Combining Ability of Six Extra-Early Quality Protein Maize (QPM) Inbred Lines

By

OFORI, PETER AMOAKO

(10358600)

THIS THESIS/DISSERTATION IS SUBMITTED TO THE UNIVERSITY OF GHANA, LEGON, IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF MPHIL CROP SCIENCE DEGREE

DEPARTMENT OF CROP SCIENCE,

SCHOOL OF AGRICULTURE

COLLEGE OF AGRICULTURE AND CONSUMER SCIENCES

UNIVERSITY OF GHANA, LEGON

JUNE, 2013

DECLARATION

I, Ofori Amoako Peter, hereby declare that except for references to other people's work which have been duly cited, this thesis is the result of my own work and that it has neither in part nor in whole been presented elsewhere.

OFORI AMOAKO PETER SIGNATURE ……

(STUDENT) DATE…….....

PROF. K. OFORI SIGNATURE……

(SUPERVISOR) DATE…….....

DR. K. OBENG-ANTWI SIGNATURE……...

(SUPERVISOR) DATE…….....

ABSTRACT

Six extra-early QPM inbred lines from IITA were investigated using a partial diallel cross design. The objectives were to assess the hybrids and their parents for their agronomic performance. The six parents along with their hybrids (15) were evaluated using a Randomized Complete Block Design (RCBD) with three replications per site in four locations. Genetic correlations, general combining ability (GCA) and specific combining ability (SCA) effects as well as mid-parent heterosis were determined. Stability of grain yield and its relationship with other agronomic traits across four locations were also determined. Results of combined analysis of variance (ANOVA) revealed significant environmental effect for all the traits studied. Significant additive effect was observed for only grain yield whilst non-significant GCA and SCA effects were identified for all other traits. The GCA estimate identified parental lines P1, P3 and P5 as the high combiners for grain yield. The highest values for SCA and mid-parent heterosis for grain yield were observed in the crosses P1xP4, P5xP6, P1xP5 and P4xP6. The additive main effects and multiplicative interaction (AMMI) analysis revealed non-significant genotype by environment interaction (GEI) for grain yield whilst genotypic and environmental main effects were highly significant. However, the contribution of the environment was higher which suggests that anyone of the locations used in this study can be used for subsequent evaluations in order to manage the limited resources available for the testing programme.

DEDICATION

To my mum, Maame Akua Tiwaah.

ACKNOWLEDGEMENT

I would like to express my profound gratitude to the Almighty God who gave me the ability to complete this work. I thank Dr. Badu-Apraku of IITA for providing me with the germplasm for this study. I am very grateful to my supervisory team; Prof. K. Ofori and Dr. K. Obeng-Antwi for their invaluable support, advice and encouragement especially during my research and thesis writing. Special thanks go to the Staff of Maize Division of Crops Research Institute (CSIR-CRI). To Messrs Kankam Robert, A.C.K. Atta, Kwame Asamoah, Danso Coffie (CRI, Ejura), Odame (CRI, Pokuase) and Titus (CRI, Akomadan) for their stimulating technical support in my research work.

I appreciate the enormous support from the families of Dr. Obeng-Antwi and Mr. Owusu-Nketia. I am grateful to Mrs. Evelyn Adu Kwarteng whose help will always be remembered. I am indebted to Messrs. Adofo, Barfi, Martin-Luther Tengan, Emmanuel Amponsah, Martin Teye, and Moses Adenusi for their contributions in diverse ways throughout this study.

Furthermore, I thank Prof. E.Y. Danquah, Prof. S.K. Offei and Prof J. Ofosu-Anim, for their motivations and encouragements in my stay on campus. My gratitude goes to Drs. Martin Yeboah (WACCI), Emmanuel Moses, Grace Borfery, Osei Kingsley, Marshack Abdulai (SARI), Stephen Amoah, Mrs. Adelaide Agyemang and Prof. Richard Akromah (KNUST) for their assistance and suggestions in times of difficulties. I would also like to acknowledge the love and friendship of Mrs. Stella Ofori Amoako. In fact, your contribution could never be forgotten.

Finally, my heartfelt appreciation goes to my mum, Maame Akua Tiwaah, and my siblings Messrs Kwaku Gyimah, Tweneboah Kodua, Kofi Ampartey, Kwasi Odame, Madams Ama Owusuwaa and Abena Gyankoma - thank you all for your love, care, and prayers.

LIST OF ABBREVIATIONS

AMMI	Additive Main Effects and Multiplicative Interaction
ANOVA	Analysis of Variance
ASI	Anthesis-Silking Interval
CD	Cob Diameter
CL	Cob Length
Cm	Centimeter
COV_G	Genetic Covariance
COV_P	Phenotypic Covariance
CRI	Crops Research Institute
CSIR	Council for Scientific and Industrial Research
CIMMYT	International Center for Maize and Wheat Improvement
d.f	Degrees of Freedom
DAG	Days After Germination
DTA	Days to Anthesis
DTS	Days to Silking

E	Pooled error
EHT	Ear Height
EMS	Expected Mean Squares
EPP	Number of Ears per Plant
F_1	First Filial Generation
F_6	Sixth Filial Generation
FAO	Food and Agriculture Organization of the United Nations
FAOSTAT	Food and Agriculture Organization Statistical Databases
G	Genotype
G L	Genotype by Location Interaction
GCA	General Combining Ability
GDP	Global Development Program
G×E	Genotype by Environment Interaction
GY	Grain Yield
Ha	Hectare
IGC	International Grains Council
IITA	International Institute of Tropical Agriculture

Kg	Kilogram
kg/ha	Kilogram per Hectare
L	Location
LA	Leaf Area
MiDA	Millennium Development Authority
MoFA	Ministry of Food and Agriculture
MP	Mid Parent
MPH	Mid Parent Heterosis
MS	Means Squares
NH_4SO_4	Sulphate of Ammonia
NKR	Number of Kernel per Row
NM	Normal Maize
NPK	Nitrogen Phosphorous Potassium
NRC	Number of Rows per Cob
OPV's	Open-Pollinated Varieties
PC	Principal Component
PC1	Principal Component One

PC2	Principal Component Two
PCA	Principal Component Analysis
PHT	Plant Height
POST	Parliamentary Office of Science and Technology
QPM	Quality Protein Maize
RCBD	Randomized Complete Block Design
REPH	Relative Ear Position over Plant Height
r_g	Genetic Correlation
RL	Root Lodging
r_P	Phenotypic Correlations
S S	Sum of Squares
SA	South Africa
SCA	Specific Combining Ability
SL	Stem Lodging
TAMU	Texas Aggie Team University
TGW	Thousand Grain Weight
V_E	Variance due to Error

V_G	Genotypic Variance
V_{GL}	Variance due to Genotype by Location Interaction
V_{GLR}	Variance due to Genotype, Location and Replication
VP	Phenotypic Variance
WAP	Weeks After Planting

TABLE OF CONTENT

LIST OF TABLES

LIST OF FIGURES

CHAPTER ONE

1.0 INTRODUCTION

Maize is an important staple cereal crop in the world (Michael *et al.*, 1999; Vivek *et al.*, 2007; Moaveni *et al.*, 2011) with an annual estimated global production of 828 million Mt (IGC, 2012). Its production spans over 100 million hectares across 125 developed and developing countries (FAOSTAT, 2010). It is estimated that 94 countries depend on maize for at least 30% of their total daily calories (CIMMYT and IITA, 2011). In sub-Saharan Africa, about 12 countries depend on maize for at least one fifth of their total daily calories intake, and up to 60 % for their total daily protein intake (Krivanek and Vivek, 2006).

Maize is a major food security crop in Ghana (MiDA, 2010), and had a positive mean annual production growth rate from 1997 to 2009. It ranked highest in total production and consumption among the cereal crops (MoFA, 2010). It is an important source of carbohydrate and can be cultivated in all agro-ecological zones in Ghana. It is readily available, less expensive, easy to manage, and is used in preparation of different forms of food including gruels, porridge, and pastes (Morris *et al.*, 1999; Badu-Apraku *et al.*, 2006). It is also a major source of feed for poultry and livestock and serves as raw material in the brewing, starch, and flour-milling industries (Tengan, 2010; Obeng-Antwi *et al.*, 2012).

Although maize plays an important role in Ghanaian food systems, there is some nutritional deficiency present in the normal maize (NM) varieties. These varieties do not have enhanced protein level and are considered as low quality protein maize. There is paucity of two specific

essential amino acids - lysine and tryptophan, which are prerequisite to human dietary protein requirement. These essential amino acids are known to be part of the building blocks of proteins in humans and monogastric animals (Vivek *et al*., 2008) and are mostly required by children for rapid growth (Millward and Rivers, 1989). Hence the over reliance on normal maize as a major food component predisposes consumers, especially children and pregnant women to diseases (Vivek *et al.,* 2007). In Ghana, and some sub-Saharan Africa countries, protein deficiency especially in children causes Kwashiorkor, a disease characterized by initial growth failure, irritability, skin lesions and oedema. In the livestock industry, especially in monogastrics production, the use of low quality protein maize as feed source introduces an extra cost in the form of protein supplements necessary to meet dietary protein requirements.

The interventions for mitigating protein deficiency from low protein quality maize can be very expensive (Vivek *et al.,* 2007), especially in a developing country like Ghana. Hugo *et al* (2010) and POST (2010) suggested bio-fortification as a potentially reliable intervention method. Great stride have been made towards improving the nutritional content of major staple crops such as maize, rice and wheat (Hawkes and Ruel, 2006; GDP, 2011). In the early 1900s, efforts were made towards screening maize germplasm to identify genotypes with fortified endosperm of high levels of lysine and tryptophan. Two main challenges encountered in this pursuit were difficulty in identifying specific genes controlling the traits (amino acid profile of maize) and lack of prerequisite knowledge in genetic techniques to enhance backcross programmes for protein quality improvement in maize (Sofi *et al.,* 2009). This necessitated increased research activities in most recognized institutions including International Center for Maize and Wheat Improvement (CIMMYT) Mexico and the Council for Scientific and Industrial Research-Crops Research

Institute (CSIR-CRI), Ghana. This resulted in production of outstanding line with significantly high nutritive value was selected but unfortunately had other undesirable characteristics such as soft kernels which make grains highly susceptible to insect and fungal attack was developed.

In 1992, 'Obatanpa', an open-pollinated quality protein maize (QPM) variety with acceptable agronomic characters was released by CSIR-CRI for commercial cultivation in Ghana. The challenge with open-pollinated QPM variety is the gradual loss of integrity as QPM due to the recessive gene (*opaque-2*) conferring the high quality protein profile. This can be subjected to contamination through cross-pollination with non-QPM maize (Vivek *et al.*, 2008). The use of QPM maize as a major source of dietary protein requirement and improving livelihood of many people such as weaning children, sick children and sick adults and livestock industry (Krivanek and Vivek, 2006) requires high yields guaranteed to sustain demands. Hybrid production is one important way of achieving and retaining combined attributes of high quality protein and yields of QPM varieties. In Ghana, five medium maturing (110 days) three-way QPM hybrids have been developed by CSIR-CRI for commercial cultivation. There is still better opportunity to be explored through hybrid development. Single cross hybrids for instance are known to exhibit highest hybrid vigour compared to any hybrid types (Khalil *et al.,* 2010).

The advent of changes in climatic conditions coupled with unpredictable rainfall pattern and incidence of pest and disease pose threats to crop production especially grains (FAO, 2007). These demand the development of an adapted extra-early maturing QPM hybrid with improved nutritional qualities and high yield potential in Ghana to improve livelihood of farmers. Combining ability study via diallel crosses is an important tool used by many plant breeders for developing

hybrid maize varieties and offers an opportunity in identification and selection of potential inbred lines and parental combinations (Hallauer, 1990).

The goal of this study was to assess the relative importance of general combining ability (GCA) and specific combining ability (SCA) of six extra-early IITA QPM inbred lines and single cross hybrids. The specific objectives were to:

(1) assess the yield and agronomic performance of extra-early maturing F1 QPM hybrids and their parents,

(2) determine the stability of the hybrids across various locations,

(3) determine the genetic correlations between grain yield and other agronomic traits,

(4) estimate the GCA and SCA effects for grain yield and other agronomic traits and

(5) identify cross combinations expressing high hybrid vigour.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Morphology of the maize plant

Maize belongs to the tribe Maydeae of the grass family *Poaceae*. It is an annual crop possessing stover architecture similar to other grasses (Surányi and Mándy, 1955). It has a cylindrical stout stalk differentiated into internodes by its nodes. The number and length of internodes determines the height of the stem and can vary from (1-6) m long bearing approximately 14 nodes. The varied height may be dependent on the variety type and growing conditions. Usually, early maturing varieties are shorter, and late maturing ones are taller. According to Győrffy *et al.* (1965) cited by Zsubori *et al*. (2002), in prolonged growing season of about 11 months, some late maturing varieties can attain a height of 7m in a tropical environment.

Maize leaves have long broad lanceolate blades that emerge from the stalk or primary stover. The male flower is called the tassel which develops only at the terminal panicle whilst the female inflorescence is ear borne in the axils of middle leaves, approximately half way up the stem. Each ear consists of a short stout axis or cob. The spike is very dense with a number of vertical rows of very much reduced spikelets. Pollination is made possible by the very great development of the single style of each ovary forming a long thread extending up from each flower to the apex of the husk. The numerous threads emerge as a conspicuous tuft known as the silks. The upper part of each female reproductive organ – the style is receptive and wind-borne pollen germinates on its surface. The developing pollen tubes extend downwards through the whole length of the thread (silk) to reach the ovule. After successful pollination, the silks wither followed by grain

enlargement (Floyd *et al.*, 2002). The ear and the grains are enveloped in tightly packed leaves (husk) which elongates to engulf the tip or apex of the ear. The husk leaves become dry and papery but remain around the mature ear. The upper ear is called the main ear. During the growing season only the upper one or two ears are able to develop completely, except in "prolific" varieties which may have more ears. These varieties could play an important part in breeding for higher yield (Motto and Moll, 1983).

2.2 The need for QPM

Proteins which consist of amino acids are the building blocks of life (Griffiths *et al.*,, 1996; Wang and Schultz, 2005). Among the 20 amino acids required for protein synthesis, tryptophan and lysine are the only two which cannot be produced through metabolic processes by humans and monogastrics (pigs, chicken). These two amino acids have to be supplied through the diet for adequate availability of required sequence of amino acids for synthesis of proteins. Hence, these are considered as essential amino acids, whilst the remaining amino acids are considered non-essential since they can be synthesized through metabolism (Giwa and Ikujenlola, 2009; Ikujenlola, 2010).

In the developed countries, the dietary nutritional protein requirement and their sources are of great concern. The diets consumed usually contain various sources of dietary protein such as cereals, legume seeds and meat. However, in most developing countries opportunities for this flexibility are lacking. As a result, the nutritional quality of their protein source as well as the amount may be important (Shewry, 2007).

The protein composition is important for human nutrition as well as feed for livestock and poultry industry. Several feeding trials using maize with fortified lysine and tryptophan levels involving humans and monogastrics have been reported. In Ghana, Akuamoa-Boateng (2002), reported the importance of these amino acids in the diet of human beings. She observed that, children fed with superior maize protein exhibited healthier growth rate compared to those fed with normal maize. She concluded that maize with high lysine and tryptophan levels is an important and reliable food that can meet nutritional needs of people especially those who cannot afford supplementary protein-rich foods. In a feeding study, pigs fed with high lysine/tryptophan maize gained weight at roughly twice the rate of pigs fed solely on normal maize with no additional protein supplements (Osei *et al.*, 1999a). Similar results in other nutrition evaluations also confirmed the role of QPM in poultry feed (Osei *et al.*, 1999b; Zhai, 2002; Onimisi *et al.*, 2009). An equal quantity of high lysine maize substituted for normal maize in feeds can maintain the amino acid balance and decrease the use of synthetic lysine thereby reducing the cost of feeding (Burgoon *et al.*, 1992).

Quality protein maize contains twice the amount of lysine (>4.0%) and tryptophan (>0.8%) in the whole grain compared to normal maize (Krivanek *et al.*, 2007). Currently, QPM maize germplasm stands to be used severally as donor stocks where they are utilized in various breeding programs to improve upon the existing non-QPM lines or as extract lines for hybrid production (Okello *et al.*, 2006).

2.3 Maize storage protein and nutritional quality of QPM

The maize kernel is composed of a pericarp (6%), an endosperm (82%), and a germ (12%). The endosperm of maize grain is highly fortified with about 71% starch but appreciable amount of germ proteins is contained both in its endosperm and embryo. In normal maize, zeins protein contributes the greater proportion of various endosperm storage proteins with an average of 60%, followed by glutelins (34%), albumins (3%), and globulins (3%) (Sofi *et al.,* 2009; Salamini and Soave, 1982). These three storage proteins constitute the non-zein proteins. All these storage proteins are appreciably rich in balanced proportions of amino acid content and are abundantly rich in lysine and tryptophan except zeins (Vasal, 2000; Prassana *et al.,* 2001). The maize endosperm storage protein (zeins) is called prolamins (Ngaboyisonga, 2008) and it is found only in maize grain (Sofi *et al.,* 2009). Prolamins are alcohol soluble proteins (Shewry and Halford, 2002; Gupta *et al.,* 2009).

The maize endosperm is made up of two distinct regions with varied physical characteristics. The outermost layer is called aleurone layer which contains specialized cells that produce hydrolytic enzymes. Aleurone layer is embedded within starch-rich endosperm possessing vitreous and starchy regions. The zein proteins contained in the vitreous region form insoluble coalescences called protein bodies in the lumen of rough endoplasmic reticulum and are closely compacted between starch grains towards maturation (Gibbon and Larkins, 2005). There are four classes of zeins. The major class (α-zeins) and three other minor classes β, γ, and δ zeins. The zeins protein accounts for the largest proportion of storage protein and consist of vital amino acids such as glutamine, leucine and proline but is devoid of two essential amino acids; lysine and tryptophan (Sofi *et al.,* 2009).

2.4 Lysine and tryptophan mutants and their genetics

Improving on the protein content of major staple crops has long been a great concern. In the early 1900, efforts were geared towards screening germplasm to identify lines with fortified endosperm of high levels of lysine and tryptophan. Two main constraints were identified from this effort. These are the difficulty in identifying specific genes controlling the traits (amino acid profile of maize) and lack of prerequisite knowledge in the genetic technique which hindered the use of backcross programmes to enhance protein quality in maize (Sofi *et al.*, 2009).

In the 1920s, the Connecticut Experiment Station in the USA identified naturally occurring mutant maize with soft, opaque grains and was named by Connecticut researchers' as opaque 2 (o-2) (Singleton, 1939; Vietmeyer, 2000). In the 1960s, Oliver Nelson and Edwin Mertz at Purdue University also identified *opaque-2* maize lines with high protein levels and discovered that the *opaque-2* trait is controlled by homozygous recessive alleles. Further biochemical analysis indicated that these lines had significantly higher biological value of maize protein in grain endosperm compared to normal maize (Krivanek *et al.*, 2007). These discoveries excited many scientists such that between the 60s and 70s, numerous natural maize mutants with higher levels of lysine and tryptophan were identified. These include *opaque-2* (*o2*), *floury-2* (*fl2*), *opaque-7* (*o7*), *opaque-6* (*o6*), and *floury-3* (*fl3*) (Vivek *et al.*, 2008). The improved maize mutants possessed altered genetic framework of endosperm storage protein composition. In order to confer higher levels of these essential amino acids, the presence of another set of genes, called enhancers, were required. The enhancers which consist of minor modifying loci confer higher levels of lysine and tryptophan in the maize endosperm. The *o2* mutant was identified to be non-zeins fraction enhancer thereby increasing the level of lysine and tryptophan by repressing the synthesis of zeins

fraction especially the alpha- zeins (Damerval and de Vienne, 1993; Sofi *et al.*, 2009; Gaziola *et al.*, 1999).

According to Crow and Kermicle, (2002) for the *opaque-2* locus, the homozygous recessive mutant *o2*, was identified with higher levels of lysine and tryptophan content than the concentrations in either homozygous dominant (*O2O2*) or heterozygous (*O2o2*). The dominant allele *O2* encodes a transcriptional activator that regulates the expression of α-zein gene and a ribosome inactivating protein (Lohmer *et al*., 1991; Kodrzycki *et al.*, 1989). Therefore, in a given quantity of protein from *o2o2* maize, the proportion of non-zeins is higher, which induces *o2* maize to possess higher lysine and tryptophan concentration. The average levels of lysine in total endosperm proteins for normal (NM) and *o2* maize is 2% and 4%, respectively. However, across diverse genetic backgrounds, the levels range from 1.5 - 2.8% in normal maize and 2.6 – 6.5% in their *o2* converted counterparts (Moro *et al*., 1996).

2.5 Pleiotropic effects associated with opaque-2 mutants

Although the advent of these mutants excited scientists to conduct further research works to develop maize with preferred protein content, this dream was shattered due to the identification of negative pleiotropic effects (Lauderdale, 2002). These defects were: reduced grain yield compared to normal maize (Toro *et al.*, 2003), soft, chalky endosperm, and susceptibility to diseases and insects associated with higher storage losses (Micic-Ignjatovic *et al.*, 2008). Singh and Venkatesh, (2006) indicated that the effect of reduced kernel weight associated with yield decline due to decreased density per unit volume resulted from the starch being loosely packed with a lot of air spaces.

Through the effort of CIMMYT, CSIR-CRI and a few research institutes, these problems were gradually resolved. Maize varieties with superior protein quality and desirable agronomic characters were developed through the adoption of conventional breeding techniques. Thus they were able to introduce opaque-2 maize types endowed with increased grain yield, vitreous endosperm accompanied with disease and insect resistance and improved storage qualities similar to those of superior normal maize varieties. The new, normal-looking, normal-tasting *opaque-2* types were renamed "Quality Protein Maize or QPM" (Vivek *et al*., 2008).

2.6 Hybrid performance and heterosis

Heterosis, normally considered as miraculous phenomenon in agriculture, was introduced by Shull (1952). The author defined it as the interpretation of increased vigour, size, fruitfulness, speed of development, resistance to disease and insect pests, or climatic rigors of any kind, manifested by crossbred organisms as compared with corresponding inbreds, it is by the specific results of unlikeness in the constitutions of the uniting parental gametes. Falconer and Mackay (1996) also defined heterosis as the difference in performance of hybrid and the mean performance of the two parents. This difference is often called mid-parent heterosis. In effect, heterosis restores reduced vigour associated with inbreeding and leads to higher performance of progenies over the parents. Heterosis has been found to be controlled by dominance complementation, locus-specific over-dominance (Shull, 1908; Crow, 1948) and epistasis effects (Lippman and Zamir, 2006). Other studies have also proved that the superiority of hybrid performance over their parents is correlated or associated with heterozygosity to buffer against deleterious recessive alleles and provide genetic

plasticity to adapt to varied environments (Woolf and Markow, 2003). Although its basis is masked with divergent views, its evidence has continuously been showed over the past years in agricultural productivity as a result of increased hybrid production (Duvick, 1999; Duvick, 2001). In maize production, it is estimated that the range of heterosis contributes at least 15% - 50% to the total yields with modern higher-yielding inbreds and with improved agronomic techniques significant linear growth performance can be achieved (Lippman and Zamir, 2006).

Tulu (2001) reported the extent of genetic diversity among seven inbred populations on the basis of yield heterosis of their F1 progenies. He identified high levels of yield heterosis among F1 progenies over mid-parent and high-parent which ranged from 36% to 55.3%. Two heterotic populations (KCB and Abo-Bako) which had higher genetic diversity were selected for subsequent breeding programme. The outcome of such crosses will always be associated with higher heterosis (Munguma and Pollak, 1988). Rodrigues and Chaves (2002) assessed 19 yellow QPM populations with varied grain characteristics in partial diallel fashion in four environments. Significant differences in grain yield existed among varieties and average heterosis depicting that best hybrid combinations can be predicted using means of parental populations.

The work done by Amiruzzaman *et al.* (2010) on combining ability studies of 7 inbreds showed the range of their standard heterosis from -17.60 to 9.71%; -20.41 to 8.04%; -13.89 to 7.54% and -6.17 to 14.48% for yield per plant, number of kernels per ear, length of ear, ear diameter and 1000-kernel weight, respectively. Amanullah *et al.* (2011) estimated the heterotic effects for 30 F1 progenies produced from diallel crosses of six inbreds of maize at the Agricultural Research Institute, Dera Ismail Khan. All traits studied revealed positive heterotic ranges. Twenty one

crosses had positive heterosis for grain yield which ranged from 0.39 % to 16.86 %; 16 hybrids ranged from 0.14% to 5.39% for days to maturity; 19 hybrids values ranged from 0.33% to 7.60% for plant height; 13 hybrids ranged from 0.80% to 14.69 % for ear height; kernels per ear ranged from 0.06% to 19.92% and 1000 seed weight was 12.92%.

2.7 Combining ability

The term combining ability was first introduced and further refined as general combining ability (GCA) and specific combining ability (SCA) by Sprague and Tatum (1942). GCA distinguishes between the mean performances of parents in cross combinations whiles SCA is the deviation of individual crosses from the average performance of the parents involved. GCA and SCA represent the additive and non-additive portions of genotypic variance respectively (Hallauer and Miranda, 1988). The method used to analyse crosses, or parents and the crosses on the basis of SCA and GCA concepts is diallel mating design (Griffiths, 1956). Hayman (1954) and Stoskopf *et al.* (1993) defined "diallel cross" as the set of all possible matings between several genotypes.

The estimates from GCA and SCA provide an assessment of relative merits of the individual genotypes in cross combinations to guide in selection and testing schemes. Thus, diallel analysis is among the genetic-statistical approaches developed to assist in selection of parents based on their combining ability and the potential to produce promising segregating populations (Okello *et al*., 2006). Combining ability for yield and other traits such as disease resistance and high protein concentration play significant role in the identification of appropriate parents for hybrid development. Diallel mating designs have been extensively used in breeding programs for the

evaluation of genetic potential of parents that range from inbred lines to wide genetic base varieties (Hallauer and Miranda, 1988; Stoskopf *et al.*, 1993; Bernardo, 2002).

Bhatnagar *et al.* (2004) realized the importance of QPM and collected seven white and nine yellow QPM inbred lines from CIMMYT; Texas A&M University (TAMU); and the University of Natal, South Africa (SA) for combining ability studies. They observed no significant differences in GCA effects for grain yield but the converse on the basis of agronomic traits and kernel quality. The inbred lines received from TAMU had positive GCA effects on traits such as earlier maturity, shorter plants, and less moisture content compared to CIMMYT and SA lines. In terms of best-yielding hybrids and highest SCA effects, inter-crosses from different breeding programmes were identified for both yellow and white inbred lines.

Woyengo *et al.* (2001), assessed the performance of topcross hybrids on the basis of yield and disease reaction in two environments. One hundred and forty-four topcross hybrids were developed using 72 inbred lines and two synthetic varieties ECAVIL-17 and ECAVIL-18 resistant to the three foliar diseases: leaf spot, leaf blight and rust. A synthetic variety tester Ecavil 17 crossed with two topcross hybrid lines 70 and 44 out yielded significantly ($P < 0.05$) (9.82 t/ha and 10.26 t/ha) compared with the best check KH634A which recorded a mean grain yield of 7.03 t/ha. Six inbred lines had significant ($P < 0.05$) positive GCA effect for grain yield but negative GCA effects for the three diseases. GCA mean squares for inbred lines were significant ($P < 0.01$) for all the traits while GCA due to testers was only significant ($P < 0.05$) for leaf blight disease. SCA due to line x tester was significant ($P < 0.01$) for leaf spot disease and grain yield. The combining ability estimates indicated that there were predominant influences of additive over non-additive

gene action since the GCA and SCA ratios for all the traits were greater than one. As suggested by Scott *et al.* (2009), the presence of both additive and non-additive genetic effects is important for determining the performance of QPM hybrids. Deitos *et al.* (2006) evaluated the yield and combining ability of maize cultivars (AG4051, AL30, AL25, D270, D170, and AG1051) in three contrasting environments. According to F test analysis; there were significant differences in effects of hybrids and environment interactions. They observed the possibility of yield increase in various locations by capitalizing on the genotype x environment interaction, selecting and recombining cultivars for each site. Among the cultivars and their hybrid combinations, AG1051 and AG4051 x AL30, respectively had the best mean performance in the three locations.

Ojo *et al.* (2007) also used diallel to estimate combining ability and heterosis for grain yield and yield components (ear length, ear diameter and shelling percentage) of seven parental inbreds. Hybrid means were observed to be significantly higher than the parental means for all traits except shelling percentage. Crosses involving tropical x (tropical x temperature) lines produced hybrids with the highest heterosis for all the traits. GCA and SCA mean squares were not significantly different for the yield components. GCA mean squares were however, highly significant for grain yield. Additive gene action indicated preponderance over non-additive gene action for grain yield. They identified inbred line 3 (tropical parent three) to produce the highest GCA effect and hybrid combinations involving inbred 3 with inbred lines 5 and 6 (tropical X temperate) were recommended for subsequent hybrid breeding programme. Aliu *et al*. (2008) explored diallel studies on leaf area (LA) of ten inbred lines. The F1 hybrid combinations with maximum and minimum leaf areas were L6xL10, xg=788.6 cm^2 and L4xL5, xgj=558.9 cm^2 respectively. When these values were compared with the experimental mean LA value for F1 generation (μ= 678.8

cm^2), the maximum and minimum mean differences respectively were + 109.8 cm^2 or 17% and - 119.9 cm^2 or - 18%. The total variability between genotypes was ± 35%, with high significance. They found the GCA and SCA significant at (P 0.01). Higher value for GCA obtained was L2= +31.326, while with lower combination, the value was L4 = – 38.069. For the SCA the higher values was + 156.73. Ji *et al.,* (2006) used diallel-mating designs to obtain genetic information on five parental lines by determining the combining ability for plant and ear heights. They also calculated relative ear position over plant height (REPH) from plant and ear heights. By using Griffiths method 2, GCA was significant in plant height whilst SCA was highly significant in all the three measurements. Average heterosis for REPH, plant and ear heights were 21.6%, 33.3% and 61.9%, respectively. The traits with low heterosis showed higher ratios of GCA/SCA and vice versa. There were significant differences for plant height, ear height and REPH between the parents and the hybrids. REPH can be used as selection criterion over plant and ear heights in the breeding program for low ear height. This was because parents with lower REPH produced hybrids with significantly lower REPH.

Zare *et al*. (2011), also assessed seven inbred lines of maize using Griffiths' method 1. The seven parents and their 42 hybrids were evaluated in two different environments using Randomized Complete Block Design (RCBD) with three replications. The parents and F1s were assessed on important traits such as days from emergence to silking, days from emergence to physiological maturity, plant height, ear height, area of ear leaf, ear length, area of flag leaf, number of rows per ear, number of kernels per row and grain yield. They found that effect of environment on these traits were significant. Similar results were obtained for almost all the traits studied. The ratio σ^2

GCA/ σ^2 SCA ratios revealed the importance of additive gene effects over non-additive gene effects for most of the traits.

2.8 Correlations between grain yield and other agronomic traits in maize

Correlation measures the degree of association between two or more characters and is measured by a correlation coefficient (Hallauer and Miranda, 1988). This could be genetic or environmental (non-genetic) in nature. Genetic correlation is associated with the breeding values of two characters (Falconer, 1989) and their measurements can be identified directly in a number of individuals in a population (Hallauer and Miranda, 1988). For instance if two variables, X and Y are said to be correlated, then values of Y are associated with increase or decrease in values of X. In this sense, association of these two variables can either be positive or negative. When values of X causes an increase or are associated with high values of Y, a positive correlation exists. When high values of X are associated with low values of Y, a negative correlation exists.

Yield is a complex trait determined by several component characters. Therefore, there is the need to consider other contributing traits when selecting for yield. The knowledge of correlation between yield and its component characters and among the component characters is essential for yield improvement programmes (Vidya and Oommen, 2002). The relationship between yield and its components have been studied in maize through correlation analysis (Jayakumar *et al.*, 2007). Ear girth was positively correlated with grain yield. Similar observations were made for kernel rows, grains per row, grain weight, ear length, shelling percentage and crude protein. Plant height was also significantly and positively associated with grain yield whilst days to maturity, days to

silking and days to tasselling were negatively correlated with grain yield. In a related study, Ali *et al*. (2010) reported correlation coefficients among traits in genotypic and phenotypic studies in F1 hybrids produced from diallel crosses. They indicated that, grain yield was positively associated with number of kernels per row (0.589), ear length (0.465) and leaf area index (0.497). Rafiq *et al.* (2010) studied genotypic correlation coefficient of ear diameter, 100-grain weight, ear length, rows per ear and grains per row significantly correlated with grain yield. According to path analysis, highest direct effect on grain yield was exhibited by 100-grain weight followed by grains per row, kernel rows per ear, ear length and ear diameter. Most of the traits exerted positive indirect effects through 100- seed weight, kernel rows per ear and grains per row. They therefore concluded that traits such as grains per row, 100-grain weight, grain rows per ear, ear length and ear diameter could be used as target traits to improve maize grain yield.

Yousuf and Saleem (2001) also assessed 74 S1 families obtained from maize population C-17 to estimate the genotypic and phenotypic correlation coefficients between various traits. Grain yield per plant showed weak negative significant genotypic correlation with plant height, number of kernel rows per ear and number of kernels per row and positive weak correlation with days to flowering. Srećkov *et al*. (2010) reported on the relationship between grain yield and morphological traits using two testcross populations formed by crossing progenies of NSU1 population after 16 cycles of phenotypic recurrent selection and observed a medium to strong positive correlation between grain yield per plant and 100- kernel weight. There was also a strong positive correlation between ear height and length for NSU1 x 568/II NS population. Conversely, a strong negative relationship was established between ear height and kernel row number in population NSU1×B73. The path coefficient analysis detected high significant direct effect on

grain yield established for ear height (p1=-0.403**) and kernel row number (p3=0.390**) in the test-cross population where inbred line 568/II NS was used as a tester. The second tester (B73) population path analysis also showed high significant desirable influence of ear length (p2=0.394**) and 100-kernel weight (p4=0.573**) on grain yield. Bahoush and Abbasdokht, (2008) assessed interdependence of grain yield and its components in maize hybrids at the Agricultural Research Station in Shahrood, Iran. Their results showed a positive correlation between grain yield and a number of important traits. These included number of grains per ear 100 grain weights and ear length. However, ear height had weak and negative correlation with grain yield.

2.9 G × E Interactions (GEI) and stability analysis

Grain yield in nature, routinely exhibits GXE Interaction (Khalil *et al.*, 2011) which necessitates evaluation of cultivars in multiple environments (Kang, 2004; Fan *et al.*, 2007). Crop cultivars are grown in diverse environments of different soil types, soil fertility levels, moisture levels, temperatures and cultural practices. During production, all these cumulated conditions constitute the growing environment for the crop varieties (Abdulai *et al.*, 2007). This poses a serious challenge to plant breeders in the identification and selection of appropriate genotypes to perform consistently in multiple environments (Ngaboyisonga, 2008). Selection is therefore, usually ineffective since genotypes may fail to exhibit the same relative performance in varied environments (Knight, 1970). It has also been shown by Comstock and Moll (1963) that correlation between phenotypic and genotypic values was significantly reduced by GEI affecting progress of selection. This is because, relative rankings for major traits often varies across multiple

environments hence possibility of identifying single superior genotype poses difficulties if not impossible (Khalil *et al.,* 2011; Abdulai *et al.*, 2007). Stability analysis defines the true performance of a cultivar when reproduced at distinct environments (Brown and Caligari, 2008). As indicated by Khalil *et al.* (2011), several stability statistic studies have been done to partition GEI which includes regression analysis (Gauch, 1988), multivariate analysis (Westcoff, 1987), cluster analysis (Crossa *et al*., 1991), additive main effect and multiplicative interaction (AMMI) model (Gauch, 1992) and GGE-biplot (Yan, 1999).

In North-West Pakistan, Khalil *et al*. (2011) evaluated grain yield stability of seven maize single cross hybrids across three locations using GGE biplot. They observed significant differences in hybrids main effect and GEI. The GGE biplot statistical analysis revealed outstanding hybrids ranked on the basis of average grain yield across locations with ICI-974 as the best followed by Pioneer-3025 and Hi-Corn. For stability analysis, ICI-974 and Pioneer-3025 were the most stable hybrids across locations, whilst remaining hybrids were ranked inferior. In Ethiopia, Worku *et al.* (2001) also studied the response of 20 genotypes of maize to nine varied environments. Variances due to genotypes, environments and GEI were significant. Most of the genotypes were unstable in the studied environments and none of the outstanding genotypes had stable yields in these environments but had specific environmental adaptabilities. Abdulai *et al.* (2007) evaluated four open-pollinated varieties (OPV's) and eight hybrids to assess their yield stability and to determine their response to GEI across eight locations in Ghana. GE effects were contributed by climatic factors. Among the genotypes, seven out of the nine were stable when the regression coefficient b-values were used. Two hybrids (GH24 x 1368) x 5012 and (GH22 x 1368) x 5012 were stable across all locations when the b-values and the deviations from regression (s^2d) were used.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental Site

Field evaluation of 15 F_1 single crosses and their parents plus a check (single cross hybrid) was conducted at Crops Research Institute (CRI) – Fumesua which is located at the forest ecological zone of Ghana with coarse sandy-loam soil. The experiment was replicated in three other out-stations of the Institute. These were Ejura in the forest transition zone with fine coarse sandy-loam soil, Pokuase and Akomadan in the coastal savannah and semi-deciduous forest ecological zones respectively with coarse sandy-loam soil for both locations (Sallah *et al.*, 2004).

3.2 Experimental materials

The genetic materials used for this study were obtained from the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. They were made up of six extra-early QPM F_6 inbred lines (Table 1). For each inbred line, eight rows of 5m length were planted using the recommended spacing of 75cm between rows and 40cm within row giving approximately 14 plants per row (Sallah *et al*., 2004). Two plants were planted per hill and later thinned to one stand. Incomplete diallel crosses involving F_1 single crosses were made by hand-pollination using bulk pollen from each line. The first rows for each parent population were sibbed to increase seed of the lines.

Prior to flowering and silk emergence, the shoots were bagged using transparent polythene bags (shoot bags) to prevent contamination. Tassel bagging was done a day before pollination using

tassel or pollinating bags to collect pollen. Pollination was done by carefully depositing pollen on emerged silks. Cross inscriptions were made on pollinating bags for easy identification of similar cross combinations during harvesting. The pollination bags stayed on the ear until full maturity to prevent any contamination that could occur after manual pollination. After pollination, off types, plants with severe disease symptoms or plants with malformations were eliminated. At harvesting, crosses of the same parents were bulked whilst malformed and diseased ears were rejected. The harvested ears were dried and shelled manually. The F_1 single cross hybrids and their parents were processed and stored in cold room prior to field evaluation.

Table 1: List of parental inbred lines and their pedigrees

Name	Pedigree	Designation
TZEEQI 1	TZEE-W Pop x 1368 STR S7 Inb 40 x Pool 15 SR QPM BC1S5 (18) 2-5-1-1	P_1
TZEEQI 2	TZEE-W Pop x 1368 STR S7 Inb 40 x Pool 15 SR QPM BC1S5 (3/4) 3-7-3-7	P_2
TZEEQI 7	TZEE-W Pop x 1368 STR S7 Inb 40 x Pool 15 SR QPM BC1S5 (7) 4-10-1-1	P_3
TZEEQI 6	TZEE-W Pop x 1368 STR S7 Inb 40 x Pool 15 SR QPM BC1S5 (7) 1-10-1-10	P_4
TZEEQI 8	TZEE-W Pop x 1368 STR S7 Inb 40 x Pool 15 SR QPM BC1S5 (7) 6-10-4-5	P_5
TZEEQI 12	TZEE-W Pop x 1368 STR S7 Inb 40 x Pool 15 SR QPM BC1S5 (7) 10-10-10-10	P_6

Table 2: List of genotypes evaluated in the study

No.	Genotype	No.	Genotype
1.	**P1xP1**	12.	**P3xP3**
2.	P1xP2	13.	P3xP4
3.	P1xP3	14.	P3xP5
4.	P1xP4	15.	P3xP6
5.	P1xP5	16.	**P4xP4**
6.	P1xP6	17.	P4xP5
7.	**P2xP2**	18.	P4xP6
8.	P2xP3	19.	**P5xP5**
9.	P2xP4	20.	P5xP6
10.	P2xP5	21.	**P6xP6**
11.	P2xP6	22.	Check (GH110)

Parental lines bolded

3.3 Field trial management

For each of the three locations, trial fields were ploughed and harrowed before planting. The entries were arranged in randomized complete block design (RCBD) with three replications. A plot consisted of two-rows of 5m long each. The rows were spaced 75cm apart while hills were spaced 40cm, as recommended by Sallah *et al.* (1998). Hence, a planting density of approximately 66,000 plants/ha was achieved in each trial. Three seeds were sown per hill and later thinned to two plants per hill at three weeks after planting (WAP). Cultural practices such as fertilization, weeding, pest and disease control were accomplished using normal field management practices. Manual weeding at all sites was carried out as and when necessary. NPK (15-15-15) and sulphate of ammonia

(NH_4SO_4) fertilizers were applied at 2 and 4 weeks after emergence respectively supplying 90kg/ha of nitrogen and 37.5kg/ha each of phosphorus and potassium.

3.4 Data collection

For each plot, five plants were randomly sampled for data on agronomic and morphological characters. Border plants on each row as well as non-competitive plants were excluded. At 14 days after emergence (DAE), number of seedlings established per plot was recorded. The number of days from planting to 50% anthesis and full emergence of silks were also recorded and designated as Anthesis (AD) and silking (SD), respectively. Anthesis–silking interval (ASI) was calculated as the difference between number of days to 50% silking and anthesis (SD–AD). Plant and ear heights were recorded 14 days after silking using a graduated measuring pole. A measure from the ground level to the flag leaf node was considered as the plant height whilst ear height was taken as the measurement from the ground level to the node bearing the uppermost ear. Number of ears per plant (EPP) was computed as the ratio of number of ears to the number of harvested plants. Disease assessment for Helminthosporium maydis (leaf blight), Puccinia polysora (rust) and maize streak were carried out 21 days after flowering. This was also rated on 1-5 scale; where 1 = no incidence, 2 = incidence, 3 = mild severe, 4 = severe and 5 = highly severe (Bello *et al.,* 2012). Root and stalk lodging (RL and SL) parameters were taken at physiological maturity. Root lodging was determined as the percentage of plants leaning at an angle greater than 45^o from the vertical whilst stalk lodging (SL) was recorded as the percentage of plants with broken stalks at or below the main ear at maturity.

At harvest, the total number of plants and ears harvested per plot were counted and recorded. The ears were visually rated on a Scale of 1–5; where 1 = good, large ears with well-filled kernels, no cracks and vitreous appearance to 5 = poor, small ears with poorly-filled kernels and an opaque appearance, and this was recorded as ear aspect. Using a weighing Scale, field weight was taken after dehusking. Grain moisture (g kg^{-1} moisture of the grain at harvest) was measured using a moisture meter. Shelled grain weight per plot was determined and used to estimate grain yield (GY) (adjusted to 12.5% grain moisture and expressed in tons per hectare). Thousand (1000) kernel weights were determined for each plot. Cob diameter was measured at mid-portion along the cob (n=5) whilst cob length was measured as length of the cob (n=5) from the base to the tip using callipers. The kernel number per row and number of rows per cob were counted and averages recorded for each plot.

3.5 Data analysis

Individual analyses of variance (ANOVA) per location or environment and across environments for agronomic traits were carried out using Genstat version 9.2. Genotypes were considered as fixed effects whilst environments and replications were treated as random effects. For each agronomic and morphological trait, an individual ANOVA was conducted to determine the statistical significance for parents and their crosses at each environment and across environments. Combining ability test involving parents and their F_1 progenitors were used to assess their performance.

Diallel analysis was conducted using the DIALLEL-SAS program (Zhang and Kang, 1997). Griffiths (1956) linear Model1 and Method 2 were used for analysis of variance as follows: $X_{ijk} = \mu + r_k + g_i + g_j + s_{ij} + e_{ijk}$; where X_{ijk} is the observed performance of the cross between i^{th} and j^{th} parents in the k^{th} replication, μ the population mean, r_k the replication effect, g_i the GCA effect for the i^{th} parent, g_j the GCA effect for the j^{th} parent, s_{ij} the SCA effect for the cross between i^{th} and j^{th} parents, and e_{ijk} is the experimental error for the X_{ijk} observation (Hallauer and Miranda, 1988). Means were compared using the least significant difference (Steel and Torrie, 1980). A simple linear phenotypic correlation between traits was computed using Genstat version 9.2.

Table 3: Format of ANOVA for GCA and SCA according to Griffiths' Method 2

Source	Degrees of freedom (d.f.)	Sum of squares (S.S.)
GCA	$n-1$	$\frac{1}{n+2}\left[\sum(y_i + y_{ii})^2 - \frac{4}{n}y_{..}^2\right]$
SCA	$\frac{n(n-1)}{2}$	$\sum\sum y_{ij}^2 - \frac{1}{n+2}\sum(y_i + y_{ii})^2 + \frac{2}{(n+1)(n+2)}y_{..}^2$
Error	$\left[\frac{n(n+1)}{2} - 1\right] \times (r-1)$	$\frac{\text{Total S. S.} - \text{Treatment S. S.} - \text{Replication S. S.}^*}{r}$

*S.S. out of base ANOVA (*Aliu *et al.*,2009*)*

Table 4: Format for analysis of variance on plot mean basis across locations

Sources of variation	Degrees of freedom	Means squares (MS)	Expected means squares (EMS)
Replication (R)	r-1	M_R (M1)	$\delta^2_E + GL\delta^2_R$
Location (L)	l-1	M_L (M2)	$\delta^2_E + R\delta^2_{GL} + GR\delta^2_L$
Genotype (G)	g-1	M_G (M3)	$\delta^2_E + R\delta^2_{GL} + RL\delta^2_G$
G × L	(l-1)(g-1)	M_{GL} (M4)	$\delta^2_E + R\ \delta^2_{GL}$
Pooled error (E)	(l-1)(g-1)r	M_E (M5)	δ^2_E

Genotypic and phenotypic variances were calculated as explained below according to Obilana and Fakorede, (1981).

Table 5: Computing estimates of variance components

Variance component	Determination method
Replication (R)	(M1 – M5)/GL
Location (L)	(M2- M4)/GR
Genotype (G)	(M3 – M4)/RL
G × L	(M4-M5)/M5
Pooled error (E)	M5

$$VP = \frac{VE}{rl} + \frac{VGL}{l} + VG$$

Where,

VG = Genotypic variance

VP= Phenotypic variance

VGL= Variance due to genotype X location

VGLR = Variance due to genotype, location and replication

r = Replication

l = Location

VE= Variance due to error

3.6 Estimation of heterosis

The estimates of heterosis over the mid parent heterosis was calculated using Aliu et al., (2009)

Mid Parent Heterosis (MPH) = $\frac{F_1 - M_P}{M_P} \times 100$

Where: F_1 is the mean of the F_1 hybrid performance and MP = mid parent value of the particular F1 cross $\left[\frac{P_1+P_2}{2}\right]$, where P_1 and P_2 are the means of the inbred parents.

3.7 Correlation coefficient

Estimates of correlation coefficients were determined to show the degree of association between yield and its components, and among yield components. The genetic (r_G) and phenotypic correlations (r_P) between two characters, X and Y, were estimated according to Akhtar *et al.* (2011).

$$r_G = \frac{COV_{G(XY)}}{\sqrt{V_{G(X)} \cdot V_{G(Y)}}}$$

Where,

$COV_{G(XY)}$ = Genetic covariance among trait X and Y.

$V_{G(X)}$ and $V_{G(Y)}$ = Genetic variance for trait X and Y, respectively.

$$r_P = \frac{COV_{P(XY)}}{\sqrt{V_{P(X)} \cdot V_{P(Y)}}}$$

Where,

$COV_{P(XY)}$ = Phenotypic covariance among traits X and Y

$V_{P(X)}$ and $V_{P(Y)}$ = Phenotypic variance for traits X and Y, respectively.

3.8 Stability of the genotypes

The grain yield of individual genotypes was analysed using additive main effects and multiplicative interactions (AMMI) statistical model (MATMODEL 2.0 (Gauch, 1993) to obtain analysis of variance and mean estimates of AMMI. The pictographic analysis of genotype x

environment was done using GGE Biplot. No - scaling and tester – centered model was used for E and G x E interaction bi-plot analysis (Yan and Tinker, 2006).

CHAPTER FOUR

4.0 RESULTS

4.1 Performance of genotypes across four locations

4.1.1 Number of days to anthesis

The interaction of genotype by location effect was not significant for number of days to 50% anthesis (Table 6). Also differences among genotypes were not significant for this trait. However, there were significant ($p < 0.05$) differences among the locations. Days to anthesis ranged from 48-52, 49-51, 45-50 and 48-50, respectively at Akomadan, Ejura, Fumesua and Pokuase.

4.1.2 Number of days to silking

There were no significant differences among genotypes for days to 50% silking (Table 7). The average for all the genotypes across the four locations was 52 days. That for the parents and hybrids was 52 days. Silking date ranged from 51-55, 52-56, 48-52 and 42-53, respectively at Akomadan, Ejura, Fumesua and Pokuase.

4.1.3 Anthesis-silking interval

No significant differences were observed among the genotypes for anthesis-silking interval. The mean interval was approximately 3 days with the least anthesis-silking interval less than a day (Table 8). It was 3 days for the parents, and about a day to 3 days for the hybrids. There were however significant differences ($p<0.01$) for location and genotype × location interaction ($P<0.05$).

The least anthesis-silking interval was at Fumesua (2 days) whilst the longest was at Akomadan, Ejura and Pokuase (3days).

Table 6: Days to anthesis for inbreds and their hybrids at four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	49	51	46	48	49
P1xP2	49	50	50	49	49
P1xP3	49	51	47	50	49
P1xP4	49	51	47	47	49
P1xP5	50	50	49	48	49
P1xP6	49	50	48	49	49
P2xP2	48	51	47	50	49
P2xP3	51	49	48	49	49
P2xP4	48	51	48	48	49
P2xP5	50	50	47	49	49
P2xP6	48	50	49	48	49
P3xP3	49	50	48	46	48
P3xP4	50	50	47	48	49
P3xP5	49	50	48	48	48
P3xP6	50	50	49	48	49
P4xP4	52	53	49	50	51
P4xP5	51	52	48	48	50
P4xP6	50	51	48	49	50
P5xP5	50	50	47	48	49
P5xP6	51	50	47	50	50
P6xP6	49	51	45	49	49
Check	50	51	48	48	49
Grand mean	50	51	48	49	49
Parental mean	50	51	47	49	49
Hybrid mean	50	50	48	49	49
Lsd $_{(0.05)}$	3	2	3	2	1

Parental lines bolded

Table 7: Days to silking for inbreds and their hybrids at four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	52	53	49	51	51
P1xP2	51	53	52	51	52
P1xP3	52	54	50	52	52
P1xP4	52	54	50	49	51
P1xP5	53	53	51	51	52
P1xP6	52	53	51	53	52
P2xP2	52	55	49	52	52
P2xP3	54	52	51	42	50
P2xP4	51	54	50	50	51
P2xP5	52	53	50	51	52
P2xP6	51	53	51	51	52
P3xP3	52	53	50	50	51
P3xP4	52	53	50	51	52
P3xP5	51	53	49	51	51
P3xP6	53	53	51	51	52
P4xP4	55	56	51	53	54
P4xP5	53	55	51	51	52
P4xP6	53	54	51	51	52
P5xP5	52	53	50	52	52
P5xP6	52	54	50	52	52
P6xP6	52	55	48	51	51
Check	52	54	50	51	52
Grand mean	52	54	50	51	52
Parental mean	53	54	49	51	52
Hybrid mean	52	53	51	51	52
Lsd $_{(0.05)}$	3	2	3	8	2

Parental lines bolded

Table 8: Anthesis-silking intervals for inbreds and their hybrids across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	3	3	3	3	3
P1xP2	3	3	2	2	3
P1xP3	3	3	3	3	3
P1xP4	3	3	3	2	3
P1xP5	3	3	2	3	3
P1xP6	3	3	3	3	3
P2xP2	3	3	2	2	3
P2xP3	2	3	2	2	2
P2xP4	2	3	2	2	3
P2xP5	3	3	3	3	3
P2xP6	3	3	2	3	3
P3xP3	2	3	2	3	3
P3xP4	2	3	3	3	3
P3xP5	3	3	2	3	3
P3xP6	2	3	2	3	3
P4xP4	3	3	1	3	3
P4xP5	3	3	3	2	3
P4xP6	3	3	3	2	3
P5xP5	2	3	2	3	3
P5xP6	2	3	3	2	3
P6xP6	3	3	3	2	3
Check	2	3	2	3	3
Grand mean	3	3	2	3	3
Parental mean	3	3	2	3	3
Hybrid mean	3	3	3	3	3
$LSD_{(0.05)}$	1	1	1	1	1

Parental lines bolded

Table 9: Performance of genotypes for vegetative traits across four locations

Genotype	PHT	EHT	RL	RST	BLT	STK
P1xP1	174.0	80.5	4.7	2.2	1.8	1.2
P1xP2	168.0	70.8	1.5	2.1	2.0	1.4
P1xP3	160.2	67.4	6.1	1.8	1.8	1.6
P1xP4	169.8	72.9	3.7	2.4	1.9	1.1
P1xP5	170.0	75.3	3.7	1.9	1.9	1.4
P1xP6	170.7	76.7	5.3	2.2	1.8	1.6
P2xP2	164.0	71.9	4.2	2.0	1.7	1.3
P2xP3	174.1	76.6	5.2	2.1	1.7	1.2
P2xP4	170.7	74.5	4.5	2.1	2.0	1.3
P2xP5	171.0	75.4	6.3	2.3	1.8	1.3
P2xP6	162.4	70.4	4.7	2.0	1.8	1.2
P3xP3	178.0	81.68	3.5	2.0	1.8	1.1
P3xP4	161.4	69.6	5.5	2.3	1.8	1.1
P3xP5	169.2	75.5	4.0	2.2	2.0	1.1
P3xP6	157.6	70.6	3.3	2.0	1.7	1.3
P4xP4	162.0	71.3	2.4	2.2	1.9	1.6
P4xP5	167.2	75.0	2.4	2.0	1.6	1.3
P4xP6	161.6	79.2	2.1	2.5	1.8	1.3
P5xP5	157.4	65.9	6.4	1.8	2.0	1.4
P5xP6	175.8	77.3	4.3	2.3	1.7	1.3
P6xP6	172.2	69.0	3.2	2.3	1.8	1.4
Check	173.5	77.5	4.1	2.2	1.8	1.7
Mean	167.8	73.9	4.1	2.1	1.8	1.3
Parental mean	168.0	73.8	4.0	2.2	1.8	1.4
Hybrid mean	167.0	73.7	4.0	2.2	1.8	1.3
Lsd $_{(0.05)}$ G	14.6	11.8	3.6	0.6	0.4	0.4
Lsd $_{(0.05)}$ L	6.2	5.0	1.5	0.2	0.2	0.1
Lsd $_{(0.05)}$ G x L	29.2	23.7	7.2	1.1	0.8	0.7

Parental lines bolded, (G) genotype, (L) location, (G x L) genotype x location interaction, (PHT) plant height, (EHT) ear height, (RL) root lodging, (RST)rust disease (BLT) blight disease, and (STR) streak disease

Table 10: Performance of genotypes for reproductive traits across four locations

Genotype	GY	DTA	DTS	ASI	SL	TGW	NRC	NKR	CL	CD
P1xP1	2.4	49	51	3	0.7	0.2	13	29	13.1	3.9
P1xP2	2.1	49	52	3	1.8	0.2	14	28	12.6	3.8
P1xP3	2.5	49	52	3	1.5	0.2	13	28	12.9	3.9
P1xP4	2.5	49	51	3	0.6	0.2	14	29	12.9	3.8
P1xP5	2.7	49	52	3	1.0	0.2	14	31	13.0	3.9
P1xP6	2.0	49	52	3	1.6	0.2	13	29	13.0	3.9
P2xP2	2.4	49	52	3	0.9	0.2	13	29	12.8	3.9
P2xP3	2.5	49	50	0	0.9	0.2	13	29	12.5	3.7
P2xP4	2.1	49	51	3	2.4	0.2	13	30	13.2	3.9
P2xP5	2.2	49	52	3	1.1	0.2	13	28	12.7	3.8
P2xP6	2.0	49	52	3	1.7	0.2	13	27	12.3	3.8
P3xP3	2.5	48	51	3	1.0	0.2	13	29	12.8	3.8
P3xP4	2.1	49	52	3	1.3	0.2	13	28	12.4	3.7
P3xP5	2.3	48	51	3	2.3	0.2	13	29	12.6	3.8
P3xP6	2.1	49	52	3	2.1	0.2	13	27	12.6	3.8
P4xP4	1.5	51	54	3	1.3	0.2	13	29	12.8	3.6
P4xP5	2.1	50	52	3	0.6	0.2	13	29	12.9	3.8
P4xP6	2.0	50	52	3	1.0	0.2	13	28	12.8	3.8
P5xP5	2.4	49	52	3	1.3	0.2	13	28	12.6	3.8
P5xP6	2.5	50	52	3	0.8	0.2	14	30	13.2	3.9
P6xP6	2.1	49	51	3	0.8	0.2	14	28	12.3	3.9
Check	2.4	49	52	3	0.8	0.2	14	29	12.6	3.9
Mean	2.2	49	52	3	1.2	0.2	13	29	12.8	3.8
Parental mean	2.3	49	52	3	1.0	0.2	13	29	12.7	3.9
Hybrid mean	2.2	49	52	3	1.2	0.2	13	28	12.7	3.8
Lsd $_{(0.05)}$ G	0.5	1	2	1	1.7	0	1	2	0.9	0.2
Lsd $_{(0.05)}$ L	0.2	1	1	0	0.7	0	0	1	0.4	0.1
Lsd $_{(0.05)}$ G x L	1.0	3	4	1	3.4	0	2	4	1.7	0.4

Parental lines bolded, (G) genotype, (L) location, (G x L) genotype x location interaction, (GY) grain yield, (DTA) days to anthesis, (DTS) days to silking, (ASI) anthesis-silking interval, (TGW) thousand grain weight, (NRC) number of rows per cob, and (NKR) number of kernels per row, (CL) cob length, (CD) diameter and (SL) stem lodging

4.1.4 Plant height

There were no significant differences in plant height among all the genotypes across all the locations. The plant height averaged 167.9cm and ranged between 157.4cm to 178.0cm for parents and 157.6cm to 175.8cm for the hybrids (Table 11). There were significant differences ($P<0.05$) among individual locations with Akomadan having the highest mean plant height (183.5cm) which was not significantly different from Pokuase (181.8cm) Fumesua (170.1cm) and Ejura (135.5cm). Among the parents, P3 was the tallest followed by P1, P6, P2, P4 and P5. Hybrid P5xP6 was the tallest but was not significantly different from others except P1xP3 and P3xP6.

4.1.5 Ear height

The analysis of variance showed no significant differences among genotypes for ear height across the four locations. Mean ear heights ranged from 65.9cm to 81.7cm for parental lines and 67.4cm to 79.2cm for hybrids but there were no significant differences between the parents and their respective hybrids (Table 12). However, there were highly significant differences ($p<0.01$) for mean ear height among the four locations. The highest mean ear height was recorded at Pokuase (84.7cm) and was significantly different from other locations. However, the mean ear height for Fumesua (76.7cm) and Akomadan (73.8cm) were significantly ($p<0.01$) higher than at Ejura (60.2cm).

Table 11: Plant height across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	193.7	134.3	182.7	185.3	174.0
P1xP2	182.2	134.0	183.9	171.7	168.0
P1xP3	176.5	130.0	169.5	165.0	160.3
P1xP4	191.1	135.0	174.2	178.7	169.8
P1xP5	173.5	144.3	170.7	191.3	170.0
P1xP6	191.9	143.3	167.1	180.3	170.7
P2xP2	188.1	138.7	160.7	168.7	164.1
P2xP3	200.6	145.7	166.7	183.5	174.1
P2xP4	164.5	131.7	188.0	198.7	170.7
P2xP5	191.7	136.7	173.5	182.0	171.0
P2xP6	163.5	139.0	161.4	185.6	162.4
P3xP3	190.7	152.0	180.6	188.7	178.0
P3xP4	157.7	136.3	155.7	195.7	161.4
P3xP5	188.9	146.3	154.5	187.0	169.2
P3xP6	175.5	140.3	143.3	171.1	157.6
P4xP4	176.1	114.0	172.2	185.8	162.0
P4xP5	189.1	121.7	165.4	192.7	167.2
P4xP6	179.9	109.3	181.7	175.4	161.6
P5xP5	168.5	133.7	170.3	157.1	157.4
P5xP6	205.5	139.7	188.8	169.3	175.8
P6xP6	196.3	129.7	172.7	189.9	172.2
Check	192.3	145.3	159.4	197.0	173.5
Mean	183.5	135.5	170.1	181.8	167.8
Parental mean	185.6	133.7	173.2	179.3	167.9
Hybrid mean	182.1	135.6	169.6	181.9	167.3
Lsd $_{(0.05)}$	28.5	33.4	24.9	27.7	14.6

Parental lines bolded

Table 12: Ear height across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	86.8	60.7	90.7	83.7	80.5
P1xP2	70.6	54.7	78.1	79.7	67.8
P1xP3	66.7	50.0	74.1	78.7	67.4
P1xP4	74.0	57.7	77.7	82.3	72.9
P1xP5	72.1	59.7	81.5	88.0	75.3
P1xP6	75.9	61.0	79.8	90.0	76.7
P2xP2	77.2	59.0	74.7	76.7	71.9
P2xP3	79.7	65.3	77.5	84.0	76.6
P2xP4	64.5	47.3	92.3	94.0	74.5
P2xP5	76.1	57.0	83.4	85.0	75.4
P2xP6	62.5	62.7	69.6	86.7	70.4
P3xP3	79.1	74.7	84.0	89.0	81.7
P3xP4	58.9	56.7	73.3	89.7	69.6
P3xP5	83.2	61.3	66.9	90.7	75.5
P3xP6	67.4	63.3	67.9	83.7	70.6
P4xP4	71.9	47.3	78.1	87.7	71.3
P4xP5	79.9	57.7	75.4	87.1	75.0
P4vP6	72.3	79.3	83.9	81.3	79.2
P5xP5	59.2	66.0	69.5	69.0	65.9
P5xP6	89.0	59.0	89.4	71.8	77.3
P6xP6	75.9	58.7	48.5	93.0	69.0
Check	81.3	66.3	71.6	90.7	77.5
Mean	73.8	60.2	76.7	84.7	73.9
Parental mean	75.0	61.1	74.3	83.2	73.4
Hybrid mean	72.9	59.5	78.1	85.2	73.9
Lsd $_{(0.05)}$	18.4	30.8	22.1	20.6	11.8

Parental lines bolded

4.1.6 Assessment of common maize diseases

No significant differences were observed for the prevalence and severity of rust and blight among the genotypes in all the locations but differences among the locations were significant. The severest symptoms were scored at Fumesua and Pokuase for rust and blight, respectively whilst Ejura and Fumesua recorded the least score for rust and blight (Tables 13 and 14). There was significant differences ($p<0.01$) between genotypic reactions for maize streak virus disease across the locations. However, there was no incidence of streak disease at Pokuase but, incidence was recorded at Fumesua, Ejura and Akomadan (Table 15).

4.1.7 Lodging

No significant differences were observed among the genotypes for stem and root lodge in across the locations (Tables 16 and 17). The grand mean stem and root lodging were 1.2% and 4.1% respectively. Stem lodging in the genotypes ranged between 0.7% and 1.3% for parents, whilst that of the hybrids was from 0.6% to 2.4% (Table 16). Similarly, the root lodging ranged between 2.4% to 6.4% for the parents, and 1.5% to 6.3% for the hybrids (Table 17). Fumesua and Ejura recorded the highest for stem and root lodging, respectively.

Table 13: Rust disease assessment across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	1.3	2.3	3.0	2.0	2.2
P1xP2	2.7	1.7	2.0	2.0	2.1
P1xP3	1.3	1.0	2.7	2.0	1.8
P1xP4	3.0	1.3	2.7	2.7	2.4
P1xP5	2.0	1.3	2.7	1.7	1.9
P1xP6	1.7	1.7	3.0	2.3	2.2
P2xP2	2.3	1.3	3.0	1.3	2.0
P2xP3	2.0	2.3	2.3	1.7	2.1
P2xP4	2.0	1.7	2.3	2.3	2.1
P2xP5	3.0	2.0	2.0	2.3	2.3
P2xP6	1.7	1.7	2.7	2.0	2.0
P3xP3	1.7	1.0	3.3	2.0	2.0
P3xP4	1.7	3.0	2.7	2.0	2.3
P3xP5	1.3	2.7	2.0	2.7	2.2
P3xP6	2.0	2.3	2.0	1.7	2.0
P4xP4	2.0	1.7	3.0	2.0	2.2
P4xP5	1.7	2.0	2.7	1.7	2.0
P4vP6	2.0	2.0	3.0	3.0	2.5
P5xP5	1.3	1.3	2.7	2.0	1.8
P5xP6	2.3	2.0	3.3	1.7	2.3
P6xP6	2.7	1.3	3.0	2.0	2.3
Check	1.7	1.3	3.0	2.7	2.2
Mean	2.0	1.8	2.7	2.1	2.1
Lsd $_{(0.05)}$	1.2	1.1	1.2	0.9	0.9

Parental lines bolded, disease assessment scale (1-5); where 1 = no incidence, 2 = incidence, 3 = mild severe, 4 = severe and 5 = highly severe

Table 14: Blight disease assessment across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	2.0	1.3	1.0	2.7	1.8
P1xP2	2.0	2.7	1.3	2.0	2.0
P1xP3	2.0	2.3	1.0	2.0	1.8
P1xP4	2.0	2.3	1.0	2.3	1.9
P1xP5	1.7	3.0	1.0	2.0	1.9
P1xP6	2.0	2.0	1.0	2.3	1.8
P2xP2	2.3	1.0	1.3	2.0	1.7
P2xP3	2.0	1.7	1.0	2.0	1.7
P2xP4	2.3	2.7	1.0	2.0	2.0
P2xP5	2.0	1.3	1.0	2.7	1.8
P2xP6	2.0	1.7	1.3	2.3	1.8
P3xP3	2.0	2.0	1.3	2.0	1.8
P3xP4	2.3	1.3	1.0	2.3	1.7
P3xP5	2.0	1.7	1.7	2.7	2.0
P3xP6	2.3	1.0	1.0	2.3	1.7
P4xP4	2.3	2.3	1.0	2.0	1.9
P4xP5	2.0	1.3	1.0	2.0	1.6
P4vP6	2.0	1.7	1.0	2.3	1.8
P5xP5	2.0	2.7	1.0	2.3	2.0
P5xP6	2.0	2.3	1.0	1.3	1.7
P6xP6	2.0	2.0	1.0	2.0	1.8
Check	2.0	2.0	1.0	2.3	1.8
Mean	2.1	2.0	1.1	2.2	1.8
Lsd $_{(0.05)}$	0.2	1.1	0.4	0.8	0.4

Parental lines bolded, disease assessment scale (1-5); where 1 = no incidence, 2 = incidence, 3 = mild severe, 4 = severe and 5 = highly severe

Table 15: Streak disease assessment across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	1.0	1.7	1.0	1.0	1.2
P1xP2	1.3	2.0	1.3	1.0	1.4
P1xP3	1.7	2.7	1.0	1.0	1.6
P1xP4	1.3	1.0	1.0	1.0	1.1
P1xP5	1.7	2.0	1.0	1.0	1.4
P1xP6	2.0	2.3	1.0	1.0	1.6
P2xP2	1.7	1.3	1.3	1.0	1.3
P2xP3	1.3	1.0	1.3	1.0	1.2
P2xP4	1.0	2.3	1.0	1.0	1.3
P2xP5	1.0	1.7	1.3	1.0	1.3
P2xP6	1.0	1.3	1.3	1.0	1.2
P3xP3	1.0	1.3	1.0	1.0	1.1
P3xP4	1.3	1.0	1.0	1.0	1.1
P3xP5	1.0	1.3	1.0	1.0	1.1
P3xP6	1.3	1.7	1.3	1.0	1.3
P4xP4	1.3	3.0	1.0	1.0	1.6
P4xP5	1.0	2.0	1.0	1.0	1.3
P4vP6	1.7	1.7	1.0	1.0	1.3
P5xP5	1.3	2.3	1.0	1.0	1.4
P5xP6	1.3	1.7	1.0	1.0	1.3
P6xP6	1.7	2.0	1.0	1.0	1.4
Check	1.3	3.0	1.3	1.0	1.7
Mean	1.3	1.8	1.1	1.0	1.3
Lsd $_{(0.05)}$	0.7	1.1	0.5	0.0	0.3

Parental lines bolded, disease assessment scale (1-5); where 1 = no incidence, 2 = incidence, 3 = mild severe, 4 = severe and 5 = highly severe

Table 16: Stem lodging across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	0.3	0.0	1.7	0.7	0.7
P1xP2	0.0	0.7	5.3	1.0	1.8
P1xP3	0.0	0.0	1.7	4.3	1.5
P1xP4	0.3	0.0	2.0	0.0	0.6
P1xP5	0.0	0.0	3.7	0.3	1.0
P1xP6	0.0	0.0	5.3	1.0	1.6
P2xP2	0.3	0.0	3.0	0.3	0.9
P2xP3	0.0	0.0	3.0	0.7	0.9
P2xP4	0.0	0.0	4.7	5.0	2.4
P2xP5	0.0	0.0	3.7	0.7	1.1
P2xP6	0.0	0.3	5.3	1.0	1.7
P3xP3	0.0	0.7	3.0	0.3	1.0
P3xP4	0.3	0.0	3.7	1.3	1.3
P3xP5	0.3	0.0	7.7	1.0	2.3
P3xP6	0.3	0.7	7.0	0.3	2.1
P4xP4	0.0	0.7	3.7	0.7	1.3
P4xP5	0.7	0.0	1.7	0.0	0.6
P4vP6	0.0	0.0	4.0	0.0	1.0
P5xP5	0.0	1.3	3.3	0.7	1.3
P5xP6	0.0	0.0	2.0	1.3	0.8
P6xP6	0.3	0.0	2.7	0.0	0.8
Check	0.3	0.0	3.0	0.0	0.8
Mean	0.2	0.2	3.7	0.9	1.2
Parental mean	0.2	0.5	2.9	0.5	1.0
Hybrid mean	0.1	0.1	4.1	1.2	1.4
$Lsd_{(0.05)}$	0.7	0.9	6.0	3.4	1.7

Parental lines bolded

Table 17: Root lodging across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	9.0	7.0	2.7	0.0	4.7
P1xP2	3.7	2.3	0.0	0.0	1.5
P1xP3	7.3	14.0	2.3	0.7	6.1
P1xP4	3.7	7.7	3.3	0.0	3.7
P1xP5	6.0	5.3	3.3	0.0	3.7
P1xP6	5.7	9.3	6.0	0.3	5.3
P2xP2	5.0	5.7	5.0	1.0	4.2
P2xP3	6.3	7.0	7.3	0.0	5.2
P2xP4	6.3	9.3	2.0	0.3	4.5
P2xP5	9.3	13.0	2.3	0.7	6.3
P2xP6	5.0	11.3	2.3	0.0	4.7
P3xP3	4.3	9.0	0.0	0.7	3.5
P3xP4	2.3	12.7	6.7	0.3	5.5
P3xP5	3.3	9.0	3.3	0.3	4.0
P3xP6	3.3	8.0	1.3	0.7	3.3
P4xP4	1.0	7.3	1.3	0.0	2.4
P4xP5	5.3	3.7	0.3	0.3	2.4
P4vP6	3.3	3.7	0.7	0.7	2.1
P5xP5	4.3	17.3	2.7	1.3	6.4
P5xP6	3.0	9.7	4.0	0.7	4.3
P6xP6	2.7	5.0	4.7	0.3	3.2
Check	2.3	9.7	4.3	0.0	4.1
Mean	4.7	8.5	3.0	0.4	4.1
Parental mean	4.4	8.6	2.7	0.6	4.1
Hybrid mean	4.9	8.4	3.0	0.3	4.2
$Lsd_{(0.05)}$	5.3	10.7	5.7	1.1	3.6

Parental lines bolded

4.1.8 Grain yield

The analysis of variance revealed significant differences ($P<0.01$) among the genotypes for grain yield per hectare across the four locations. With the grand mean of 2.23 t/ha, the parental and

hybrid grain yield means were 2.20 t/ha and 2.23 t/ha respectively. The grain yield of the genotypes ranged from 1.45 t/ha to 2.45 t/ha for parents and 1.99 t/ha to 2.70 t/ha for the hybrids (Table 18).

Among the parents (inbreds), P3 produced the highest grain yield whilst P4 gave the lowest. For the hybrids, P1xP5 emerged as the highest yielding hybrid across the four locations and P2xP6 had the lowest among the hybrids. There were also significant differences ($P<0.05$) among the four locations with Akomadan producing the highest grain yield of 3.05 t/ha followed by Fumesua (2.47 t/ha), Pokuase (1.87 t/ha) and Ejura (1.54 t/ha). Genotype x location interaction effect was not significant.

4.1.9 Thousand grain weight

The analysis of variance indicated no significant differences among the genotypes and GXE effect for thousand grain weight. However, there were significant differences ($p<0.01$) among locations. Thousand grain weights at Akomadan (0.33kg) was significantly higher than at Fumesua (0.20kg), Pokuase (0.18kg) and Ejura (0.16kg) (Table 19).

Table 18: Grain yield (t/ha) across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	4.27	1.50	2.37	1.47	2.40
P1xP2	2.70	1.30	2.73	1.77	2.13
P1xP3	3.27	1.50	3.00	2.07	2.46
P1xP4	3.23	1.87	2.53	2.20	2.46
P1xP5	3.97	1.60	2.83	2.40	2.70
P1xP6	3.07	1.93	2.10	0.90	2.00
P2xP2	2.80	1.67	2.70	2.23	2.35
P2xP3	3.00	2.03	2.67	2.13	2.46
P2xP4	2.60	1.27	2.60	1.80	2.07
P2xP5	3.37	1.50	2.23	1.70	2.20
P2xP6	2.80	1.20	2.13	1.83	1.99
P3xP3	3.03	1.80	2.67	2.30	2.45
P3xP4	2.43	1.73	2.27	1.83	2.07
P3xP5	3.37	1.70	1.93	2.03	2.26
P3xP6	2.67	1.50	2.27	1.97	2.10
P4xP4	1.60	0.73	1.90	1.57	1.45
P4xP5	3.50	1.10	2.07	1.70	2.09
P4vP6	2.67	1.40	2.40	1.57	2.01
P5xP5	3.03	1.83	2.90	1.97	2.43
P5xP6	3.40	1.80	2.90	2.00	2.53
P6xP6	3.30	1.17	2.20	1.77	2.11
Check	3.03	1.73	2.90	1.90	2.39
Grand mean	3.05	1.54	2.47	1.87	2.23
Parental mean	3.01	1.45	2.46	1.89	2.20
Hybrid mean	3.07	1.56	2.44	1.86	2.23
Lsd $_{(0.05)}$	1.27	0.98	0.91	1.00	0.51

Parental lines bolded

Table 19: Thousand grain weight (kg) across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	0.33	0.15	0.19	0.16	0.21
P1xP2	0.32	0.15	0.18	0.19	0.21
P1xP3	0.32	0.16	0.25	0.19	0.23
P1xP4	0.31	0.16	0.20	0.18	0.21
P1xP5	0.32	0.16	0.20	0.19	0.22
P1xP6	0.32	0.17	0.21	0.15	0.21
P2xP2	0.34	0.16	0.19	0.19	0.22
P2xP3	0.32	0.16	0.19	0.20	0.22
P2xP4	0.32	0.16	0.19	0.17	0.21
P2xP5	0.31	0.16	0.20	0.19	0.22
P2xP6	0.34	0.16	0.19	0.18	0.22
P3xP3	0.34	0.16	0.21	0.16	0.22
P3xP4	0.34	0.16	0.21	0.16	0.21
P3xP5	0.34	0.15	0.19	0.16	0.22
P3xP6	0.32	0.16	0.21	0.18	0.21
P4xP4	0.33	0.15	0.19	0.17	0.21
P4xP5	0.31	0.16	0.19	0.18	0.21
P4vP6	0.32	0.16	0.17	0.19	0.22
P5xP5	0.33	0.17	0.22	0.17	0.22
P5xP6	0.33	0.16	0.19	0.18	0.21
P6xP6	0.32	0.16	0.18	0.17	0.21
Check	0.33	0.15	0.21	0.16	0.21
Grand mean	0.33	0.16	0.20	0.18	0.21
Parental mean	0.33	0.16	0.20	0.17	0.22
Hybrid mean	0.32	0.16	0.20	0.18	0.22
Lsd $_{(0.05)}$	0.02	0.01	0.04	0.03	0.02

Parental lines bolded

4.1.10 Cob length and diameter

There were no significant differences among genotypes for cob length. With the grand mean of 12.8cm, it ranged between 12.3cm to 13.1cm for the parents and 12.3cm to 13.2cm the hybrids (Table 20). On the other hand, significant differences ($p<0.01$) existed among the locations. The cob length at Akomadan (13.1cm) was significantly ($p<0.01$) longer than Fumesua (12.8cm), Pokuase (12.9cm) and Ejura (12.2cm). No significant differences were observed among the genotypes for cob diameter. The cob diameter varied from 3.6cm to 3.9cm for parental lines and 3.7cm to 3.9cm for the hybrids (Table 21). Again, there were significant differences ($p<0.05$) among locations for the cob diameter. The bigger cob was recorded at Akomadan (4.0cm) and Fumesua (4.0cm), followed by Pokuase (3.7cm) and Ejura (3.5cm).

4.1.11 Number of rows per cob and number of kernels per row

No statistical differences were observed among the genotypes ($P>0.05$) but, significant differences ($p<0.05$) existed among the locations. Mean number of rows per cob ranged between 13 and 14 rows for inbreds and hybrids (Table 22). Akomadan and Fumesua (14 rows) had the same mean number of rows per cob and was same at Pokuase and Ejura (13 rows). At Akomadan, there were significant differences ($p<0.05$) between P1xP1 (15 rows) and P5xP5 (11 rows); and P1xP4 (15 rows) and P3xP6 (12 rows) among parental lines and hybrids respectively. There were significant differences among genotypes across all locations but no significant differences ($p<0.05$) existed among locations for number of kernels per row. Mean number of kernels per row for parental lines and hybrids ranged from 28 to 29, and 27 to 31 kernels, respectively (Table 23). The mean number

of kernels per row at Akomadan (30 kernels) and Ejura (29 kernels) were significantly ($p<0.01$) different from Fumesua (28 kernels) and Pokuase (28 kernels).

Table 20: Cob length (cm) across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	13.9	12.1	12.8	13.6	13.1
P1xP2	11.8	12.0	14.0	12.5	12.6
P1xP3	14.0	12.6	12.6	12.5	12.9
P1xP4	13.5	12.2	13.2	12.9	12.9
P1xP5	13.2	11.8	13.4	13.6	13.0
P1xP6	13.6	12.9	12.3	13.0	13.0
P2xP2	12.9	12.4	13.0	12.7	12.8
P2xP3	13.3	11.8	12.3	12.5	12.5
P2xP4	12.6	12.3	14.1	13.8	13.2
P2xP5	13.0	12.5	12.8	12.7	12.7
P2xP6	12.4	11.0	12.4	13.3	12.3
P3xP3	12.8	12.6	12.6	13.2	12.8
P3xP4	12.2	12.8	11.9	12.9	12.4
P3xP5	13.2	12.1	12.1	12.9	12.6
P3xP6	12.7	12.8	12.3	12.5	12.6
P4xP4	13.0	11.5	13.2	13.3	12.8
P4xP5	13.5	13.1	11.9	12.9	12.9
P4vP6	12.8	11.9	13.9	12.4	12.8
P5xP5	12.6	12.8	12.2	12.7	12.6
P5xP6	14.3	12.3	12.9	13.2	13.2
P6xP6	12.8	11.3	12.6	12.6	12.3
Check	13.0	12.2	12.4	12.9	12.6
Mean	13.1	12.2	12.8	12.9	12.7
Parental mean	13.0	12.1	12.7	13.0	12.7
Hybrid mean	13.1	12.3	12.8	12.9	12.8
$Lsd_{(0.05)}$	1.4	2.4	1.5	1.7	0.9

Parental lines bolded

Table 21: Cob diameter (cm) across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	4.3	3.6	4.0	3.6	3.9
P1xP2	4.1	3.3	4.4	3.6	3.8
P1xP3	4.2	3.7	4.0	3.7	3.9
P1xP4	4.0	3.2	4.1	3.7	3.8
P1xP5	4.2	3.5	4.2	3.7	3.9
P1xP6	4.0	3.8	4.1	3.4	3.8
P2xP2	4.3	3.3	4.3	3.7	3.9
P2xP3	3.9	3.6	3.9	3.5	3.7
P2xP4	4.1	3.5	4.1	3.9	3.9
P2xP5	4.0	3.6	3.9	3.9	3.8
P2xP6	4.1	3.1	4.1	3.8	3.8
P3xP3	3.9	3.7	4.1	3.6	3.8
P3xP4	3.7	3.6	3.7	3.6	3.7
P3xP5	4.1	3.7	4.0	3.6	3.8
P3xP6	3.7	3.8	3.9	3.7	3.8
P4xP4	3.8	3.1	3.9	3.7	3.6
P4xP5	4.3	3.5	3.7	3.7	3.8
P4vP6	4.0	3.4	3.9	3.7	3.8
P5xP5	3.7	3.9	4.1	3.7	3.8
P5xP6	4.1	3.6	4.0	3.9	3.9
P6xP6	4.2	3.6	3.8	4.0	3.9
Check	4.0	3.7	4.0	3.8	3.9
Mean	4.0	3.5	4.0	3.7	3.8
Parental mean	4.0	3.5	4.0	3.7	3.8
Hybrid mean	4.0	3.5	4.0	3.7	3.8
$Lsd_{(0.05)}$	0.4	0.5	0.4	0.5	0.2

Parental lines bolded

Table 22: Number of rows per cob across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	15	13	13	13	13
P1xP2	14	12	14	14	14
P1xP3	13	13	14	12	13
P1xP4	15	13	14	13	14
P1xP5	14	14	14	12	14
P1xP6	14	14	13	13	13
P2xP2	14	12	14	13	13
P2xP3	13	12	13	12	13
P2xP4	14	13	14	14	13
P2xP5	14	13	13	14	13
P2xP6	14	12	14	13	13
P3xP3	13	13	14	13	13
P3xP4	13	14	13	13	13
P3xP5	13	13	13	14	13
P3xP6	12	14	14	13	13
P4xP4	14	12	13	14	13
P4xP5	14	13	13	13	13
P4vP6	13	13	13	13	13
P5xP5	11	14	13	13	13
P5xP6	13	12	15	14	14
P6xP6	15	14	13	13	14
Check	14	13	13	14	14
Mean	14	13	14	13	13
Parental mean	14	13	13	13	13
Hybrid mean	14	13	14	13	13
$Lsd_{(0.05)}$	2	2	2	2	1

Parental lines bolded

Table 23: Number of kernel per row across four locations

Genotype	Akomadan	Ejura	Fumesua	Pokuase	Mean
P1xP1	31	30	28	27	29
P1xP2	30	25	29	28	28
P1xP3	29	30	27	26	28
P1xP4	31	28	29	29	29
P1xP5	31	32	29	30	31
P1xP6	31	30	27	26	29
P2xP2	31	30	27	28	29
P2xP3	32	31	27	27	29
P2xP4	29	28	31	30	30
P2xP5	29	29	27	27	28
P2xP6	28	25	26	28	27
P3xP3	28	31	28	29	29
P3xP4	28	30	26	27	28
P3xP5	30	31	26	29	29
P3xP6	28	30	25	26	27
P4xP4	29	25	30	30	29
P4xP5	32	29	28	27	29
P4vP6	28	27	29	26	28
P5xP5	27	30	29	28	28
P5xP6	32	30	29	28	30
P6xP6	31	26	28	27	28
Check	32	30	27	28	29
Mean	30	29	28	28	29
Parental mean	30	29	28	28	29
Hybrid mean	30	29	28	28	29
$Lsd_{(0.05)}$	4	5	4	5	2

Parental lines bolded

4.2. Stability analysis for the genotypes across four locations

4.2.1 Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield

In the AMMI analysis of stability and adaptability for grain yield (Table 24), two PCA axes were generated to decompose genotype × environment interaction and both were not significant. On the other hand, the main effects of genotype and environment were significant at (P<0.01) and (P<0.001), respectively but the contribution of environment (35.8%) was higher than genotypes (10.4%).

Table 24: AMMI Analysis of grain yield

Source	DF	SS	MS	F	F_prob	% of total $_{ss}$
Total	263	155797429	592386			
Treatments	87	89778856	1031941	2.74	0.001	
Genotypes	21	16206650	771745	2.05	0.01	10.40
Environment	3	55432532	18477511	52.75	0.00000	35.78
Block	8	2802021	350253	0.93	0.49257	
Interaction	63	18139674	287931	0.77	0.88866	
IPCA1	23	10621260	461794	1.23	0.22806	
IPCA2	21	4462626	212506	0.56	0.93696	
Residual	19	3055787	160831	0.43	0.98307	
Error	168	63216552	376289			

(SS) Sum of squares, (MS) Mean square, (DF) Degree of freedom, and F-test used to measure significant at 0.01 F probability level.

4.2.2 Mean performance and stability analysis of genotypes using GGE biplot

The combined means of the genotypes across the four locations were used for the biplot analysis. At Akomadan and Pokuase, P1 (1) and P3 (12) respectively emerged as the best whiles P1xP5 (5) was the best genotype at both Fumesua and Ejura (Fig1).

The most stable genotype was P5xP6 (20) but was not significantly different from P1xP5 (5) which was the best yielding genotype (Fig 2). Although P2xP6 (11) was more stable across all locations, it was low yielding. The least stable genotypes were P1xP1 (1) and P1xP6 but P1xP1 (1) was high yielding whilst P1xP6 was low yielding.

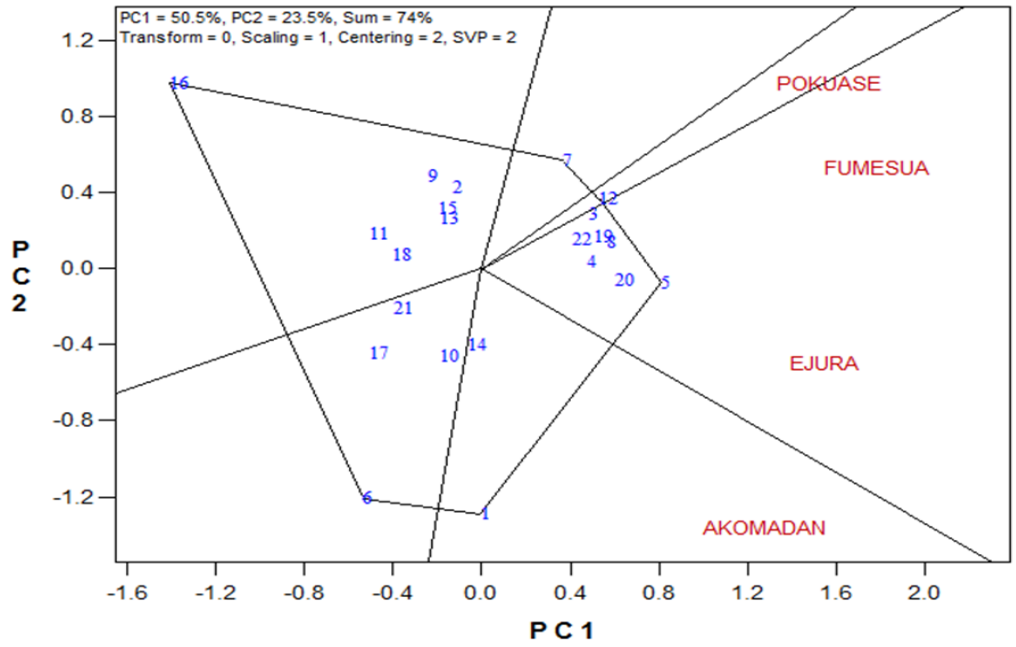

Figure 1: Biplot for grain yield across the four locations (For genotypes names refer to Table 2)

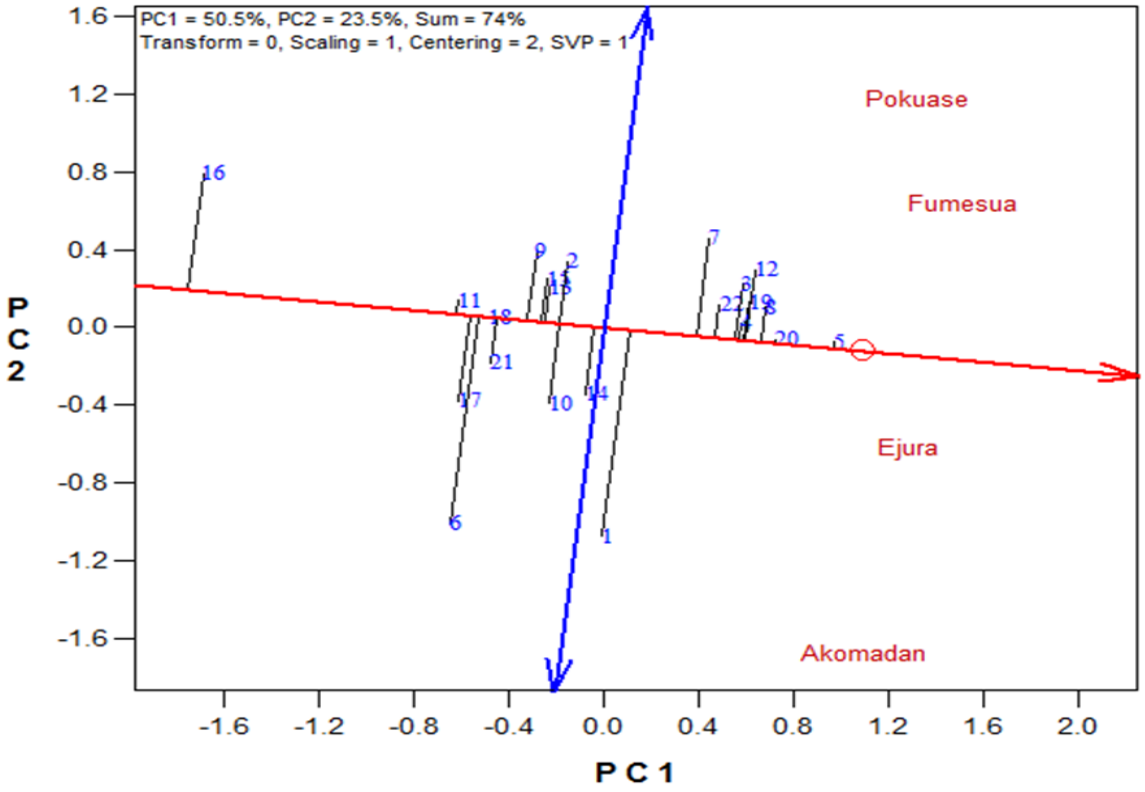

Figure 2: GGE biplot for average grain yield and stability of maize genotypes (For genotypes names refer to Table 2)

4.3 Phenotypic correlation among traits across the locations

Results from phenotypic correlation showed that grain yield had a highly positive correlation ($P<0.001$) with plant height, ear height, cob length, cob diameter and number of rows per cob at Ejura and Akomadan (Tables 25 and 27). At Ejura, root lodging had high significant ($P<0.01$) and positive correlation with grain yield, plant height, ear height, and cob diameter (Table 25).

In addition, grain yield showed highly positive correlation with thousand grain weight and number of kernels per row across the locations (Table 29). At flowering there was a highly significant ($P<0.001$) positive association between days to 50% anthesis and silking at each location and

across locations. However, DTS and DTA correlated negatively ($P<0.05$) with plant height, ear height, cob length, cob diameter, and stem lodging across all the locations. There was no association between days to silking and number of kernels per row (Table 29).

The combined analysis of phenotypic associations between plant height and ear height showed positive and highly significant ($P<0.001$) correlation, and both had similar association with cob length, cob diameter, number of rows per cob and number of kernels per row. On the other hand, plant height and ear height had negative and highly significant ($P<0.01$) correlation with root lodging (Table 29). Thousand grain weight significantly ($P<0.01$) correlated positively with plant height, cob length, cob diameter, number of rows per cob and number of kernels per row across all the locations. It was however observed to have negative and highly significant ($P<0.01$) correlation with stem lodging. The association between cob length and cob diameter was significant ($P<0.001$) positive, and both traits correlated similarly with number of rows per cob at each location except Akomadan (Table 29).

Table 25: Phenotypic correlation matrix of measured traits at Ejura

	GY	DTA	DTS	ASI	PHT	EHT	TGW	CL	CD	NRC	NKR	SL
GY	-											
DTA	-0.51***	-										
DTS	-0.49***	0.97***	-									
ASI	0.05	0.04	0.29*	-								
PHT	0.65***	-0.75***	-0.74***	-0.11	-							
EHT	0.39***	-0.58***	-0.55***	0.04	0.6***	-						
TGW	0.27*	-0.21	-0.23	-0.11	0.15	0.18	-					
CL	0.61***	-0.33**	-0.33**	-0.07	0.52***	0.31*	0.27*	-				
CD	0.59***	-0.31*	-0.3*	-0.02	0.51***	0.31*	0.29*	0.65***	-			
NRC	0.39***	-0.32**	-0.32**	-0.05	0.41***	0.21	0.26	0.37**	0.64***	-		
NKR	0.71***	-0.34**	-0.33**	0	0.53***	0.22	0.34**	0.69***	0.64***	0.4***	-	
SL	0.08	-0.09	0.05	-0.12	-0.02	0.08	-0.09	-0.01	0.08	0.15	-0.22	-
RL	0.41***	-0.37**	-0.37**	-0.07	0.49**	0.34**	0.22	0.25*	0.35**	0.27	0.23	0.14

(GY) grain yield, (DTA) days to 50% anthesis (DTS) days to 50% silking, (ASI) anthesis-silking interval, (PHT) plant height, (EHT) ear height, (TGW) thousand grain weight, (CL) cob length, (CD) diameter, (NRC) number of rows per cob, (NKR) number of kernels per row, (SL) stem and (RL) root lodging
=significant (P<0.05), **=high significant (P<0.01), *= highly significant (P<0.001)*

Table 26: Phenotypic correlation matrix of measured traits at Fumesua

	GY	DTA	DTS	ASI	PHT	EHT	TGW	CL	CD	NRC	NKR	SL
GY	-											
DTA	-0.17	-										
DTS	-0.13	0.91***	-									
ASI	0.11	-0.26*	0.16	-								
PHT	0.45***	-0.27*	-0.13	0.32**	-							
EHT	0.44***	-0.24*	-0.14	0.25*	0.77**	-						
TGW	0.24	-0.14	-0.19	-0.11	-0.23	-0.17	-					
CL	0.3*	0.13	0.12	-0.03	0.42***	0.41***	-0.24	-				
CD	0.35**	0.15	0.11	-0.1	0.15	0.22	-0.1	0.53***	-			
NRC	0.18	0.11	0.18	0.15	0.13	0.23	-0.13	0.25*	0.51***	-		
NKR	0.12	-0.08	-0.08	0.01	0.53***	0.41***	-0.29	0.44**	0.19	0.19	-	
SL	-0.18	0.23	0.32**	0.19	-0.15	-0.1	-0.11	0.05	0.1	0.17	-0.3*	-
RL	-0.05	-0.17	-0.17	0	-0.17	-0.04	0.17	-0.23	-0.1	-0.02	-0.14	-0.11

(GY) grain yield, (DTA) days to 50% anthesis (DTS) days to 50% silking, (ASI) anthesis-silking interval, (PHT) plant height, (EHT) ear height, (TGW) thousand grain weight, (CL) cob length, (CD) diameter, (NRC) number of rows per cob, (NKR) number of kernels per row, (SL) stem and (RL) root lodging

=significant (P<0.05), **=high significant (P<0.01), *= highly significant (P<0.001)*

Table 27: Phenotypic correlation matrix of measured traits at Akomadan

	GY	DTA	DTS	ASI	PHT	EHT	TGW	CL	CD	NRC	NKR	SL
GY	-											
DTA	-0.18	-										
DTS	-0.21	0.91***	-									
ASI	-0.09	-17	0.24*	-								
PHT	0.53***	0.03	0.01	-0.04	-							
EHT	0.54***	0.04	0.05	0.03	0.84***	-						
TGW	-0.13	0	0.01	0.01	-0.02	0.06	-					
CL	0.52***	0.14	0.13	-0.01	0.51***	0.63***	-0.03	-				
CD	0.62***	-0.34***	-0.25*	0.21	0.32**	0.45***	-0.1	0.43***	-			
NRC	0.3*	-0.16	-0.05	0.26*	0.3*	0.37**	-0.31	0.11	0.48***	-		
NKR	0.32**	0.17	0.16	-0.02	0.51***	0.55***	-0.07	0.46***	0.33**	0.47**	-	
SL	0.04	0.19	0.21	0.06	-0.09	0.08	-0.14	-0.05	0.1	0.29*	0.12	-
RL	0.12	0.06	0.09	0.1	-0.03	0.04	0.12	0.01	0.29*	0.14	0.18	0.15

(GY) grain yield, (DTA) days to 50% anthesis (DTS) days to 50% silking, (ASI) anthesis-silking interval, (PHT) plant height, (EHT) ear height, (TGW) thousand grain weight, (CL) cob length, (CD) diameter, (NRC) number of rows per cob, (NKR) number of kernels per row, (SL) stem and (RL) root lodging

=significant (P<0.05), **=high significant (P<0.01), *= highly significant (P<0.001)*

Table 28: Phenotypic correlation matrix of measured traits at Pokuase

	GY	DTA	DTS	ASI	PHT	EHT	TGW	CL	CD	NRC	NKR	SL
GY	-											
DTA	-0.22	-										
DTS	-0.34**	0.86***	-									
ASI	-0.25*	-0.13	0.41***	-								
PHT	0.06	-0.24	-0.25*	-0.05	-							
EHT	0.12	-0.21	-0.22	-0.04	0.91***	-						
TGW	0.18	0.08	-0.05	-0.23	-0.24	-0.21	-					
CL	0.46***	-0.13	-0.13	-0.01	0.2	0.28*	-0.07	-				
CD	0.47***	0.05	-0.07	-0.22	0.14	0.24	0.13	0.53***	-			
NRC	0.22	-0.24	-0.23	-0.12	0.2	0.29*	-0.18	0.37**	0.47***	-		
NKR	0.6***	-0.24	-0.35**	-0.25*	0.16	0.26*	-0.03	0.73***	0.44***	0.33**	-	
SL	0.14	0.11	0.17	0.14	0.11	0.2	-0.09	0.21	0.36**	0.16	0.1	-
RL	-0.01	-0.05	-0.08	-0.06	-0.35**	0.31**	0.03	-0.21	-0.02	-0.16	-0.15	-0.1

(GY) grain yield, (DTA) days to 50% anthesis (DTS) days to 50% silking, (ASI) anthesis-silking interval, (PHT) plant height, (EHT) ear height, (TGW) thousand grain weight, (CL) cob length, (CD) diameter, (NRC) number of rows per cob, (NKR) number of kernels per row, (SL) stem and (RL) root lodging

=significant (P<0.05), **=high significant (P<0.01), *= highly significant (P<0.001)*

Table 29: Phenotypic correlation matrix of measured traits across all the locations

	GY	DTA	DTS	ASI	PHT	EHT	TGW	CL	CD	NRC	NKR	SL
GY	-											
DTA	-0.27***	-										
DTS	-0.3***	0.94***	-									
ASI	-0.15*	0.04	0.39***	-								
PHT	0.56***	-0.43***	-0.44***	-0.12	-							
EHT	0.33***	-0.39***	-0.38***	-0.08	0.74***	-						
TGW	0.61***	0.01	-0.01	-0.07	0.38***	0.05	-					
CL	0.47***	-0.15*	-0.16	-0.08	0.49***	0.43***	0.15**	-				
CD	0.68***	-0.27***	-0.3***	-0.17**	0.47***	0.34***	0.42***	0.55***	-			
NRC	0.34***	-0.2**	-0.17**	0.04	0.3***	0.26***	0.12**	0.31***	0.55***	-		
NKR	0.39***	0.01	0	-0.02	0.27***	0.16**	0.16**	0.54***	0.36***	0.34***	-	
SL	0.04	-0.16**	-0.17**	-0.06	0.05	0.14**	-0.16**	0.07*	0.25***	0.17**	-0.19**	-
RL	0.02	0.13**	0.17**	0.13*	-0.23**	-0.18**	0.01	-0.07	0.02	0.06	0.19**	-0.14*

(GY) grain yield, (DTA) days to 50% anthesis (DTS) days to 50% silking, (ASI) anthesis-silking interval, (PHT) plant height, (EHT) ear height, (TGW) thousand grain weight, (CL) cob length, (CD) diameter, (NRC) number of rows per cob, (NKR) number of kernels per row, (SL) stem and (RL) root lodging

=significant (P<0.05), **=high significant (P<0.01), *= highly significant (P<0.001)*

4.4 Combining ability

When the genotypic sum of squares was partitioned into general combining ability (GCA) and specific combining ability (SCA), only GCA was found to be significant ($p< 0.01$) and for only grain yield. Estimates of GCA effects indicated parental performances of the traits across all the locations (Tables 30 and 31). For days to flowering (anthesis and silking), the highest and lowest GCA values were observed for P4 and P3, respectively. However, P4 had the least GCA values for grain yield, thousand grain weight, cob diameter, plant height and root lodging whilst P3 had the least for stem lodging. P5 had the highest parental GCA value for grain yield, number of kernels per row and root lodging. P1 was the best general combiner for plant height, ear height, cob length, cob diameter and number of rows per cob but exhibited the least and negative value for anthesis-silking interval. P6 had the least GCA effect for cob length and number of kernels per row but had the highest observed GCA value for anthesis-silking interval. The crosses P1xP4 and P5xP6 had the highest SCA effect for grain yield but P1xP4 had the highest negative SCA effects for both days to anthesis and silking (Table 33 and 34). Similarly, P5xP6 had the highest SCA effects for anthesis-silking interval, plant height, cob length and number of kernels per row. The cross combinations P1xP5 and P1xP6 had the least SCA values for anthesis-silking interval with the latter combination emerging as the least for grain yield. P1xP3 gave high negative SCA effects for both plant and ear heights and high positive value for root lodging. P4 also produced negative SCA effects for stem lodging in all crosses except for P2xP4, which had positive SCA effects for both stem and root lodging. P1xP4 however had a high positive SCA effect for cob length, cob diameter, number of rows per cob and number of kernels per row. Similarly, P5xP6 had positive SCA effects for all the traits estimated with the exception of stem and root lodging.

Table 30: Estimates of general combining ability (GCA) of parents for vegetative traits

Parents	PHT	EHT	RL
P1	1.783	1.019	0.076
P2	0.225	-0.547	0.191
P3	0.760	0.911	0.264
P4	-2.215	-0.249	-0.747
P5	-0.544	-0.674	0.576
P6	-0.010	-0.460	-0.361

(PHT) plant height, (EHT) ear height, and (RL) root lodging.

Table 31: Estimates of general combining ability (GCA) of parents for reproductive traits

Parents	GY	DTA	DTS	ASI	TGW	CL	CD	SL	NRC	NKR
P1	0.122	-0.128	-0.122	-6.875	-0.001	0.173	0.034	-0.135	0.135	0.361
P2	-0.003	-0.045	0.014	-2.875	0.000	-0.061	0.020	0.104	0.021	-0.087
P3	0.084	-0.253	-0.247	0.000	0.003	-0.086	-0.024	0.156	-0.177	-0.139
P4	-0.247	0.424	0.337	2.000	-0.003	0.055	-0.073	-0.052	-0.042	-0.045
P5	0.134	0.017	0.024	3.375	0.001	0.029	0.028	-0.052	-0.042	0.372
P6	-0.091	-0.014	-0.007	4.375	-0.002	-0.110	0.015	-0.021	0.104	-0.462

(GY) grain yield, (DTA) days to 50% anthesis (DTS) days to 50% silking, (ASI) anthesis-silking interval, (TGW) thousand grain weight, (CL) cob length, (CD) diameter (SL) stem lodging (NRC) number of rows per cob, and (NKR) number of kernels per row.

Table 32: Specific combining ability (SCA) effects for grain yield

Parents	P1	P2	P3	P4	P5	P6
P1	-0.068	-0.218	0.028	0.360	0.220	-0.255
P2		0.132	0.153	0.093	-0.155	-0.138
P3			0.057	0.005	-0.184	-0.118
P4				-0.280	-0.020	0.122
P5					-0.059	0.257
P6						0.132

Table 33: Specific combining ability (SCA) effects for vegetative traits

Hybrids	PHT	EHT	RL
P1xP2	-1.542	-3.395	-2.906
P1xP3	-9.794	-8.254	1.604
P1xP4	2.715	-1.543	0.198
P1xP5	1.260	1.299	-1.125
P1xP6	1.394	2.417	1.479
P2xP3	5.631	-0.695	0.573
P2xP4	5.223	2.580	0.917
P2xP5	3.819	1.624	1.427
P2xP6	-5.331	2.915	0.698
P3xP4	-4.679	-2.333	1.844
P3xP5	1.500	-4.718	-0.979
P3xP6	-10.650	1.607	-0.708
P4xP5	2.492	-3.558	-1.552
P4xP6	-3.675	6.236	-0.948
P5xP6	8.888	4.744	-0.021

(PHT) plant height, (EHT) ear height, and (RL) root lodging

Table 34: Specific combining ability (SCA) effects for reproductive traits

Hybrids	GY	DTA	DTS	ASI	TGW	CL	CD	SL	NRC	NKR
P1xP2	-0.218	0.420	0.100	0.750	-0.005	-0.263	-0.030	0.519	0.237	-0.743
P1xP3	0.028	0.461	0.527	-1.125	0.012	0.095	0.065	0.217	-0.232	-0.774
P1xP4	0.360	-0.799	-0.973	-2.125	0.001	-0.037	-0.011	-0.491	0.299	0.382
P1xP5	0.220	0.274	0.423	-2.500	0.002	0.047	0.013	-0.074	0.132	1.299
P1xP6	-0.255	0.305	0.621	-2.500	0.001	0.136	-0.016	0.478	-0.180	0.216
P2xP3	0.153	0.628	0.808	-0.125	0.002	-0.130	-0.072	-0.606	-0.451	1.007
P2xP4	0.093	-0.716	-0.775	-1.125	-0.004	0.438	0.127	1.103	0.164	0.997
P2xP5	-0.155	-0.143	-0.046	-1.500	0.000	0.022	-0.040	-0.231	0.164	-1.003
P2xP6	-0.138	-0.362	-0.348	-1.500	0.004	-0.306	-0.069	0.321	0.018	-1.170
P3xP4	0.005	-0.591	-0.432	0.000	0.001	-0.279	-0.053	-0.033	-0.055	-0.868
P3xP5	-0.184	-0.435	-0.536	-0.375	-0.009	-0.120	0.013	0.884	0.278	0.132
P3xP6	-0.118	0.597	0.329	-0.375	0.004	0.044	-0.050	0.686	-0.034	-0.618
P4xP5	-0.020	0.305	0.214	0.625	-0.003	0.031	0.037	-0.574	-0.190	0.039
P4xP6	0.122	0.003	-0.004	0.625	0.000	0.053	-0.009	-0.189	-0.336	-0.628
P5xP6	0.257	0.409	0.225	1.250	0.002	0.488	0.040	-0.356	0.164	1.455

(GY) grain yield, (DTA) days to 50% anthesis (DTS) days to 50% silking, (ASI) anthesis-silking interval, (TGW) thousand grain weight, (CL) cob length, (CD) diameter (SL) stem lodging (NRC) number of rows per cob, and (NKR) number of kernels per row.

4.5 Mid-parent heterosis

The mid parent heterosis estimates for the respective 15 hybrid combinations are shown in Tables 35 and 36. For grain yield, the highest positive mid-parent heterosis was observed in the hybrid P1xP4 followed by P4xP6, P1xP5, P5xP6, P2xP4, P4xP5, P2xP3 and P1xP3 whilst the remaining hybrids had negative estimates. Mid-parent heterosis for grain yield ranged from -15.16 to 26.15% with an average estimate of 0.99% for the 15 hybrids (Table 36). For days to flowering, it ranged between -2.41% and 2.08% for DTA, and -3.24 to 1.94% for DTS with an averages of 0.21% and 0.25% for days to anthesis and silking respectively. The average estimate of mid-parent heterosis for anthesis-silking interval was -6.96% and ranged from -85.19 to 10.55%. Most of the hybrids had negative mid-parent heterosis for plant height except for P1xP5, P2xP3, P2xP4, P2xP5, P3xP5, P4xP5, and P5xP6. Similarly except for 7 hybrids (P1xP2, P1xP3, P1xP4, P2xP3, P2xP6, P3xP4 and P3xP6). The average estimate of mid-parent heterosis for plant height was -0.36% and ranged from of -9.99% to 6.70%. A range of -12.71 to 14.56% with an average of 1.25% was observed for the ear height (Table 35). For thousand grain weight, the range was -2.33 to 6.98% with 0.47% as the average for 15 hybrids. Cob length and cob diameter had 0.41% and 0.42% for average mid-parent heterosis estimate for 15 hybrids and ranged from -2.58 to 5.66% and -3.08 to 3.59% respectively (Table 36). The mid-parent value for number of rows per cob also ranged from -4.09 to 6.55% with an average of 0.47%, whilst number of kernels per row had an average of -0.12% and ranged from -5.54 to 6.51%. Stem and root lodging respectively had a mid-parent heterosis range of -54.26 to 137.71% and -66.06 to 85.81% with averages of 45.09% and 6.15%, respectively.

Table 35: Mid-parent heterosis estimates for vegetative traits

Hybrids	PHT	EHT	RL
P1xP2	-0.64	-7.11	-66.06
P1xP3	-8.97	-12.71	48.84
P1xP4	-0.15	-3.89	3.53
P1xP5	2.57	2.91	-33.81
P1xP6	-1.41	2.6	35.97
P2xP3	1.8	-0.21	34.1
P2xP4	4.72	4.1	36.57
P2xP5	6.23	9.38	19.55
P2xP6	-3.4	-0.16	27.25
P3xP4	-5.09	-8.95	85.81
P3xP5	0.89	2.33	-19.35
P3xP6	-9.99	-6.33	-0.15
P4xP5	4.7	9.36	-45.25
P4xP6	-3.29	12.94	-25.22
P5xP6	6.7	14.56	-9.49
Mean	-0.36	1.25	6.15

(PHT) plant height, (EHT) ear height, and (RL) root lodging.

Table 36: Mid-parent heterosis estimates for reproductive traits

Hybrids	GY	DTA	DTS	ASI	TGW	CL	CD	SL	NRC	NKR
P1xP2	-10.32	1.11	0.4	-11.82	-2.33	-2.55	-1.29	120.25	2.51	-3.01
P1xP3	1.44	1.97	1.71	2.9	6.98	-0.11	1.04	79.64	-2.22	-3.32
P1xP4	26.15	-2.18	-2.47	-7.75	0	-0.04	0.4	-39.58	2.51	3.35
P1xP5	11.8	1.11	0.4	4.66	2.33	1.21	0.77	0	6.55	6.51
P1xP6	-11.31	1.46	1.94	10.39	0	1.81	-1.03	122.54	0.92	0.44
P2xP3	2.5	1.55	-3.24	-85.19	0	-2.23	1.3	-4.17	-4.09	1.73
P2xP4	8.95	-2.41	-0.56	-1.57	-2.33	3.33	3.32	123.04	1.28	2.61
P2xP5	-6.49	-0.16	-0.89	1.57	0	0.91	-1.03	-0.03	2.56	-2.62
P2xP6	-10.76	-0.33	-0.41	10.55	-2.33	-2.07	-3.08	100	-0.3	-5.54
P3xP4	-6.15	-1.76	-1.44	4.43	0	-2.58	-1.48	18.22	-1.59	-4.03
P3xP5	-15.16	-0.34	-0.57	-4.3	-2.33	-0.79	0	93.13	2.19	0.87
P3xP6	-7.89	2.08	1.39	-10.39	2.33	0.36	0.94	137.71	-0.75	-3.79
P4xP5	7.73	-0.09	-0.39	-6.18	2.33	1.58	2.01	-54.26	-0.65	1.75
P4xP6	12.92	-0.41	-0.55	-2.91	4.76	1.63	3.59	0	-3.42	-2.93
P5xP6	11.45	1.54	0.96	-8.83	-2.33	5.66	0.78	-20.19	1.54	6.19
Mean	0.99	0.21	-0.25	-6.96	0.47	0.41	0.42	45.09	0.47	-0.12

(GY) grain yield, (DTA) days to 50% anthesis (DTS) days to 50% silking, (ASI) anthesis-silking interval, (TGW) thousand grain weight, (NRC) number of rows per cob, and (NKR) number of kernels per row

CHAPTER FIVE

5.0 DISCUSSION

5.1 Performance of parental lines and hybrids

Generally, the yield performance of the hybrids was quite low. This is because QPM hybrids are noted to have low yields compared with non-QPM hybrids (Bhatnagar *et al*., 2003). The check (GH 110) used in this study is a single cross QPM hybrid between Entries 6 and 70 (inbred lines) from CRI. This single cross hybrid is used as female parent to produce three-way QPM hybrids which include Mamaba, Etubi and Enibi. The crosses P1×P5, P5×P6, P1×P3, P2×P3 and P1×P4 which had very good yields have very high potential as female parents in subsequent QPM three-way cross hybrids. Significant variations among hybrids and inbred lines for grain yield were identified across all the environments. The yields of some of the inbred lines (P1, P2, P3, and P5) were appreciably higher than the rest hence these parental lines may serve as valuable materials for QPM hybrid maize development and improvement. Again, their genetic potential may also be tapped by crossing them with other genetically different inbred lines or populations.

The cross P2×P3 had the least anthesis-silking interval suggesting a hybrid with good nick. This study also revealed high levels of lodging with root lodging being on the average higher than stem lodging. Although lodging is genetically influenced, environmental conditions and timing of harvest can also play a major role (Glover *et al.*, 2005). For instance, in this study, Ejura was the latest site to be harvested and increased frequency of lodging was clearly manifested. Lodging may also be attributed to pest attack. This is because at Akomadan, a significant presence of termites on the experimental field was associated with the lodging. Termites gradually degraded and weakened the root system and sometimes the stem, thereby

making the maize plant highly susceptible to lodging. The highly significant environmental effects on several traits including grain yield, suggests that these traits are influenced by environmental conditions. This confirms the significant environmental effects for grain yield and number of rows per cob reported by Soengas *et al.* (2003)

The non-significant genotype × environment interaction effects for all the traits except anthesis-silking interval indicates that the genotypes performed similarly across the environments. The existence of significant genotype × environment interaction for anthesis-silking interval suggests the relative performance of the genotypes with respect to flowering and pollen shed will be unstable under different environmental conditions.

5.2 Combining ability and heterosis

The significance of general combining ability (GCA) and specific combining ability (SCA) plays a vital role in developing appropriate breeding approaches. As proposed by Hallauer and Miranda (1988), general and specific combining ability estimates respectively provide relative genetic effects of additive gene and non-additive gene actions (dominance and epistasis). The results indicated highly significant additive gene action for grain yield indicating that further progress can be achieved in these genotypes through recurrent selection methods. This result corroborates the finding of Musila *et al.* (2010), who also found significant GCA and non-significant SCA effects for grain yield. Baker (1978) and Ojo *et al.* (2007) suggested that the non-significant differences in SCA estimate permit maximum utilization of GCA in predicting the performance of single cross hybrids. Again, Mhike *et al.* (2011) suggested possibility of exploring early testing of the genotypes due to the predominance of additive gene to non-additive gene actions. This method becomes more efficient and effective for selecting

promising hybrids based on their predictions from GCA effects. This presupposes that, early testing of the selected genotypes from the testcrosses from the studied population can be done for grain yield because of the predominance of GCA variances to SCA variances. The application of early testing becomes necessary since additive gene action is not affected by inbreeding depression. Hence traits that are under control of additive gene action will not suffer from inbreeding.

This assertion reflected in grain yield where the best performing hybrids (P1×P5 and P1×P3) were crosses between three inbred lines (P1, P3 and P5) with the highest GCA estimates for grain yield (0.122, 0.084 and 0.134 t/ha^{-1}, respectively) suggesting that these parents are potentially superior (Woyengo *et al.*, 2001). These parental lines had positive GCA effects for grain yield, indicating the presence of favourable alleles for grain yield. In addition, P1 was a good combiner for reduced days to flowering (both anthesis and silking), anthesis-silking interval, stem lodging and increased number of rows per cob, number of kernels per row, cob length and cob diameter. Consequently, P1 proved to be the best combiner for early maturity and high yields. Similarly, P3 had reduced days to flowering whilst P5 had reduced plant height, ear height and stem lodging suggesting that they have good potentials for use in maize improvement programmes. Although P4 and P6 were poor combiners for grain yield, both parents exhibited negative GCA effects for plant height, ear height, root and stem lodgings which suggests that these parents can be used for reduced plant height and lodging tolerance improvement. For increased grain yield, it is desirable to make selection based on yield components (Zare *et al.*, 2011). Hence P1 was the suitable genetic resource for cob length, cob diameter and number of rows per cob; P3 for thousand-grain weight, and P5 for number of kernels per row. In similar studies, non-significant GCA effects have been identified for plant height and cob length (Zare *et al.*, 2011). As suggested by Simmonds (1979), GCA effects of

parental lines also provide substantive information for selecting outstanding parents to make desirable crosses for advance breeding programmes.

The non-significant SCA effects observed in this study is possibly due to the use of parental lines that are related as proposed by Hill (1983). Similarly, non-significant SCA has been reported for grain yield (Filho *et al.,* 1981; Ojo *et al.,* 2007). To exploit the genetic potentials of these parents, they could be crossed with distantly related inbreds or populations. The SCA estimate gives heterotic response of parental interaction (heterosis) for specific traits (Zare *et al.,* 2011). The high SCA and mid-parent heterosis values for grain yield observed in the following combinations: P1×P4, P5×P6, P1×P5 and P4×P6 suggests that these crosses are suitable for increased grain yield. This was manifested in yield components such as number of kernels per row, number of rows per cob, cob length and diameter where positive SCA and mid-parent heterosis values were observed. The mid parent heterosis for some crosses were negative for days to anthesis and silking indicating earliness in maturity. The maximum negative heterosis for days to flowering recorded for P1×P4, P3×P4, P2×P4, P2×P5, P4×P6 and P4×P5 suggests that the parental lines involved in these crosses may be useful for producing extra-early maturing QPM hybrids. The advent erratic climatic conditions also poses serious threat to existing early maturing varieties there by making them susceptible to biotic and abiotic factors hence the promising hybrid combinations can be useful germplasm to replace them. Earliness in maturity also offers opportunity to utilize minor season cropping where the short rainy periods can efficiently be used for maize cultivation. High negative mid-parent heterosis for plant height was exhibited in the crosses P1×P3, P1×P4, P3xP4 and P3×P6 which also means that the parents could be used as germplasm source for developing short varieties.

5.3 Correlation among traits

Correlation analysis is an important tool for estimating the value and association of various characters with grain yield (Edmeades *et al*., 1997). The genetic association among traits plays a vital role in improving selection efficiency in plant breeding programmes. In selection programmes, grain yield and some yield components (such as number of rows per cob, cob length and diameter) are among the most economic traits usually targeted by plant breeders. The studies on relationships among yield and related characters could be important strategy for crop improvement. Therefore, special preferences should be given to these parameters when formulating indirect selection indices for grain yield improvement in maize.

The corroborative reports of significant positive correlation between grain yield and other yield components suggests that any one of the traits could be used to select indirectly for grain yield. For instance, Yousuf and Saleem, (2001), affirmed the opportunity to select plant height, number of kernels per row cob length (Ali *et al*., 2010) thousand-grain weight, cob diameter, and number of rows per cob (Rafiq *et al*., 2010) indirectly for grain yield. On the other hand, the strong positive correlation between traits (days to anthesis and silking; plant height and ear height) suggests that each of two pairs of traits may either be controlled by the same or similar genes or by genes with pleiotropic effect on these traits or may be controlled by closely linked genes (Brown and Caligari, 2008). However, both days to anthesis and silking exhibited negative significant correlation with grain yield, plant height, ear height, cob diameter and stem lodging. Hence, flowering days seems undesirable for indirect selection for these traits. The negative significant association between days to flowering and grain yield agrees with Jayakumar *et al.* (2007). Depending on the breeder's objectives, the strong positive association between plant height and ear height as well as their relationship with other traits (thousand-grain weight, cob length, cob diameter, number of rows per cob, number of kernels per row

and root lodging) can play a major role in formulating selection indices. The positive correlation among some yield components (thousand-grain weight, cob length, cob diameter, number of rows per cob and number of kernels per row) suggests their usefulness for indirect selection.

5.4 Stability of grain yield in hybrids

The magnitude and nature of genotype by environment (GE) effect displayed by additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield in the main effects showed higher environmental effects than the genotypic effects. According to Easwari and Sheela (1998), and Cach *et al.* (2006) as cited by Ssemakula *et al.* (2007), the predominance of environmental effect over genotypic effect was because yield is a polygenic trait and, therefore, subject to much influence from the environment.

As observed in the AMMI analysis, the non-significant GE interaction implies that the genotypes had similar responses across the environments in which they were evaluated and that all the genotypes can reliably be assessed under anyone of the locations used for this study in future or advance evaluation trials (Yan and Tinker, 2006). In other words, it is unnecessary to assess these genotypes simultaneously in the multi- environments used for the study in subsequent evaluations, thereby offering an opportunity to manage the limited resources available for the testing programme (Tonk *et al.*, 2011).

CHAPTER SIX

6.0 CONCLUSION AND RECOMMENDATIONS

The study identified valuable genetic materials which can be exploited for subsequent breeding activities. The GCA estimates identified parental lines P1, P3 and P5 as the best combiners for grain yield. Again, P1 was the most suitable parent for increased cob length, cob diameter, number of rows per cob and reduced anthesis-silking interval; P3 for thousand-grain weight and reduced days to flowering (anthesis and silking days), and P5 for number of kernels per row, and reduced plant height and ear height. Hence, these parents may be used in hybridization programmes as donors of the superior traits indicated.

The crosses P1×P5, P5×P6, P1×P3, P2×P3 and P1×P4 were the best performing hybrids as well as for exploiting hybrid vigour. Therefore, they can be further evaluated for possible release for commercial production by farmers. Alternately, they can be utilized as females for development of three-way cross hybrids. The correlation among studied traits especially the positive association between grain yield and other essential yield components (such as thousand-grain weight, cob length, cob diameter, number of rows per cob and number of kernels per row) gives a positive indication that these traits could be considered in developing selection indices in maize improvement programmes.

The non-significant genotype × environment interaction revealed by AMMI suggests that the relative performance of the genotypes in grain yield did not change across all environments hence anyone of the locations used in this study can be used for subsequent evaluations. The study also identified the Akomadan experimental site as a lodging prone area because of high prevalence of organic degraders (termites), a situation likely to have an adverse effect in any future research activities in that site.

REFERENCES

Abdulai, M. S. Sallah, P.Y.K., and Safo-Kantanka D. O. (2007). Maize grain yield stability analysis in full season lowland maize in Ghana. *International Journal of Agriculture and Biology* 9(1): 41-45.

Akhtar N., Mehmood T., Ahsan M., Aziz A., Ashraf M., Ahmad S., Asif M. and Safdar E. (2011). Estimation of correlation coefficients among seed yield and some quantitative traits in wheat (*Triticum aestivum* L.). *African Journal of Agricultural Research* 6(1): 152-157

Akuamoa-Boateng, A. (2002). Quality Protein Maize: Infant feeding trial in Ghana. *Ghana Health Service*, Ashanti, Ghana. 1-17.

Ali A.W., Azzam H. K., and AL-Ahmad S. A., (2010.). Genetic variances, heritability, correlation and path coefficient analysis in yellow maize crosses (*Zea mays* L.) *Agriculture and Biology Journal of North America* 1(4): 630-637 http://www.scihub.org/ABJNA (Accessed on 22-11-2011)

Aliu S., Fetahu S., Salillari A., Rozman, L. (2008). General and specific Combining ability studies for leaf area (LA) in some Maize Inbreed Lines (*Zea mays* L.) in Agro ecological Conditions in *Kosova. Notulae Botanicae Horti Agrobotanici Cluj-Napoca* 36 (1): 38-41 *www.notulaebotanicae.ro* (Accessed on *4-11-2011)*

Aliu, S., Fetahus, S., Kaciu, S., and Salillari, A. (2009). Combining ability study for Yield Kernel per ear of maize (*Zea mays* L.) hybrid. *44th Craotian and 4th International Symposium on Agriculture* 476- 480.

Amanullah, S. J., Mansoor M., and Khan M. A. (2011). Heterosis studies in diallel crosses of maize. *Sarhad Journal of Agriculture* 27(2): 207-211.

Amiruzzaman M., Islam M.A., Hassan L. and Rohman M.M. (2010). Combining Ability and Heterosis for Yield and Component Characters in Maize. *Academic Journal of Plant Sciences* 3 (2): 79-84.

Badu-Apraku B., Twumasi-Afriyie S., Sallah P.Y.K., Haag W., Asiedu E., Marfo K.A., Dapaah S. and Dzah B.D. (2006). Registration of "Obatanpa GH" maize. *Crop Science Journal* 46: 1393-1394.

Bahoush M. and Abbasdokht H., (2008). Correlation Coefficient Analysis between Grain Yield and Its Components in Corn (*Zea mays* L.) Hybrids. *International Meeting on Soil Fertility Land Management and Agroclimatology* 263-265.

Baker, R.L., (1978). Issues in diallel analysis. *Crop Science Journal* 18: 533–536.

Bello, O. B., Azeez M. A., Abdulmaliq, S. Y., Ige, S. A. Mahamood, J., Oluleye F., Afolabi,M.S. (2012). Yield and disease reactions of quality protein maizevarieties in the southern Guinea savanna agro-ecology of Nigeria. *Journal of Agricultural Science* Vol. 2(3), pp. 32-41.

Bernardo R. (2002). *Breeding for quantitative traits in plants*. Stemma Press, Woodbury, Minnesota, USA. 369.

Bhatnagar S., Betran F.J., and Rooney L.W., (2004) Combining abilities of quality protein maize inbreds. *Crop Science Journal* 44: 1997-2005.

Bhatnagar, S., Betran F. J., and Transue D.K., (2003) Agronomic performance, aflatoxin accumulation and protein quality of subtropical and tropical QPM hybrids in Southern U.S. *Maydica* 48: 113-124.

Brown, J., and Caligari, P. (2008). *An introduction to plant breeding*. Blackwell Publishing Ltd, Oxford, UK.

Burgoon, KG, Hansen JA, Knabe D.A, Bockhol AJ.(1992). "Nutritional value of quality protein maize for starter and finisher swine", *Journal of Animal Science* 70(3): 811-817.

Cach, N.T., Lenis, J.I., Perez, J.C., Morante, N., Calle, F., amd Ceballos, H. (2006). Inheritance of useful traits in cassava grown in sub-humid conditions. *Plant Breeding Journal* 125:177-182.

CIMMYT and IITA, (2011). Maize - Global Alliance for Improving Food Security and the Livelihoods of the Resource-poor in the Developing World. *Proposal submitted to CGIAR Consortium Board*.

Comstock, R.E., and Moll, R.H. (1963). Genotype-environment interactions. p. 164–196. In W.D. Hanson and H.F. Robinson (ed.) Statistical genetics and plant breeding. *National Academy of Sciences– National Research Council Publication.* 982. NAS-NRC, Washington, DC.

Crossa, J., P., Fox, .N., Pfeiffer, W.H., Rajaram, S. and H.G. Gauch. (1991). AMMI adjustment for statistical analysis of an international wheat yield trial. *Theoretical and Applied Genetic Journal* 81:27–37.

Crow, J.F., (1948). Alternative hypotheses of hybrid vigor. *Journal of Genetics.* 33: 477–487

Crow, J.F., and Kermicle J. (2002). Oliver Nelson and quality protein maize. *Journal of Genetics* 160:819.

Damerval, C., and de Vienne, D. (1993). Quantification of dominance for proteins pleitropically affected by *opaque-2* in maize. *Heredity Journal* 70: 38-51.

Deitos A., Arnhold E., Mora F., and Miranda G.V., (2006). Yield and combining ability of maize under different ecogeographic conditions. *Crop Breeding and Applied Biotechnology* 6: 222-227.

Duvick, D. N. (1999). Heterosis: Feeding People and Protecting Natural Resources. pp. 19-29. In J. G. Coors and S. Pandey (ed.) The Genetics and Exploitation of Heterosis in Crops. *American Society of Agronomy*, Inc., *Crop Science Society of America*, Inc., *Soil Science Society of America*, Inc., Madison, WI. http://www.biotech-info.net/heterosis_duvick1.pdf (Accessed on 03-05-2012).

Duvick D.N. (2001). Biotechnology in the 1930s: the development of hybrid maize. *Nature Review Genetics Journal* 2: 69–74.

Easwari, A.C.S. and Sheela M.M. (1998). Genetic analysis in diallel cross of inbred lines of cassava. *Madras Agriculture Journal* 85: 264-268.

Edmeades, G.O., Bola˜nos, J., Chapman, S.C., (1997). Value of secondary traits in selecting for drought tolerance in tropical maize. CIMMYT, El Batán, Mexico, March 25–29. 222–233.

Falconer D.S. (1989). *Introduction to quantitative genetics*. 3rd edition. John Wiley and Sons Inc. New York.

Falconer, D. S. and Mackay T. F. C. (1996). *Introduction to quantitative genetics*.

4th edition. Longman, Essex, England.

Fan, X., Kang S.M., Chen, H., Zhang Y., Tan J., and Xu, C. (2007). Yield stability of maize hybrids evaluated in multi-environment trials in Yunnan, China. *Agronomy Journal* 99:220-228.

FAO (2007). Global change impacts on agriculture, forestry and soils: The programme of the global change and terrestrial ecosystems core project of IGBP. *Department of Plant Sciences*, University of Oxford, UK. (www.fao.org/docrep/w5183e/w5183e0e.htm)

FAOSTAT (2010). *Statistical databases and data-sets of the Food and Agriculture Organization of the United Nations*. http://faostat.fao.org/default.aspx (Accessed on 02-04-2010).

Filho V. N., Elto Gama E.G., Vianna R. T., and Môro J. R., (1981). General and specific combining ability for yield in a diallel cross among 18 maize populations *(Zea mays* L.) *Revista Brasileira De Genetica* (4): 571·577

Floyd, N., Horst W. J., Puigdomenech P., and Riveill N. (2002). Maize. *Interactive European Network for Industrial Crops and their Applications (IENICA).* http://www.ienica.net/crops/maize.pdf (Accessed on 7-12-2011)

Gauch, H.G. Jr. (1988). Model selection and validation for yield trials with interaction. *Biometrics* 44: 705-715.

Gauch, H.G. Jr. (1992). AMMI and related models. In: Gauch, H.G. (ed.) Statistical analysis of regional trials. *Elsevier Science Publishers*, Netherlands.

Gauch, H.G. (1993). Matmodel Version 2.0: AMMI and related analysis for two-way data matrices. *Microcomputer power*, Ithaca, New York, USA.

Gaziola, S.A., Alessi E.S., Guimaraes P.E.O, Damerval C. and Azevedo R.A. (1999). Quality Protein maize: A biochemical study of enzymes involved in metabolism. *Journal of Agricultural and food Chemistry* 47: 1268-1275

Gibbon, B.C. and Larkins B.A. (2005). Molecular genetic approaches to developing quality protein maize. *Trends in Genetics* 21: 227-233.

Giwa, E.O.and Ikujenlola A.V. (2009). Application of Quality Protein Maize in the formulation of broiler's finisher feed. *Journal of Science, Food and Hospitality* 1(1): 47-50.

Global Development Program (GDP), (2011). Agricultural development: Strategy overview. *Bill and Mellinda Gates Foundation*. http://www.gatesfoundation.org (Accessed on 23-04-2012).

Glover, M. A., Willmot D.B, Darrah L.L., Hibbard B.E., and Xhu, X. (2005). Diallel analysis of agronomic traits using Chinese and U.S maize germplasm. *Crop Science Journal* 45: 1096 – 1102.

Griffiths, B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Science* 9: 463–493.

Griffiths, A.J.F., J.H. Miller, D.T. Suzuki, R.C. Lewontin and W.M. Gelbart. 1996. The nature of the gene. *An Introduction to Genetic Analysis* (6th edn.). W.H. Freeman and Co., NY. 345-358.

Gupta, H. S., Agrawal P. K., Mahajan V., Bisht G. S., Kumar A., Verma P., Srivastava A., Saha S., Babu R., Pant M. C. and Mani V. P. (2009). Quality protein maize for nutritional security: rapid development of short duration hybrids through molecular marker assisted breeding. *Current science* 96 (2): 230-237

Győrffy, B.-I'só, I.-Bölöni, I. (1965): Kukoricatermesztés. (Corn growing.) *Mezőgazdasági Kiadó*, Budapest.

Hallauer, A.R. (1990). Methods used in developing maize inbreds. *Maydica* 35: 1-16.

Hallauer, A.R. and Miranda, J.B. (1988). *Quantitative genetics in Maize breeding*. Iowa State Univ. Press, Ames.

Hallauer, A.R., Russell W.A. and Lamkey K.R. (1988). Corn Breeding. In: G.F. Sprague and J.W. Dudley (ed.) Corn and Corn Improvement. *Agronomy Monograph* (18) 3rd edition. Madison, WI53711, USA.

Hayman, B.I., (1954). The theory and analysis of diallel crosses. *Genetics* 39: 789-809.

Hawkes, C. and Ruel, M.T., (2006). "Agriculture and nutrition linkages: old lessons and new paradigms", *Understanding the links between agriculture and health*. Focus 13: brief 4 of 16.

Hill, Jr., R.R. (1983). Heterosis in population crosses of Alfalfa. *Crop Science Journal* 23: 48–50.

Hugo, D. G., Nilupa G., K., and Dennis F. (2010). Extension and adoption of biofortified crops: Quality protein maize in East Africa. *Contributed Paper presented at the Joint 3rd African Association of Agricultural Economists (AAAE) and 48th Agricultural Economists Association of South Africa (AEASA) Conference*, Cape Town, South Africa 19-23.

IGC *(International Grain Council)*, (2012). Grain market report: Highlight GMR No. 419. (http://www.igc.int/downloads/gmrsummary/gmrsumme.pdf (Accessed on 08-03-2012)

Ikujenlola, A.V. (2010). Effects of Malting and Fermentation on the Nutritional Qualities of complementary Foods produced from Maize varieties and Soybean grains. *Doctor of Philosophy Thesis submitted Obafemi Awolowo University Ile-Ife,* Nigerian.

Jayakumar, J., Sundaram T., Arun P. D. and Ragu R. R.A. (2007).Correlation studies in maize (*Zea mays* L.) evaluated for grain yield and other yield attributes. *International Journal Agriculture Science* (2): 57-60

Ji, H. C, Cho, J.W. and Yamakawa, T .(2006). Diallel Analysis of Plant and Ear Heights in Tropical Maize (*Zea mays* L.) *Journal of the Faculty Agriculture, Kyushu University* 51 (2): 233–238.

Kang, M.S. (2004). Breeding: Genotype-by-environment interaction. In R.M. Goodman (ed.) *Encyclopedia of plant and crop science*. Marcel-Dekker, New York 218–221.

Khalil, I. A., Rahman, H., Saeed, N., Khan, N. U., Durrishawar, Nawaz, I., Ali F., Sajjad, M. and Saeed, M. (2010). Combining ability in maize single cross hybrids for grain yield: a graphical analysis. *Sarhad Journal of Agriculture* Vol.26, No.3.

Khalil, I.A.Rahman, H.U. Naveed-Ur-Rehman, Arif M., Khalil I. H.,Iqbal M., Atullah H., Afridi K.,Sajjad M., and Ishaq M. (2011). Evaluation of maize hybrids for grain yield stability in North-West Pakistan. *Sarhad Journal of Agriculture* 27(2): 213-218.

Knight, R., (1970). The measurement and interpretation of genotype environment interactions. *Euphytica* 19: 225–35

Kodrzycki R., Boston, R., and Larkins, B. A. (1989). The *opaque-2* mutation of maize differentially reduces zein gene transcription. *Plant Cell* 1: 105-114

Krivanek, A. and Vivek, B. (2006). Science behind breeding QPM. *CIMMYT*, Mexico.

Krivanek, A.F., Groote, D., Gunaratna H., Diallo A.O., and Friesen, D., (2007). Breeding and disseminating quality protein maize (QPM) for Africa. *Africa Journal of Biotechnology* 6: 312–324.

Lauderdale, J., (2002). Issues regarding targeting and adoption of quality protein maize. *CIMMYT Working Paper* 31.

Lippman, Z. B. and Zamir, D. (2006) Heterosis: Revisiting the magic. *Trends in Genetics* Vol.23 No.2 www.sciencedirect.com, (Accessed on 4-11-2011)

Lohmer, S., Maddaloni, M., Motto, M., Di Fonzo, N., Hattings, H., Salamini, F., and Thompson, R. D. (1991). The maize regulatory locus *opaque-2* encodes a DNA binding protein which activates the transcription of the b-32 gene. *EMBO Journal* 10: 617- 624.

Mhike, X., Lungu, D. M., and Vivek, B. (2011). Combining ability studies amongst AREX and CIMMYT maize (*Zea mays L.*) inbred lines under stress and non-stress conditions. *African Journal of Agricultural Research* 6(8): 1952-1957.

Michael, L.M., Rosert, T. and Dankyi, A.A. (1999). Adoption and impacts of improved Maize production technology: A case study of the Ghana Grains Development Project. *CIMMYT Economics Program* Paper 9

Micic-Ignjatovic, D., Stankovic G., Markovic K., Lazic-Jancic V. and Denic M. (2008). *Quality protein maize – QPM. – Genetika* 40(3): 205-214.

MiDA (*Millenium Development Authority*) report, (2010). http://mida.gov.gh/site/wp-content/uploads/2010/07/Food_Grain_BOM_Final_Draft2.pdf (Accessed on 21-03-2012).

Millward, D., and Rivers, J.P.W. (1989). The need for indispensable amino acids: The concept of the anabolic drive. *Diabetes Metabolism Reviews* 5:191-212.

MoFA (Ministry of Food and Agriculture), (2010). Agriculture in Ghana*:* Facts and Figures. *Statistical Research and Information Directorate (SRID).*

Moaveni, P., Lotfi, M., Farahani, and Maroufi, K., (2011). Effect of spraying TiO_2 nano particles on some of physiological and chemical parameters in maize (*Zea mays* Lo), *International Journal of Biosciences (IJB)* 1(4): 63-67

Moro, G.L., Habben, J.E., Hamaker, B.R., and Larkins, B.A. (1996). Characterization of the variability in lysine content for normal and opaque-2 maize endosperm. *Crop Science Journal*36:1651-1659.

Morris, M.L., Tripp, R., and Dankyi, A.A. (1999). Adoption and Impacts of Improved Maize Production Technology: A Case Study of the Ghana Grains Development Project. *CIMMYT Economics Program* Paper 99-01.

Motto, M. and Moll, R.H. (1983). Prolificacy in maize: A review. *Maydica* 28:53-76.

Munguma, C. and Pollak, L.K. (1988). Heterotic patterns among ten Corn Belt and exotic maize populations. *Crop Science Journal* 28:500-504.

Musila, R.N., Diallo, A.O., Makumbi, D., and Njoroge, K., (2010). Combining ability of early-maturing quality protein maize inbred lines adapted to Eastern Africa. *Field Crops Research* 119: 231–237.

Ngaboyisonga, C. (2008). Quality Protein Maize under stress environments: Gene action and Genotype × environment effects. *Doctor of Philosophy Thesis, Department of Plant Science and Crop Protection, University of Nairobi, Kenya.*

Obeng-Antwi, K., Craufurd, P., Menkir, A., Ellis .H. & Sallah, P.Y.K. (2012). Phenotypic Diversity in Maize Landraces in Ghana. *International Journal of Science and Advanced Technology* 2 (5): 39-70.

Obilana, A and Fakorede, M. B. (1981). Heritability: A treatise. *Samaru Journal of Agricultural Research* 1: 72-82.

Ojo, G.O.S., Adedzewa, D.K. and Bello, L.L. (2007). Combining ability estimates and heterosis for grain yield and yield components in maize (*Zea mays* L.). *Journal of sustainable development in Agnananthe and environment* 3:49-57.

Okello, D.K., Manna, R., Imanywoha, J., Pixley, K. and Edema, R. (2006). Agronomic performance and breeding potential of selected inbred lines for improvement of protein Quality Adopted Ugandan maize Germplasm. *African Crop Science Journal* 14(1): 37-47.

Onimisi, P.A., Omage, J.J., Dafwang, I.I. and Bawa, G.S. (2009) Replacement Value of Normal Maize with Quality Protein Maize (Obatampa) in Broiler Diets. Pakistan Journal of Nutrition 8 (2): 112-115.

Osei, S. A., Dei H. K., and Tuah A. K., (1999b). Evaluation of quality protein maize as a feed ingredient for layer pullet. *Journal of Animal. Feed Science*. 8: 181-189.

Osei. A., Okai, D. B. and Tuah. A. K. (I999a). Quality Protein Maize as the sole source of amino acids in the diets of starter pigs: A preliminary survey. Journal of University of Science and Technology 19: 1- 4.

POST, *Parliamentary Office of Science and Technology* (2010). Biofortification of Foods. POSTNOTE 367 November 2010. (http://www.parliament.uk/briefing-papers/POST-PN-367.pdf (Accessed on 08-03-2012)

Prasanna B.M., Vasal S.K., Kassahun B., and Singh N.N. (2001). Quality Protein Maize. *Current Science* 81:1308 – 1319.

Rafiq, C. M., Rafique, M., Hussain, A. and Altaf, M.(2010). Studies on heritability, correlation and path analysis in maize (*Zea mays* L.) Journal of Agricultural Research 48(1): 35-38.

Rodrigues, M. C. and Chaves, L.J. (2002). Heterosis and its components in crosses among high quality protein maize populations. *Crop Breeding and Applied Biotechnology* 2(2): 281-290.

Salamini, F. and Soave, C. (1982). In *Maize for Biological Research* (ed. Sheridan, W. F.), University of North Dakota Press 155–160.

Sallah, P.Y.K., Obeng-Antwi, K., Twumasi-Afriyie, S., Asiedu, E.A., Boa-Amponsem, K., Ahenkora, K. and Agyeman, A., (1998). Agronomic potentials of recently released maize varieties in Ghana. I. Extra-early maturing maize varieties. *Presented at the First Biennials NARS Workshop, Accra International Conference Centre* 16-20, NARP Secretariat, CSIR, Accra.

Sallah, P.Y.K., Abdulai, M.S., and Obeng-Antwi, K. (2004). Genotypes and environment interactions in three maturity groups of maize cultivars. *African Crop Science Journal* 12(2): 95 -104.

Scott, M.P., Peterson J.M., Hallaurer, A.R. (2009). Evaluation of combining ability of quality Protein maize derived from U.S. Public inbred lines. *Maydica* 54: 499-456.

Shewry, P. and Halford, N. (2002). Cereal seed storage proteins: structure, properties and role in grain utilization. *Journal of Experimental Botany* 53: 947-958.

Shewry, P.R., (2007) Improving the protein content and composition of cereal grain. *Journal of Cereal Science* 46: 239–250.

Shull, G. H. (1952). Beginnings of the heterosis concept. pp. 14-48. *In*: Heterosis J. W. Gowen, *Iowa State College Press*, Ames.

Shull, G.H. (1908). The composition of field of maize. *American Breeders Association Representatives.* 4, 296–301

Simmonds, N.W., (1979). *Principles of Crop Improvement*. Longman, London.

Singh, N. N., and Venkatesh S., (2006). Development of quality protein maize inbred lines. In: Heterosis in Crop Plants. Ed. Kaloo G, Rai M, Singh M, Kumar S. *Research Book Center*, New Delhi, 102-113.

Singleton, W.R. (1939). Recent Linkage Studies In Maize: V. Opaque endosperm-2 (o2): Connecticut Experiment Station, New Haven. *Genetics* 24:61.

Soengas, P, Ordás, B., Malvar, R.A, Revilla, P., and Ordás, A. (2003). Heterotic patterns among flint maize populations. *Crop Science Journal* 43: 844-849.

Sofi, P. A., Shafiq, A. W., Rather A. G. and Shabir, H. W. (2009). Review article: Quality protein maize (QPM), Genetic manipulation for the nutritional fortification of maize. *Journal of Plant Breeding and Crop Science* 1(6): 244-253.

Sprague, G.F. and Tatum, L.A. (1942). General versus specific combining ability in single crosses of corn. *Journal of American Society of Agronomy* 34: 923-932.

Srećkov, Z., Boćanski, J., Aleksandra, N., Ivica, Đ.and Mirjana, V., (2010). Correlation and Path Coefficient Analysis of Morphological Traits of Maize (*Zea mays* L.) Research *Journal of Agricultural Science* 42 (2).

Ssemakula, G., Dixon, A.G.O. and Maziya-Dixon, B. (2007). Stabiltiy of total carotenoid concentration and fresh yield of selected yellow-fleshed cassava (*Manihot esculenta* Crantz). *Journal of Tropical Agriculture* 45 (1-2): 14-20.

Steel, R.G.D. and Torrie, J.H., (1980). Principles and Procedures of Statistics, *A Biometrical Approach*. 2nd Edition. McGraw Hill Inc., New York, Toronto, London.

Stoskopf, N. C., Tomes, D. T. and B. R. Christie, (1993). Plant Breeding: Theory and Practice. *Westview Press*, Oxford, UK.

Suranyi, J. and Mandy, G.Y. (1955). Akukoria. (Corn) Magyarorszag Kulturfloraja. (Culture flora of Hungary) *Akademiai Kiado*, Budapest.

Tengan, K.M.L. (2010). Conversion of Okomasa - a normal open pollinated variety to quality protein maize using the backcross approach. *Master's Thesis. Faculty of Agriculture, College of Agriculture and Renewable Natural Resources, Kwame Nkrumah University of Science and Technology*, Kumasi, Ghana**.**

Tonk, F. A., Ilker, E., and Tosun, M. (2011) Evaluation of genotype x environment interactions in maize hybrids using GGE biplot analysis. *Crop Breeding and Applied Biotechnology* 11: 1-9.

Toro, A., Medici, L., Sodek, L., Lea P. and Azevedo R. (2003). Distribution of soluble amino-acids in maize endosperm mutants. *Scientia Agricola* 60: 91-96.

Tulu, L. (2001). Heterosis and genetic diversity in crosses of seven Eastern African maize (*Zea mays* L.) population. *Seventh eastern and Southern Africa Regional maize conference*, 11th -15th February, 125-129.

Vasal, S.K. (2000). Quality protein maize story. Proceedings of workshop on Improving Human nutrition through agriculture. The Role of International Agricultural Research, *International Rice Research Institute (IRRI)* 1-16.

Vidya, C. and Oommen, S. K (2002). Correlation and path analysis in yard-long bean. *Journal of Tropical Agriculture* 40: 48-50.

Vietmeyer, N.D (2000). A drama in three long acts: the story behind the story of the development of quality-protein maize. *Diversity* 16: 29-32.

Vivek, B., Krivanek, P.R N., Twumasi-Afriyie, S., Diallo, A. (2007). Breeding Quality Protein Maize (QPM): Protocols for developing QPM cultivars, *CIMMYT*. Mexico.

Vivek, B.S., Krivanek, A.F., Palacios-Rojas, N., Twumasi-Afriyie, S. and Diallo, A.O. (2008). Breeding Quality Protein Maize (QPM): Protocols for Developing QPM Cultivars. *CIMMYT*, Mexico, DF.

Wang, L. and Schultz, P. G. (2005). Expanding the Genetic Code: Protein science, *Angewandte Chemie International* 44: 34–66.

Westcoff, B. (1987). A method of analysis of the yield stability of crops. *Journal of Agricultural Science* 108: 267–274.

Woolf, C.M. and Markow, T.A. (2003). Genetic models for developmental homeostasis: historical perspectives. In Developmental Instability – Causes and Consequences. *Oxford University Press* 99–114.

Worku, M., Zelleke H., Taye G., Tolessa B., Wolde L., Abera, W., Guta A., and Tuna H. (2001). Yield stability of maize (*Zea mays* L.) genotypes across locations. *Southern Eastern and South Africa Regional Maize Conference* 11th -15th February. 139-142.

Woyengo, V.W., Odongo, O.M. and Ajanga, S.I. (2001) Combining ability analysis of 72 maize inbred lines and development of Topcross hybrids resistant to follar diseases. *Master Science Thesis submitted University of Nairobi*, Kenya.

Yan, W. 1999. Methodology of cultivar evaluation based on yield trial data-with special reference to winter wheat in Ontario. *Doctor Philosophy Thesis submitted to University of Guelph*, Ontario, Canada.

Yan, W. and Tinker, N. A. 2006. Biplot analysis of multi-environment trial data: Principles and applications. *Journal of Plant Science* 86: 623–645.

Yousuf, M. and Saleem, M. (2001). Correlation analysis of S1 families of maize for grain yield and its components International. *Journal of Agriculture and Biology* 3 (4): 387-388

Zare, M., Choukan, R., Heravan, E.M., Bihamta, R.M., and Ordookhani, K., (2011). Gene action of some agronomic trats in corn (*Zea mays* L.) using diallel cross analysis. *African Journal of Agricultural Sciences* 6(3): 693-703.

Zhai, Shao-Wei., (2002). Nutritional evaluation and utilization of quality protein maize Zhong Dan 9409 in laying hen feed. *Master Science Thesis submitted to Northwestern Agricultural and Forestry University of Science and Technology, Shaanxi* 712100, P. R. China.

Zhang, Y., and Kang, M.S., (1997). DIALLEL-SAS: a SAS program for Griffiths's diallel analyses. *Agronomy Journal* 89: 76–182.

Zsubori, Z., Gyenes-Hegyi, Z., Illés, O., Pók, I., Rácz, F., and Szőke, C. (2002). Inheritance of Plant and Ear height in maize (*Zea mays* L.). *Agricultural Research Institute of the Hungarian Academy of Sciences*, Martonvásár. http://www.date.hu/acta-agraria/2002-08i/zsubori.pdf (Assed on 08-05-2012).