  $i$ ,  $m_i$  and  $s_i$  are the mean and standard deviation of trait  $i$  in a population, and  $x_{ij}$  is the value of the trait  $i$  measured on genotype  $j$ . Typical weights in managed drought experiments were allocated as follows: grain yield = +5 ears per plant = +3 ASI = -2. Under low nitrogen experiment the weights were allocated as follows: grain yield weight = +5, ears per plant = +2, ASI = -1 and leaf senescence = -2 (Bänziger *et al.*, 2000). Using these weights and standardized means, a multi-trait selection index ( $I$ ) was computed based on the model  $I = b_1P_1 + b_2P_2 + \dots + b_nP_n$  where  $P_i$  is the observed standardized value of the trait  $i$  and  $b_i$  is the weight given to that trait in the selection index (Bänziger *et al.*, 2000). The best genotypes were selected based on multi-trait selection index and subjected to genotype main effects and genotype by environment interaction (GGE) biplot analysis (Yan *et al.*, 2000) to visualize the performance and stability of the genotypes across environments. Correlation coefficients between morpho-physiological traits and final grain yield were computed using SAS (SAS, 1997).

### **3.3 Results and discussion**

#### **3.3.1 Analysis of Variance across well-watered environment**

Analysis of variance across well watered environments revealed significant differences ( $P < 0.05$ ) for all traits among early quality protein maize (QPM) top cross hybrids suggesting that selection for superior genotypes can safely be practiced with respect to the traits used in this study (Table 3.1). Genotype by environment interaction was significant for all traits except anthesis date (AD), silking date (SD), anthesis silking

interval (ASI), rust (*Puccinia sorghi*) and root lodging (RL). This suggests that selection both within and across environments selection can be practiced and superior genotypes for individual site and across sites can be identified (Table 3.1). Bänziger *et al.* (1997) recommended traits to be used as selection criteria under well watered environment which include grain yield, root lodging (RL), stalk lodging (SL), husk cover (HC), gray leaf spot (GLS), turcicum blight (ET) and maize streak virus (MSV). Early QPM top cross hybrids showed reasonable tolerance to diseases across well watered environments as indicated by significant differences among the genotypes for all the diseases scored in this study. The significant genotype by environment (GxE) interactions could be explained by variation in soil and climatic conditions in different environments and their interaction with the genotypes. Genotype by environment (GxE) interactions did not have significant effect on anthesis date and silking date and therefore the early QPM top cross hybrids had similar maturity dates across well watered environments (Table 3.1). Bänziger and Cooper (2001) reported that GxE interactions originate from variable plant stand, variable soil water holding capacity, and genetic variation in flowering time and this may lead to overestimation of genetical and statistical parameters (Sharma, 1995).

**Table 3. 1 Mean squares for analysis of variance across well-watered environment**

Source	df	GY	AD	SD	ASI	RL	SL	EPP
Env	2	1677.22***	1481.90***	439.05***	651.65***	405.11***	50430.58***	1.44***
Rep (Env)	3	3.96*	9.54*	8.06	5.58*	122.36**	4714.82***	0.07***
Genotype	129	3.91***	10.68***	14.70***	3.43***	31.34*	232.77***	0.02***
Env (Gen)	258	1.92***	2.95	4.02	2.09	23.77	179.55***	0.01***
Error	387	1.16	2.87	3.736	2.16	24.19	92.01	0.01

**Table 3.1 continued Mean squares for ANOVA across well-watered environment**

Source	df	GLS	ET	EA	df	ER	MSV	HC
Env	1	76.92***	77.69***	43.27***	2	18264.33***	388.07***	6171.01***
Rep (Env)	2	2.06***	0.02	0.04	3	33.49	0.32***	21.49
Genotype	129	0.78***	0.04**	0.33***	129	69.04**	0.16**	107.43***
Env (Gen)	129	0.47***	0.05***	0.25***	258	71.76***	0.17***	61.63**
Error	258	0.25	0.03	0.16	387	46.32	0.12	46.29

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

GY-grain yield AD-anthesis date, SD-silking date ASI-anthesis silking interval, RL-root lodging, SL-stem lodging EPP-ears per plant, GLS-gray leaf spot (*Cercospora zea-maydis*), ET-*Exserohilum turcicum*, EA-ear aspect, ER-ear rot, MSV-maize streak virus

### 3.3.2 Analysis of Variance across managed drought stress environment

Analysis of variance across managed drought stress environment varied significantly among the traits as presented in Table 3.2. Significant difference ( $P < 0.05$ ) among early quality protein (QPM) maize top cross hybrids were observed for all traits except ears per plant (EPP), turcicum blight (ET), ear rot (ER) and ear aspect (EA). Genotypes by environment interactions were significant ( $P < 0.05$ ) for all traits except for gray leaf spot, turcicum blight, husk cover (HC) and ear rot. Lack of significant difference among early QPM top cross hybrids for gray leaf spot calls for screening of diverse germplasm to identify early QPM top cross hybrids that are resistant or tolerant to gray leaf spot under drought conditions. Perhaps backcrossing early QPM genotypes with resistance sources of germplasm could provide QPM hybrids resistant to foliar diseases. International Institute of Tropical Agriculture (IITA), has developed twenty maize (*Zea mays* L.) inbred lines with resistance to foliar diseases and adaptation to tropical mid altitudes (Reg. no. GP-379 to GP-398, PI 635122 to PI 635141). The lines are at the  $S_8$  to  $S_9$  stages of inbreeding and confer combined resistance to gray leaf spot (caused by *Cercospora zea-maydis*), Maize streak virus (MSV), turcicum blight (caused by

*Exserohilum turcicum*) and common rust (caused by *Puccinia sorghi*); diseases prevalent in the mid altitude ecology in West and Central Africa (Everett *et al.*, 1994a).

Environments performed differently as indicated by significant differences for environment in the ANOVA (Table 3.2). This might partly explain the significant GxE interactions for grain yield and other secondary traits in this study. However, abiotic and biotic stresses have been reported to cause increased GxE interactions (Kang, 1998). The author suggested that improving genotypes resistance/tolerance to stress minimizes GxE interactions. Similarly, Tollenaar and Lee (2002) reported that improvement in maize grain yield is associated with increased stress tolerance which reduces GxE interactions. Bänziger and cooper (2001), reported that GxE interactions are common under drought stress and the interactions originate from environmental variation in the timing and severity of water deficits, genetic variation in flowering time and nutrient deficiencies and toxicities whose occurrence interact with water deficits. Selection approaches under drought stress have been recommended and grain yield, ears per plant, anthesis silking interval and leaf senescence have been used as selection criteria under managed drought stress experiments (Bänziger *et al.*, 2000).

**Table 3.2 Mean squares for analysis of variance across managed drought environment**

Source	df	GY	AD	RL	SL	EPP
Env	2	1635.53***	11262.07***	25601.46***	17160.54***	40.18***
Rep (Env)	3	1.600	39.50**	268.54	44.12	0.15**
Genotype	129	1.11**	29.99***	203.54***	133.25**	0.04
Env (Gen)	258	1.45***	18.77***	183.81***	128.11**	0.05**
Error	387	0.74	7.66	132.4	90.82	0.03

GY-grain yield; AD-anthesis date; RL-root lodging; SL-stem lodging; EPP-ears per plant

**Table 3.2 continued: Analysis of Variance across managed drought environment**

Source	df	SD	ASI	ER	EA	HC
Env	2	3501.66***	4436.81***	63781.71***	95.43***	101.29***
Rep (Env)	3	12.03	19.23*	732.85	0.62	0.41
Genotype	129	31.42***	22.63***	641.33	0.57	0.53*
Env (Gen)	258	25.05***	23.27***	681.37	0.60*	0.48
Error	387	6.73	5.7	692.21	0.47	0.41

Source	df	GLS	PS	ET	MSV
Env	2	505.11***	30.77***	7.39***	238.28***
Rep (Env)	3	0.05	1.25***	0.45**	0.01
Genotype	129	2.17	0.29***	0.14**	0.18***
Env (Gen)	258	1.95	0.24***	0.1	0.19***
Error	387	2.14	0.12	0.09	0.02

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

SD-silking date, ASI-anthesis silking interval, ER-ear rot, EA-ear aspect, HC-husk cover, GLS-gray leaf spot (*Cercospora zea-maydis*), PS-*Puccinia sorghi*, ET-*Exserohilum turcicum*, MSV-maize streak virus

### 3.3.3 Analysis of Variance under Low nitrogen environment

Results of analysis of variance under low nitrogen stress are presented in Table

3.3. Significant differences ( $P < 0.05$ ) were observed among early QPM top cross hybrids for husk cover (HC) and ear rot (ER) but not for grain yield and other secondary traits and this call for testing of more QPM hybrids in diverse environments to identify sources of tolerance to low nitrogen stress. However, the results of this study are based on a single low nitrogen stress environment and therefore there is a need for testing the early QPM top cross hybrids across many low nitrogen sites to obtain conclusive results. Low nitrogen conditions have been reported in farmer's field in the tropics. Farmers in the tropics use little fertilizer because of the high cost of fertilizer, inaccessibility to credit facilities and unpredictable weather conditions and therefore breeding for low nitrogen remains a critical option to alleviate low nitrogen stress in the tropics (Heisey and

Mwangi, 1996). Perhaps testing of a large number of germplasm will identify sources of tolerance to low nitrogen stress

**Table 3.3 Mean squares for analysis of variance under low nitrogen environment**

Source	df	GY	AD	SD	ASI	RL	SL	EPP	HC	ER	SEN
Rep	1	3.75***	1080.39***	1246.08***	8.56	14.3	0.10	0.75***	180.61*	121.73*	0.39***
Genotype	129	0.27	48.04	67.98	13.1	5.41	3.20	0.03	66.20*	34.04*	0.01
Error	129	0.26	53.24	80.36	11.6	5.72	2.70	0.03	45.84	24.77	0.01

\*\*\* \*\* \* Indicate significance at 0.001 0.01 and 0.05 respectively

GY-grain yield, AD-anthesis date, SD-silking date, ASI-anthesis silking, RL-root lodging, SL-stem lodging, EPP-ears per plant, HC-husk cover, ER-ear rot EA-ear aspect

### **3.3.4 Performance of early quality protein maize top cross hybrids across drought and low nitrogen environments**

The average grain yield across managed drought stress experiment was 2.3 t/ha (Table 3.4) which falls within the limits stipulated by Bolanos and Edmeades (1996) who indicated that the average grain yield under abiotic stress has to be between 20% and 30% of the average grain yield under optimal conditions. Similar results have been reported by Campos *et al.* (2004). Grain yield ranged from 1.25 t/ha to 3.22 t/ha and the highest yielding genotype was genotype 19. The checks, genotype 129 (Susuma) and 130 (Pool 15 QPM SR) had a grain yield of 2.8 t/ha and 2.3 t/ha respectively. In this study therefore some early QPM top cross hybrids performed better than the checks (Table 3.4). The high grain yield of the best hybrids across managed drought stress may be attributed to combined factors of high ears per plant and a reduced anthesis silking interval (ASI) which are key secondary traits associated with drought tolerance (Bänziger *et al.*, 2000).

The average days to anthesis (AD) was 70.4 days with a range of 59.2 days to 76.3 days whereas the average days to silking (SD) was 76.6 days with a range of 67.3 days to 83.0 days (Table 3.4). Maturity under drought is a critical factor as drought

escape is not uncommon among hybrids and therefore to determine drought tolerant genotypes, selection has to be done in reference to maturity grouping (Diallo, personal communication). The best hybrid across managed drought stress experiment had an average AD of 70.4 days and therefore it can reliably be categorized as drought tolerant. The average ASI was 6.9 days with a range of 2.4 days to 16.5 days (Table 3.4). In this study, the best performing hybrids had short ASI which agrees with previous studies by Edmeades *et al.* (1997) who reported that a long ASI is associated with drought susceptibility, low harvest index, slow ear growth and bareness.

On average, root lodging (RL) was high (13.6%) compared to stalk lodging (SL) which recorded 4.1%. Ear aspect (EA) scores which indicate uniformity of ears, size of ears and how well the ears are filled were low for most of the best early QPM top cross hybrids across managed drought stress environments. The average EA score was 2.6 with a range of 1.5 to 3.6 (Table 3.4).



**Table 3.4 Grain yield and secondary traits for the best 20 early quality protein maize top cross hybrids across managed drought stress**

GEN	grain yield (t/ha)	AD	SD	ASI	EPP	RL	SL	ER	EA	HC
19	3.22	70.5	77.3	6.8	0.8	9.5	2.8	11.0	1.9	14.0
90	3.17	71.8	77.3	5.5	0.8	21.2	4.0	17.8	2.6	12.0
89	3.07	66.3	72.7	6.3	0.7	7.8	4.8	20.9	3.1	2.8
79	3.02	66.7	71.2	4.5	0.8	19.6	6.6	12.6	1.9	2.5
80	2.97	72.7	79.3	6.6	0.7	6.1	2.8	5.4	2.9	3.7
73	2.93	68.7	76.3	7.6	0.6	15.6	4.0	17.0	2.8	4.0
14	2.90	69.3	76.0	6.6	0.6	8.3	4.0	9.6	2.0	8.1
60	2.85	69.5	75.5	6.0	0.7	20.1	5.8	14.6	2.0	8.4
56	2.85	72.2	78.2	6.0	0.7	5.4	3.0	24.5	2.8	8.6
122	2.82	71.7	75.0	3.3	0.6	28.8	6.3	15.1	2.0	4.9
12	2.82	72.7	78.5	5.9	0.6	12.2	6.4	13.1	2.9	9.4
53	2.80	71.8	78.5	6.7	0.7	18.1	2.3	14.9	2.5	2.6
37	2.80	72.7	78.7	6.0	0.8	35.5	4.4	14.4	2.1	7.2
25	2.80	76.3	83.0	6.7	0.6	16.1	3.1	14.4	2.5	9.0
91	2.77	70.7	77.7	7.0	0.7	5.7	1.0	8.7	2.2	6.4
98	2.75	67.5	73.5	6.0	0.8	9.6	7.4	20.5	2.1	9.7
11	2.73	70.2	76.5	6.3	0.7	6.8	2.1	8.4	2.3	4.4
71	2.68	67.3	75.6	8.3	0.6	7.4	5.8	13.1	2.5	4.4
10	2.67	67.7	72.8	5.1	0.6	10.7	5.8	12.7	3.5	2.5
30	2.62	70.7	77.7	8.4	0.7	14.4	3.9	12.7	2.3	2.5
Check 1	2.80	76.3	83.0	6.7	0.6	16.1	3.1	14.4	2.5	9.0
Check 2	2.28	66.7	73.8	7.2	0.6	4.2	6.2	20.3	2.9	7.0
Mean	2.26	70.4	76.6	6.9	0.6	13.6	4.1	16.3	2.6	6.8
MIN	1.25	59.2	67.3	2.4	0.4	0.9	0.0	1.8	1.5	2.4
MAX	3.22	76.3	83.0	16.5	0.8	48.0	10.6	32.0	3.6	15.9
LSD(0.05)	0.68	4.3	16.5	4.1	0.2	16.5	5.7	0.7	0.7	6.2

AD-anthesis date; SD-silking date; ASI-anthesis silking interval; EPP-ears per plant; RL-root lodging; SL-stem lodging; ER-ear rot; EA-ear aspect; HC-husk cover, Check 1-Susuma; Check 2-Pool 15 QPM SR; MIN-minimum value recorded in the experiment; MAX-maximum value recorded in the experiment

The average grain yield and secondary traits of the best 20 early QPM hybrids under low nitrogen stress are presented in Table 3.5. The average grain yield was 1.3 t/ha with a range of 0.4 t/ha to 2.4 t/ha. The best early QPM top cross hybrid (genotype 75) had a grain yield of 2.4 t/ha. The best 20 genotypes used in this study had a higher grain yield than all the checks (Table 3.5). The checks, genotype 129 (Susuma) and 130 (Pool 15 QPM SR) yielded

1.0 t/ha and 1.5 t/ha respectively (Table 3.5). Based on mean performance, the impact of stress on grain yield was high under low nitrogen stress (1.3 t/ha) as compared to drought stress (2.3 t/ha). Uhart and Andrade (1995) reported that low nitrogen condition in the soil reduce leaf area index, leaf area duration, radiation interception and radiation use efficiency which perhaps explains the low grain yields recorded in this study. Presterl *et al.* (2003) reported a grain yield reduction of 37% under low nitrogen compared to high nitrogen. In this study however, grain yield under low nitrogen was 22 % of grain yield under optimal condition (Table 3.5).

Nitrogen stress reduces final grain number by increasing kernel abortion (Lemcoff and Loomis, 1986; Pearson and Jacobs, 1987; Uhart and Andrade, 1995b). Around 85% of the abortion occurs during the first 20 days after female flowering (Monneveux *et al.*, 2005). This increase in grain abortion is closely related to a lack of post-flowering nitrogen uptake by the crop. Nitrogen deprivation reduces leaf area index and hence radiation interception. It also accelerates senescence of lower leaves (Moll *et al.*, 1994), decreases radiation use efficiency (Uhart and Andrade, 1995a), and increases ASI (Jacobs and Pearson, 1991, Edmeades *et al.*, 2000). Bänziger and Lafitte (1997) and Bänziger *et al.* (2000) proposed ASI and foliar senescence as secondary traits for improving maize for low nitrogen target environments. The average anthesis silking interval increased from 1.8 days under optimal conditions to 7.8 days under low nitrogen conditions which contrasts with earlier reports by Zaidi *et al.* (2004) who reported a high increase in ASI under drought stress compared to low nitrogen stress. The average days to anthesis were 69.8 days with a range of 63.5 days to 77.7 days whereas the average days to silking were 77.6 days with a range of 68 days to 88 days (table 3.5)

**Table 3.5 Grain yield and secondary traits for the best 20 early quality protein maize top cross hybrids under low nitrogen**

Gen	grain yield (t/ha)	AD	SD	ASI	EPP	RL	SL	ER	EA	HC
75	2.4	66.0	70.0	4.0	1.0	0.0	0.0	0.0	2.3	8.2
124	2.3	65.0	69.0	4.0	1.0	0.0	0.0	0.0	2.8	10.6
63	2.3	68.0	71.0	3.0	0.9	0.0	5.3	3.0	3.0	2.7
41	2.2	67.5	74.5	7.0	1.0	0.0	0.0	0.0	2.5	13.2
22	2.1	65.5	70.0	4.5	0.9	0.0	0.0	0.0	2.8	5.6
33	2.1	72.0	74.5	2.5	1.0	0.0	0.0	5.9	2.0	2.8
68	2.0	69.5	74.5	5.0	0.9	0.0	0.0	0.0	2.3	2.7
108	2.0	63.5	68.0	4.5	1.0	0.0	0.0	3.2	2.8	0.0
128	2.0	68.0	72.5	4.5	0.9	0.0	0.0	0.0	3.0	13.6
65	1.9	63.5	70.0	6.5	1.0	3.0	0.0	2.8	2.3	14.7
122	1.9	69.5	76.0	6.5	1.0	0.0	0.0	0.0	3.3	2.7
18	1.9	71.5	75.0	3.5	0.8	0.0	2.7	0.0	2.5	0.0
86	1.9	67.5	71.5	4.0	0.8	2.5	5.0	3.4	2.5	12.5
87	1.8	65.0	72.0	7.0	1.0	0.0	0.0	0.0	2.3	11.2
36	1.8	66.5	72.5	6.0	1.0	0.0	0.0	0.0	2.8	0.0
19	1.8	67.5	72.5	5.0	0.9	0.0	0.0	6.1	2.3	7.9
79	1.8	69.5	74.5	5.0	0.8	2.8	0.0	5.6	2.5	5.3
72	1.7	70.5	77.5	7.0	0.8	0.0	0.0	0.0	2.5	2.7
97	1.7	70.5	78.0	7.5	1.0	2.7	0.0	3.0	2.0	5.3
88	1.7	69.0	74.0	5.0	0.9	0.0	0.0	0.0	2.8	0.0
Check 1	1.0	73.5	84.0	10.5	0.8	0.0	0.0	0.0	2.0	0.0
Check 2	1.5	68.0	76.5	8.5	0.8	0.0	0.0	5.9	2.0	10.8
MEAN	1.3	69.8	77.6	7.8	0.8	0.8	0.4	3.3	2.5	7.0
MIN	0.4	63.5	68.0	2.0	0.5	0.0	0.0	0.0	1.8	0.0
MAX	2.4	77.5	88.0	15.5	1.1	8.4	7.9	20.7	3.8	29.0
LSD (0.05)	1.1	7.3	0.7	5.9	0.4	4.7	3.3	9.8	0.9	13.4

AD-anthesis date; SD-silking date; ASI-anthesis silking interval; EPP-ears per plant; RL-root lodging; SL-stem lodging; ER-ear rot; EA-ear aspect; HC-husk cover, Check 1-Susuma; Check 2-Pool 15 QPM SR; MIN-minimum value recorded in the experiment; MAX-maximum value recorded in the experiment

The observed effects of low nitrogen and drought stress on grain yield and agronomic traits confirmed that these abiotic stresses are major factors limiting maize production in the tropics. Genotypic differences for grain yield were observed among early QPM top cross hybrids under managed drought stress whereas under low nitrogen stress, there was no significant differences among the genotypes. However, some hybrids ranked among the best 20 appeared both under drought and low nitrogen stress. These hybrids include genotype 19, 79 and 122 (Table 3.4 and Table 3.5). These results indicate that perhaps physiological mechanisms under these two stresses are similar. Bänziger *et al.* (1999) reported that drought tolerant populations perform well under nitrogen deficient conditions. They also showed that gains from selection under well-fertilized drought stressed conditions did not diminish as the level of nitrogen stress increased.

High yielding genotypes across managed drought and low nitrogen conditions were associated with high EPP and a short ASI and this confirms the utility of secondary traits in breeding for tolerance to drought and low nitrogen. Kamara *et al.* (2004) investigated physiological basis for tolerance of maize genotypes to drought and reported that a shorter ASI, the stay green, reduced bareness and increased biomass results in high grain yield. Similarly, Lafitte and Edmeades (1994) and Bänziger *et al.* (1999) reported a high correlation between these traits and grain yield. Drought and low nitrogen increased ASI and this agrees with results of Edmeades (1993) who reported that a characteristic of maize under environmental stresses such as low nitrogen and drought is an increase in the ASI. However, for better performing genotypes, a short ASI is desirable as it leads to increased partitioning of assimilates to the developing ears resulting in high grain yield (Edmeades *et al.*, 1993).

### 3.3.5 Performance of early quality protein maize top cross hybrids across well watered environments

Performance of early QPM top cross hybrids across well watered environment varied significantly among hybrids (Table 3.6). The average grain yield was 5.8 t/ha with a range of 3.8 t/ha to 7.9 t/ha. The check, genotype 129 (Susuma) and 130 (Pool 15 QPM SR) had a grain yield of 4.9 t/ha and 5.6 t/ha respectively. The average days to anthesis (AD) was 66.3 days whereas the average days to silking were 68.1 days (Table 3.6). A short anthesis silking interval (ASI) was recorded with an average ears per plant (EPP) of 0.9 ears. The average ear aspect (EA) score was 2.6 with a range of 1.9 to 3.3 (Table 3.6). The checks recorded high ear aspect score compared to the early QPM top cross hybrids. Lower EA scores are desirable as they indicate uniform, big and well filled ears. Among the best 20 hybrids, most hybrids had high EPP and lower scores of EA. Husk cover (HC) problem was more pronounced across well watered environment compared to drought stress and low nitrogen environment. This could be attributed to less competition for photo-assimilate flux into the developing ears and hence the plants have the capacity to fully fill their ears. Similar results have been reported by Betran *et al.* (2003c).

High yields of QPM compared to normal checks have been reported. Srinivasan *et al.* (1997) and Akande and Lamidi (2006) reported that QPM hybrids compared well with most popular non QPM commercial checks and in some cases, yield advantage of QPM hybrids was as high as 60% over checks. In this study similar results were obtained where the best 20 early QPM top cross hybrids recorded high grain yields compared to the checks. Thus, there is a potential of releasing QPM hybrid varieties for commercial production with an added benefit of quality protein over normal maize. Across well watered environments, genotypes showed a reasonable level of tolerance to diseases as indicated by the disease incidence scored on a scale of 1 to 5 (Table 3.6). Gray leaf spot (GLS- *Cercospora zea-maydis*) recorded an average score of 2.4 whereas rust (PS-*Puccinia sorghi*) and turicum blight (ET-

*Exserohilum turcicum*) recorded a score of 1.4. The early QPM top cross hybrids showed the least incidence of maize streak virus (MSV) disease with an average score of 0.7. The checks recorded similar results (Table 3.6)

**Table 3.6 Grain yield and secondary traits for the best 20 early quality protein maize top cross hybrids across well watered environment**

Gen	GY (t/ha)	Secondary traits									Disease scores			
		AD	SD	ASI	EPP	RL	SL	HC	ER	EA	GLS	PS	ET	MSV
49	7.9	69.2	70.0	0.8	1.0	0.8	2.6	16.0	7.7	2.0	2.9	1.3	1.5	0.8
105	7.8	66.5	68.2	1.7	1.0	2.4	11.8	7.1	7.7	1.9	2.6	1.1	1.5	0.8
30	7.7	66.8	68.5	1.7	1.0	7.0	12.1	10.1	9.3	2.2	2.4	1.1	1.4	0.6
88	7.6	69.3	71.8	2.5	1.0	2.9	5.8	9.2	4.4	2.3	2.6	1.5	1.4	0.8
113	7.4	65.0	66.5	1.5	1.0	2.1	4.7	7.1	4.6	2.2	3.0	1.4	1.4	0.6
77	7.3	65.7	68.3	2.7	1.0	1.5	22.1	2.4	3.1	2.3	2.4	1.6	1.3	0.8
25	7.2	66.7	67.5	0.8	1.0	4.6	18.2	6.4	2.5	2.3	2.6	1.0	1.4	0.9
9	7.2	66.3	67.3	1.0	1.0	4.1	5.6	1.9	3.2	2.3	2.5	1.3	1.5	0.6
42	7.1	66.3	67.2	0.8	1.0	2.4	8.3	5.3	6.9	2.2	1.8	1.0	1.3	0.8
59	7.1	65.2	66.2	1.0	1.0	0.6	1.9	7.7	4.7	2.5	2.6	1.3	1.5	0.9
46	7.0	65.0	67.5	2.5	0.9	0.0	13.9	4.0	6.0	2.2	2.9	1.1	1.5	0.8
90	7.0	67.3	69.3	2.0	1.0	0.8	19.6	9.4	9.2	2.2	3.0	1.4	1.4	0.8
28	7.0	66.0	67.7	1.7	1.0	0.0	9.1	3.1	7.9	2.1	2.3	1.8	1.4	0.6
2	6.9	68.8	70.7	1.8	1.0	3.0	10.6	4.7	12.0	2.5	1.9	1.3	1.3	0.6
122	6.8	66.5	69.0	2.5	1.0	1.3	10.6	11.4	3.4	2.3	2.9	1.4	1.5	0.6
109	6.7	67.3	69.3	2.0	1.0	5.0	11.5	9.6	5.4	2.3	2.1	1.4	1.6	0.8
71	6.7	63.8	65.0	1.2	0.9	0.0	21.8	4.9	7.2	2.3	2.8	1.6	1.5	0.8
114	6.7	67.3	68.5	1.2	1.0	2.7	19.5	6.8	9.2	2.0	2.5	1.6	1.5	0.8
37	6.7	65.0	67.0	2.0	1.0	0.8	9.9	4.7	11.5	2.6	2.4	1.3	1.3	0.6
18	6.6	66.8	68.8	2.0	1.0	1.6	6.9	8.0	10.3	2.3	2.9	1.5	1.5	1.0
Check 1	4.9	70.5	73.0	2.5	1.0	2.7	5.0	0.0	5.3	2.7	2.3	1.5	1.4	0.6
Check 2	5.6	65.7	67.3	1.7	0.9	3.3	6.2	17.9	9.2	2.8	2.4	1.5	1.4	0.8
MEAN	5.8	66.3	68.1	1.8	0.9	2.6	10.7	6.1	8.5	2.6	2.4	1.4	1.4	0.7
MIN	7.9	71.0	73.0	3.8	1.1	10.0	27.8	20.6	18.3	3.3	3.4	4.8	1.6	1.0
MAX	3.8	63.0	65.0	0.3	0.7	0.0	1.0	0.0	0.8	1.9	1.5	1.0	1.3	0.5
LSD(0.05)	1.2	1.9	2.2	1.7	0.1	5.6	10.9	7.7	7.7	0.5	0.7	0.9	0.2	0.3

GY-grain yield, AD-anthesis date, SD-silking date, ASI-anthesis silking interval, EPP-ears per plant, RL-root lodging, SL-stem lodging, HC-husk cover, ER-ear rot, EA-ear aspect; GLS-gray leaf spot (*Cercospora zae-maydis*), PS-*Puccinia sorghi*, ET-*Exserohilum turcicum*, MSV-maize streak virus, MIN-minimum value recorded in the experiment, MAX-maximum value recorded in the experiment

### 3.3.6 Correlation Analysis among traits

The results of correlation analysis among various traits are presented in Table 3.7. Across well-watered environment grain yield was significantly ( $P < 0.05$ ) correlated with ears per plant (EPP), ASI and silking date. Similarly, correlation between silking date (SD) and anthesis date (AD) was high and significant. The correlation between grain yield and ASI was negative but very low with strength of correlation ( $R^2$ ) of 1.5 %. This indicates that ASI is less preferred as a trait for selection as compared to EPP under well-watered environment. Under stress conditions (managed drought and low nitrogen environments), ASI, ears per plant, anthesis date and silking date were significantly correlated with grain yield (Table 3.7). The correlation between grain yield and ASI was negative and high under low nitrogen (-0.678) as compared to drought (-0.356) indicating the importance of ASI as a secondary trait for selection under low nitrogen stress. Similar results have been reported by Bänziger *et al.* (2000). Similarly, correlation between grain yield and EPP was positive and relatively high under low nitrogen as compared to managed drought environment (Table 3.7) This conforms to previous findings that selection for reduced ASI and increased EPP would lead to better performance under drought and low nitrogen environment (Bänziger *et al.*, 2000). Anthesis silking interval (ASI) was strongly correlated to silking date under low nitrogen (0.56) than under managed drought (0.20). However, the correlation between ASI and anthesis date was not consistent under stress with a negative correlation observed under managed drought and a positive correlation under low nitrogen environment (Table 3.7).

**Table 3.7 Correlation coefficient and Coefficient of determination (in parentheses) for grain yield and other secondary traits across well watered, managed drought and Low N environments**

	well-watered				managed drought				low nitrogen			
	GY	ASI	EPP	AD	GY	ASI	EPP	AD	GY	ASI	EPP	AD
<b>ASI</b>	-0.12 (0.02)				-0.36*** (0.13)				-0.68*** (0.46)			
<b>EPP</b>	0.48*** (0.23)	-0.085 (0.01)			0.649*** (0.42)	-0.63 (0.4)			0.74*** (0.55)	-0.616*** (0.379)		
<b>AD*</b>	0.082 (0.007)	0.07 (0.01)	-0.08 (0.01)		0.69*** (0.48)	-0.63** (0.4)	0.62*** (0.39)		-0.37*** (0.14)	0.15 (0.02)	-0.275** (0.08)	
<b>SD<sub>↓</sub></b>	0.04 (0.001)	0.49*** (0.235)	-0.13 (0.02)	0.84*** (0.709)	0.48*** (0.23)	0.20*** (0.04)	0.11** (0.01)	0.63*** (0.4)	-0.61*** (0.37)	0.56*** (0.32)	-0.50** (0.25)	0.90*** (0.81)

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

GY-grain yield, ASI-anthesis silking interval, EPP-ears per plant, AD-anthesis date SD-silking date



### 3.3.7 Multi-trait selection and genotype plus genotype by environment (GGE) biplot analysis

The ranking of quality protein maize based on an index are presented in Table 3.8. Based on the index genotype 75 was the best under low nitrogen with an average yield of 2.4 t/ha while entry 90 had an outstanding performance under managed drought with a mean yield of 3.2 t/ha. Among the best 20 genotypes based on the multi-trait selection index, 5 genotypes were common both under low nitrogen and managed drought indicating a level of tolerance to the two stresses. These were 79, 89, 108, 124 and 128 (Table 3.8).

**Table 3.8 Ranking of the best 20 early quality protein maize hybrids based on Multi-trait selection index**

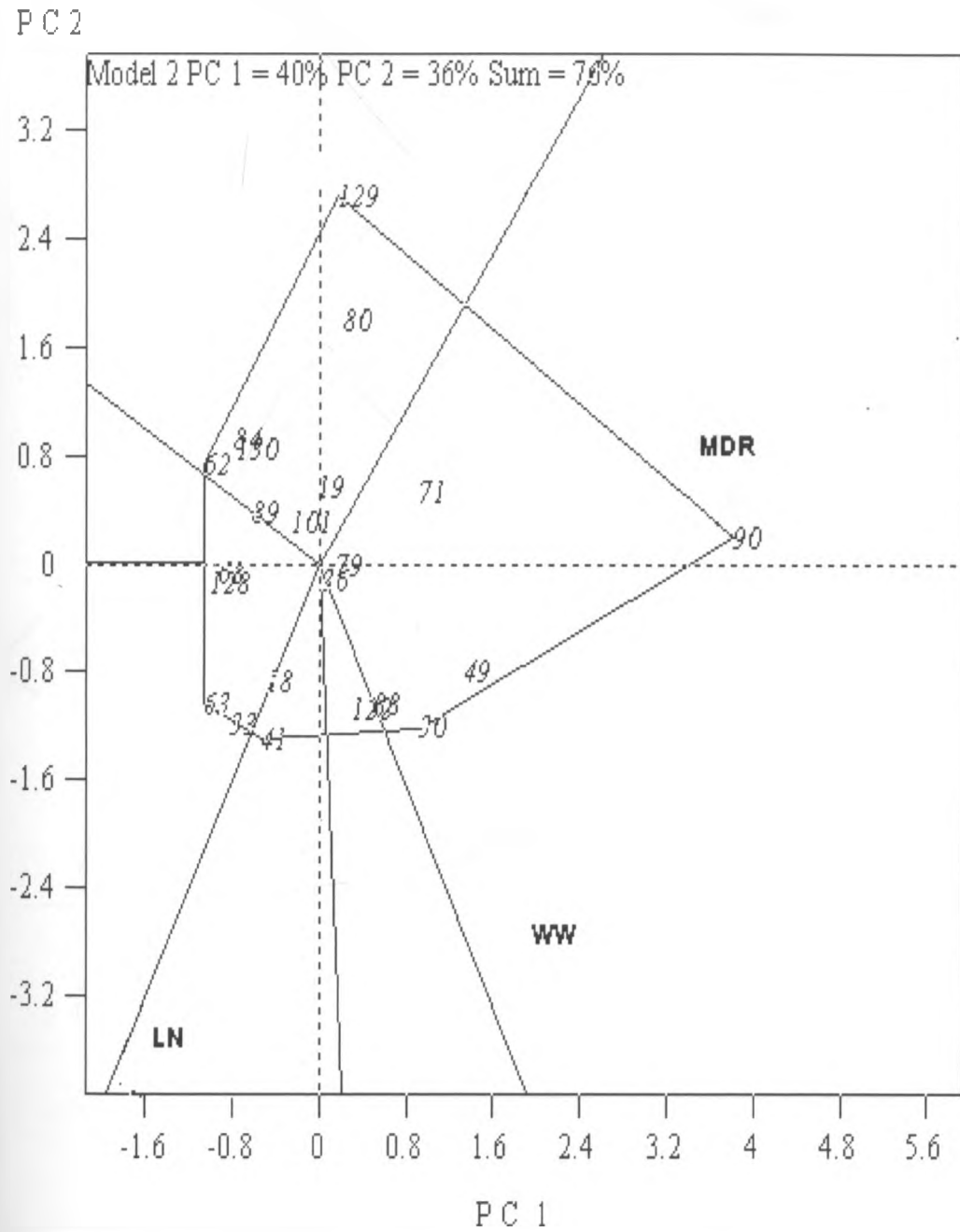
Low nitrogen stress			Managed drought stress		
Genotype	Grain yield (t/ha)	Index	Genotype	Grain yield (t/ha)	Index
75	2.4	8.9	90	3.2	1.8
124	2.3	8.6	89	3.1	-1.6
63	2.3	9.4	79	3.0	4.0
41	2.2	4.8	56	2.9	-1.7
33	2.1	9.0	12	2.8	5.9
22	2.1	7.0	37	2.8	1.5
108	2.0	6.7	53	2.8	-1.7
68	2.0	6.0	10	2.7	-0.2
128	2.0	6.2	120	2.6	0.8
65	1.9	4.3	84	2.6	5.5
122	1.9	4.2	26	2.6	0.2
18	1.9	6.7	107	2.5	0.8
86	1.9	6.1	124	2.4	-0.1
19	1.8	4.7	118	2.4	1.7
79	1.8	4.7	108	2.4	-1.0
97	1.7	4.5	128	2.4	1.4
62	1.7	7.1	49	2.4	-0.9
67	1.7	6.8	32	2.3	8.2
9	1.7	5.6	117	2.2	5.7
89	1.7	4.6	94	2.2	-0.9
MEAN	1.3			2.26	
MIN	0.4			1.25	
MAX	2.4			3.22	
LSD (0.05)	1.1			0.68	

MIN-minimum value recorded in the experiment, MAX-maximum value recorded in the experiment

The GGE biplot analysis explained 76% of variation with principal component 1 (PC1) score of 40% and PC2 of 36% (Figure 1). Since the vertex of a biplot explains a winning cultivar in a mega environment (Yan *et al.*, 2006) entry 90 was the best genotype under managed drought and well-watered environment although it performed relatively better under drought compared to well watered environment. Under low nitrogen environment, entry 41 was the winning genotype but only slightly higher than entry 18 in close proximity (Figure 1). Other entries that performed better under drought and well watered environment include entry 49, 71 and 88 (Figure 1)

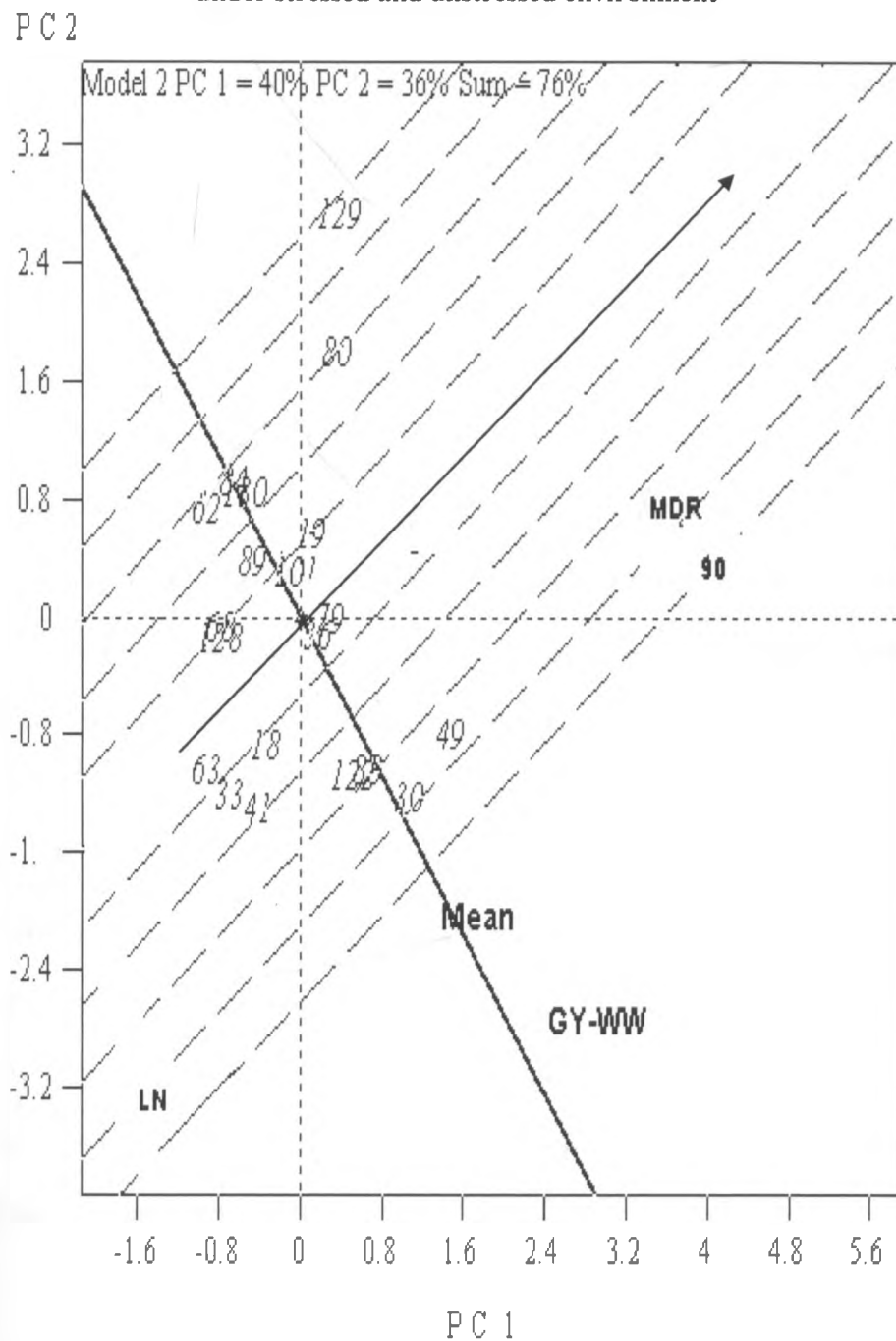
Figure 2 displays the performance and stability of genotypes across stressed and unstressed environments. The arrow on the abscissa indicates direction of high performance. The abscissa approximates genotype contribution to G and the ordinate approximate genotypes' contribution to GE, which is a measure of stability or instability (Yan *et al.*, 2006). Entry 79 was the most stable genotype as it was located on the abscissa (Figure 2). This indicates that its rank was highly consistent across environment compared to other entries. In contrast, entry 129 (check) and entry 90 were the least stable genotypes with above average mean performance (Figure2). Well-watered environment and low nitrogen stress environment had a higher discriminating power and representative of the genotype as indicated by the environment vector (length of a perpendicular from location of an environment to the abscissa). Environment with longer vector have a more discriminating power and are well represented by PC1 and PC2 (Yan *et al.*, 2006). Managed drought environment had a low power of discrimination among genotype (Figure2).

**Figure 1** Biplot view of which won where among early quality protein maize top cross hybrids under stressed and unstressed conditions



WW-well watered environment, LN-low nitrogen stress environment, MDR-managed drought stress environment, PC1-Principal Component 1, PC2- Principal Component 2

**Figure 2** Biplot view of performance and stability of early quality protein maize hybrids under stressed and unstressed environment



WW-well watered environment, LN-low nitrogen stress environment, MDR-managed drought stress environment, PC1-Principal Component 1, PC2- Principal Component 2

### 3.4 Conclusions and Recommendations

Results of preliminary evaluation indicate that differences among early QPM inbred lines can be identified by early generation testing of germplasm in the target environments. Among environments used in this study, significant difference for grain yield among early QPM top cross hybrids were observed for drought and well watered environments. No significant difference was observed among the QPM top cross hybrids under low nitrogen environment. This calls for testing of diverse genotypes to identify sources of tolerance to low nitrogen stress and perhaps introgression of genes for tolerance to low nitrogen stress from non QPM maize germplasm. Most early QPM top cross hybrids yielded higher than experimental check (Susuma and Pool 15QPM). The best hybrid under well watered environment was genotype 49 with a grain yield of 7.9 t/ha whereas the best hybrid under drought (genotype 19) yielded 3.2 t/ha of grain yield. Low nitrogen stress reduced grain yield more than drought stress and the highest yielding top cross hybrid under low nitrogen (genotype 75) yielded 2.4 t/ha. Results of this study indicate that superior early QPM hybrids can be identified at early generation and this reduces extra costs of evaluating increased number of genotypes at advanced generations. Across well watered environments, most hybrids yielded higher than the checks. Similarly, hybrids that yielded higher than checks across managed drought stresses environments were identified.

## CHAPTER FOUR

### 4.0 Genetic Analysis among Early Quality Protein Maize Inbred Lines under Stress and Non-Stress Conditions

#### 4.1 Introduction

Quality protein maize describes a range of maize cultivars with twice the content of limiting amino acid lysine and tryptophan compared with conventional maize and has been developed to help alleviate human nutrition in areas where maize is the major protein source in the diet, as in various parts of sub-Saharan Africa (SSA) (Krivanek *et al.*, 2007). International Maize and Wheat Improvement Center (CIMMYT) together with other stakeholders have developed QPM that has improved kernel quality characteristics over opaque-2 soft genotypes by introducing modifier genes and selecting for a hard vitreous endosperm in opaque-2 germplasm (Vasal, 2000). Efforts by CIMMYT and other stakeholders face challenges of drought. Losses due to drought in the tropics are estimated at 40% which is equivalent to 24 million tons per hectare (Edmeades *et al.*, 1992). One of the major CIMMYT programs is development of early maturing drought stress tolerant maize in order to alleviate hunger in SSA. The breeding approach of screening and selection of inbred lines under managed stress and multilocation testing of progenies in representative sample environments has facilitated development of early QPM inbred lines adapted to stress prone environments. Thus, information on agronomic performance and combining abilities of the early QPM inbred lines will facilitate the development of early QPM hybrids adapted to drought prone ecologies. The objective of this study was therefore to:

1. Determine the general and specific combining ability of early QPM inbred lines under drought stress and well watered environment
2. Identify superior early QPM top cross and three-way hybrids adapted to drought stress conditions.

## **4.2 Materials and Methods**

### **4.2.1 Germplasm**

A total of 50 early Quality Protein Maize (QPM) inbred lines selected based on top cross hybrid performance were advanced to S<sub>4</sub> before being crossed to three testers namely, CML144/CML159, ECA-QPOPE and Susuma. A total of 150 early QPM hybrids were generated comprising two sets of early QPM top cross hybrids and one set of three-way cross hybrids. The crossing was done in different blocks and at different times for each tester to avoid contamination of pollen. All females (early QPM inbred lines) were detassled before pollen shed and only males (testers) were the source of pollen. All rows were planted at a spacing 0.8 m x 0.2 m with two rows of male planted after every four rows of female and an additional two rows of male planted around the block to ensure sufficient pollen availability. One hundred and fifty early QPM hybrids (100 top cross hybrids and 50 three-way hybrids) were evaluated across four environments under drought and well-watered conditions. Six standard checks namely Check 1 (CML 144/CML 159//CML 181), Check 2 (CML 144/CML 159//Susuma), Check 3 (CML 144/CML 159// CML 176), Check 4 (CML 144/CML 159//CML 511), Check 5 (Susuma) and Check 6 (ECA-QPOPE) were included in all experiments.

### **4.2.2 Experimental sites, design and treatments**

This trial was carried out in 2007 across four environments. Three environments namely Embu (37.41<sup>0</sup> E, 0.4490S, 1510 m asl, 1200 mm rainfall); Kiboko (37.75<sup>0</sup> E, 2.15<sup>0</sup> S, 975 m asl, 530 mm rainfall) both in Kenya and Namulonge (32.35<sup>0</sup>E, 0.32<sup>0</sup> N, 1150 m asl, 530 mm rainfall) in Uganda were under well watered conditions. Experiments in all the three environments were carried out during the normal rainy season under well-watered conditions except for the well watered experiment in Kiboko

where irrigation was applied to avoid any moisture stress. In addition, one experiment was carried out in Kiboko during the dry season (June-October 2007) under managed drought conditions. This is the season consistently free of rainfall during vegetative and reproductive stages, allowing the control of stress level by withdrawing or delaying irrigation during flowering and grain filling period. Experiments under well-watered environments were carried out during October and February (2007/2008) period under rainfall conditions except Kiboko (dry mid altitude zone) where irrigation was applied after every four days to avoid moisture stress.

All experiments were planted using Alpha (0,1) lattice design (Patterson and Williams, 1976) with two replicates for each environment and six plots per incomplete block giving 26 blocks in each replication. The experimental unit was one 4-metre row plot. A total of 156 entries (150 early QPM hybrids and 6 standard checks) were planted with two seeds per hill every 20 cm in single rows spaced 80 cm apart and later thinned to one plant per hill two weeks after emergence to achieve a population density of 63,000 plants per hectare. The parents were planted side by side both under drought and non drought environment using a similar spacing.

#### **4.2.3 Agronomic practices and stress management**

In all experiments, 27 kg/ha of nitrogen and 60 kg/ha of phosphorus were applied as diammonium phosphate (DAP) during planting and at 4 weeks after emergence. Additional N was applied as calcium ammonium nitrate (CAN) at a rate of 60 kg/ha of nitrogen. Granular furadan (2,3-dihydro-2,2-dimethyl-7-benzofuranyl methylcarbamate) was applied in all experiments during planting at a rate of 24.7 kilograms active



ingredients per hectare to control soil borne insect pests. All experiments were maintained free of weeds by hand weeding.

Drought stress in managed drought experiment was achieved by withdrawing water 14 days before flowering to the end of flowering. The need for additional irrigation was determined based on population means for anthesis-silking interval (ASI) (Bänziger *et al.*, 2000). Based on this principle for management of drought experiments, an additional irrigation is not required if the average ASI is less than 3 days. An additional irrigation is applied two weeks after male flowering is complete if the average ASI is 3 to 5 days. For average ASI of 5 to 8 days, an additional irrigation is applied 7 days after male flowering is complete and for ASI greater than 8 days, an additional irrigation is applied when 80-100% of the plots have completed male flowering (Bänziger *et al.*, 2000). Average pollination dates and estimates of period to initiate drought stress were predicted based on previous data of standard hybrids

#### **4.2.4 Data collection**

During crop growth and maturity, measurements were recorded on the following agronomic traits: Grain weight was measured at harvest and used to calculate grain yield (expressed in tonnes per hectare (t/ha) and adjusted to 12.5% moisture content). Grain moisture content (percentage) at harvest was measured using a moisture meter. Silking date (days from planting to 50% silking) and anthesis date (days from planting to 50% pollen shed) were recorded during flowering. Anthesis silking interval was calculated as the difference between silking and anthesis dates ( $ASI = SD - AD$ ). Plant height (distance in centimeters (cm) from the ground to the top of tassel) and ear height (distance in cm from the ground level to the node bearing the main ear) were recorded

before harvest from representative plants within a plot. Ear aspect scores were recorded at harvest for each plot on a scale of one to five where 1 was scored for clean, uniform, large, and well-filled ears and 5 for rotten, variable, small, and partially filled ears. Before harvesting, root lodging defined as the percentage of plants with root lodging and stalk lodging (SL) defined as percentage of plants with stalk lodging were recorded for each plot. Ear rot (ER) scores were recorded at harvest as the percentage of ears that are rotten and ears per plant (EPP) were recorded at harvest as the ratio of number of ears to number of plants harvested. An ear means a cob with at least one fully developed grain. Husk cover (HC) was recorded before harvest as number of ears with open tips. Diseases (maize streak virus, gray leaf spot, rust and *Exserohilum turcicum*) were scored under well watered environments on a scale of 1-5 where 1 = no visible infection, 2 = a few scattered infection on leaves below the ear, 3 = many infection on leaves below the ear, with a few spreading above the ear, 4 = severe infection on all but uppermost leaves, and 5 = severe infection on all leaves with most of the leaf tissue being necrotic.

#### **4.2.5 Data analyses**

Individual analysis of variance was performed for each experiment with PROC GLM procedure from SAS (SAS institute Inc., 1997). Genotypes were considered fixed effects and replicates, plots and incomplete blocks within replicates as random factors. Combined analysis of variance across sites (drought and non drought environments) were performed with PROC GLM procedure of SAS (SAS institute Inc., 1997) to examine the partitioning of total sum of squares to genotypes, line, tester and line by tester interaction, and to assess the contribution of the three components to total variance. Multi-trait selection adapted to fieldbook software (Fieldbook version 8.4.4, 2006) was used to rank

genotypes based on performance per se and least significant difference (LSD) and identify the best yielding genotypes. Mean separation was done in SAS by least significant difference (LSD).

Hybrids and inbred lines under drought were classified into maturity groups using Fieldbook program to isolate genotypes that would have escaped drought. Adjusted means were used to calculate General Combining Ability (GCA) effects of male and females and Specific Combining Ability (SCA) effects using excel macro developed by Dr. Dan Makumbi of CIMMYT following Kempthorne method of line by tester analysis for combining ability (Kempthorne, 1957). Standard errors were used to compute t-values and two tailed t-test was used to test the significance of GCA and SCA effects. The restriction imposed on combining ability effects are:  $\sum g_i=0$ ,  $\sum g_{ij}=0$  where  $\sum g_i$  is the summation of GCA and  $\sum g_{ij}$  is summation of SCA and i and j are lines and testers respectively. Contributions of lines, testers and line x tester interaction to hybrid variance and estimation of genetic components (variance of SCA and GCA, covariance of half sib and full sib) were computed following a method described by Kempthorne (Kempthorne, 1957). Correlation analysis between morpho-physiological traits and grain yield were computed using SAS (SAS institute Inc., 1997). Adjusted means for grain yield were used for calculation of additive and dominance variance based on a model by Sharma (1995)

## **4.3 Results and Discussions**

### **4.3.1 Analysis of Variance**

Early Quality Protein Maize (QPM) hybrid and inbred lines were evaluated both under drought and non drought environments to compare their performance and match the

performance *per se* of the inbred lines and their combination in hybrids. Analysis of variance (ANOVA) under managed drought experiment revealed significant differences ( $P < 0.05$ ) among early QPM hybrids (genotypes) for grain yield (GY), ears per plant (EPP), anthesis date (AD), anthesis silking interval (ASI) and ear aspect (EA) (Table 4.1). Partitioning of total sum of squares into lines, testers and line by tester revealed significant differences ( $P < 0.05$ ) among early QPM inbred lines for all traits except root lodging, husk cover and ear rot. Significant differences among testers were observed for all traits except grain yield, stalk lodging, husk cover, ear rot and ear aspect (Table 4.1).

**Table 4.1 Mean squares of early quality protein maize hybrids under managed drought stress environment**

source	df	GY	EPP	AD	SL	RL	HC	ER	SD	ASI	EA
Rep	1	59.41***	1.84***	132.00***	8.13	0.42	53	2.73	576.30***	306.82***	12.74***
Entry	155	2.04***	0.07***	15.95***	4.08	1.4	30.7	6.24	36.03***	15.30**	0.70*
Gen.	149	2.05***	0.07**	14.27***	1.45	4.17**	31.5	6.48	32.67**	14.56**	0.71*
Line(L)	49	2.79***	0.11***	17.09***	4.14*	1.32	37.41	5.48	2764.59***	23.54***	1.01**
Tester(T)	2	2.97	0.15*	393.48***	5.89	5.00*	13.6	4.01	449.95***	34.43*	1.1
L x T	98	1.66*	0.06	5.13	4.14*	1.44	28.95	7.02	1590.48	10.60	0.54
Checks	5	0.84	0.02	21.08	2.01	0.00	2.97	0.00	58.52	14.67	0.48
Error	155	1.11	0.05	6.05	2.70	1.55	33.20	6.76	19.73	10.46	0.54

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

GY-grain yield (t/ha), EPP-ears per plant, AD-anthesis date, SL-stalk lodging, RL- root lodging, HC-husk cover, ER-ear rot, SD-silking date, ASI-anthesis-silking interval, EA-ear aspect

Analysis of variance across non drought experiment revealed significant differences ( $P < 0.05$ ) among early QPM hybrids (genotypes) for all traits except root lodging (RL), stalk lodging (SL), turcicum blight (*Exserohilum turcicum*) and plant aspect (PA) indicating that selection can be practiced among the hybrids with respect to these traits (Table 4.2). Similarly, among entries (genotypes plus checks), significant differences were observed for all traits except root lodging, stalk lodging, ear rot (ER), turcicum blight (*E. turcicum*) and plant aspect (PA). The early QPM inbred lines were

highly significant ( $P < 0.01$ ) for most traits except root lodging and stalk lodging whereas line by tester interactions were significant for anthesis silking interval, rust (*Puccinia sorghi*) and maize streak virus (MSV) disease. This agrees with the results of relative contribution of lines, testers and their interaction to hybrid variance which indicated that the testers had high contribution followed by the early QPM inbred lines. This suggests that variability in performance of hybrids under non drought experiment was largely due to the independent contribution of the inbred lines and testers with minimal contribution of their interactions.

The checks were significantly different in grain yield, anthesis date (AD), silking date (SD) and husk cover (HC). Across non drought experiments, environments differed significantly for all traits except root lodging (Table 4.2). Differences among environments indicate that selection for superior genotypes can be practiced for specific environments across non drought experiments and the differences could be attributed to differences in soil and climatic conditions which interacted significantly with the genotypes (Table 4.2). The interaction of environment and entry, environment and genotype, environment and inbred line, and environment and tester was significant for grain yield and varied considerably across secondary traits recorded in this study. The interaction of lines, testers and environment was not significant. Similarly, the interaction of checks and environment was not significant (Table 4.2).

**Table 4.2 Mean squares of early quality protein maize hybrids across non drought environments**

Source	df	GY	AD	ASI	RL	SL	EPP	HC
Env	2	3982.88***	15297.51***	41.71***	0.00	1640.77***	0.64***	2095.79***
REP(Env)	3	15.02***	30.16**	7.92*	4.41	219.43***	0.00	210.18*
Entry	155	6.39***	43.47***	5.64***	1.79	15.03	0.02***	193.22***
Genotypes	149	6.11***	37.67***	5.64***	1.80	14.01	0.02***	188.50***
Line	49	4.32***	30.62***	6.29***	2.00	15.13	0.02***	373.87***
Tester	2	254.63***	1593.55***	122.81***	0.33	31.25	0.06**	1974.23***
Line*Tester	98	1.93	9.44	2.928*	1.73	13.09	0.01	59.42
Checks	5	10.11***	68.51***	4.04	1.71	34.27	0.02	257.62**
Env*Entry	310	2.23***	8.25	2.70*	1.89	15.19	0.01**	91.23***
Env*gen	298	2.26***	8.34	2.67*	1.88	14.10	0.02**	92.58***
Env*Line	98	3.00***	8.06	2.87*	2.24	15.52	0.01*	141.28***
Env*Tester	4	16.43***	40.15***	1.70	2.55	31.28	0.03*	595.76***
Env*Line*Tester	196	1.60	7.84	2.59	1.69	13.04	0.01**	57.89
Env*checks	10	1.32	4.36	2.13	2.55	34.27	0.01	55.58
Error	445	1.61	7.68	2.22	1.94	13.94	0.01	57.47

**Table 4.2 continued: Mean squares of early quality protein maize hybrids across non drought environments**

Source	df	GLS	MSV	ET	PS	PA	ER	EA	SD
Env	2	106.68***	45.10***	147.11***	103.34***	181.45***	26.84**	69.35***	14368.02***
REP(Env)	3	8.32**	1.31***	2.42***	7.08***	0.46**	3.78	1.08**	9.15
Entry	155	0.31***	0.44***	0.16	0.07***	0.11	4.94	0.40***	37.40***
Genotypes	149	0.31***	0.40***	0.16	0.07***	0.11	4.88*	0.41***	32.82***
Line	49	0.71***	0.42***	0.20	0.10***	0.12	6.17**	0.60***	33.73***
Tester	2	0.43***	2.47***	0.58*	0.53***	0.49**	8.80	7.18***	1073.78***
Line*Tester	98	0.11	0.35*	0.13	0.05*	0.10	4.15	0.18	11.12*
Checks	5	0.29	1.14	0.09	0.07	0.13	2.79	0.16	63.51***
Env*Entry	310	0.30	0.43***	0.14	0.07***	0.08	4.70	0.22	10.88**
Env*gen	298	0.30	0.39***	0.14	0.08***	0.08	4.75*	0.21	10.88**
Env*Line	98	0.69	0.41*	0.17	0.10***	0.10	5.30*	0.24	10.73
Env*Tester	4	0.48	2.22*	0.69*	0.44***	0.13	1.31	0.28	36.64**
Env*Line*Tester	196	0.11	0.35*	0.12	0.05*	0.07	4.54	0.19	10.43*
Env*checks	10	0.12	1.14	0.09	0.03	0.03	1.33	0.14	9.38**
Error	445	0.13	0.35	0.18	0.04	0.09	3.86	0.20	8.47

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

GY-grain yield (t/ha), AD-anthesis date, ASI-anthesis-silking interval, RL-root lodging SL-stalk lodging, EPP-ears per plant, HC-husk cover, GLS-gray leaf spot (*Cercospora zea-maydis*), MSV-maize streak virus, PS-rust (*Puccinia sorghi*), ET-*Exserohilum turcicum*, ER-ear rot, EA-ear aspect, SD-silking date,

Combined ANOVA across sites indicated significant differences ( $P < 0.05$ ) among early QPM hybrids (genotypes) for all traits except root lodging (RL), stalk lodging (SL) and ear rot (Table 4.3). The early QPM inbred lines were highly significant ( $P < 0.001$ ) for all traits except for root lodging, stalk lodging and ear rot (ER). Similar results were recorded for testers. Line by tester interactions were significant ( $P < 0.05$ ) for grain yield, anthesis date (AD), anthesis silking interval (ASI) and highly significant ( $P < 0.001$ ) for ears per plant (EPP) (Table 4.3). Checks were significant ( $P < 0.05$ ) for grain yield, anthesis date, husk cover (HC) and highly significant ( $P < 0.001$ ) for silking date. Entries (hybrids plus checks) were significant for all traits except root lodging; stalk lodging, ears per plant, husk cover and ear rot (Table 4.3). Environment by entry interactions were significant for grain yield, ASI and ear aspect. Similarly, genotype (hybrids) by environment interactions were highly significant ( $P < 0.001$ ) for grain yield, ASI, EPP, husk cover and significant ( $P < 0.05$ ) for ear rot and ear aspect (EA). Environment by line interactions were highly significant ( $P < 0.001$ ) for all traits except anthesis date, root lodging and stalk lodging whereas environment by tester interactions were significant ( $P < 0.05$ ) for all traits except for ASI, root lodging and stalk lodging. The interaction of environment by line by tester (Environment\*Line\*Tester) was significant for EPP whereas environment by checks interaction was not significant for all traits (Table 4.3).

**Table 4. 3 Mean squares for grain yield and other secondary traits among early quality protein maize hybrids across sites (drought and non drought)**

Source	df	GY	AD	ASI	SD	RL	SL	EPP	HC	ER	EA
Env	3	5288.98***	11995.01***	1647.50***	15981.36***	0.18	978.81***	17.58***	11044.64***	26.91***	67.32***
REP(Env)	4	26.45***	55.62***	84.80***	291.23***	3.08	148.99***	0.46***	174.70**	9.01*	4.83***
Entry	155	5.39***	53.61***	10.66***	29.54***	1.46	11.02	0.03	165.36	4.49	0.50***
Genotype	149	5.33***	46.01***	10.87***	20.66**	1.48	10.18	0.03***	162.22***	4.59	0.52***
Line	49	4.51***	40.39***	15.95***	30.60***	1.72	11.51	0.04***	308.68***	5.22	0.87***
Tester	2	184.97***	1979.29***	149.89***	189.81***	2.68	14.39	0.02	1636.23***	6.18	4.71***
Line*Tester	98	2.07*	9.37*	5.38*	11.85	1.34	9.43	0.02***	59.12	4.22	0.26
Checks	6	6.19*	84.28*	7.07	109.45***	1.11	29.22	0.01	173.32*	0.18	1.93
Env*entry	465	2.50***	7.44	5.22***	16.72	1.81	11.64	0.03	80.24	4.37	0.35**
ENV*gen	447	2.44***	7.54	5.14**	16.90	1.82	11.05	0.03***	80.92***	4.50*	0.35*
ENV*Line	147	2.85***	7.81	6.78***	22.39***	1.92	11.64	0.04***	128.52***	4.95*	0.42**
ENV*Tester	6	35.29***	29.35***	2.17	137.17***	2.60	27.01*	0.08***	520.58***	4.88	1.43***
ENV*Line*Tester	294	1.57	6.96	4.26	11.51	1.76	10.42	0.02*	48.12	4.26	0.29
ENV*Checks	15	2.36	4.12	4.77	9.48	1.55	20.78	0.02	63.60	0.29	1.01
Error	583	1.48	7.30	4.08	15.12	1.83	10.20	0.02	51.41	3.84	0.29

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

GY-grain yield (t/ha), AD-anthesis date, ASI-anthesis-silking interval, SD-silking date, RL-root lodging SL-stalk lodging, EPP-ears per plant, HC-husk cover, ER-ear rot, EA-ear aspect,



### 4.3.2 Contribution of Lines, Testers and their Interaction to total Variance

Estimates of the contribution of the lines, testers and their interactions to total variance indicated that line by tester interactions had a high contribution for grain yield variance under drought to a tune of 53.4 % (Table 4.4). The early QPM inbred lines and the testers had a contribution of 44.7 % and 2.0 % respectively suggesting that variability observed for grain was largely due to the inbred lines and their interaction with the tester (Table 4.4). Contribution of testers was minimal for all secondary traits except anthesis date (AD) where contribution of the tester was similar to the female parents. The results under drought condition suggest that perhaps a breeding program should focus on improving the inbred lines (female parents) to obtain meaningful gain to selection under drought condition. However, to improve on maturity, the program should aim to improve both the early QPM inbred lines and the testers.

Under non drought experiment, the tester had a high contribution to hybrid variance (56.0 %) for grain yield whereas the inbred line and the inbred line by tester interactions recorded 23.25 % and 20.76 % respectively (Table 4.4). Similar results were recorded for anthesis date and silking date. Inbred line by tester interactions had a high contribution to hybrid variance for root lodging (RL), stalk lodging (SL), ears per plant (EPP), ear rot (ER), rust (PS-*Puccinia sorghi*), turcicum blight (ET-*Exserelohilum turcicum*), maize streak virus (MSV) disease and plant aspect (PA). The early QPM inbred lines recorded high contribution to hybrid variance for husk cover (HC), ear aspect (EA) and gray leaf spot (GLS) (*Cercospora zae-maydis*) (Table 4.4).

Across sites (drought and non drought), testers had high contribution to hybrid variance for grain yield and anthesis date. The early QPM inbred lines recorded a high contribution for husk cover, ASI, ear aspect and ear rot. The line by tester interactions was

important for root lodging; stem lodging, ears per plant and silking date. Across all sites, high contribution to hybrid variance for grain yield was due to testers and the results of across site may be attributed to many sites used for non drought conditions as compared to drought experiment. The contribution of the early QPM inbred lines and the line by tester interactions were 27.9 % and 25.5 % respectively.

The results under drought indicate that grain yield, root lodging, stalk lodging, ears per plant, husk cover, ear rot and ear aspect are not dependent on any single parent but on the interaction of genes from both parents controlling the traits. It is evident that there is a need to further improve both parents (inbred lines and tester) if higher yield levels are to be attained under well watered conditions. This is because both parents influence the variances of most of the traits evaluated across non drought conditions. Similar results have been reported by Ordonez *et al.* (2005).

**Table 4. 4 Contribution (in percentage) of Lines, Testers and their Interaction to hybrid variance**

Trait	non drought			drought			Across sites		
	Line(L)	Tester(T)	LxT	Line(L)	Tester(T)	LxT	Line(L)	Tester(T)	LxT
GY	23.3	56.0	20.8	44.7	2.0	53.4	27.9	46.6	25.5
AD	26.7	56.8	16.5	39.4	37.0	23.6	28.9	57.7	13.4
RL	36.6	0.2	63.2	30.0	4.6	65.4	38.1	2.4	59.5
SL	35.5	3.0	61.5	32.7	1.9	65.4	37.2	1.9	60.9
EPP	41.3	5.5	53.3	47.3	2.7	50.0	46.7	0.9	52.5
HC	65.2	14.1	20.7	39.0	0.6	60.4	62.5	13.5	23.9
ASI	36.7	29.2	34.1	51.0	3.1	45.9	48.6	18.6	32.8
EA	48.4	23.5	28.1	47.1	2.1	50.8	55.2	12.2	32.6
SD	33.8	43.9	22.3	57.5	9.4	33.1	37.5	1.8	60.7
ER	41.6	2.4	56.0	27.8	0.8	71.3	49.3	12.5	38.2
GLS	74.5	1.9	23.6	-	-	-	-	-	-
PS	44.2	9.8	46.1	-	-	-	-	-	-
ET	41.1	5.0	54.0	-	-	-	-	-	-
MSV	34.7	8.3	57.0	-	-	-	-	-	-
PA	35.2	6.0	58.8	-	-	-	-	-	-

GY-grain yield (t/ha), AD-anthesis date, RL-root lodging SL-stalk lodging, EPP-ears per plant, HC-husk cover, ASI-anthesis-silking interval, EA-ear aspect , SD-silking date, ER-ear rot, GLS-gray leaf spot, PS-*Puccinia sorghi*, ET-*Exserelohilum turcicum*, MSV-maize streak virus, PA-plant aspect, dash (-) indicate traits recorded only under non drought experiment

### 4.3.3 Performance *per se* of early quality protein maize Inbred lines and Hybrids

The average grain yield under non drought environment was 8.0 t/ha with a range of 5.6 t/ha to 10.7 t/ha (Table 4.5) whereas the average grain yield under managed drought stress was 2.1 t/ha with a range of 0.3 t/ha to 5.0 t/ha (Table 4.6). The trial mean of 2.1 t/ha under drought was 20.4% of the trial mean under non drought condition. This level of stress has been classified as intermediate stress (Bänziger *et al.*, 2000) and falls within the stipulated limits recommended by Bolanos and Edmeades (1996) who indicated that the average grain yield under abiotic stress has to be between 20% and 30% of the average grain yield under optimal conditions. Similar results have been reported by Campos *et al.* (2004).

Drought increased days to 50% anthesis (AD) and silking (SD) by 5 days and 9 days respectively (Table 4.6). Consequently, the anthesis silking interval (ASI) was increased by drought from 1 day to 6 days suggesting that hybrid had a longer growing cycle under drought as compared to non drought conditions. An opposite trend was reported by Zaidi *et al.* (2004). Short ASI under drought stress has been associated with partitioning of assimilates to the developing ears at the reproductive phase (Edmeades *et al.*, 1993) and this could explain why hybrids with short ASI had high grain yield. Ears per plant (EPP) which is strongly correlated with grain yields under drought (Betran *et al.*, 2003) were 1.0 and 0.6 under non drought (Table 4.5) and drought condition (Table 4.6) respectively. Root lodging, stalk lodging and ear rot were similar under both drought and non drought condition. The average ears aspect score was 2.7 (Table 4.5) and 3.2 (Table 4.6) under non drought and drought conditions respectively. This is expected because under drought condition there is reduction in size of the ears and an increase in the number of barren ears. Husk cover problem seems to be more pronounced under non

drought condition (13.9%) as compared to drought condition (2.6%) and perhaps this could be attributed to the ability of hybrids to fully fill their ears as there is less competition for photoassimilate flux to the developing ears.

The average grain yield for checks under non drought conditions was 8.97 t/ha with a range of 7.1 t/ha to 10.7 t/ha (Table 4.5). Under drought conditions grain yield for checks ranged from 0.7 t/ha to 2 t/ha with an average yield of 1.4 t/ha (Table 4.6). The best check under non drought condition yielded poorly under drought conditions. Conversely, the least yielding check under non drought condition was the best under drought conditions. This inconsistency in performance among the experimental checks clearly indicates lack of drought tolerance traits and perhaps lack of quantitative trait loci (QTLs) that are linked to drought tolerance. Therefore some experimental hybrids used in this study would perform better under both drought and non drought condition.

**Table 4.5 Performance of best 20 early quality protein maize hybrids across non drought conditions**

Gen.	Line	Tester	GY	AD	SD	ASI	EPP	RL	SL	HC	ER	EA	GLS	PS	ET	MSV
12	15	3	10.1	60.0	60.3	1.0	0.9	0.0	0.0	18.4	0.0	1.9	1.9	1.9	2.1	0.5
97	43	1	9.9	66.0	65.7	0.0	1.1	1.3	2.4	11.4	0.0	2.3	2.1	1.8	1.8	0.5
93	45	1	9.9	67.0	66.2	-1.0	1.1	2.5	1.3	8.8	0.7	2.2	1.5	1.5	2.1	1.3
52	28	1	9.9	65.0	64.5	0.0	1.1	0.0	1.2	14.3	2.8	2.8	2.1	1.8	1.9	0.5
5	13	3	9.8	63.0	64.7	2.0	1.0	0.0	0.0	7.6	0.8	2.3	1.6	1.4	2.1	0.5
58	44	1	9.6	67.0	66.0	-1.0	1.1	0.0	2.5	4.2	0.0	2.3	1.8	1.6	2.0	0.8
3	38	3	9.6	63.0	64.7	2.0	1.0	0.0	1.2	11.6	2.7	2.3	1.4	1.6	2.1	0.5
8	44	3	9.6	59.0	62.2	3.0	1.1	0.0	0.0	6.7	0.0	2.2	2.1	1.6	2.1	0.5
66	46	1	9.6	67.0	66.3	-1.0	1.1	0.0	2.4	20.9	0.0	2.3	1.4	1.6	1.9	1.3
81	7	1	9.6	66.0	64.2	-1.0	1.1	0.0	2.6	22.7	0.0	2.4	2.0	1.6	1.9	0.9
53	38	1	9.4	67.0	67.8	1.0	1.1	0.0	1.2	18.8	2.3	2.3	1.6	1.8	1.8	1.1
47	43	3	9.4	62.0	64.2	2.0	1.0	0.0	2.4	12.1	2.3	2.5	2.0	1.6	1.8	1.3
10	25	3	9.4	64.0	64.2	0.0	1.0	0.0	1.3	11.8	0.0	2.5	1.8	1.9	2.1	0.5
26	36	3	9.4	61.0	60.8	0.0	1.0	1.2	1.2	11.5	0.7	2.4	1.6	2.0	1.9	0.8
15	40	3	9.3	63.0	62.5	-1.0	1.1	0.0	0.0	10.8	0.0	2.8	1.4	1.6	1.9	0.8
54	6	1	9.3	68.0	69.3	2.0	1.1	0.0	1.3	14.8	0.0	2.3	1.9	1.4	1.9	0.8
64	21	1	9.3	64.0	64.0	0.0	1.0	0.0	6.3	19.4	2.0	2.9	1.8	1.8	1.9	0.5
2	28	3	9.3	61.0	62.3	1.0	1.1	0.0	1.2	12.5	0.7	2.7	2.1	1.8	2.1	0.5
71	30	1	9.2	65.0	65.7	1.0	1.0	0.0	1.3	21.8	0.0	2.5	1.6	1.6	2.0	1.3
70	29	1	9.2	63.0	63.7	0.0	1.1	0.0	0.0	14.0	0.0	2.5	2.0	1.6	1.6	0.5
Check 1			10.7	68.0	68.0	0.3	1.1	0.0	1.2	21.8	0.0	2.5	2.1	1.5	1.8	1.8
Check 2			8.4	70.0	69.0	-1.2	1.0	0.0	6.4	7.7	0.9	2.8	1.5	1.6	2.1	0.5
Check 3			8.9	71.0	71.0	0.7	1.1	1.2	2.5	6.5	0.0	2.7	1.4	1.6	1.9	1.3
Check 4			10.1	70.0	70.0	0.2	1.1	0.0	7.5	5.0	0.0	2.5	1.6	1.6	2.0	1.5
Check 5			8.6	67.0	68.0	1.3	1.1	0.0	3.7	5.2	0.0	2.8	1.8	1.9	1.9	0.8
Check 6			7.1	62.0	62.0	0.3	1.0	1.3	0.0	12.9	1.6	2.8	1.5	1.8	2.1	0.5
mean			8.0	62.9	63.8	0.9	1.0	0.3	1.8	13.9	0.7	2.7	1.7	1.7	2.0	0.7
Max			10.7	71.0	71.0	4.2	1.2	4.6	9.5	31.7	3.6	3.5	2.4	2.1	2.9	2.0
Min			5.6	56.8	57.2	-1.5	0.8	0.0	0.0	4.2	0.0	1.9	1.4	1.4	1.5	0.5
LSD			1.7	4.1	4.2	1.5	0.1	1.9	5.2	12.3	2.0	0.5	1.0	0.5	0.1	0.1

GY-grain yield (t/ha), AD-anthesis date, SD-silking date, ASI-anthesis-silking interval, EPP-ears per plant, RL-root lodging SL-stalk lodging, HC-husk cover, ER-ear rot, EA-ear aspect, GLS gray leaf spot, PS-rust (*Puccinia sorghi*), ET-turcicum blight (*Exserelohilum turcicum*), MSV-maize streak virus,

**Table 4. 6 Performance of best 20 early quality protein maize hybrids under managed drought stress environment**

Gen.	Line	tester	GY	AD	SD	ASI	EPP	RL	SL	HC	ER	EA
12	15	3	5.0	65.0	68.0	3.0	0.9	0.0	0.0	5.3	0.0	1.8
11	4	3	4.9	66.5	67.5	1.0	1.0	0.0	0.0	5.8	0.0	1.5
35	22	3	4.3	65.5	66.5	1.0	1.0	2.8	0.0	2.8	0.0	2.0
5	13	3	4.3	66.0	70.5	4.5	0.8	0.0	0.0	2.7	3.6	2.8
135	22	2	4.1	64.5	65.5	1.0	1.0	0.0	5.3	8.2	0.0	2.3
121	30	2	4.0	63.0	64.5	1.5	1.0	2.8	0.0	5.8	0.0	2.5
10	25	3	3.9	67.5	71.0	3.5	0.7	0.0	0.0	0.0	0.0	2.5
90	16	1	3.9	68.0	73.5	5.5	0.8	0.0	0.0	5.5	0.0	2.5
103	38	2	3.8	65.5	69.0	3.5	0.9	0.0	0.0	0.0	0.0	2.5
94	39	1	3.8	68.0	70.0	2.0	0.8	0.0	10.5	7.9	0.0	2.3
52	28	1	3.8	67.5	70.5	3.0	0.7	0.0	2.8	0.0	0.0	3.0
64	21	1	3.7	67.5	71.0	3.5	0.8	0.0	0.0	2.7	0.0	2.5
122	31	2	3.6	65.0	67.0	2.0	0.9	0.0	5.3	0.0	0.0	2.5
106	9	2	3.6	64.0	69.0	5.0	0.8	0.0	0.0	0.0	0.0	2.3
17	50	3	3.6	68.5	72.5	4.0	0.8	0.0	0.0	0.0	0.0	2.3
76	36	1	3.5	68.0	70.5	2.5	0.8	0.0	0.0	5.3	0.0	2.8
29	2	3	3.5	63.5	69.5	6.0	0.8	0.0	0.0	13.8	0.0	2.5
81	7	1	3.5	67.5	73.0	5.5	0.6	0.0	0.0	2.7	0.0	2.5
112	15	2	3.5	64.5	67.5	3.0	0.8	0.0	2.8	5.6	3.0	2.5
33	11	3	3.4	66.0	71.0	5.0	0.7	2.7	0.0	5.6	0.0	2.3
Check 1			0.7	75.0	81.0	6.0	0.3	0.0	0.0	0.0	0.0	4.3
Check 2			1.4	73.5	81.0	7.5	0.4	0.0	0.0	0.0	0.0	3.5
Check 3			1.0	75.0	86.5	11.5	0.3	0.0	0.0	2.7	0.0	3.5
Check 4			1.1	73.0	80.0	7.0	0.5	0.0	2.7	2.7	0.0	3.5
Check 5			2.0	71.0	76.5	7.1	0.4	0.0	0.0	0.0	0.0	3.5
Check 6			2.0	66.5	70.5	4.0	0.6	0.0	0.0	0.0	0.0	2.8
mean			2.1	67.8	73.2	5.7	0.6	0.3	0.5	2.6	0.5	3.2
MAX			5.0	75.0	86.5	13.5	1.0	3.0	10.5	29.4	10.0	4.5
MIN			0.3	56.5	61.5	1.0	0.2	0.0	0.0	0.0	0.0	1.5
LSD (0.05)			2.1	4.9	4.2	4.9	0.4	2.5	3.2	11.2	3.7	1.5

GY-grain yield (t/ha), AD-anthesis date, SD-silking date, ASI-anthesis-silking interval, EPP-ears per plant, RL-root lodging, SL-stalk lodging, HC-husk cover, ER-ear rot, EA-ear aspect, MIN-minimum value recorded in the experiment, MAX-maximum value recorded in the experiment

Average grain yields across sites (drought and non drought) was 6.5 t/ha with a range of 4.7 t/ha to 8.8 t/ha (Table 4.7). The best hybrid across sites was genotype 12 (L15 x T3) with grain yield of 8.8t/ha (Table 4.7). Tester 1(CML 144 xCML159) and tester 3 (Susuma) dominated the best hybrids used in this study (Table 4.7). The least yielding hybrid involved tester 2 (ECA-QPOPE) indicating that the early QPM inbred lines expressed high heterosis when crossed to tester 1 and tester 3 as compared to tester 2. Among the best 20 hybrids across sites, 11 hybrids involved early QPM inbred lines crossed to tester 3 while 9 hybrids involved early QPM inbred lines crossed to tester 1(Table 4.7). Prolificacy was on average one ear per plant (Table 4.7) and ear aspect scores ranged from 1.9 to 3.3 (Table 4.7). The best hybrid (genotype 12) had the least ear aspect scores indicating that the cobs for this hybrid were well filled, uniform and large with a flint or semi flint texture (Table 4.7). Anthesis silking interval ranged from -0.9 to 5.4 with majority of high yielding hybrids recording short ASI (Table 4.7). Average anthesis date was 64 days with a range of 58 days to 69 days (Table 4.7) whereas average silking date was 66 days with a range of 58 days to 70 days (Table 4.7). The average ASI was 2 days. Checks varied in performance with the best check (genotype 151) yielding 8.2 t/ha of grain yield, which is lower than the best hybrids used in this study (Table 4.7).

**Table 4. 7 Performance of the best 20 early quality protein maize hybrids across sites (Drought and non drought)**

Gen	Line	Tester	GY	AD	SD	ASI	EPP	ER	EA	RL	SL	HC
12	15	3	8.8	61.1	64.8	1.1	0.9	0.0	1.9	0.0	0.0	15.1
5	13	3	8.4	63.6	66.1	2.5	1.0	1.5	2.4	0.0	0.0	6.4
52	28	1	8.3	65.3	62.5	0.8	1.0	2.1	2.8	0.0	1.7	10.7
81	7	1	8.0	66.0	66.0	0.4	1.0	0.0	2.4	0.0	1.8	17.7
10	25	3	8.0	65.0	66.9	0.9	0.9	0.0	2.5	0.0	0.8	8.8
8	44	3	8.0	60.6	65.0	3.5	1.0	0.0	2.3	0.0	0.0	6.5
93	45	1	7.9	67.8	65.5	0.8	1.0	0.5	2.4	1.7	0.8	8.1
64	21	1	7.9	64.9	66.8	0.9	1.0	1.5	2.8	0.0	4.2	15.2
66	46	1	7.9	68.3	67.4	0.6	1.0	0.0	2.3	0.0	2.5	17.1
15	40	3	7.8	63.8	65.1	0.6	1.0	0.0	2.7	0.9	0.0	8.8
11	4	3	7.8	63.1	63.9	0.3	1.0	0.6	2.1	0.0	0.0	9.8
3	38	3	7.8	63.6	65.4	2.8	0.9	2.0	2.4	0.9	1.6	8.7
26	36	3	7.8	62.3	66.8	0.8	0.9	0.5	2.6	0.8	0.8	8.6
97	43	1	7.7	67.1	66.6	2.4	0.9	0.0	2.8	0.8	1.6	8.6
39	14	3	7.7	65.1	69.6	3.5	0.9	1.2	2.6	0.8	0.0	9.2
58	44	1	7.6	68.6	65.7	0.9	0.9	0.0	2.7	0.0	1.7	3.2
47	43	3	7.5	63.5	67.4	3.9	0.9	1.8	2.7	0.0	1.6	9.1
33	11	3	7.5	63.5	67.5	3.0	0.9	1.2	3.2	0.9	1.6	9.3
53	38	1	7.5	67.8	65.6	2.8	0.9	1.8	2.6	0.0	0.8	14.1
76	36	1	7.4	65.4	63.3	0.5	0.9	0.0	2.6	0.0	1.7	12.4
Check 1			8.2	69.4	71.1	1.8	0.9	0.0	2.9	0.0	0.8	16.4
Check 2			6.7	70.8	71.8	1.0	0.9	0.7	3.0	0.0	4.3	5.8
Check 3			6.9	71.8	75.1	3.4	0.9	0.0	2.9	0.8	1.7	5.5
Check 4			7.9	70.5	72.4	1.9	1.0	0.0	2.8	0.0	5.9	4.4
Check 5			7.0	67.6	70.0	2.8	0.9	0.0	3.0	0.0	2.5	3.9
Check 6			5.8	62.8	64.0	1.3	0.9	1.2	2.8	0.9	0.0	9.6
Mean			6.5	64.1	66.2	2.1	0.9	0.6	2.8	0.3	1.4	11.1
MAX			8.8	69.1	70.0	5.4	1.1	3.3	3.3	3.0	6.4	26.6
MIN			4.7	58.0	57.6	-0.9	0.7	-0.1	1.9	0.0	0.0	3.2
LSD (0.05)			1.2	2.6	8.6	1.1	0.2	1.9	0.6	1.5	3.7	7.0

GY-grain yield (t/ha), AD-anthesis date, SD-silking date, ASI-anthesis-silking interval, EPP-ears per plant, ER-ear rot, EA-ear aspect, RL-root lodging, SL-stalk lodging, HC-husk cover,



The average grain yield for inbred line under drought was 1.7 t/ha with a range of 0.0 t/ha to 3.2 t/ha (Table 4.8). Under non drought condition the average grain yield was 3.9 t/ha with a range of 1.8 t/ha to 6.5 t/ha (Table 4.9). Superior early QPM inbred line under drought stress condition (inbred line 38) was also the best under non drought condition indicating clearly the genotypic strength of the inbred line. On average inbred lines flowered 2 days earlier under non drought as compared to drought conditions. However, an opposite trend was observed for ASI where it increased from 1.0 under non drought condition to 2.3 days under drought conditions. Prolificacy as indicated by ears per plant was 0.8 (Table 4.8) and 1.0 (Table 4.9) under drought and non drought respectively. Root lodging, stalk lodging, husk cover and ear rot were slightly higher under non drought (Table 4.9) compared to drought condition (Table 4.9). Ear aspect was similar under both drought and non drought conditions. Among the best twenty early QPM inbred lines under managed drought, eleven inbred lines produced superior hybrid under managed drought stress conditions indicating their consistency for drought tolerance. These inbred lines included line number 2, 4, 7, 11, 13, 15, 21, 22, 31, 36, 38 and 50 (Table 4.8). This consistency confirms earlier reports by Bänziger *et al.* (1999) that selection of inbred lines for tolerance to drought increases the gain in selection and the drought tolerance trait can be conferred by the parents to the hybrids.

**Table 4. 8 Performance of the best 20 early quality protein maize inbred lines under managed drought stress**

Gen	Inbred line	GY	AD	SD	ASI	EPP	SL	HC	ER	EA
1	38	3.2	68.0	70.3	2.3	1.0	0.0	3.0	0.0	1.6
19	15	3.1	64.3	65.8	1.4	1.0	8.4	0.0	0.0	1.2
51	2	2.9	63.9	66.3	2.4	1.0	0.0	16.7	3.4	1.1
55	7	2.8	68.3	69.6	1.2	0.8	0.0	8.8	0.0	1.3
68	22	2.7	67.3	68.9	1.6	1.4	3.4	0.0	0.0	2.0
40	36	2.7	67.6	67.2	-0.4	1.1	0.0	0.0	0.0	1.3
37	31	2.7	69.7	70.6	0.9	1.1	0.0	7.2	0.0	2.2
3	13	2.3	68.6	70.7	2.0	1.2	0.0	0.0	0.0	2.7
70	19	2.3	67.9	71.6	3.8	0.9	0.0	13.9	0.0	2.4
61	11	2.3	69.3	70.7	1.4	1.0	0.0	0.0	2.5	2.1
7	44	2.3	72.0	71.7	-0.2	0.9	2.7	0.0	0.0	2.7
28	40	2.2	68.2	69.6	1.3	0.9	0.0	3.0	0.0	2.8
32	50	2.1	70.7	70.7	0.0	1.1	3.2	0.0	3.0	2.8
77	18	2.1	70.3	71.0	0.8	0.8	0.0	0.0	0.0	2.4
38	32	2.1	66.9	72.8	5.9	0.9	0.0	0.0	0.0	2.1
49	1	2.1	68.8	70.8	2.0	0.9	0.0	0.0	7.2	2.5
22	21	2.1	63.2	67.7	4.4	1.0	0.0	11.6	0.0	1.6
83	43	2.0	70.2	73.3	3.1	0.8	0.0	3.4	0.0	2.3
15	4	2.0	75.0	72.1	-2.9	1.0	0.0	0.0	0.0	2.0
74	14	1.9	71.6	72.1	0.5	0.7	0.0	0.0	0.0	2.1
Check 1		0.0	-	-	-	0.1	0.0	0.0	0.0	4.9
Check 2		0.5	78.8	83.7	4.9	0.3	0.0	2.8	0.0	3.8
Mean		1.7	69.1	71.4	2.3	0.8	1.0	3.6	0.7	2.6
MAX		3.6	78.8	83.7	9.1	1.4	25.0	25.3	7.2	4.9
MIN		0.0	60.1	62.6	-2.9	0.1	0.0	0.0	0.0	1.1
LSD (0.05)		1.1	2.9	2.7	3.0	0.4	10.3	11.9	4.3	0.9

Dash indicate a missing value, GY-grain yield (t/ha), AD-anthesis date, SD-silking date, ASI-anthesis-silking interval, EPP-ears per plant, SL-stalk lodging, HC-husk cover, ER-ear rot, EA-ear aspect, MIN-minimum value recorded in the experiment, MAX-maximum value recorded in the experiment

**Table 4. 9 Performance of the best 20 early quality protein maize inbred lines under non drought environment**

Gen	inbred line	GY	AD	SD	EPP	ASI	RL	SL	HC	ER	EA	PA
1	38	6.5	68.8	70.3	0.9	1.5	0.0	2.6	9.5	-0.5	1.5	2.5
83	43	6.2	71.2	71.7	1.0	0.5	0.0	24.3	2.5	8.1	2.2	2.5
61	11	6.0	71.0	70.5	1.0	-0.5	0.0	3.0	17.5	2.4	2.5	2.0
84	47	5.7	74.8	76.3	1.0	1.5	0.0	-0.4	2.4	-0.5	2.0	2.6
82	42	5.5	72.3	71.3	1.2	-1.0	0.0	9.5	0.0	0.0	1.5	2.0
3	13	5.3	72.9	71.9	1.2	-1.0	0.0	9.1	0.0	0.3	1.5	1.7
77	18	5.3	74.3	72.8	1.0	-1.5	0.0	0.3	0.0	0.2	2.8	1.7
70	19	5.2	70.1	70.6	1.1	0.5	0.0	-0.3	23.6	8.0	3.0	2.3
69	23	5.0	66.6	67.6	1.1	1.0	2.4	-0.5	11.2	-0.1	3.0	1.8
51	2	5.0	65.6	65.1	1.1	-0.5	0.0	3.5	2.9	-0.4	2.0	1.3
55	7	4.9	69.2	70.7	1.0	1.5	0.0	7.5	12.1	6.3	2.2	2.0
60	10	4.8	72.9	72.4	1.1	-0.5	0.0	-0.6	12.5	-0.3	2.0	2.3
81	41	4.8	69.4	71.9	0.9	2.5	2.4	-1.1	0.0	-0.4	1.8	2.3
28	40	4.7	70.4	70.4	0.8	0.0	0.0	16.0	2.5	0.0	2.0	2.6
68	22	4.7	67.2	67.2	1.1	0.0	2.8	-0.8	0.0	4.3	3.0	2.0
22	21	4.6	62.8	65.3	1.1	2.5	0.0	-0.8	9.8	2.9	2.0	1.8
37	31	4.5	70.0	69.0	1.0	-1.0	2.8	6.4	0.0	3.4	1.5	1.7
6	8	4.5	69.0	71.5	0.9	2.5	0.0	-0.5	5.1	0.1	2.5	2.4
33	27	4.5	69.7	70.2	0.9	0.5	0.0	0.7	14.3	-0.1	2.7	2.0
19	15	4.4	65.6	69.1	0.9	3.5	0.0	-0.8	7.8	3.1	2.2	1.5
Check 1		3.7	84.2	83.7	1.2	-0.5	0.0	0.0	0.0	2.1	2.3	2.4
Check 2		6.1	85.3	84.3	0.9	-1.0	0.0	0.9	7.5	-0.1	2.5	1.8
Mean		3.9	71.2	71.5	1.0	0.9	0.9	5.4	5.0	2.9	2.6	1.9
Max		6.5	85.3	84.3	1.2	16.5	13.9	52.5	39.6	17.3	3.7	2.6
Min		1.8	52.6	65.1	0.8	-3.5	0.0	-1.5	-0.1	-0.5	1.5	1.0
LSD (0.05)		1.6	5.7	5.3	0.2	5.9	4.8	9.8	10.1	7.6	0.9	0.8

GY-grain yield (t/ha), AD-anthesis date, SD-silking date , EPP-ears per plant, ASI-anthesis-silking interval, RL-root lodging SL-stalk lodging, HC-husk cover, ER-ear rot, EA-ear aspect, PA-plant aspect, MIN-minimum value recorded in the experiment, MAX-maximum value recorded in the experiment

#### 4.3.4 Correlation between grain yield and morpho-physiological traits

Results of correlation between grain yield (GY) and secondary traits under drought are presented in the Table 4.10. Negative and significant ( $P < 0.05$ ) correlations were observed between grain yield (GY) and anthesis date (AD), anthesis silking interval (ASI), silking date (SD) and ear aspect (EA). Correlation between grain yield and anthesis-silking interval was 65% while correlation between grain yield and anthesis date was 46% (Table 4.10). Correlation between grain yield and silking date was 66%. Ears per plant (EPP) were strongly correlated with grain yield ( $r = 0.88$ ). Similar results were reported by Betran *et al.* (2003a) who reported a correlation of 0.86 between ears per plant and grain yield. No significant correlation was observed between grain yield and root lodging (RL) and grain yield and stalk lodging (SL) under managed drought stress. Correlation between ASI and EPP was high and significant ( $r = -0.72$ ). This is consistent with previous studies by Bolanos and Edmeades (1996) who reported a correlation of -0.6.

Betran *et al.* (2003a) reported that variation for ASI was much greater under drought stress than under well-watered conditions. Positive correlations between grain yield and ears per plant (EPP) are expected because grain yield is a dependent variable of EPP. Bolanos and Edmeades (1996) reported a correlation of 0.73 between EPP and grain yield and -0.48 between ASI and grain yield. A greater ASI is related to less assimilate being partitioned to developing ears resulting in slower ear growth, increased kernel abortion and decreased kernel growth (Edmeades *et al.*, 1993). Blum (1988) reported that under stress condition, the heritability of ASI and EPP is maintained or increased and that of grain yield falls due to decrease in genotypic variance and the correlation between grain yield and this two traits increase. This is in agreement with this study which

indicated high correlation between grain yield and EPP and grain yield and ASI. Although the correlation between grain yield and root lodging was positive, it was not significant. The expected direction of correlation is towards negative values. The positive correlation might be attributed to zero value recorded for over 90% of the plots.

Across non drought experiment, grain yield was significantly ( $P < 0.05$ ) correlated with anthesis date (AD), anthesis silking interval (ASI), ears per plant (EPP), ear rot (ER), ear aspect (EA) and silking date (SD) (Table 4.11). Correlation between grain yield and EPP was high and stronger under managed drought experiment (0.88) compared to non drought experiment (0.35) (Table 4.11) Sharma (1995) indicated that at genetic level, negative correlation arises from repulsion linkage of genes controlling the traits involved. Conversely, a positive correlation occurs due to coupling phase of linkage although in both type of correlation pleiotropy may play a role in determining the correlation. Transient genetic correlation may be due to linkage disequilibrium rather than pleiotropy. No correlation ( $r = 0$ ) indicates that genes concerned are located far apart on the same chromosome or they are located on different chromosomes.

The correlation between grain yield and ear aspect (EA) under non drought experiment was high and significant ( $P < 0.05$ ) (Table 4.10). Ear aspect scores indicate how well ears are filled, uniformity of ears, size and texture of ears. The strong correlation between grain yield and ear aspect scores indicates the reliability of the trait in selecting maize hybrids. Correlation between EPP and ASI was negative and significant (Table 4.11). This agrees with previous studies (Bolanos and Edmeades, 1996; Bänziger *et al*, 2000) which indicated that an increase in ASI especially under drought stress results in an increase in bareness hence less EPP. Correlation among secondary traits varied considerably both under drought and non drought conditions. However, strong

correlations were observed under drought as compared to non drought environment (Table 4.11).

Across site analysis revealed significant ( $P < 0.05$ ) correlation between grain yield and ASI (-0.56) (Table 4.12). Similarly, the correlation between grain yield and ear aspect was strong and significant (-0.70). Ears per plant were positively correlated to grain yield. Both anthesis date and silking date were negatively correlated to grain yield although the correlation was weak (-0.10 and -0.29 respectively). The correlation between EPP and ASI was strong and significant (-0.70) (Table 4.12). An increase in ASI leads to an increase in barren ears and poorly filled ears hence low yields (Betran *et al.*, 2003). Root lodging, stalk lodging and ear rot were weakly correlated with grain yield (Table 4.12). Husk cover was positively correlated with grain yield under drought and non drought conditions. Perhaps this correlation between husk cover and grain yield may be attributed to well filled cobs especially under well watered environment where plants have little competition for photo- assimilate flux to the developing ear. Thus selection for high grain yield coupled with low husk cover should be practiced in QPM breeding programme.

**Table 4.10 Correlation matrix between traits under managed drought stress environment**

Trait	GY	AD	ASI	RL	SL	EPP	HC	ER	EA
AD	-0.46***								
ASI	-0.65***	0.27***							
RL	0.11	-0.09	-0.09						
SL	0.18**	-0.16**	-0.13*	-0.07					
EPP	0.88***	-0.49***	-0.72***	0.09	0.17**				
HC	0.28***	-0.09	-0.19**	0.02	-0.01	0.28***			
ER	-0.06	0.02	-0.06	-0.05	0.04	-0.11*	0.04		
EA	-0.83***	0.39***	0.58***	-0.13*	-0.17**	-0.80***	-0.23***	-0.02	
SD	-0.66***	0.76***	0.83***	-0.1	-0.17**	-0.72***	-0.19**	-0.09	0.57***

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

**Table 4. 11 Correlation matrix between traits across non drought environments**

Trait	GY	AD	ASI	RL	SL	EPP	HC	ER	EA
AD	0.19***								
ASI	-0.21***	-0.21***							
RL	0.02	-0.01	-0.01						
SL	-0.06	0.39***	-0.04	0.02					
EPP	0.35***	0.03	-0.11***	0.06	-0.07				
HC	0.05	-0.21	-0.03	-0.05	-0.15***	0.04			
ER	0.07*	0.05	0.04	-0.06	-0.06	0.03	0.04		
EA	-0.74***	-0.11***	0.20***	-0.04	0.06	-0.23***	-0.02	0.03	
SD	0.14***	0.97***	0.04	-0.01	0.39***	0.00	-0.22***	0.06	-0.06*

**Table 4. 12 Correlation matrix between traits across sites (drought and non drought environments)**

Trait	GY	AD	ASI	RL	SL	EPP	HC	ER	EA
AD	-0.10***								
ASI	-0.56***	0.15***							
RL	0.01	-0.02	-0.02						
SL	0.14***	0.28***	-0.15***	0.00					
EPP	0.69***	-0.31***	-0.74***	0.03	0.15***				
HC	0.35***	-0.32***	-0.35***	-0.04	-0.04	0.43***			
ER	0.09**	0.03	-0.04	-0.04	0.01	0.08**	0.07*		
EA	-0.70***	0.09**	0.46***	-0.06*	-0.09**	-0.55***	-0.21***	0.00	
SD	-0.29***	0.91***	0.54***	-0.02348	0.19***	-0.54***	-0.41***	0.01	0.24***

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

GY-grain yield (t/ha), AD- anthesis date, ASI-anthesis silking interval, RL-root lodging, SL- stalk lodging, EPP-ears per plant, HC-husk cover, ER-ear rot, EA-ear aspect

#### 4.3.5 Estimates of General and Specific Combining Ability Effects and Variances

General combining ability of male ( $GCA_m$ ) and general combining ability of female ( $GCA_f$ ) parent varied considerably among the lines and traits.  $GCA_f$  for grain yield under drought ranged from -1.43 to 1.47 t/ha (Table 4.13). Among the 50 early QPM inbred lines used in this study, 24 inbred lines recorded positive  $GCA_f$  for grain yield. Anthesis silking interval which is strongly associated with drought tolerance varied among hybrids. Eighteen early QPM inbred lines with positive  $GCA_f$  for grain yield had a negative  $GCA$  for ASI (Table 4.13). A short ASI is associated with drought tolerance under drought stress. Thus, selection will aim at hybrids with short ASI or inbred lines

with negative GCA for ASI (Bänziger *et al.*, 2000).  $GCA_f$  for AD ranged from -6.05 to 3.28 whereas  $GCA_f$  for SD ranged from -7.35 to 6.32.  $GCA_f$  for EPP ranged from -0.27 to 0.32 (Table 4.13). Both tester 1 (CML 144 x CML 159) and tester 3 (Susuma) recorded a positive  $GCA_m$  for grain yield with considerable variation of  $GCA_m$  for secondary traits (Table 4.13).

Most superior hybrids under drought involved inbred lines with positive  $GCA_f$  for grain yield. The results of this study suggests that additive gene effects were predominant for grain yield and strongly confirms the importance of determining combining ability of germplasm in a breeding programme (Betran *et al.*, 2003). Matching per se performance of an inbred line and GCA is very important as it confirms whether additive or non additive genetic effects are operative (Sharma, 1995). Therefore inbred lines with positive GCA and high grain yield are desired in a breeding programme. In this study, several inbred lines under drought were identified based on per se performance of the inbred line, its GCA and performance in hybrid combination. The hybrids include inbred line 2,4,13,15,22,36 and 40 (Table 4.8)



**Table 4. 13 Estimates of general combining ability effects among early quality protein maize inbred lines under managed drought stress (MDR) environment**

Inbred line	GY	AD	SD	ASI	EPP	EA	ER	RL	SL	HC
1	-0.05	-1.39	-1.69	-0.03	-0.07	0.24	-0.51	-0.29	-0.52	-0.88
2	0.85*	-4.22***	-4.35**	-0.38	0.18*	-0.59*	-0.51	-0.29	1.41*	1.95**
3	-1.19**	1.78*	5.31**	3.28**	-0.18*	0.41	-0.51	-0.29	-0.52	-0.88
4	0.95*	0.95	-3.52*	-4.7***	0.20*	-0.67*	-0.51	-0.29	-0.52	10.02***
5	0.31	-1.39	-1.18	-0.05	-0.02	-0.26	0.67	0.59	-0.52	-1.75**
6	-0.82*	1.95*	3.15*	0.95	-0.18*	0.16	-0.51	0.54	-0.52	-0.86
7	0.55	-0.72	-1.35	-0.88	0.02	-0.42	-0.51	-0.29	-0.52	0.07
8	-0.92*	1.95*	5.48**	3.29**	-0.15	0.58*	0.77	-0.29	0.36	-2.63***
9	0.45	-1.05	-0.18	0.62	0.07	-0.42	-0.51	1.52**	-0.52	-2.63***
10	-0.30	-0.89	-2.18	-1.55	-0.02	0.16	-0.51	-0.29	-0.52	-1.75**
11	0.19	-1.72*	-2.53	-0.70	0.03	-0.42	-0.51	0.59	-0.52	0.12
12	0.20	-1.39	-2.52	-1.38	0.12	-0.26	-0.51	-0.29	-0.52	-1.75**
13	0.95*	0.61	-2.36	-2.53*	0.08	0.16	0.67	-0.29	1.23*	0.02
14	-0.28	1.78*	3.48*	1.45	-0.03	0.16	-0.51	-0.29	0.36	-1.70**
15	1.53***	-1.72*	-3.68*	-2.21*	0.22**	-0.92**	0.47	-0.29	0.41	0.97
16	0.48	-0.22	0.14	2.29*	0.02	-0.52*	2.15*	-0.29	-0.52	0.12
17	-0.94*	3.28*	5.65**	2.12*	-0.23**	0.49	-0.51	-0.29	-0.52	-2.63***
18	0.00	-0.55	0.48	0.79	0.05	-0.26	-0.51	0.64	0.36	-1.75**
19	-0.61	0.61	0.13	0.66	-0.08	0.83**	-0.51	0.69	-0.52	2.84***
20	0.46	-0.39	-1.35	-1.21	0.05	-0.09	0.47	-0.29	-0.52	-2.63***
21	0.46	-1.72*	-2.68	-1.21	0.13	-0.17	2.82**	-0.29	0.36	0.12
22	1.47***	-1.22	-5.52**	-4.55***	0.32***	-0.76**	-0.51	0.64	1.23*	3.67***
23	-0.12	-6.05	-7.35***	-1.55	-0.02	0.16	-0.51	-0.29	1.35*	2.27***
24	-0.59	-0.89	0.65	1.29	-0.07	0.66*	-0.51	0.59	-0.52	4.74***
25	0.45	0.95	0.32	-0.88	0.00	-0.26	-0.51	-0.29	-0.52	-2.63***

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

GY-grain yield (t/ha), AD-anthesis date, SD-silking date, ASI-anthesis silking interval, EPP-ears per plant, EA-ear aspect, ER-ear rot, RL-root lodging, SL-stalk lodging, HC-husk cover

**Table 4.13 Continued: GCA effects among early quality protein maize inbred lines under MDR environment**

Inbred line	GY	AD	SD	ASI	EPP	EA	ER	RL	SL	HC
26	-1.20**	2.28	6.30***	3.99**	-0.23**	0.83**	-0.51	-0.29	0.31	-2.6***
27	-0.38	0.61	-0.86	-0.70	-0.02	0.24	-0.51	-0.29	-0.52	-0.78
28	0.49	-2.22**	-1.18	0.79	0.02	0.33	-0.51	-0.29	2.23***	-2.63***
29	-1.43***	0.45	3.47*	2.97**	-0.27**	0.99***	-0.55	-0.29	-0.52	-0.86
30	-0.04	-1.05	-3.19*	0.12	-0.02	0.06	2.49**	0.64	-0.52	-0.71
31	0.64	0.11	-1.02	-1.38	0.15*	-0.26	-0.51	0.64	1.23*	1.09
32	-0.75*	1.11	4.48**	3.12**	-0.20*	0.16	-0.51	-0.29	-0.52	1.85**
33	-0.43	-1.22	1.48	2.45*	-0.07	0.24	-0.51	-0.29	-0.52	2.69***
34	0.35	-0.39	-2.02	-1.88	0.18*	-0.34	-0.51	-0.29	-0.52	0.30
35	-0.04	1.61	1.65	-0.21	0.02	0.16	0.60	-0.29	-0.52	1.97**
36	1.05**	-0.39	-3.52	-3.38**	0.13	-0.09	1.34	-0.29	-0.52	2.82***
37	-0.28	0.95	0.48	-0.71	-0.05	0.33	-0.51	-0.29	-0.52	-1.75**
38	0.44	-0.05	-0.18	-0.38	0.03	-0.26	-0.51	0.64	0.31	-2.63***
39	-0.16	0.61	-0.69	-1.03	-0.03	-0.17	-0.51	0.59	2.98	1.75**
40	0.74*	-0.89	-2.85	-2.21*	0.17*	-0.17	-0.51	0.64	-0.52	4.55***
41	-0.90*	1.28	4.47**	2.45*	-0.23**	0.40	0.32	-0.29	-0.52	1.09
42	0.03	-0.05	-1.52	-1.71	0.17*	-0.26	2.27*	0.64	1.25*	-0.71
43	-0.09	1.28	1.81	1.45	-0.10	-0.10	2.49**	-0.29	-0.52	-1.75*8
44	0.40	0.95	-1.19	-0.86	0.00	-0.26	-0.51	-0.29	-0.52	2.12**
45	0.34	1.11	0.98	-0.38	0.10	-0.42	-0.51	-0.29	-0.52	0.22
46	-0.55	2.28**	4.47**	2.66*	-0.08	0.24	1.00	-0.29	0.41	1.15
47	-0.46	2.45**	6.32***	3.62**	-0.13	0.16	-0.51	-0.29	0.36	-2.63***
48	-0.67	0.61	-0.52	-1.38	-0.10	0.41	-0.51	-0.29	-0.52	-2.63***
49	-0.63	-0.89	-2.18	-1.55	0.15*	0.16	-0.51	0.64	0.46	-2.63***
50	0.03	1.11	2.65	1.29	0.02	-0.34	-0.51	-0.29	-0.52	-1.75**
Tester1	0.01	0.62	0.71*	0.04	-0.01	-0.01	-0.48	0.2	-0.08	-0.11
Tester2	-0.18	0.47	0.16	-0.13	-0.03	0.1	0.45	-0.29	0.1	-0.42
Tester3	0.17	-1.08**	-0.87*	0.09	0.03	-0.09	0.03	0.09	-0.02	0.54

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

GY-grain yield (t/ha), AD-anthesis date, SD-silking date, ASI-anthesis silking interval, EPP-ears per plant, EA-ear aspect, ER-ear rot, RL-root lodging, SL-stalk lodging, HC-husk cover

$GCA_f$  under non drought condition ranged from -1.05 t/ha to 1.09 t/ha. Inbred line 44 had the highest positive  $GCA_f$  for grain yield (1.09 t/ha) with positive and significant  $GCA_f$  for anthesis date (AD) and Silking date (SD) (Table 4.14). This inbred line had a high grain yield with all three testers under non drought condition. Among 50 early QPM inbred lines used in this study, 21 inbred lines exhibited positive  $GCA_f$  for grain yield under non drought condition (Table 4.14). Tester 1 (CML 144 x 159) showed positive  $GCA_m$  for grain yield whereas tester 3 (Susuma) had negative GCA for grain yield (Table 4.14). Tester 2 (ECA-QPOPE) recorded zero value for GCA. Positive GCA matched with performance per se is an indicator of additive genetic effects while SCA signify predominance of non additive genetic effects (dominance and epistasis). High grain yield under non drought could be explained by long period of photoassimilate flux into the developing ears as indicated by anthesis date and silking date.  $GCA_f$  for ears per plant (EPP) was low and ranged from -0.08 to 0.08 while that of anthesis silking interval (ASI) ranged from -1.60 to 1.23 (Table 4.14).  $GCA_f$  for SD ranged from -3.37 to 2.58. Ear aspect scores range from -0.44 to 0.42.  $GCA_f$  for stalk lodging (SL) and root lodging (RL) varied considerably for most inbred lines (Table 4.14). Most superior hybrids under non drought involved inbred lines with positive  $GCA_f$  for grain yield indicating predominance of additive genetic effects. The best inbred lines under non drought conditions include inbred line 13, 17, 28, 38 and 44.

**Table 4. 14 Estimates of general combining ability effects among early quality protein maize inbred lines across non drought conditions**

Inbred Line	GY	AD	SD	ASI	EPP	EA	ER	RL	SL	HC
1	-0.13	-1.16	-0.76	0.40	0.00	0.06	0.73	0.22	0.26	-4.55
2	-0.95**	-3.27***	-3.37	-0.10	-0.04	0.14	0.04	0.17	-0.09	1.77
3	-0.57	1.45*	0.85	-0.60*	-0.03	0.25*	0.70	-0.25	-0.48	0.22
4	0.30	0.95	-0.65	-1.60***	-0.01	-0.44***	-0.40	-0.25	-1.77*	-1.81
5	-0.22	-2.05**	-1.81**	0.23	0.02	0.08	-0.67	0.15	2.37**	-2.72
6	0.58	2.12**	2.58***	0.46	0.01	-0.22*	-0.67	-0.25	-1.35	7.15
7	-0.02	-0.66	-0.15	0.51	-0.04	0.00	-0.67	0.62*	-0.05	8.50
8	-0.15	1.79**	1.97**	0.18	0.02	-0.06	0.35	-0.25	0.61	1.22
9	0.39	-1.44*	-1.15	0.29	0.02	-0.25*	-0.37	-0.25	0.76	-3.09
10	-0.61	0.29	-0.31	-0.660*	-0.01	0.11	-0.67	-0.25	-0.14	8.65
11	0.00	-0.77	-0.53	0.23	-0.03	0.42***	-0.13	-0.25	1.56	-0.03
12	-0.47	0.18	0.19	0.01	-0.03	0.22*	-0.67	0.15	-0.58	-2.71
13	1.00**	1.68**	1.80**	0.12	0.06*	-0.19	-0.40	-0.25	-1.35	-5.27
14	-0.08	1.06	1.74**	0.68*	-0.03	0.08	1.19*	0.17	0.03	-2.60
15	0.43	-1.49*	-2.09**	-0.60*	0.00	-0.28*	-0.67	-0.25	-1.77*	2.11
16	-0.31	0.68	1.91**	1.23***	0.00	-0.17	0.14	-0.25	-0.54	-2.82
17	0.57	0.62	0.47	-0.15	0.01	0.08	0.20	-0.25	-0.37	-5.08
18	0.20	0.18	0.58	0.40	-0.01	0.14	0.65	1.69***	0.01	-1.76
19	-0.25	0.51	0.97	0.46	0.04	0.11	0.57	0.22	1.89*	8.25
20	-0.54	-1.71**	-0.87	0.85**	0.02	-0.11	0.26	-0.25	1.02	-7.70
21	-0.16	-1.77**	-0.65	1.12***	-0.07**	0.31**	0.28	-0.25	0.71	4.69
22	-0.34	-0.82	-1.37*	-0.54	0.02	0.06	-0.67	-0.25	0.19	-0.01
23	-1.05**	-0.99	-1.37*	-0.38	0.06*	0.22*	-0.67	-0.25	-0.98	-3.14
24	-0.31	-0.82	0.41	1.23***	-0.01	0.03	-0.37	-0.25	-0.58	3.55
25	0.48	1.56**	1.08	-0.49	-0.02	-0.19	-0.67	-0.25	-0.04	0.33
26	-0.33	2.18**	1.63**	-0.54	0.01	0.08	0.91	0.15	-0.54	-5.40

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

GY-grain yield (t/ha), AD-anthesis date, SD-silking date, ASI-anthesis silking interval, EPP-ears per plant, EA-ear aspect, ER-ear rot, RL-root lodging, SL-stalk lodging, HC-husk cover

**Table 4.14 continued: Estimates of GCA effects among early quality protein maize inbred lines across non drought conditions**

Inbred Line	GY	AD	SD	ASI	EPP	EA	ER	RL	SL	HC
27	0.18	-0.16	-0.37	-0.21	-0.04	0.11	-0.11	-0.25	-0.98	10.70
28	0.72*	-1.05	-0.92	0.12	0.04	0.03	0.82	-0.25	-0.55	2.11
29	0.00	-1.21*	-1.03	0.18	0.02	0.14	-0.37	-0.25	-0.49	0.48
30	-0.26	-0.38	-0.42	-0.04	-0.03	0.08	0.52	-0.25	0.83	6.52
31	0.15	-0.27	-0.98	-0.71	0.02	0.17	-0.13	0.15	1.59*	2.95
32	-0.02	0.95	2.08**	1.12***	-0.01	-0.22*	0.14	0.19	-0.93	4.10
33	-0.54	-1.38*	-0.76	0.62*	0.03	0.17	-0.02	1.02**	2.51**	0.83
34	-0.47	-1.16*	-1.09	0.07	-0.01	0.11	-0.10	-0.25	-1.28	-2.03
35	0.19	-2.55***	-3.03***	-0.49	-0.01	0.19	0.04	-0.25	-0.93	7.65
36	0.49	-0.99	-1.76**	-0.77**	-0.05	-0.06	-0.43	0.15	-0.14	0.73
37	-0.10	0.23	0.02	-0.21	0.01	-0.17	-0.68	0.17	1.21	-1.59
38	0.83*	0.68	1.35*	0.68*	-0.03	-0.33**	0.99*	-0.25	-0.97	1.77
39	-0.44	-0.16	-0.26	-0.10	0.01	0.03	-0.21	0.15	0.47	-5.39
40	0.26	0.79	-0.53	-1.32***	0.02	0.08	-0.42	-0.25	0.48	-2.00
41	0.27	0.79	0.91	0.12	-0.03	0.22*	1.03*	-0.25	-1.37	-6.62
42	-0.40	0.01	-0.37	-0.38	0.04	-0.22*	0.13	-0.25	0.30	-1.57
43	0.92*	0.29	0.41	0.12	0.04	-0.11	0.11	0.17	0.65	-1.93
44	1.09**	0.12	0.47	0.35	0.03	-0.31**	-0.39	0.17	-0.10	-6.31
45	0.07	1.68**	1.08	-0.60*	0.08**	0.03	1.42**	0.58*	-1.35	-0.01
46	0.25	1.79**	1.30*	-0.49	-0.02	-0.19	-0.37	-0.25	-0.51	6.70
47	0.61	1.29*	1.80**	0.51	-0.08**	-0.11	-0.10	0.15	3.39***	-3.50
48	-0.32	-0.10	-0.76	-0.65*	0.01	-0.11	0.91	-0.25	-1.37	-1.27
49	-0.55	-0.05	-0.65	-0.60*	0.05*	0.06	-0.45	-0.25	0.31	-3.87
50	-0.33	2.56***	2.40**	-0.15	-0.01	-0.06	-0.67	1.12**	0.42	-6.22
T1	0.42	0.85	0.95	0.10	0.01	-0.05	0.08	-0.12	0.49	-1.49
T2	0.00	0.58	0.14	-0.45	0.00	-0.06	-0.09	0.16	-0.23	-0.11
T3	-0.43	-1.43*	-1.09	0.35	-0.01	0.11	0.01	-0.04	-0.26	1.59

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

GY-grain yield (t/ha), AD-anthesis date, SD-silking date, ASI-anthesis silking interval, EPP-ears per plant, EA-ear aspect, ER-ear rot, RL-root lodging, SL-stalk lodging, HC-husk cover

Table 4.15 shows the GCA effects of early QPM inbred lines across sites (drought and non drought). Positive GCA effects for grain yield were recorded for 23 inbred lines. Inbred line 13 had the highest positive and significant ( $P < 0.001$ ) GCA for grain yield (0.99 t/ha) with positive GCA for EPP and negative GCA for ASI (Table 4.15). A total of 5 inbred lines had positive and significant GCA for grain yield. These include inbred line 13, 15, 28, 38 and 44 (Table 4.15). GCA for EPP ranged from -0.08 to 0.10. GCA for AD ranged from -3.51 to 2.20 whereas GCA for SD ranged from -3.23 to 2.81. GCA for ASI ranged from -2.38 to 1.62 (Table 4.15). General combining ability (GCA) across sites varied considerably among the hybrids. However, hybrids involving inbred lines with positive and significant GCA coupled with high grain yield were identified. The hybrids include genotype 5, 8, 12, 26, 52, 53 and genotype 58. These hybrids recorded high grain yield and high and significant GCA for grain yield. Thus, these entries are potential hybrids for advanced yield testing and consequent release.

**Table 4. 15 Estimates of general combining ability effects among early quality protein maize inbred lines across sites (Drought and non drought)**

Inbred Line	GY	AD	SD	ASI	EPP	EA	ER	RL	SL	HC
1	-0.11	-1.22*	0.02	0.29	-0.02	0.10	0.47	0.22	0.26	-3.61
2	-0.50	-3.51***	-0.49	-0.17	0.01	-0.05	-0.05	0.17	-0.09	1.83
3	-0.73*	1.54**	1.68*	0.37	-0.07*	0.28*	0.44	-0.25	-0.48	-0.04
4	0.46	0.95	-1.62*	-2.38***	0.04	-0.51**	-0.38	-0.25	-1.77*	1.16
5	-0.09	-1.88**	-1.95*	0.16	0.01	-0.01	-0.29	0.15	2.37**	-2.46
6	0.23	2.08**	0.97	0.58	-0.04	-0.13	-0.58	-0.25	-1.35	5.16*
7	0.12	-0.67	0.01	0.16	-0.03	-0.11	-0.58	0.62*	-0.05	6.41**
8	-0.34	1.83**	1.30	0.95	-0.03	0.10	0.50	-0.25	0.61	0.27
9	0.41	-1.34	0.22	0.37	0.03	-0.30*	-0.36	-0.25	0.76	-2.96
10	-0.53	-0.01	0.34	-0.84	-0.01	0.12	-0.58	-0.25	-0.14	6.06*
11	0.05	-1.01	0.60	0.00	-0.02	0.20	-0.18	-0.25	1.56*	0.02
12	-0.30	-0.21	0.30	-0.34	0.01	0.10	-0.58	0.15	-0.58	-2.46
13	0.99**	1.41*	-0.48	-0.54	0.06*	-0.11	-0.09	-0.25	-1.35	-3.93
14	-0.13	1.24	1.22	0.87	-0.03	0.10	0.81	0.17	0.03	-2.36
15	0.70*	-1.55**	-1.24	-1.01	0.05	-0.45**	-0.34	-0.25	-1.77*	1.84
16	-0.12	0.45	0.05	1.49**	0.00	-0.15	0.02	-0.25	-0.54	-2.07
17	0.19	1.29*	1.43	0.41	-0.05	0.18	0.07	-0.25	-0.37	-4.45
18	0.15	-0.01	-0.57	0.49	0.01	0.03	0.41	1.68***	0.01	-1.74
19	-0.33	0.53	0.57	0.50	0.01	0.28*	0.35	0.22	1.89*	6.91**
20	-0.29	-1.38*	-0.03	0.33	0.02	-0.11	0.36	-0.25	1.02	-6.42**
21	0.00	-1.76**	0.18	0.53	-0.02	0.18	0.96	-0.25	0.71	3.56
22	0.11	-0.92	-0.78	-1.55**	0.10*	-0.15	-0.58	-0.25	0.19	0.92
23	-0.82*	-2.26**	-1.99	-0.67	0.04	0.20	-0.58	-0.25	-0.98	-1.77
24	-0.37	-0.84	0.80	1.24*	-0.03	0.18	-0.36	-0.25	-0.58	3.86
25	0.47	1.41*	1.01	-0.59	-0.01	-0.22	-0.58	-0.25	-0.04	-0.39

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

GY-grain yield (t/ha), AD-anthesis date, SD-silking date, ASI-anthesis silking interval, EPP-ears per plant, EA-ear aspect, ER-ear rot, RL-root lodging, SL-stalk lodging, HC-husk cover

**Table 4.15 Continued: Estimates of GCA among early quality protein maize inbred lines across sites (Drought and non drought)**

Inbred Line	GY	AD	SD	ASI	EPP	EA	ER	RL	SL	HC
26	-0.55	2.20**	1.73*	0.59	-0.05	0.26*	0.60	0.15	-0.54	-4.69
27	0.04	0.03	-3.23**	-0.33	-0.04	0.14	-0.16	-0.25	-0.98	7.85**
28	0.66*	-1.34	-1.41	0.28	0.03	0.10	0.54	-0.25	-0.55	0.94
29	-0.36	-0.80	0.44	0.87	-0.05	0.35**	-0.38	-0.25	-0.49	0.16
30	-0.21	-0.55	-1.20	-0.01	-0.03	0.12	0.29	-0.25	0.83	4.72*
31	0.27	-0.17	-0.82	-0.88	0.05	0.06	-0.18	0.15	1.59*	2.50
32	-0.20	0.99	0.76	1.62**	-0.06	-0.13	0.03	0.19	-0.93	3.56
33	-0.51	-1.34*	-0.20	1.08*	0.01	0.18	-0.10	1.02**	2.51**	1.31
34	-0.27	-0.96	-0.24	-0.42	0.04	-0.01	-0.15	-0.25	-1.28	-1.44
35	0.13	-1.51**	1.39	-0.42	0.00	0.18	0.23	-0.25	-0.93	6.25**
36	0.63	-0.84	-1.24	-1.42**	0.00	-0.07	0.06	0.15	-0.14	1.26
37	-0.14	0.41	0.43	-0.34	-0.01	-0.05	-0.59	0.17	1.21	-1.61
38	0.73*	0.49	-0.99	0.41	-0.01	-0.32*	0.66	-0.25	-0.97	0.69
39	-0.37	0.03	-0.56	-0.33	0.00	-0.03	-0.24	0.15	0.47	-3.59
40	0.38	0.37	-0.70	-1.55**	0.05	0.01	-0.39	-0.25	0.48	-0.34
41	-0.02	0.91	2.81**	0.92	-0.08	0.33*	0.69	-0.25	-1.37	-5.39*
42	-0.29	-0.01	0.76	-0.72	0.07*	-0.24	0.71	-0.25	0.30	-1.34
43	0.67*	0.53	0.09	0.45	0.00	-0.05	0.00	0.17	0.65	-1.87
44	0.92**	0.33	-0.90	0.04	0.02	-0.31	-0.37	0.17	-0.10	-4.19
45	0.14	1.54**	0.14	-0.55	0.08*	-0.09	0.98*	0.58*	-1.35	0.06
46	0.05	1.91**	0.98	0.29	-0.04	-0.09	0.02	-0.25	-0.51	5.33*
47	0.34	1.58**	1.01	1.28*	-0.10	-0.05	-0.15	0.15	3.39***	-3.26
48	-0.42	0.08	-0.66	-0.84	-0.02	0.01	0.60	-0.25	-1.37	-1.59
49	-0.57	-0.26	-1.41	-0.84	0.07*	0.08	-0.41	-0.25	0.31	-3.54
50	-0.24	2.20**	1.47	0.20	0.00	-0.13	-0.58	1.12***	0.42	-5.09*
T1	0.42	0.85	0.95	0.10	0.01	-0.05	0.08	-0.12	0.49	-1.49
T2	0.00	0.58	0.14	-0.45	0.00	-0.06	-0.09	0.16	-0.23	-0.11
T3	-0.43	-1.43*	-1.09	0.35	-0.01	0.11	0.01	-0.04	-0.26	1.59

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

GY-grain yield (t/ha), AD-anthesis date, SD-silking date, ASI-anthesis silking interval, EPP-ears per plant, EA-ear aspect, ER-ear rot, RL-root lodging, SL-stalk lodging, HC-husk cover



Specific combining ability (SCA) effects for grain yield varied across lines and testers. Under non drought condition, the best specific combiner recorded SCA of 1.23 t/ha whereas under drought the best specific combiner recorded SCA of 2.00 t/ha (Table 4.16). Previous studies have reported varying results for SCA. Bhatnagar *et al.* (2004) and San Vicente *et al.* (1998) reported that SCA effects for grain yield were highly significant while GCA effects were not significant. Vasal *et al.* (1993) reported predominance of additive genetic effects in CIMMYT's subtropical maize germplasm. Similarly, Beck *et al.* (1991) reported predominance of additive genetic effects in subtropical and temperate intermediate maturity germplasm. Contrasting reports about GCA and SCA may be explained by differences in genetic background of materials used in the studies. In this study however, good specific combiners under non drought environment include genotype 8, 12, 54, 71 and genotype 93 (Table 4.16). These hybrids recorded high and significant ( $P < 0.05$ ) SCA effects for grain yield and high grain yield under non drought conditions. There were significant variations of SCA effects for grain yield under drought environment suggesting that non additive genetic effects were important under managed drought stress conditions. Many combinations had positive and significant SCA effects for grain yield (Table 4.16) and good specific combiners under drought include genotype 5, 11, 12, 15, 35, 52, 105, 109, 112 and entry 121 (Table 4.16). This results contrast with previous findings by Betran *et al.* (2003) who reported that under drought stress condition additive genetic effects are more important than non additive genetic effects. Perhaps this may be attributed to differences in genetic materials used in the study.

**Table 4. 16 Specific combining ability effects for grain yield among the best 20 early quality protein maize hybrids**

managed drought environment					non drought environment					Across drought and non drought				
Gen.	IL	T	SCA	GY	Gen.	IL	T	SCA	GY	Gen.	IL	T	SCA	GY
12	15	3	1.23*	5.0	12	15	3	1.23**	10.1	12	15	3	1.22**	8.8
11	4	3	1.72**	4.9	52	28	1	0.44	9.9	5	13	3	0.58	8.4
29	13	3	1.05	4.3	97	43	1	0.30	9.9	52	28	1	0.66*	8.3
135	22	3	0.57	4.3	93	45	1	1.10**	9.9	81	7	1	0.90*	8.0
126	22	2	0.51	4.1	5	13	3	0.43	9.8	10	25	3	0.65	8.0
121	30	2	1.88***	4.0	8	7	1	0.88*	9.6	8	44	3	0.19	8.0
35	25	3	1.14*	3.9	3	38	3	0.38	9.6	64	21	1	0.91*	7.9
5	16	1	1.44**	3.8	58	44	1	-0.15	9.6	93	45	1	0.79*	7.9
15	28	1	1.34*	3.8	66	44	3	0.06	9.6	66	46	1	0.82*	7.9
109	39	1	2.00***	3.8	81	46	1	0.61	9.6	11	4	3	0.48	7.8
112	38	2	1.20*	3.8	10	25	3	0.50	9.4	3	36	3	0.27	7.8
105	21	1	1.26*	3.6	26	36	3	0.48	9.4	26	38	3	0.17	7.8
94	31	2	0.80	3.6	53	38	1	-0.10	9.4	15	40	3	0.58	7.8
26	7	1	0.99	3.5	47	43	3	0.07	9.4	39	14	3	0.93*	7.7
10	36	1	0.52	3.5	15	6	1	0.06	9.3	97	43	1	0.07	7.7
90	9	2	0.95	3.5	54	21	1	0.80*	9.3	58	44	1	-0.35	7.6
17	2	3	0.35	3.5	2	28	3	0.17	9.3	33	11	3	0.60	7.5
52	50	3	1.23*	3.5	64	40	3	0.68	9.3	53	38	1	-0.26	7.5
86	26	1	-0.43	3.4	70	29	1	0.51	9.2	47	43	3	0.01	7.5
33	15	2	-0.23	3.4	71	30	1	0.80*	9.2	76	36	1	-0.19	7.4

\*\*\* \*\* \* Indicate significance at 0.001, 0.01 and 0.05 respectively

Gen- Genotype, SCA-Specific combining ability, GY-grain yield (t/ha), T-tester, IL-early QPM inbred line

#### 4.4 Conclusion and Recommendations

It is evident from the results of this study that variability exists among early QPM hybrids under drought and non drought environments. This is indicated by variation in performance of hybrids under these environments and differences in combining ability of early QPM inbred lines across drought and non drought environments. Genetic variations are the basis of genetic improvement in any crop. Crossing of diverse early QPM inbred lines provided sufficient variability for an effective selection of desirable traits. Suitable inbred lines and their specific combinations therefore may be selected on the basis of combining ability effects with better mean performance. Early QPM hybrids that performed better under

drought and non drought environments were identified. Promising early QPM hybrids namely genotype 5, 12 and 52 performed better under both drought and non drought conditions and involved early QPM inbred lines with positive general combining ability (GCA) for grain yield. These genotypes are potential hybrids for advanced testing and consequent release.

Owing to unpredictability of drought farmers require maize genotypes that perform better under drought and non drought conditions to mitigate against effects of yield losses due to drought and the risk of hunger. Information on general and specific combining ability is important in designing a breeding program. In this study, several early QPM inbred lines recorded positive and significant GCA for grain yield and therefore they form a potential breeding stock for drought tolerant germplasm. Inbred line 15 was superior under both drought and non drought conditions with positive and significant GCA for grain yield and high grain yield. Other potential early QPM inbred lines identified in this study include inbred line 2, 4, 13, 22, 36 and inbred line 40. The estimates of high general combining ability suggest the importance of additive genetic variance whereas estimates of high specific combining ability suggest the importance of non additive genetic variance. In this study, predominance of additive genetic effects was evident with all traits recording positive additive variance and negative dominance variance. Results of combining ability indicated predominance of additive genetic variance with majority of early QPM inbred lines recording positive GCA for grain yield. However a breeding program that utilizes both additive and dominance genetic variance will be desirable since high yielding early QPM hybrids recorded high and significant SCA indicating predominance of non additive genetic variance.

## CHAPTER FIVE

### 5.0 General Discussion, Conclusions and Recommendations

Results of this study indicates that variability for drought tolerance exists among early Quality Protein maize (QPM) inbred lines and therefore inbred lines with high general combining ability (GCA) can be utilized for future breeding activities. However for future studies, the experiments under drought should be replicated across many sites to minimize the effects of genotype by environment interactions. Most early QPM hybrids performed better than the experimental checks both under drought and well watered environment.

Under drought, high grain yield was associated with high ears per plant (EPP) and short anthesis silking interval (ASI). Genotype 12 (Line<sub>15</sub> x Tester<sub>3</sub>) was superior hybrid both under drought and non drought conditions. This genotype involved early QPM inbred line 15 crossed to tester 3 (Susuma). The GCA for grain yield of inbred line 15 was positive and highly significant and its seed production under drought and non drought conditions was 3.1 t/ha and 4.4 t /ha respectively.

Under drought conditions, the hybrid produced 5.0 t/ha of grain yield whereas under non drought environment the hybrid produced 10.1 t/ha of grain yield. Thus, genotype 12 is a potential hybrid for advanced yield testing and consequent release. Other potential QPM hybrids for advanced yield trial and consequent release include genotype 5, 12, 39, 52, 64, 66, 81 and genotype 93. These hybrids had high grain yield and recorded significant specific combining ability (SCA) across environments. Among the three testers used in this study, tester 3 (Susuma) produced superior hybrids followed by tester 1 (CML 144 x CML 159). Tester 2 (ECA-QPOPE) produced low yielding hybrids. Thus, Susuma act as better testers for production of drought tolerant QPM hybrids. This

may be attributed to the wide genetic background of Susuma and the hybrid vigour of the single cross hybrid (CML 144 x CML 159).

In this study, testers were used as male parents (pollen parents) while early QPM inbred lines were used as female parents. However, for purposes of economic seed production of the superior QPM hybrids, testers should be used as female and inbred lines as male parents. The testers have high hybrid vigour compared to inbred lines. The low hybrid vigour in inbred lines is due to inbreeding depression. The flowering dates of both the testers and the inbred lines should be observed in order to synchronize pollen shed and silk emergence. Hybrids with short days to anthesis may have escaped drought as a result of their earliness whereas hybrids with long days to anthesis require a long growing season. Thus, selection of drought tolerant hybrids should be based on maturity. Inbred line 2, 4, 13, 15, 22, 36 and inbred line 40 recorded high general combining ability (GCA) and per se performance under drought and can be utilized as breeding stock for future breeding of drought tolerant QPM hybrids.

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## CHAPTER SEVEN: APPENDICES

### Appendix 1 Specific combining ability effects for grain yield across non drought stress conditions

Gen	Line	Tester	SCA	GY	Gen	Line	Tester	SCA	GY
12	15	3	1.23**	10.1	69	26	1	0.08	8.8
52	28	1	1.10**	9.9	9	35	3	0.6	8.8
97	43	1	0.44	9.9	76	36	1	0.22	8.8
93	45	1	0.3	9.9	99	48	1	0.38	8.8
5	13	3	0.43	9.8	4	6	3	0.56	8.7
81	7	1	0.61	9.6	63	20	1	-0.27	8.7
3	38	3	0.38	9.6	61	4	1	0.55	8.6
58	44	1	0.88*	9.6	7	8	3	-0.25	8.6
8	44	3	-0.15	9.6	46	24	1	1.06**	8.6
66	46	1	0.06	9.6	18	27	3	0.47	8.6
10	25	3	-0.1	9.4	74	33	1	0.35	8.6
26	36	3	0.07	9.4	59	35	1	-0.41	8.6
53	38	1	0.5	9.4	45	41	3	-0.06	8.6
47	43	3	0.48	9.4	148	47	2	0.05	8.6
54	6	1	0.80*	9.3	51	5	1	0.06	8.5
64	21	1	0.17	9.3	82	10	1	-0.43	8.5
2	28	3	0.68	9.3	40	16	3	0.4	8.5
15	40	3	0.06	9.3	92	18	1	-0.48	8.5
70	29	1	0.80*	9.2	72	37	3	0.4	8.5
71	30	1	0.51	9.2	95	41	1	-0.35	8.5
56	4	2	0.21	9.1	38	1	1	0.21	8.4
39	14	3	-0.02	9.1	1	5	3	0.15	8.4
41	17	3	0.80*	9.1	75	34	1	-0.56	8.4
68	27	1	0.12	9.1	65	40	1	0.31	8.4
91	17	1	-0.14	9.0	80	3	1	-0.74*	8.3
78	24	3	-0.27	9.0	105	13	2	-0.03	8.3
60	34	3	0.44	9.0	48	16	2	0.25	8.3
44	39	3	-0.32	9.0	42	18	3	-0.28	8.3
98	47	1	1.01**	9.0	67	50	1	0.2	8.3
33	11	3	0.34	8.9	17	50	3	0.35	8.3
55	13	1	-0.78	8.9	28	1	3	-0.19	8.2
73	32	1	0.77*	8.9	84	12	1	-0.01	8.2
77	37	1	0.49	8.9	86	23	1	-0.08	8.2
100	49	1	0.21	8.9	122	31	2	0.59	8.2
11	4	3	0.47	8.8	23	32	3	1.10**	8.2
6	9	3	0.01	8.8	108	44	2	0.09	8.2
37	19	3	-0.42	8.8	49	3	2	-0.02	8.1

**Appendix 1 continued: Specific combining ability effects for grain yield across non drought stress conditions**

Gen	Line	Tester	SCA	GY	Gen	Line	Tester	SCA	GY
62	15	1	-1.08**	8.1	94	39	1	-0.15	7.3
87	19	1	-0.31	8.1	131	7	2	-1.15**	7.2
14	21	3	-0.17	8.1	31	7	3	0.27	7.2
27	31	1	-0.3	8.1	133	11	2	0.03	7.2
88	42	3	-0.15	8.1	135	22	2	0.18	7.2
83	11	1	-0.65	8.0	109	35	2	0.59	7.2
89	14	1	-0.43	8.0	107	8	2	-0.6	7.1
90	16	1	-0.36	8.0	36	23	3	0.26	7.1
20	29	2	-0.66	8.0	110	25	2	-0.12	7.1
57	8	1	-0.61	7.9	102	28	2	-0.36	7.1
142	18	2	-0.15	7.9	115	40	2	-0.22	7.1
85	22	1	0.71*	7.9	134	12	2	0.43	6.9
35	22	3	-0.44	7.9	118	27	2	-0.03	6.9
79	2	1	-0.75*	7.8	123	32	2	-0.26	6.9
104	6	2	-0.84*	7.8	125	34	2	0.37	6.9
19	26	3	0.06	7.8	120	29	3	-0.2	6.8
22	31	3	-0.23	7.8	143	45	2	-0.15	6.8
145	41	2	0.55	7.8	139	14	2	-0.15	6.7
16	46	3	0.21	7.8	138	24	2	-0.16	6.7
141	17	2	0.16	7.7	146	42	2	0.08	6.7
96	42	1	-0.63	7.7	127	45	3	0.03	6.7
29	2	3	0.19	7.6	140	47	3	-0.01	6.7
30	3	3	-0.22	7.6	128	1	2	-0.28	6.5
111	9	1	0.33	7.6	101	5	2	-0.17	6.5
13	20	3	-0.27	7.6	121	30	2	-0.35	6.5
43	37	2	-0.90*	7.6	144	39	2	-0.06	6.5
32	10	3	-0.42	7.5	137	19	2	0.02	6.4
34	12	3	0.23	7.5	119	26	2	-0.03	6.4
21	30	3	-0.37	7.5	124	33	2	-0.22	6.4
103	38	2	-0.63	7.5	130	48	3	-0.24	6.4
147	43	2	-0.28	7.5	117	50	2	-0.29	6.4
116	46	2	-0.31	7.5	149	48	2	-0.36	6.3
50	49	3	-0.27	7.5	132	10	2	-0.13	6.2
106	9	2	-0.06	7.4	114	21	2	-0.65	6.2
25	25	1	-0.44	7.4	113	20	2	-0.29	6.1
24	33	3	0.01	7.4	150	49	2	-0.47	6.0
126	36	2	-0.52	7.4	129	2	2	-0.25	5.8
112	15	2	-0.95*	7.3	136	23	2	-0.37	5.6

**Appendix 2 Specific combining ability effects for grain yield under managed drought stress conditions**

Gen	Line	Tester	SCA	GY	Gen	Line	Tester	SCA	GY
12	15	3	1.23*	5.0	147	43	2	-0.22	2.0
11	4	3	1.72**	4.9	101	5	2	-0.52	2.0
35	22	3	1.05	4.3	115	40	2	-0.79	2.0
5	13	3	0.57	4.3	34	12	3	0.32	2.0
135	22	2	0.51	4.1	82	10	1	-0.16	2.0
121	30	2	1.88***	4.0	9	35	3	0.16	2.0
10	25	3	1.14*	3.9	31	7	3	-0.43	1.9
90	16	1	1.44**	3.8	28	1	3	-0.22	1.9
103	38	2	1.34*	3.8	102	28	2	-1.15*	1.9
94	39	1	2.00***	3.8	109	35	2	-0.75	1.9
52	28	1	1.20*	3.8	65	40	1	0.45	1.9
64	21	1	1.26*	3.6	18	27	3	-0.87*	1.9
122	31	2	0.8	3.6	62	15	1	0.54	1.8
106	9	2	0.99	3.5	63	20	1	-0.37	1.8
17	50	3	0.52	3.5	96	42	1	0.22	1.8
76	36	1	0.95	3.5	75	34	1	0.01	1.8
29	2	3	0.35	3.5	113	20	2	-0.16	1.8
81	7	1	1.23*	3.5	74	33	1	-0.13	1.7
112	15	2	-0.43	3.4	23	32	3	0.73	1.7
33	11	3	-0.23	3.4	133	11	2	-0.3	1.7
22	31	3	0.98	3.4	85	22	1	0.42	1.7
36	23	3	0.52	3.4	143	45	2	-0.86*	1.7
92	18	1	1.42**	3.3	61	4	1	0.06	1.7
15	40	3	0.19	3.3	134	12	2	-1.24*	1.6
105	13	2	1.29*	3.3	3	38	3	-0.73	1.6
39	14	3	0.28	3.3	79	2	1	0.35	1.6
8	44	3	0.94*	3.2	114	21	2	-0.08	1.6
129	2	2	0.22	3.2	6	9	3	-0.02	1.5
51	5	1	0.58	3.2	98	47	1	-1.27*	1.5
126	36	2	-0.15	3.0	93	45	1	-0.22	1.4
26	36	3	1.5	2.9	25	25	1	-0.93*	1.4
43	37	2	0.44	2.9	60	34	3	0.47	1.4
127	45	3	1.09	2.9	46	24	1	0.43	1.4
13	20	3	0.36	2.9	88	42	3	0.11	1.4
125	34	2	0.2	2.9	136	23	2	-0.22	1.4
108	44	2	-0.37	2.9	145	41	2	-0.18	1.4
66	46	1	0.33	2.9	47	43	3	-0.34	1.3



**Appendix 2 continued: Specific combining ability effects for grain yield under managed drought stress conditions**

Gen	Line	Tester	SCA	GY	Gen	Line	Tester	SCA	GY
37	19	3	-1.30*	1.3	27	31	1	-0.96*	1.2
48	16	2	0.36	2.8	72	37	3	0.22	1.2
140	47	3	0.8	2.8	117	50	2	-1.32*	1.2
40	16	3	-0.17	2.7	42	18	3	-0.93*	1.2
84	12	1	0.22	2.7	91	17	1	-0.25	1.2
146	42	2	0.99*	2.6	4	6	3	-1.05*	1.2
56	4	2	-0.12	2.6	97	43	1	-0.85*	1.2
111	9	1	-0.07	2.6	83	11	1	-0.75	1.2
131	7	2	0.46	2.6	118	27	2	-0.82*	1.1
149	48	2	0.35	2.6	144	39	2	-0.62	1.1
128	1	2	1.21*	2.6	19	26	3	-0.87*	1.1
14	21	3	0.36	2.6	59	35	1	-0.46	1.1
100	49	1	-1.00*	2.5	150	49	2	-0.01	1.1
124	33	2	0.63	2.5	107	8	2	-0.64	1.0
32	10	3	0.05	2.4	132	10	2	-0.19	1.0
142	18	2	0.09	2.4	123	32	2	-0.84*	1.0
137	19	2	0.45	2.4	44	39	3	-0.59	1.0
38	1	1	-0.25	2.4	99	48	1	-0.39	1.0
78	24	3	-1.09*	2.3	138	24	2	-1.13*	1.0
104	6	2	-0.2	2.3	54	6	1	0.12	0.9
57	8	1	0.86*	2.3	45	41	3	-0.17	0.9
110	25	2	-0.02	2.3	148	47	2	0.16	0.9
67	50	1	-0.05	2.3	20	29	2	-0.80*	0.9
53	38	1	-0.18	2.3	120	29	3	0.03	0.9
55	13	1	0.82*	2.3	24	33	3	-0.97*	0.9
50	49	3	-0.57	2.2	80	3	1	-0.49	0.9
141	17	2	-0.39	2.2	71	30	1	-0.54	0.8
68	27	1	-0.24	2.2	7	8	3	-1.04*	0.8
2	28	3	-0.47	2.2	139	14	2	-1.07*	0.8
89	14	1	0.53	2.1	87	19	1	-0.54	0.8
49	3	2	-0.28	2.1	41	17	3	-0.57	0.8
130	48	3	-0.16	2.1	73	32	1	-0.42	0.7
58	44	1	0.64	2.1	95	41	1	-0.3	0.7
21	30	3	-0.53	2.1	86	23	1	-1.22*	0.6
119	26	2	-0.23	2.1	30	3	3	-0.58	0.5
116	46	2	-0.17	2.0	16	46	3	-1.28*	0.4
77	37	1	-0.65	2.0	70	29	1	-0.58	0.3
1	5	3	0.78	2.0	69	26	1	-0.27	0.3

**Appendix 3 Specific combining ability for Grain yield across sites (drought and non drought environment)**

Gen	Inbred line	tester	SCA	GY	Entry	Inbred line	tester	SCA	GY
12	15	3	1.22**	8.8	122	31	2	1.02**	7.1
5	13	3	0.58	8.4	105	33	1	0.57	7.1
52	28	1	0.66*	8.3	100	49	1	0.71	7.1
81	7	1	0.90*	8.0	17	50	3	0.5	7.1
10	25	3	0.65	8.0	61	4	1	-0.45	7.0
8	44	3	0.19	8.0	82	10	1	0.54	7.0
64	21	1	0.91*	7.9	91	17	1	-0.15	7.0
93	45	1	0.79*	7.9	35	17	3	-0.06	7.0
66	46	1	0.82*	7.9	41	22	3	0.03	7.0
11	4	3	0.48	7.8	44	29	1	0.33	7.0
3	36	3	0.27	7.8	77	37	1	0.17	7.0
26	38	3	0.17	7.8	70	39	3	0.48	7.0
15	40	3	0.58	7.8	46	16	1	0.04	6.9
39	14	3	0.93*	7.7	40	16	3	0.1	6.9
97	43	1	0.07	7.7	73	32	1	0.05	6.9
58	44	1	-0.35	7.6	75	34	1	0.14	6.9
33	11	3	0.6	7.5	65	40	1	-0.45	6.9
53	38	1	-0.26	7.5	90	42	3	0.35	6.9
47	43	3	0.01	7.5	28	1	3	0.04	6.8
76	36	1	-0.19	7.4	4	6	3	-0.27	6.8
56	9	1	-0.12	7.3	59	35	1	-0.39	6.8
60	25	1	-0.17	7.3	108	44	2	0.16	6.8
2	28	3	-0.19	7.3	99	48	1	0.21	6.8
9	35	3	0.25	7.3	7	8	3	0.13	6.7
98	47	1	-0.08	7.3	62	12	1	-0.05	6.7
78	1	1	0.29	7.2	84	15	1	-1.06**	6.7
51	5	1	0.28	7.2	38	24	3	0.25	6.7
54	6	1	0.01	7.2	48	26	1	0.24	6.7
6	9	3	-0.12	7.2	69	31	1	-0.59	6.7
92	18	1	0.02	7.2	22	31	3	-0.43	6.7
63	20	1	0.44	7.2	23	32	3	0.07	6.7
68	27	1	0.16	7.2	45	41	3	-0.17	6.7
18	13	1	-0.89*	7.1	72	47	2	0.59	6.7
37	13	2	0.31	7.1	148	47	3	-0.51	6.7
74	19	3	0.53	7.1	67	50	1	-0.1	6.7
55	27	3	0.2	7.1	42	18	3	-0.46	6.6
71	30	1	0.35	7.1	88	24	1	-0.09	6.6

**Appendix 3 continued: Specific combining ability for Grain yield across sites (drought and non drought environment)**

Gen	Inbred line	tester	SCA	GY	Entry	Inbred line	tester	SCA	GY
103	38	2	0.09	6.6	109	35	2	0.13	6.0
95	41	1	-0.43	6.6	115	40	2	-0.13	6.0
29	2	3	0.23	6.6	21	46	3	-0.95*	6.0
1	5	3	-0.17	6.6	50	49	3	-0.25	6.0
80	3	1	0.18	6.5	131	7	2	0.02	5.9
14	21	3	-0.32	6.5	116	11	2	0.13	5.9
85	22	1	-0.6	6.5	121	30	2	0.34	5.9
27	2	1	-0.1	6.4	125	34	2	0.39	5.9
49	8	1	-0.28	6.4	133	46	2	0.13	5.9
13	9	2	0.24	6.4	30	3	3	-0.31	5.8
96	18	2	0.44	6.4	24	12	2	0.32	5.8
43	20	3	-0.16	6.4	110	25	2	-0.48	5.8
135	22	2	0.57	6.4	134	33	3	-0.58	5.8
79	37	3	-0.32	6.4	127	37	2	0.15	5.8
94	39	1	-0.22	6.4	143	45	2	-0.2	5.7
142	42	1	-0.36	6.4	101	5	2	-0.11	5.6
147	43	2	-0.08	6.4	107	8	2	0.15	5.6
106	45	3	-0.59	6.4	140	16	2	-0.14	5.5
57	48	3	-0.06	6.4	146	42	2	0.01	5.5
104	6	2	0.26	6.3	118	27	2	-0.36	5.4
83	11	1	-0.73	6.3	123	32	2	-0.12	5.4
34	12	3	-0.27	6.3	128	1	2	-0.32	5.3
89	14	1	-0.54	6.3	124	19	2	-0.16	5.3
87	15	2	-0.16	6.3	120	29	2	-0.06	5.3
112	19	1	-0.37	6.3	137	33	2	0.01	5.3
86	23	1	0.13	6.3	114	3	2	0.13	5.2
126	36	2	-0.08	6.3	139	14	2	-0.39	5.2
145	41	2	0.6	6.3	113	20	2	-0.28	5.2
111	4	2	-0.03	6.2	130	21	2	-0.59	5.2
141	17	2	0.21	6.2	138	24	2	-0.16	5.2
36	23	3	0.13	6.2	149	48	2	-0.16	5.2
19	26	3	-0.16	6.2	119	2	2	-0.12	5.1
20	29	3	-0.27	6.2	129	26	2	-0.07	5.1
25	7	3	-0.92*	6.1	117	39	2	-0.26	5.1
32	10	3	-0.24	6.1	144	50	2	-0.4	5.1
31	34	3	-0.52	6.1	132	10	2	-0.3	4.9
102	28	2	-0.47	6.0	136	23	2	-0.26	4.7
16	30	3	-0.69*	6.0	150	49	2	-0.46	4.7

#### Appendix 4 Performance of Hybrids across non drought environment

Gen	Line	Tester	GY	AD	SD	ASI	EPP	RL	SL	HC	ER	EA	GLS	PS	ET	MSV
12	15	3	10.1	60.0	60.0	1.0	0.9	0.0	0.0	18.4	0.0	1.9	1.9	1.9	2.1	0.5
52	28	1	9.9	66.0	66.0	0.0	1.1	1.3	2.4	11.4	0.0	2.3	2.1	1.8	1.8	0.5
97	43	1	9.9	67.0	66.0	-1.0	1.1	2.5	1.3	8.8	0.7	2.2	1.5	1.5	2.1	1.3
93	45	1	9.9	65.0	65.0	0.0	1.1	0.0	1.2	14.3	2.8	2.8	2.1	1.8	1.9	0.5
5	13	3	9.8	63.0	65.0	2.0	1.0	0.0	0.0	7.6	0.8	2.3	1.6	1.4	2.1	0.5
81	7	1	9.6	67.0	66.0	-1.0	1.1	0.0	2.5	4.2	0.0	2.3	1.8	1.6	2.0	0.8
3	38	3	9.6	63.0	65.0	2.0	1.0	0.0	1.2	11.6	2.7	2.3	1.4	1.6	2.1	0.5
58	44	1	9.6	66.0	64.0	-1.0	1.1	0.0	2.6	22.7	0.0	2.4	2.0	1.6	1.9	0.9
8	44	3	9.6	59.0	62.0	3.0	1.1	0.0	0.0	6.7	0.0	2.2	2.1	1.6	2.1	0.5
66	46	1	9.6	67.0	66.0	-1.0	1.1	0.0	2.4	20.9	0.0	2.3	1.4	1.6	1.9	1.3
10	25	3	9.4	67.0	68.0	1.0	1.1	0.0	1.2	18.8	2.3	2.3	1.6	1.8	1.8	1.1
26	36	3	9.4	62.0	64.0	2.0	1.0	0.0	2.4	12.1	2.3	2.5	2.0	1.6	1.8	1.3
53	38	1	9.4	64.0	64.0	0.0	1.0	0.0	1.3	11.8	0.0	2.5	1.8	1.9	2.1	0.5
47	43	3	9.4	61.0	61.0	0.0	1.0	1.2	1.2	11.5	0.7	2.4	1.6	2.0	1.9	0.8
54	6	1	9.3	68.0	69.0	2.0	1.1	0.0	1.3	14.8	0.0	2.3	1.9	1.4	1.9	0.8
64	21	1	9.3	64.0	64.0	0.0	1.0	0.0	6.3	19.4	2.0	2.9	1.8	1.8	1.9	0.5
2	28	3	9.3	63.0	63.0	-1.0	1.1	0.0	0.0	10.8	0.0	2.8	1.4	1.6	1.9	0.8
15	40	3	9.3	61.0	62.0	1.0	1.1	0.0	1.2	12.5	0.7	2.7	2.1	1.8	2.1	0.5
70	29	1	9.2	65.0	66.0	1.0	1.0	0.0	1.3	21.8	0.0	2.5	1.6	1.6	2.0	1.3
71	30	1	9.2	63.0	64.0	0.0	1.1	0.0	0.0	14.0	0.0	2.5	2.0	1.6	1.6	0.5
56	4	2	9.1	64.0	66.0	2.0	1.0	1.3	0.0	11.3	1.6	2.7	2.1	1.6	2.3	0.8
39	14	3	9.1	63.0	65.0	2.0	1.0	0.0	0.0	7.3	0.0	2.8	1.9	1.6	1.9	0.8
41	17	3	9.1	66.0	66.0	0.0	1.0	0.0	0.0	21.1	0.0	2.4	1.8	1.6	1.8	1.8
68	27	1	9.1	64.0	66.0	2.0	1.0	0.0	2.5	10.5	0.0	2.4	1.4	1.6	2.0	0.8
91	17	1	9.0	67.0	67.0	0.0	1.0	0.0	2.7	11.8	0.0	2.3	1.8	1.6	2.1	0.8
78	24	3	9.0	66.0	66.0	0.0	1.1	0.0	2.5	11.2	0.8	2.6	1.6	1.6	1.9	1.0
60	34	3	9.0	66.0	66.0	1.0	1.1	0.0	4.2	9.6	2.6	2.7	1.6	1.8	2.0	0.8
44	39	3	9.0	66.0	65.0	-1.0	1.0	1.2	6.0	9.4	0.8	2.6	1.4	1.6	2.1	0.5
98	47	1	9.0	62.0	63.0	1.0	1.1	1.2	3.8	9.1	0.0	2.5	1.8	1.9	2.1	0.5
33	11	3	8.9	65.0	65.0	0.0	1.1	0.0	1.2	11.1	0.0	2.2	1.8	1.8	1.8	0.5
55	13	1	8.9	68.0	69.0	1.0	1.1	0.0	1.3	8.9	0.0	2.5	1.6	1.5	2.0	1.0
73	32	1	8.9	65.0	64.0	0.0	1.1	0.0	2.4	6.7	0.0	2.3	1.4	1.9	2.0	1.5
77	37	1	8.9	63.0	65.0	2.0	1.0	0.0	2.5	10.5	1.6	3.5	1.5	1.5	2.0	0.9
100	49	1	8.9	67.0	69.0	2.0	1.0	0.0	0.0	13.3	0.9	2.3	1.6	1.6	1.8	1.0
11	4	3	8.8	68.0	68.0	1.0	1.0	1.2	1.2	5.4	1.0	2.4	1.4	1.5	1.9	1.3
6	9	3	8.8	60.0	62.0	2.0	1.1	0.0	2.4	11.2	0.9	2.5	1.5	1.6	1.9	0.5
37	19	3	8.8	63.0	64.0	1.0	1.1	0.0	0.0	16.2	1.4	3.0	2.3	1.6	2.4	0.8

Appendix 4 continued: Performance of Hybrids across non drought environment

Gen	Line	Tester	GY	AD	SD	ASI	EPP	RL	SL	HC	ER	EA	GLS	PS	ET	MSV
69	26	1	8.8	62.0	62.0	0.0	1.0	0.0	0.0	11.2	0.8	2.3	2.0	1.8	2.0	0.8
9	35	3	8.8	65.0	64.0	0.0	1.0	0.0	2.5	14.8	0.0	2.5	1.8	1.8	1.8	0.5
76	36	1	8.8	63.0	64.0	1.0	1.2	0.0	5.0	28.6	0.8	2.7	1.5	1.8	2.5	1.3
99	48	1	8.8	65.0	64.0	-1.0	1.0	0.0	1.2	12.9	1.5	2.3	1.8	1.8	2.0	0.8
4	6	3	8.7	64.0	65.0	1.0	1.1	0.0	2.5	7.0	1.1	2.4	1.4	1.8	2.1	0.8
63	20	1	8.7	64.0	65.0	1.0	1.0	0.0	0.0	18.6	0.0	2.5	1.9	2.0	2.4	1.5
61	4	1	8.6	64.0	64.0	0.0	1.0	1.3	7.6	10.5	0.0	2.7	2.0	1.5	1.6	0.5
7	8	3	8.6	57.0	57.0	0.0	1.0	0.0	1.2	16.8	0.8	2.6	1.9	1.6	1.8	0.8
46	24	1	8.6	62.0	64.0	2.0	1.0	0.0	0.0	10.4	0.0	2.6	1.4	1.8	2.1	0.5
18	27	3	8.6	62.0	63.0	2.0	1.0	0.0	2.4	21.6	1.7	2.8	2.4	1.6	1.9	0.5
74	33	1	8.6	63.0	65.0	2.0	1.0	0.0	5.4	10.5	2.4	2.5	1.6	1.8	2.1	1.0
59	35	1	8.6	64.0	65.0	1.0	1.0	0.0	0.0	8.2	2.8	2.9	1.4	1.6	1.9	0.5
45	41	3	8.6	67.0	65.0	-2.0	1.1	0.0	0.0	10.9	0.0	2.3	1.9	1.6	2.3	0.5
148	47	2	8.6	62.0	63.0	1.0	1.0	0.0	1.3	11.8	0.0	2.2	1.4	1.6	1.9	0.5
51	5	1	8.5	64.0	64.0	1.0	1.1	0.0	8.6	12.5	0.0	2.6	2.0	1.6	1.9	0.5
82	10	1	8.5	66.0	65.0	0.0	1.1	0.0	2.6	15.5	0.8	2.8	1.5	1.6	2.1	0.5
40	16	3	8.5	65.0	64.0	-1.0	1.0	0.0	2.4	18.9	0.0	2.4	1.5	1.5	2.1	1.3
92	18	1	8.5	63.0	66.0	3.0	1.0	0.0	2.4	7.5	0.8	2.3	1.5	1.9	1.9	0.5
72	37	3	8.5	66.0	66.0	1.0	1.0	0.0	0.0	5.2	0.8	2.8	1.4	1.6	1.8	0.5
95	41	1	8.5	64.0	66.0	2.0	1.0	0.0	2.7	10.6	0.0	2.8	1.5	1.6	1.9	1.0
38	1	1	8.4	62.0	64.0	2.0	1.0	0.0	3.6	12.3	0.0	2.4	1.4	1.6	2.0	0.5
1	5	3	8.4	67.0	66.0	-1.0	1.0	0.0	3.1	10.6	0.8	2.6	1.4	1.6	2.1	1.5
75	34	1	8.4	60.0	62.0	2.0	1.0	0.0	2.6	12.6	0.0	2.7	2.1	1.6	2.1	0.5
65	40	1	8.4	64.0	64.0	0.0	1.1	0.0	0.0	7.1	0.0	2.4	1.4	1.6	1.8	0.5
80	3	1	8.3	67.0	67.0	0.0	1.0	2.8	1.6	4.3	0.0	2.4	1.5	1.6	1.8	2.0
105	13	2	8.3	67.0	66.0	-1.0	1.0	0.0	3.9	10.1	0.0	2.8	1.5	1.6	1.9	0.5
48	16	2	8.3	63.0	63.0	0.0	1.1	0.0	0.0	9.3	0.0	2.6	2.3	1.8	1.9	0.5
42	18	3	8.3	62.0	64.0	1.0	1.0	1.3	1.2	12.0	3.2	2.9	1.6	1.8	1.8	0.8
67	50	1	8.3	66.0	67.0	2.0	1.0	1.3	1.3	8.4	0.0	2.7	1.5	1.9	2.0	0.5
17	50	3	8.3	64.0	67.0	3.0	0.8	0.0	9.5	11.4	0.9	2.5	1.4	1.6	1.9	0.5
28	1	3	8.2	66.0	66.0	0.0	1.1	0.0	0.0	8.1	0.0	2.4	1.8	1.6	1.8	1.3
84	12	1	8.2	66.0	66.0	0.0	1.0	0.0	1.2	7.7	0.0	2.8	1.4	1.8	2.0	0.5
86	23	1	8.2	60.0	60.0	0.0	1.1	1.2	1.2	19.0	0.1	2.9	1.8	1.8	1.9	0.5
122	31	2	8.2	61.0	63.0	2.0	1.0	1.4	3.6	7.8	0.0	2.7	1.9	1.8	1.9	0.8
23	32	3	8.2	64.0	67.0	3.0	1.0	1.3	1.2	16.8	0.8	2.3	1.6	1.8	1.9	0.5
108	44	2	8.2	63.0	65.0	2.0	1.1	1.3	2.5	11.9	0.8	2.6	1.8	1.6	1.9	0.5
49	3	2	8.1	67.0	68.0	1.0	1.0	0.0	4.4	17.7	1.7	2.8	2.1	1.6	2.1	0.8

**Appendix 4 continued: Performance of Hybrids across non drought environment**

Gen	Line	Tester	GY	AD	SD	ASI	EPP	RL	SL	HC	ER	EA	GLS	PS	ET	MSV
62	15	1	8.1	67.0	67.0	1.0	1.0	0.0	1.5	16.9	0.0	2.6	1.4	1.8	2.3	0.8
87	19	1	8.1	64.0	65.0	1.0	1.1	0.0	2.6	9.0	0.0	2.7	1.6	1.5	1.9	0.5
14	21	3	8.1	62.0	66.0	4.0	0.9	0.0	0.0	16.7	0.0	2.8	2.1	2.0	2.0	0.5
27	31	1	8.1	65.0	66.0	1.0	1.1	0.0	0.0	6.8	0.0	2.5	1.8	1.8	1.9	0.8
88	42	3	8.1	62.0	63.0	1.0	1.1	0.0	0.0	10.7	0.0	2.8	2.0	1.8	2.3	0.5
83	11	1	8.0	65.0	65.0	0.0	1.0	0.0	0.0	12.5	0.0	2.8	1.5	1.5	1.9	0.5
89	14	1	8.0	63.0	65.0	2.0	1.0	0.0	2.6	13.1	0.9	2.8	1.5	1.6	2.4	0.5
90	16	1	8.0	65.0	66.0	2.0	1.0	0.0	2.6	5.5	1.6	2.7	1.8	1.6	1.8	1.0
20	29	2	8.0	66.0	68.0	2.0	1.1	0.0	1.3	11.9	0.0	2.4	1.6	1.9	2.0	0.8
57	8	1	7.9	68.0	68.0	0.0	1.1	0.0	1.8	12.6	0.0	2.4	2.0	1.6	2.3	1.5
142	18	2	7.9	65.0	65.0	0.0	1.1	0.0	0.0	10.3	0.0	2.6	1.5	1.8	2.4	1.0
85	22	1	7.9	61.0	63.0	1.0	1.1	0.0	5.9	16.3	0.0	2.8	1.8	1.8	2.4	0.5
35	22	3	7.9	63.0	64.0	1.0	1.1	4.6	1.5	13.8	0.8	2.8	1.5	1.6	2.0	0.5
79	2	1	7.8	65.0	65.0	0.0	1.1	0.0	0.0	9.4	3.0	2.9	1.5	1.9	2.5	0.5
104	6	2	7.8	61.0	62.0	1.0	1.0	0.0	1.2	15.4	0.8	2.8	2.0	1.8	2.0	1.1
19	26	3	7.8	63.0	63.0	1.0	1.0	0.0	6.3	16.1	0.8	2.8	1.5	1.6	2.3	0.5
22	31	3	7.8	66.0	67.0	1.0	0.9	0.0	1.4	16.7	0.9	2.6	1.5	1.6	1.9	0.8
145	41	2	7.8	61.0	63.0	2.0	1.0	0.0	1.2	8.4	1.5	3.0	1.8	1.8	2.0	0.5
16	46	3	7.8	64.0	65.0	1.0	1.0	0.0	0.0	29.7	0.0	2.6	2.1	1.6	2.1	0.5
141	17	2	7.7	62.0	62.0	0.0	1.1	0.0	0.0	9.6	0.0	2.8	1.6	1.9	2.1	1.0
96	42	1	7.7	66.0	66.0	0.0	1.1	0.0	3.8	9.4	1.6	2.5	1.4	1.6	1.9	0.8
29	2	3	7.6	60.0	61.0	1.0	1.0	0.0	1.2	14.5	1.4	2.8	2.0	1.9	2.1	0.5
30	3	3	7.6	63.0	65.0	1.0	1.0	0.0	0.0	15.4	1.6	2.9	1.5	1.8	2.0	0.5
111	9	1	7.6	63.0	62.0	-1.0	1.0	0.0	0.0	14.2	0.0	2.2	2.3	1.6	2.1	0.5
13	20	3	7.6	61.0	64.0	3.0	1.1	0.0	2.7	5.9	1.7	2.7	1.4	1.5	1.9	0.5
43	37	2	7.6	64.0	65.0	1.0	1.1	0.0	0.0	11.6	3.6	3.0	1.4	1.6	2.1	0.5
32	10	3	7.5	61.0	61.0	0.0	1.0	0.0	1.3	12.0	0.0	2.7	1.6	1.6	2.3	1.8
34	12	3	7.5	64.0	65.0	1.0	1.0	0.0	2.5	22.2	0.0	2.9	1.4	1.6	2.0	0.5
21	30	3	7.5	61.0	63.0	2.0	1.0	0.0	0.0	16.6	0.0	2.4	1.5	1.6	2.0	0.5
103	38	2	7.5	62.0	63.0	1.0	1.1	0.0	2.5	12.4	0.0	2.8	2.0	1.9	2.1	0.5
147	43	2	7.5	62.0	64.0	1.0	1.0	0.0	2.4	7.0	0.0	2.9	1.8	1.9	2.1	0.5
116	46	2	7.5	62.0	63.0	2.0	1.0	0.0	2.4	16.6	1.7	2.8	1.6	1.8	2.3	0.5
50	49	3	7.5	61.0	62.0	2.0	1.0	0.0	0.0	24.2	0.0	2.6	1.4	1.6	2.1	0.5
106	9	2	7.4	62.0	65.0	3.0	1.1	2.5	5.3	12.3	0.0	2.8	2.0	1.9	1.9	0.8
25	25	1	7.4	62.0	64.0	2.0	1.0	0.0	1.5	12.1	0.8	2.8	1.4	1.6	1.9	1.0
24	33	3	7.4	60.0	61.0	1.0	1.0	0.0	1.2	17.6	0.0	2.9	1.9	1.8	1.9	0.5
126	36	2	7.4	60.0	60.0	0.0	1.0	0.0	2.7	10.7	0.0	2.3	1.9	1.9	2.0	0.5
112	15	2	7.3	65.0	65.0	1.0	1.0	0.0	1.8	7.7	1.4	2.7	1.9	1.6	2.3	0.5

**Appendix 4 continued: Performance of Hybrids across non drought environment**

Gen	Line	Tester	GY	AD	SD	ASI	EPP	RL	SL	HC	ER	EA	GLS	PS	ET	MSV
94	39	1	7.3	59.0	59.0	0.0	1.0	0.0	0.0	22.9	0.0	2.8	1.8	2.0	1.9	0.8
131	7	2	7.2	60.0	63.0	3.0	1.0	0.0	1.2	22.4	0.0	2.8	2.0	1.8	2.5	1.0
31	7	3	7.2	61.0	64.0	3.0	1.0	2.6	1.3	22.2	0.0	2.8	1.6	1.6	1.8	1.5
133	11	2	7.2	60.0	60.0	0.0	1.0	0.0	0.0	15.1	0.0	2.8	1.5	1.8	1.9	0.9
135	22	2	7.2	61.0	61.0	0.0	1.1	0.0	1.3	31.7	0.0	3.0	2.1	1.5	2.1	0.5
109	35	2	7.2	59.0	60.0	1.0	1.0	0.0	7.5	18.6	0.0	2.9	1.5	1.6	2.0	1.0
107	8	2	7.1	61.0	63.0	1.0	1.1	0.0	0.0	15.0	0.0	3.1	2.0	1.6	1.9	0.5
36	23	3	7.1	61.0	61.0	0.0	1.0	0.0	3.6	14.3	0.0	2.9	1.4	1.8	1.9	0.8
110	25	2	7.1	64.0	65.0	2.0	1.1	0.0	0.0	22.2	0.7	2.9	1.9	1.6	2.9	1.3
102	28	2	7.1	62.0	64.0	2.0	1.0	0.0	1.2	19.1	0.0	2.7	1.9	1.6	1.9	0.8
115	40	2	7.1	60.0	62.0	2.0	1.1	0.0	1.3	21.2	1.0	2.7	1.9	1.8	2.0	0.8
134	12	2	6.9	61.0	62.0	2.0	1.0	1.2	0.0	18.9	0.0	2.9	1.8	1.8	1.9	0.5
118	27	2	6.9	61.0	63.0	2.0	1.0	0.0	1.3	23.9	0.8	2.7	1.5	2.1	1.9	1.0
123	32	2	6.9	61.0	61.0	1.0	1.0	0.0	0.0	31.1	0.0	3.2	2.1	1.8	2.1	0.5
125	34	2	6.9	60.0	61.0	1.0	1.0	0.0	0.0	16.4	0.9	3.1	1.4	1.6	1.8	0.8
120	29	3	6.8	62.0	63.0	1.0	1.1	0.0	0.0	21.2	1.9	2.9	1.4	1.6	1.9	1.0
143	45	2	6.8	59.0	60.0	1.0	1.0	0.0	1.2	16.0	0.0	3.1	1.9	1.8	1.9	0.5
139	14	2	6.7	63.0	64.0	1.0	1.0	0.0	2.8	17.1	2.4	2.9	2.1	1.6	2.1	0.5
138	24	2	6.7	61.0	62.0	1.0	1.0	1.3	5.1	16.9	0.0	2.7	1.9	1.8	1.8	0.8
146	42	2	6.7	62.0	64.0	2.0	1.0	0.0	0.0	13.9	1.7	2.8	1.6	2.1	2.1	0.5
127	45	3	6.7	62.0	63.0	1.0	1.1	0.0	0.0	23.3	0.9	2.8	1.4	1.8	2.0	0.5
140	47	3	6.7	61.0	61.0	1.0	1.1	0.0	1.2	15.8	0.8	2.7	1.4	1.6	2.0	0.5
128	1	2	6.5	60.0	61.0	1.0	1.0	0.0	4.2	22.8	1.9	3.0	1.6	2.0	2.0	0.8
101	5	2	6.5	59.0	61.0	2.0	1.0	0.0	0.0	9.0	3.4	2.9	2.1	1.9	2.1	0.8
121	30	2	6.5	59.0	60.0	1.0	1.0	1.2	1.2	8.4	0.0	3.0	2.3	1.6	1.5	0.5
144	39	2	6.5	62.0	62.0	1.0	1.0	0.0	1.2	8.7	0.0	2.9	2.1	2.1	2.0	0.8
137	19	2	6.4	60.0	63.0	2.0	1.1	1.4	1.6	20.1	1.2	2.9	2.0	1.9	2.0	0.5
119	26	2	6.4	63.0	64.0	1.0	1.0	0.0	0.0	16.8	2.6	3.0	1.4	1.8	1.8	1.3
124	33	2	6.4	64.0	64.0	1.0	1.1	0.0	3.8	10.3	0.0	2.8	1.4	1.8	2.1	0.5
130	48	3	6.4	62.0	63.0	1.0	1.0	0.0	2.5	10.7	0.7	2.9	1.5	1.5	2.3	0.5
117	50	2	6.4	59.0	60.0	2.0	1.1	0.0	0.0	21.5	1.9	3.0	1.5	1.9	1.8	0.5
149	48	2	6.3	61.0	62.0	1.0	1.0	0.0	0.0	14.3	3.2	2.6	2.4	1.8	2.1	1.0
132	10	2	6.2	61.0	62.0	1.0	1.0	0.0	0.0	26.5	0.0	3.0	1.4	1.8	2.1	0.8
114	21	2	6.2	57.0	59.0	2.0	1.0	0.0	1.2	19.6	0.9	3.2	1.6	1.9	2.0	1.0
113	20	2	6.1	59.0	60.0	1.0	1.0	0.0	3.3	5.7	0.0	2.6	1.4	1.6	2.1	0.5
150	49	2	6.0	63.0	64.0	1.0	1.1	0.0	2.6	11.3	0.7	3.2	1.6	1.9	2.3	0.8
129	2	2	5.8	57.0	58.0	0.0	1.0	1.3	2.6	17.0	0.0	2.8	2.4	1.8	1.9	0.8
136	23	2	5.6	58.0	59.0	1.0	1.1	0.0	2.4	9.2	0.0	3.2	2.0	1.6	1.8	0.5

## Appendix 5 Performance of Hybrids under drought environment

Gen	Line	Tester	GY	AD	RL	SL	EPP	HC	ASI	ER	EA	SD
12	15	3	5.0	65.0	0.0	0.0	0.9	5.3	3.0	0.0	1.8	68.0
11	4	3	4.9	67.0	0.0	0.0	1.0	5.8	1.0	0.0	1.5	68.0
35	22	3	4.3	66.0	2.8	0.0	1.0	2.8	1.0	0.0	2.0	67.0
5	13	3	4.3	66.0	0.0	0.0	0.8	2.7	5.0	3.6	2.8	71.0
135	22	2	4.1	65.0	0.0	5.3	1.0	8.2	1.0	0.0	2.3	66.0
121	30	2	4.0	63.0	2.8	0.0	1.0	5.8	2.0	0.0	2.5	65.0
10	25	3	3.9	68.0	0.0	0.0	0.7	0.0	4.0	0.0	2.5	71.0
90	16	1	3.8	68.0	0.0	0.0	0.8	5.5	6.0	0.0	2.5	74.0
103	38	2	3.8	66.0	0.0	0.0	0.9	0.0	4.0	0.0	2.5	69.0
94	39	1	3.8	68.0	0.0	10.5	0.8	7.9	2.0	0.0	2.3	70.0
52	28	1	3.8	68.0	0.0	2.8	0.7	0.0	3.0	0.0	3.0	71.0
64	21	1	3.6	68.0	0.0	0.0	0.8	2.7	4.0	0.0	2.5	71.0
122	31	2	3.6	65.0	0.0	5.3	0.9	0.0	2.0	0.0	2.5	67.0
106	9	2	3.5	64.0	0.0	0.0	0.8	0.0	5.0	0.0	2.3	69.0
17	50	3	3.5	69.0	0.0	0.0	0.8	0.0	4.0	0.0	2.3	73.0
76	36	1	3.5	68.0	0.0	0.0	0.8	5.3	3.0	0.0	2.8	71.0
29	2	3	3.5	64.0	0.0	0.0	0.8	13.8	6.0	0.0	2.5	70.0
81	7	1	3.5	68.0	0.0	0.0	0.6	2.7	6.0	0.0	2.5	73.0
112	15	2	3.4	65.0	0.0	2.8	0.8	5.6	3.0	3.0	2.5	68.0
33	11	3	3.4	66.0	2.7	0.0	0.7	5.6	5.0	0.0	2.3	71.0
22	31	3	3.4	67.0	2.8	0.0	0.9	8.4	3.0	0.0	2.8	70.0
36	23	3	3.4	66.0	0.0	2.8	0.8	14.7	5.0	0.0	2.5	70.0
92	18	1	3.3	69.0	2.8	0.0	0.8	0.0	3.0	0.0	2.8	72.0
15	40	3	3.3	66.0	2.8	0.0	0.7	2.8	4.0	0.0	2.5	70.0
105	13	2	3.3	67.0	0.0	0.0	0.7	2.7	3.0	0.0	3.5	70.0
39	14	3	3.3	68.0	0.0	0.0	0.7	2.8	8.0	0.0	2.3	76.0
8	44	3	3.2	65.0	0.0	0.0	0.7	5.9	6.0	0.0	2.5	70.0
129	2	2	3.2	60.0	0.0	5.8	0.9	0.0	3.0	0.0	2.3	63.0
51	5	1	3.2	68.0	2.7	0.0	0.6	0.0	4.0	0.0	2.5	72.0
126	36	2	3.0	67.0	0.0	0.0	0.7	11.1	2.0	5.6	3.3	69.0
26	36	3	2.9	67.0	0.0	0.0	0.6	0.0	3.0	0.0	3.3	70.0
43	37	2	2.9	68.0	0.0	0.0	0.8	2.7	4.0	0.0	3.0	71.0
127	45	3	2.9	69.0	0.0	0.0	0.8	2.8	6.0	0.0	2.3	75.0
13	20	3	2.9	66.0	0.0	0.0	0.8	0.0	5.0	3.0	2.5	70.0
125	34	2	2.9	66.0	0.0	0.0	0.9	0.0	2.0	0.0	2.5	68.0
108	44	2	2.9	67.0	0.0	0.0	0.6	8.4	4.0	0.0	2.5	71.0
66	46	1	2.9	72.0	0.0	2.8	0.8	5.8	5.0	0.0	2.3	77.0



**Appendix 5 continued: Performance of Hybrids under drought environment**

Gen	Line	Tester	GY	AD	RL	SL	EPP	HC	ASI	ER	EA	SD
147	43	2	2.8	67.0	0.0	0.0	0.7	2.7	4.0	0.0	2.8	71.0
101	5	2	2.8	63.0	0.0	0.0	0.7	2.7	4.0	3.6	2.8	67.0
115	40	2	2.7	66.0	0.0	0.0	0.8	8.2	3.0	0.0	3.5	68.0
34	12	3	2.7	66.0	0.0	0.0	0.7	2.7	5.0	0.0	3.0	71.0
82	10	1	2.6	69.0	0.0	0.0	0.7	2.7	4.0	0.0	2.8	73.0
9	35	3	2.6	69.0	0.0	0.0	0.7	2.8	6.0	0.0	2.8	74.0
31	7	3	2.6	67.0	0.0	0.0	0.6	2.8	5.0	0.0	2.8	72.0
28	1	3	2.6	67.0	0.0	0.0	0.5	0.0	7.0	0.0	3.0	74.0
102	28	2	2.6	63.0	0.0	2.8	0.6	0.0	9.0	0.0	3.5	72.0
109	35	2	2.6	69.0	0.0	0.0	0.7	11.0	5.0	3.4	3.0	74.0
65	40	1	2.6	69.0	0.0	0.0	0.7	10.6	4.0	0.0	3.0	73.0
18	27	3	2.5	67.0	0.0	0.0	0.8	5.6	6.0	0.0	3.0	72.0
62	15	1	2.5	69.0	0.0	0.0	0.7	0.0	5.0	0.0	2.5	73.0
63	20	1	2.4	70.0	0.0	0.0	0.6	0.0	3.0	0.0	3.5	72.0
96	42	1	2.4	70.0	0.0	0.0	0.6	0.0	4.0	8.4	2.8	74.0
75	34	1	2.4	69.0	0.0	0.0	0.7	0.0	4.0	0.0	3.0	73.0
113	20	2	2.4	67.0	0.0	0.0	0.5	0.0	7.0	0.0	3.3	74.0
74	33	1	2.3	69.0	0.0	0.0	0.7	5.3	4.0	0.0	3.3	72.0
23	32	3	2.3	68.0	0.0	0.0	0.5	5.6	8.0	0.0	3.0	76.0
133	11	2	2.3	63.0	0.0	0.0	0.8	2.7	6.0	0.0	2.8	69.0
85	22	1	2.3	70.0	0.0	0.0	0.7	7.9	2.0	0.0	3.0	71.0
143	45	2	2.3	68.0	0.0	0.0	0.6	0.0	5.0	0.0	3.0	73.0
61	4	1	2.3	71.0	0.0	0.0	0.7	29.4	1.0	0.0	3.0	72.0
134	12	2	2.3	64.0	0.0	0.0	0.7	0.0	6.0	0.0	2.8	69.0
3	38	3	2.2	67.0	2.8	2.5	0.5	0.0	5.0	0.0	2.8	72.0
79	2	1	2.2	67.0	0.0	0.0	0.5	0.0	7.0	0.0	3.0	74.0
114	21	2	2.2	65.0	0.0	2.7	0.6	2.7	5.0	10.0	3.0	69.0
6	9	3	2.2	67.0	2.8	0.0	0.6	0.0	5.0	0.0	3.0	72.0
98	47	1	2.1	72.0	0.0	0.0	0.5	0.0	10.0	0.0	3.3	81.0
93	45	1	2.1	71.0	0.0	0.0	0.7	5.8	5.0	0.0	3.0	76.0
25	25	1	2.1	71.0	0.0	0.0	0.6	0.0	5.0	0.0	3.3	76.0
60	34	3	2.1	68.0	0.0	0.0	0.7	8.8	6.0	0.0	3.0	73.0
46	24	1	2.1	71.0	0.0	0.0	0.7	0.0	4.0	0.0	2.8	74.0
88	42	3	2.1	67.0	0.0	2.7	0.8	3.0	5.0	0.0	3.0	72.0
136	23	2	2.0	63.0	0.0	2.8	0.5	0.0	3.0	0.0	3.3	66.0
145	41	2	2.0	67.0	0.0	0.0	0.5	0.0	10.0	0.0	3.5	77.0
47	43	3	2.0	68.0	0.0	0.0	0.4	0.0	9.0	0.0	3.3	77.0

**Appendix 5 continued: Performance of Hybrids under drought environment**

Gen	Line	Tester	GY	AD	RL	SL	EPP	HC	ASI	ER	EA	SD
37	19	3	2.0	67.0	3.0	0.0	0.7	5.3	6.0	0.0	3.8	73.0
48	16	2	2.0	67.0	0.0	0.0	0.6	2.8	9.0	0.0	3.3	75.0
140	47	3	2.0	69.0	0.0	0.0	0.6	0.0	8.0	0.0	2.8	77.0
40	16	3	2.0	68.0	0.0	0.0	0.4	0.0	10.0	8.0	2.2	71.0
84	12	1	2.0	70.0	0.0	0.0	0.6	0.0	3.0	0.0	3.0	73.0
146	42	2	2.0	66.0	2.8	2.7	0.8	2.8	4.0	0.0	3.0	70.0
56	4	2	1.9	69.0	0.0	0.0	0.6	2.8	1.0	0.0	3.0	70.0
111	9	1	1.9	70.0	2.7	0.0	0.5	0.0	9.0	0.0	3.0	79.0
131	7	2	1.9	67.0	0.0	0.0	0.5	2.7	5.0	0.0	3.0	71.0
149	48	2	1.9	65.0	0.0	0.0	0.6	0.0	1.0	0.0	3.0	66.0
128	1	2	1.9	64.0	0.0	0.0	0.6	5.3	7.0	0.0	3.3	71.0
14	21	3	1.9	66.0	0.0	0.0	0.7	3.0	6.0	0.0	3.5	72.0
100	49	1	1.8	69.0	0.0	0.0	0.9	0.0	3.0	0.0	3.0	71.0
124	33	2	1.8	65.0	0.0	0.0	0.5	7.9	8.0	0.0	3.3	73.0
32	10	3	1.8	68.0	0.0	0.0	0.6	0.0	5.0	0.0	3.3	72.0
142	18	2	1.8	66.0	0.0	2.7	0.6	2.7	9.0	0.0	2.5	75.0
137	19	2	1.8	66.0	0.0	0.0	0.5	5.6	6.0	0.0	4.0	68.0
38	1	1	1.7	69.0	0.0	0.0	0.4	0.0	3.0	0.0	4.0	70.0
78	24	3	1.7	68.0	2.7	0.0	0.4	5.3	6.0	0.0	3.8	74.0
104	6	2	1.7	67.0	0.0	0.0	0.5	2.7	6.0	0.0	3.3	73.0
57	8	1	1.7	70.0	0.0	2.7	0.6	0.0	4.0	0.0	3.3	74.0
110	25	2	1.7	68.0	0.0	0.0	0.5	0.0	6.0	0.0	3.0	74.0
67	50	1	1.7	71.0	0.0	0.0	0.5	0.0	7.0	0.0	3.0	78.0
53	38	1	1.6	71.0	0.0	0.0	0.4	0.0	8.0	0.0	3.5	79.0
55	13	1	1.6	73.0	0.0	5.3	0.5	2.7	2.0	0.0	3.8	72.0
50	49	3	1.6	66.0	2.8	3.0	0.6	0.0	6.0	0.0	3.3	71.0
141	17	2	1.6	70.0	0.0	0.0	0.4	0.0	6.0	0.0	3.8	76.0
68	27	1	1.5	73.0	0.0	0.0	0.5	0.0	5.0	0.0	3.5	74.0
2	28	3	1.5	66.0	0.0	2.7	0.4	0.0	8.0	0.0	4.0	74.0
89	14	1	1.4	71.0	0.0	2.7	0.6	0.0	5.0	0.0	3.3	76.0
49	3	2	1.4	67.0	0.0	0.0	0.4	5.3	10.0	0.0	3.8	77.0
130	48	3	1.4	69.0	0.0	0.0	0.5	0.0	5.0	0.0	3.8	73.0
58	44	1	1.4	75.0	0.0	0.0	0.4	0.0	5.0	0.0	3.8	75.0
21	30	3	1.4	68.0	0.0	0.0	0.4	0.0	7.0	0.0	3.5	74.0
119	26	2	1.4	67.0	0.0	2.5	0.4	0.0	10.0	0.0	3.8	77.0
116	46	2	1.4	68.0	0.0	0.0	0.5	5.6	7.0	4.6	4.0	75.0
77	37	1	1.3	70.0	0.0	0.0	0.4	0.0	5.0	0.0	3.8	75.0
1	5	3	1.3	68.0	0.0	0.0	0.4	0.0	10.0	0.0	3.5	78.0

**Appendix 5 continued: Performance of Hybrids under drought environment**

Gen	Line	Tester	GY	AD	RL	SL	EPP	HC	ASI	ER	EA	SD
27	31	1	1.2	72.0	0.0	0.0	0.4	2.8	9.0	0.0	3.5	80.0
72	37	3	1.2	69.0	0.0	0.0	0.4	0.0	7.0	0.0	3.8	76.0
117	50	2	1.2	67.0	0.0	0.0	0.5	2.7	11.0	0.0	3.3	78.0
42	18	3	1.2	68.0	0.0	0.0	0.4	0.0	8.0	0.0	3.5	75.0
91	17	1	1.2	73.0	0.0	0.0	0.4	0.0	8.0	0.0	3.8	80.0
4	6	3	1.2	69.0	2.5	0.0	0.4	2.7	6.0	0.0	3.0	75.0
97	43	1	1.2	72.0	0.0	0.0	0.3	0.0	9.0	9.0	3.2	77.0
83	11	1	1.2	70.0	0.0	0.0	0.4	0.0	4.0	0.0	3.3	72.0
118	27	2	1.1	66.0	0.0	0.0	0.4	0.0	5.0	0.0	3.8	71.0
144	39	2	1.1	67.0	2.7	0.0	0.4	0.0	5.0	0.0	3.3	72.0
19	26	3	1.1	70.0	0.0	0.0	0.4	0.0	6.0	0.0	3.8	75.0
59	35	1	1.1	71.0	0.0	0.0	0.4	0.0	6.0	0.0	4.3	77.0
150	49	2	1.1	67.0	0.0	0.0	0.7	0.0	5.0	0.0	3.8	71.0
107	8	2	1.0	69.0	0.0	0.0	0.4	0.0	12.0	3.9	4.0	81.0
132	10	2	1.0	64.0	0.0	0.0	0.4	0.0	4.0	0.0	4.0	68.0
123	32	2	1.0	68.0	0.0	0.0	0.4	7.9	10.0	0.0	3.5	77.0
44	39	3	1.0	70.0	0.0	0.0	0.4	5.3	7.0	0.0	3.5	75.0
99	48	1	1.0	72.0	0.0	0.0	0.4	0.0	8.0	0.0	4.0	79.0
138	24	2	1.0	67.0	0.0	0.0	0.4	13.9	10.0	0.0	4.3	77.0
54	6	1	0.9	73.0	0.0	0.0	0.3	0.0	9.0	0.0	3.8	82.0
45	41	3	0.9	69.0	0.0	0.0	0.4	2.7	13.0	0.0	4.0	82.0
148	47	2	0.9	70.0	0.0	2.7	0.3	0.0	11.0	0.0	4.0	81.0
20	29	2	0.9	68.0	0.0	0.0	0.4	2.7	9.0	0.0	3.8	77.0
120	29	3	0.9	66.0	0.0	0.0	0.3	2.7	12.0	-0.1	4.3	78.0
24	33	3	0.9	66.0	0.0	0.0	0.4	2.8	14.0	0.0	3.8	80.0
80	3	1	0.9	72.0	0.0	0.0	0.4	0.0	8.0	0.0	3.3	79.0
71	30	1	0.8	70.0	0.0	0.0	0.3	0.0	10.0	9.0	3.7	71.0
7	8	3	0.8	70.0	0.0	0.0	0.3	0.0	12.0	0.0	4.0	82.0
139	14	2	0.8	70.0	0.0	0.0	0.4	0.0	9.0	0.0	4.5	79.0
87	19	1	0.8	72.0	0.0	0.0	0.3	5.6	7.0	0.0	4.3	78.0
41	17	3	0.8	71.0	0.0	0.0	0.2	0.0	10.0	0.0	3.5	81.0
73	32	1	0.7	71.0	0.0	0.0	0.2	0.0	10.0	0.0	3.5	81.0
95	41	1	0.7	72.0	0.0	0.0	0.2	8.5	2.0	2.5	3.2	74.0
86	23	1	0.6	57.0	0.0	0.0	0.4	0.0	5.0	0.0	4.3	62.0
30	3	3	0.5	70.0	0.0	0.0	0.4	0.0	10.0	0.0	3.8	80.0
16	46	3	0.4	71.0	0.0	0.0	0.2	0.0	13.0	0.0	4.0	81.0
70	29	1	0.3	71.0	0.0	0.0	0.2	0.0	5.0	0.0	4.5	75.0
69	26	1	0.3	74.0	0.0	0.0	0.2	0.0	13.0	0.0	4.5	86.0

**Appendix 6 Performance per se of inbred lines across non drought environment**

Gen.	Inbred Line	GY	AD	ASI	RL	SL	EPP	HC	ER	EA
1	38	6.5	69.0	2.0	0.0	3.0	0.9	10.0	-1.0	1.5
3	21	6.2	71.0	1.0	0.0	24.0	1.0	3.0	8.0	2.0
5	3	6.0	71.0	-1.0	0.0	3.0	1.0	17.0	2.0	2.0
6	10	5.7	75.0	2.0	0.0	0.0	1.0	2.0	0.0	1.8
7	23	5.5	72.0	-1.0	0.0	9.0	1.2	0.0	0.0	2.5
13	37	5.3	73.0	-1.0	0.0	9.0	1.2	0.0	0.0	3.0
15	32	5.3	74.0	-2.0	0.0	0.0	1.0	0.0	0.0	1.5
19	13	5.2	70.0	1.0	0.0	0.0	1.1	24.0	8.0	3.5
22	24	5.0	67.0	1.0	2.0	0.0	1.1	11.0	0.0	3.3
28	12	5.0	66.0	-1.0	0.0	3.0	1.1	3.0	0.0	3.0
31	44	4.9	69.0	2.0	0.0	7.0	1.0	12.0	6.0	1.5
32	46	4.8	73.0	-1.0	0.0	-1.0	1.1	13.0	0.0	3.0
33	27	4.8	69.0	3.0	2.0	-1.0	0.9	0.0	0.0	2.0
34	45	4.7	70.0	0.0	0.0	16.0	0.8	3.0	0.0	3.3
35	33	4.7	67.0	0.0	3.0	-1.0	1.1	0.0	4.0	2.0
36	2	4.6	63.0	3.0	0.0	-1.0	1.1	10.0	3.0	2.7
37	40	4.5	70.0	-1.0	3.0	6.0	1.0	0.0	3.0	3.3
38	47	4.5	69.0	3.0	0.0	-1.0	0.9	5.0	0.0	2.5
39	15	4.5	70.0	1.0	0.0	1.0	0.9	14.0	0.0	2.7
40	16	4.4	66.0	4.0	0.0	-1.0	0.9	8.0	3.0	3.5
42	19	4.4	68.0	2.0	0.0	19.0	1.0	0.0	0.0	3.0
49	14	4.4	69.0	-2.0	0.0	5.0	1.2	0.0	2.0	3.5
51	43	4.2	69.0	0.0	0.0	11.0	0.9	3.0	6.0	3.7
54	17	4.2	76.0	-2.0	0.0	1.0	1.0	2.0	15.0	3.3
55	49	4.1	73.0	-1.0	0.0	0.0	1.0	0.0	0.0	2.0
60	1	4.0	67.0	2.0	0.0	0.0	1.0	19.0	0.0	3.0
61	9	4.0	71.0	1.0	3.0	21.0	1.0	0.0	2.0	2.7
64	4	3.9	71.0	1.0	0.0	1.0	1.0	17.0	2.0	2.2
68	18	3.9	77.0	2.0	0.0	3.0	1.1	3.0	3.0	2.7
69	42	3.8	74.0	2.0	0.0	3.0	1.0	0.0	0.0	2.0
70	31	3.7	67.0	2.0	0.0	10.0	1.0	0.0	0.0	1.5
71	50	3.7	75.0	-2.0	0.0	1.0	1.0	0.0	0.0	3.5
74	8	3.4	77.0	-1.0	3.0	17.0	1.0	0.0	0.0	2.5
75	30	3.0	73.0	2.0	2.0	9.0	0.9	0.0	0.0	2.7
76	22	2.9	70.0	2.0	0.0	21.0	0.9	0.0	0.0	3.3
77	25	2.8	76.0	0.0	0.0	0.0	0.8	0.0	6.0	2.0
79	7	2.6	70.0	0.0	0.0	8.0	0.9	0.0	6.0	2.0
80	41	2.5	72.0	2.0	3.0	0.0	1.0	0.0	3.0	3.5
81	48	2.4	73.0	2.0	3.0	0.0	0.9	0.0	6.0	2.7
82	26	2.3	75.0	-1.0	3.0	0.0	0.9	0.0	9.0	2.0
83	11	2.2	73.0	1.0	0.0	4.0	0.9	9.0	1.0	2.3
84	36	2.2	75.0	0.0	0.0	9.0	1.0	0.0	0.0	3.0
85	39	2.0	78.0	3.0	0.0	0.0	1.0	0.0	6.0	2.5
86	29	1.8	63.0	3.0	3.0	20.0	1.1	10.0	4.0	2.3