EVALUATION OF THREE-WAY HYBRID MAIZE (*Zea mays* L.) FOR GRAIN YIELD AND ASSOCIATED TRAITS IN THE SAVANNAS OF NORTHERN GHANA.

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(BSc. Agricultural Biotechnology)

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A THESIS SUBMITTED TO THE DEPARTMENT OF CROPS AND SOIL SCIENCES, FACULTY OF AGRICULTURE, KWAME NKRUMAH UNIVERSITY OF SCIENCE AND TECHNOLOGY IN PARTIAL FULFILMENT

OF THE REQUIREMENTS FOR THE DEGREE OF

MASTER OF PHILOSOPHY

IN

PLANT BREEDING

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KWAME NKRUMAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, KUMASI, GHANA

SCHOOL OF GRADUATE STUDIES

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DECLARATION

I hereby declare that except for the references cited in relation to other works, this work is the result of my own original research and that this thesis has neither in whole nor part been presented anywhere for a degree.

…… ……

KULAI AMADU MANIGBEN (STUDENT) DATE

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DR. MASHARK S. ABDULAI (CO-SUPERVISOR) DATE

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DR. ENOCK OSAKRE (HEAD OF DEPARTMENT) DATE

DEDICATION

To God be the glory.

This work is dedicated to my parents. For their endless love, support and encouragement.

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ABSTRACT

The promotion of three-way hybrid maize production in cereal dominated cropping systems are still being developed because of their wide adaptation and cheap seed prices relative to single cross hybrid. Cultivar release and recommendation require identifying high yielding and widely adapted genotypes for a diverse range of environments. This study was designed to evaluate the performances of three-way cross maize hybrids for grain yield and other important traits across five diverse environments in the savannas of Ghana. The results showed that environments (E) and genotypes (G) and interaction (G × E) effects were highly significant ($P < 0.001$) for grain yield and other important traits, with low repeatability or broad sense heritability (0.40) for grain yield across the test environments. However, Damongo (0.97) and Nyankpala (0.69) had high repeatability for grain yield. The strong phenotypic correlation between grain yield and most important traits demonstrated that selection for those traits can simultaneously be improved with grain yield. A strong genetic correlation between Manga and Wa revealed the similarity between the test environments. This implied one of the environment can be dropped to improve breeding efficiency by reducing the cost involved in multi-location testing. The interaction between genotypes and environments were crossover type of interaction revealing an inconsistent performance of hybrid genotypes across the test environments. The hybrid 14 (M1227-12) was found to be the highest yielding, with yield advantage of 10% over the commercial check SC719. The genotype and genotype-by-environment biplots analysis identified hybrids 14 (M1227-12), 23 (M1227-5) and 25 (M1124-6) as the most stable and high yielding with above

grand mean grain yield. Similarly, hybrids 21 (AS1204-46), 24 (M1428-7), 27 (M1227-2) and 34 (M1428-14) were identified as high yielding above grand mean and moderately stable. These promising three-way maize hybrids would benefit farmers and seed producers when promoted for adoption and has the potential to increase household incomes of smallholder farmers in the Savannas of Ghana.

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LIST OF ABBREVIATIONS AND ACRONYMS

AEC	Average Environment Coordinate
AMMI	Additive Main effects and Multiplicative Interaction
ANOVA	Analysis of variance
ASI	Anthesis -silking interval
BLUE	Best Linear Unbiased Estimators
BLUP	Best Linear Unbiased Predictor
CIMMYT	International Maize and Wheat Improvement Center
COI	Crossover Interactions
CSIR	Council for Scientific and Industrial Research
CV	Coefficient of Variation
DF	Degrees of Freedom
DT	Drought Tolerant
DTMA	Drought Tolerant Maize for Africa
FAO	Food and Agriculture Organization
IITA	International Institute of Tropical Agriculture
FAOSTAT	FAO Statistical Databases (United Nations)
FR	Factorial Regression
GE	Genotype-by-environment
GEI	Genotype –by-Environment Interaction
GGE	Genotype plus Genotype-by-Environment
GLM	Generalized Linear Model
IITA	International Institute of Tropical Agriculture
IPCC	Intergovernmental Panel on Climate Change
LSD	Least Significant Difference
MoFA	Ministry of Food and Agriculture
NGO	Non-governmental Organization
OGTR	Office of the Gene Technology Regulator
PCA	Principal Component Analysis
PLS	Partial Least Square
REML	Restricted. Maximum Likelihood
SARI	Savanna Agriculture Research Institute

SAS	Statistical Analysis System
SOV	Sources of Variation
SSA	Sub Sahara Africa
SV	Singular-Value
USDA	United States Department of Agriculture

CHAPTER ONE

1.0 INTRODUCTION

Maize is a principal staple food crop worldwide next to rice and wheat. It is predominantly used as food for about 1.2 billion inhabitants in Latin America and Sub-Sahara Africa (Naete, 2013; FAO, 2013). Maize is cultivated primarily for human consumption and feed for poultry and other livestock as dry forage, silage and grain. It is estimated that only 15 % maize grain is used as food worldwide. In Ghana, 85 percent of maize cultivated is used for human consumptions while the remaining 15 percent is used as feed for the poultry industry (Angelucci, 2012). However, in 2011, FAO estimates suggested that Africa consumes about 30 % of world maize as food with Sub Sahara Africa taking the lion's share (Awika, 2011). The trend of maize per capita consumption varies from country to country and from continent to continent. Analysis of FAO food balance sheet from 2007-2009 indicated that the amount of maize consumed in Africa per person in a day varies from 50-328 grams. However, Lesotho has the largest maize consumption of 328 grams per person in a day whereas in Ghana, a person consumes 53 grams of maize in a day. It is therefore not surprising that maize consumption have been forecast to surge as the average income earned per person in Ghana increases with population growth (MoFA, 2011; Ranum *et al.*, 2014).

According to FAO (2015) a total of 875 (million metric tons), 1.0 and 1.0 billion metric tons of maize was realized worldwide from 179, 186 and 183 million hectares in 2012, 2013 and 2014 respectively. Out of this total, Africa contributed 69 (8 %),70 (7 %) and 77 (7.5 %) million metric tons from 34, 36.3 and 36.9 million hectares respectively whiles Ghana realized 1.9, 1.7 and 1.7 million metric tons in 2012, 2013 and 2014 respectively. The average grain yield per unit area was 4.9, 5.5 and 5.7 tons ha^{-1} for the

world total, 2.0, 2.0 and 2.1 tons ha^{-1} in 2012, 2013 and 2014 respectively (FAO, 2015). Thus, there is variability and yield gap in average grain yield per unit area in Africa including Ghana when compared to the world average.

Grain yields continue to decline with annual yield fluctuation due to negative consequence of flooding, drought, heat, low nitrogen in the soil, salinity, acidity and aluminum toxicity of the soil, pests and disease incidence as well as issues of parasitic weeds. The effects of climate change give rise to high temperature and low rainfall and are predicted to have severe impact in Sub Sahara Africa (Smale *et al*., 2011). Furthermore, low grain yield of maize has also been attributed to lack of adoption of improved varieties and hybrids, low fertilizer application (due to high fertilizer prices, inadequate distribution network and low subsidies) and high incidences of weeds infestation (*Striga*) (Gibbon *et al*., 2007; Fisher *et al*., 2014). Research shows that drought at anthesis and grain filling stage, reduce grain yield by 90 % (Badu-Apraku *et al*., 2013). Oswald and Ransom, (2001) revealed that *Striga* infestation result in about 10-100% grain yield loses on maize fields depending on the various stress factors that affect the crop.

It is estimated that 40 % of Africa's ―corn belt‖ faces frequent drought stress leading to yield losses amounting to 10-25 % (CIMMYT, 2013). Thus, the consequences of climate change such as erratic rainfall pattern coupled with frequent drought continuously pose great danger to food security and maize production in Sub Sahara Africa. In addressing these challenges, IITA, CIMMYT and their partners instituted a widespread breeding approach, methodology and testing schemes with National Agricultural Institutes, private seed companies and NGOs. Two major strategies were adopted: Developments of extra early, early, intermediate and late maturity population, inbred line and hybrid varieties to address recurrent drought that normally occur during anthesis and grain-

filling stages as well as *Striga* infestation. And secondly, developments of hybrids that possess drought tolerant genes such as threeway cross hybrid. Three-way hybrid for drought tolerance has a wider genetic base and can be developed by gene pyramiding for drought tolerance for broad adaptation (Edmeades *et al*., 1997).

Climate change models, Crop Simulation model and Scenarios persistently envisage increased incidence of drought, erratic rainfall and high temperatures (Li *et al*., 2009; Fisher *et al*., 2014; IPCC, 2014). Climate projections shows that yields are expected to decline rapidly in maize production regions (IPCC, 2014). Maize target environments will continue to experience changing environmental conditions leading to potential losses. Therefore, maize cultivar development pipelines must take into account changing environmental conditions in target environments to maximize yields and gains.

According to ASPB (2015), agriculture faces three important challenges; (1) stability of crop yields across the multiple environment every year (2) Climate change resulting in extreme weather conditions. (3) Changing distribution of many environments. Therefore, the ability of plant breeders to identify and release genotypes or varieties that are specifically adapted or broadly adaptable are of prime importance in ever-widening range of environments and changing environmental conditions as a result of climate change.

Thus, significant changes in climatic conditions change the growing environment of most crops affecting the yields and performance of the genotypes (Li *et al*., 2011).

These conditions translate into varying response of genotypes across the environments. Changing environmental conditions translate into GEI which obscure progress from selection. Because GEI negatively affect heritability as, the bigger the GEI variance,

the smaller the heritability estimate. Therefore, gains from selection and/or the rate of genetic gain is hampered (Bänziger *et al*., 2007; Chenu *et al*., 2011; Yan, 2014). Moreover, the occurrences of GE interaction reduce correlation between phenotypic and genotypic value making valid inferences about the genetic potential of a genotype complicated (Comstock and Moll, 1963; Yan and Kang, 2003).

Multi-environment trials are routinely conducted in Guinea and Sudan Savannas of Ghana These trials persistently reveal differential response of genotypes to diverse growing conditions (Badu-Apraku *et al*., 2003). However, the data available from these trials have not been fully exploited to allow complete understanding of the genotype x environment interaction (GEl) of hybrid genotypes. There is also little information on the adaptability and stability of these three-way hybrid materials. It is therefore imperative that such information would be useful for effective evaluation of hybrid trials. This in turn will improve the rate of genetic advance from selection. Furthermore, this will help breeders in the area to identify and select superior genotypes for better adaptation and stability in their cultivar development program.

Therefore, the overall objective of the study was to investigate the performance of three-way cross hybrids in the Savannas of Ghana.

The specific objectives of the study sought:

I. To determine the magnitude of interaction between genotype and environment.

II. To estimate heritability and genetic variance of traits

III. To identify stable and high-yielding hybrids that are specific or broad adapted IV. To determine the correlation among traits and between environments

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin and botany of maize

The center of origin of maize is believed to be Mesoamerica, now modern Mexico in North America and to some extent the Caribbean (OGTR, 2008). It is believed that maize was originally domesticated from teosinte a wild relative of *Zea mays* L. (OECD, 2006). Maize is a versatile crop and has the ability to grow in a wide range of environmental conditions with altitudes ranging from sea level up to 3,800 meters. High diversity of maize can be attributed to its ability to grow in wide environmental conditions (OGTR, 2008). Maize was introduced by the Portuguese to the West African Coast in the seventeenth and eighteenth centuries (Johnson, 1997).

Maize is a flowering plant belonging to a member of the grass family Poaceae (Gramineae) with five major species (*diploperennis* HH, *luxurians*, *mays*, *nicaraguensis* HH and *perennis*) in the genus *Zea*. (USDA, 2005; OGTR, 2008). Maize is a monoecious annual plant with determinate growth habit and can grow up to four meters tall. Maize is characteristically protandrous, in that the male flower matures before the female flower. The growth of maize can be categorized into vegetative and reproductive phases of growth. The vegetative phase consists of the Seedling stage, growth stage and Tasseling initiation stage. Whiles the reproductive stage comprises of the Silking stage, Milky stage and Maturity stage. The maize inflorescences consist of the tassel and the ear. The ear develops from lateral branches from auxillary shoot buds on the stalk and produces silk receptive to pollens. The male inflorescence (tassel) produces anthers from spikelets which emerges from the florets. The anther produces pollen grains. Pollen grains per anther range from two thousand to seven thousand five hundred. A tassel can produce roughly seven thousand anthers on average. Research

suggest that each tassel can produce fourteen million pollen grains. (Bennetzen and Sarah, 2009). Environmental conditions such as cool temperatures and high humidity are suitable for pollen shed and pollen longevity. Pollen shed by tassel are captured by the fine sticky hair on the silk resulting into fertilization which eventually develop into cob (Bennetzen *and* Sarah, 2009).

2.2 Importance of maize

Maize is a principal supplier of food and food safeguard for most people in Sub Saharan Africa, Latin America and the Caribbean. It contains an estimated seventytwo percent of starch, ten percent of protein, and four percent of fat, providing 365,000 amount of energy in 100 g of maize. Maize is life, a major source of livelihood in the Sub-region. This grain account for an estimated 15 % of the total calories consumed daily, however, this differ on country basis as some consumed roughly 50 % calories every day from maize (Badu-Apraku *et al*., 2011; Ranum *et al*., 2014).

Maize grains can be described as grains with unlimited possibilities in its utilization. It can be hydrolyzed and enzymatically treated to produce high-fructose corn syrup and sweeteners. It is often used to generate ethanol for fuel and additive to gasoline. Maize is utilized in various industry from design and creative industrials to Pharmaceuticals and cosmetics. Starch from maize constitute 70 % of the kernel, used as ingredients in dyes, pigments paint, allantoin (a natural antioxidant and healing agent), soaps and antibiotic (NCGA, 2013; Dharam *et al*., 2014). Maize could be prepared or transformed into a variety of food forms, fermented and non-fermented foods. Maize grains soaked for 2-3 days are milled and fermented into corn dough used for preparation of food such as *Ga Kenkey*, *koko* (porridge) and *banku.* Dry maize grains are normally milled to produce corn flour used for preparation of *non*fermented food such as *tuo zafi* (TZ). Maize is also roasted and eaten when immature. Local breweries use maize for *pito*

production, an alcoholic beverage. Other industrial products produced from maize, include oil, beverages, glue, and products of fermentation and distillation industries (OGTR, 2008; Ranum *et al*., 2014).

2.3 Constraints of maize production in Sub-Sahara Africa

Maize grain yield losses and gap have been unprecedentedly high in the SSA compared to the rest of the world due to climate change, frequent and extreme weather conditions such as drought and erratic rainfall pattern and other related factors such as poor soil fertility (Low-Soil nitrogen) and weeds (*Striga spp*) (Bänziger *et al*., 2000; Hillel and Rosenzweig, 2002; De Schutter, 2012; Badu-Apraku *et al*., 2013). Studies by Several workers on Farmers perception of drought-related risks in West Africa established that 54% of the respondents in Mali, 43% in Benin Republic, 32% in Nigeria, and 27% in Ghana considered drought as a major factor threatening production (IITA, 2015). Moreover, a survey of expert opinion regarding maize yield constraints in Sub Sahara Africa conducted by Gibbon *et al*. (2007) reported that Soil constraints contributed 44 % to yield losses whiles weeds such as

Striga spp and drought contribute to 19 and 18 percent respectively to yield reduction.

Drought is a chief impediment to production of maize in Sub Sahara African countries' such as Ghana and the world at large. Maize is the most sensitive to drought, of all the principal staple food crop (Bänziger, 2010; Campos *et al*., 2006). Several workers (Robins and Domingo, 1953; Claassen and Shaw, 1970; Shaw, 1976;

NeSmith and Ritchie, 1992; Araus *et al*., 2008) have demonstrated in various studies that maize is sensitive and/or susceptible to drought at all stages of growth but, the most sensitive stages that lead to significant yield losses occur at the flowering and gain-filling stages. A study conducted by Denmead and Shaw (1960) revealed that drought stress that occur at grain-

filling stages reduced grain yield by 21 % whiles drought stress occurring at flowering period reduced yield by an estimated 50 %. However, it is reported that this is more serious when drought stress occurs ranging from tassel emergences to grain-filling period and can result in an estimated 90 % yield losses (Banziger *et al*., 2000). Similarly, Badu-Apraku *et al.* (2004) revealed that under drought stress, grain yield can be reduced not less than fifty-three percent. Furthermore, in a study to ascertain the impact of climate change in two zones in Ghana, Guinea Savannah and transitional zone. The study found that grain yield and biomass was reduced by 19-41 % and 11-33 % respectively as result of climate change (drought) (MacCarthy *et al*., 2013).

Striga spp is a major problem in areas where cereal crop is predominantly grown in sub-Saharan Africa infesting an estimated 40 % production area (Ejeta, 2007; Makumbi *et al*., 2015). Yield losses resulting from *Striga* infestation have been reported. For small-holder farmers, *Striga* infestations can cause yield losses to vary from twenty to eighty percent. Generally speaking, yield losses as a result of *striga* ranges from ten to hundred percent depending on the soil fertility, genotype used, prevalent weather conditions and the infestation levels have also been reported in literature (Lagoke *et al*., 1991; Kroschel, 1999; Oswald and Ransom, 2001). Ransom (1996) reported that yield losses due *Striga* infestation are as a result of damage to host photosynthetic system leading to reduced efficiency and a potent phytotoxic effect of Striga on host maize plant. The parasitic weed, *Striga hermonthica* (Del.) Benth are the most prevalent species in Guinea and Sudan Savanah (Lagoke *et al*., 1991). Several studies on obligate parasitic weed, suggest that the plants are highly reproductive, producing large amount of tiny seeds of about 500,000 each plant.

These seeds are capable of staying alive in the soil for not less than twenty years before germinating. Therefore, management and control of infestations become problematic

for commonly used approaches such as fallowing, pulling by hand, application of organic and inorganic fertilizers, seed treatments, intercropping and crop rotation (Carsky *et al*., 2000; Khan *et al*., 2000). Several workers (Vogt *et al*., 1991; Badu-Apraku *et al*., 2013; Makumbi *et al*., 2015) have explained that as population in the sub-region increases, pressure on scarce land resources also increases resulting in crop intensification. Thus, the fertility of the soil decreases whiles the seed reservoir in the soil increases resulting in yield losses.

Nitrogen is an essential element for vegetative growth in plant and a constituent of amino acids for protein synthesis (Azevedo *et al*., 2004; Kramer, 2004). However, low soil nitrogen is one of the important abiotic limitation to maize production in developing countries in Sub Sahara Africa due to intensification in land use for crop cultivation with low external input (Application of fertilizer) resulting in nutrient depletion in the soil (Ransom *et al*.,1996). As reported by Wolfe *et al*. (1988), low nitrogen stress in maize result in an estimated 10 to 50 percent yield losses. In another study, Bänziger and Lafitte (1997) reported that low soil nitrogen reduces yield by 40 %. Although nitrogenous fertilizers are available for amendment, prices are so high that small scale farmers are unable to afford.

2.4 Grain yield and yield potential

Grain yield is an important objective for almost every breeding program. Maize grain yield and maize productivity have been dwindling due to adverse effects of drought (Bänziger *et al*., 2000; Araus *et al*., 2008). However, there have been concerted effort over the years to increase grain yield under these conditions. Increase in maize grain yield over the years have been attributed to both genetic improvement and improved agronomic and/ or management practices (Araus *et al*., 2012; Tollenaar and Lee, 2011). However, 75% of improvement in yield has been ascribed to genetic gain and the rest have been attributed to improved

agronomic and management practices. One could also argue that ―yield improvement was largely due to the improvement in the genotype-by-environment interaction, as yield improvement could not have been achieved by either genetics or management practices alone‖ (Tollenaar and Lee, 2002; Duvick, 2005). According Araus *et al*. (2012), yield improvement over the years could also be attributed to breeding for drought tolerances.

Studies in the developed world revealed that genetic improvement in yield gains ranged from 60 to 90 percent while's agronomic practices takes the remaining portion (Duvick, 1999; Tollenaar *et al*., 2000; Badu-Apraku *et al*., 2015). In West and Central Africa, according Badu-Apraku *et al*. (2013), increase in grain yield, ranging from 1.1 to 2.1% yr^{-1} as result of breeding for abiotic stress such as drought, over 22 year of the selection program have been achieved.

Grain yield is a quantitative trait, a trait controlled by many genes. However, grain yield is determined by number of factors. Factors involve in dry matter accumulation or partitioning of assimilate into grain. These include Grain yield as determined by radiation, water availability, nitrogen availability, yield components, source and sink (Bänzinger *et al*., 2000).

Grain yield as determined by radiation and increased in grain yield as a result of genetic improvement are associated with direct seasonal dry matter accumulation. The more dry matter accumulated, the higher the grain yield during the growing season (Tollenaar *et al*., 1994). According to Tollenaar and Lee, (2006), seasonal dry matter accumulation is determined by duration of the life cycle, interception and utilization of incident solar radiation throughout life cycle. Thus, light interception is directed by leaf area whereas light utilization is determined by leaf-angle and photosynthesis. Under water limited conditions, grain yield is a function of

water transpired by the crop, water use efficiency and biomass/unit water transpired (Passioura, 1977; Bänzinger *et al*., 2000).

Grain yield is a function of yield potentials, flowering date to escape drought, and traits for drought tolerance (Fischer *et al*., 2003; Araus *et al*., 2008). Yield potential have been defined as the yield of an adapted crop variety or hybrid when grown under favorable conditions without growth limitations from water, nutrients, pests, or diseases. In other words, the maximum yield a crop can attain or achieve in a given environment provided there is perfect and/ or best management of agronomic and other inputs, and in the absence of manageable abiotic and biotic stresses (Evans, 1993; Evans and Fischer, 1999; Tollenaar and Lee, 2002; Lobell *et al*., 2009; Fischer *et al*., 2014). Progress in yield potential which has an impact on grain yield can be achieved through breeding. Phenotyping of physiological traits associated with novel secondary traits can be used to increase progress in yield potential. Increased sink size, harvest index and grain filling can be attributed to increase in yield potential (Evans and Fischer, 1999). According to Lobell *et al*. (2009), yield potential (for a given genotype or crop) is determined by three factors: (i) solar radiation, (ii) temperature, and (iii) water supply, depending on a given site and/or growing season.

The amount of water supply can determine the yield potential of a given crop. Hence, under irrigation and rainfall condition, provided there is adequate water supply and/or water availability, it is assumed that maximum attainable yield can be achieved (Cassman *et al*., 2003). Thus, water –limited yield potential have been proposed. Water-limited yield potential is described as the yield of an adapted crop variety or hybrid when grown under rain-fed or irrigation, favorable conditions without growth limitations from nutrients, pests, or diseases (Lobell *et al*., 2009). Hence, waterlimited yield potential is determined by the degree of water deficit, genotype, solar radiation,

and temperature and plant population. Under moderate stress (limited water supply), high yield potential often gives rise to increased yield because yield potential is associated with an increase in general stress tolerance and because it is a constitutive trait (Bänzinger *et al*., 2000). Consequently, reduction in yields to levels far below 50 % of yield potential, results in yield potentials becoming inapplicable and/or unimportant. Thus, yield potential is used as a standard measure to ensure that water deficits do not constrain yield (FAO and DWFI, 2015).

The concept of yield potential deals with conditions in which there is no biotic and abiotic stress to a crop, where the crop plant is able to express its full potential when agronomic practices and/or management conditions are ideal. However, such conditions are rarely achieved under field conditions, especially on farmers' fields. For instances, in Sub Saharan Africa where agronomic or management practices are not perfect coupled with low input, low soil fertility, *Striga* infestation and losses from insects, weeds, and diseases problems yield potential is greatly affected. Hence, under such conditions, actual farm yield is obtained where farmers make use of their average skills and technology to achieve an average yield possible. Thus, yield gap occurs when there is a difference between yield potential and actual farm yield or average yield (FAO and DWFI, 2015; Lobell *et al*., 2009). Global maize average yield is 5.2 t/ha whereas in West Africa and Ghana the average maize yield from 2008 to 2010 is 1.8 t/ha (FAO, 2013; Fischer *et al*., 2014). In addition, progress of yield potential in terms of gains for maize have been reported. Badu-Apraku *et al.* (2013), reported that, gain in grain yield, ranged from 1.1 to 2.1% yr^{-1} was made over 22 years of the selection program under drought, low soil nitrogen and *Striga*.

Quantification of yield potential in maize is important for identification of constraints to maize production that maximizes returns from investment from research and

development as well as achieving optimum yield and profitability. It also provides valuable information for understanding of the causes of yield gap so as to allow farmers to prioritize the use of their scarce resource to maximize yield and productivity as well as help formulate policies. (Cassman *et al*., 2003; Lobell *et al*., 2009; Meng *et al*., 2013). Various methods have been proposed for measuring yield potential in literature. These include Crop models, Field experiments and yield contests and Maximum farmer yields (Lobell *et al*., 2009). Estimation of yield potential can be done based on yields from farmers' fields provided the farmer keeps accurate records of yields value. These values can be used to measure yield potential for a locality. Thus farmers' yields can directly be quantified based on sampling of individual farmers' fields by comparing with best performing crops in neighboring field with similar biophysical properties or weather or climatic and biotic condition. Reasonable estimates of yield potential can be obtained when historical weather data are available. (Lobell *et al*., 2009; FAO and DWFI, 2015). Another commonly used method for measuring yield potential has been the use of crop model or simulation models to estimate yield potential (Yang *et al*., 2004). These models are often used to predict yield potential and requires a minimum set of input data by using climatic or weather data with key physiological factors to validate or calibrate field observations (yield data) over a period to obtain accurate estimates (Yang *et al*., 2004; Fischer *et al*., 2014). Field experiments and yield contests can also provide direct measure of yield potential, however, inaccuracies of design experiment coupled with lack of accurate data can restrict the reliability of yield potential (Duvick and Cassman, 1999; Meng *et al*., 2013).

In addition, yield contests provide useful information and direct estimate of yield potential for a given region. This approach motivates farmers as they are well aware that there is a price tag, recognition and reward for the ultimate winner (Duvick and

Cassman, 1999). However, because it is a contest, there is the need for independent verification to avoid cheating (Lobell *et al*., 2009). According to Fischer *et al*. (2015), there is the need for cautious interpretations of yield values as they are often recorded under very favourable conditions relative to the District or regional average conditions.

2.5 Genotype-by-Environment interaction

In quantitative genetic terms, the phenotypic expression of a character can be considered as the function of genetic make-up of the individual and a deviation as a result of the environment and interaction between genotype and environment (Comstock and Robinson, 1948; Falconer, 1989). Thus, the genotype and environment interact to produce different forms of phenotypes such that when a genotype is grown in two different environments, it turns to exhibit different responses in their phenotypic expression and performance (Kang, 2002).

Genotype by environment interaction is a common occurrence for most quantitatively inherited traits of economic importance in plant breeding program, when genotypes are evaluated across diverse environments (Cooper *et al*., 1996; Xu, 2010; Yan, 2014). Genotype by environment interaction is defined as differential responses of genotypes or cultivars and/or genotypic expression across environments (Hayward *et al*., 1993; Fox *et al*., 1997; Kang, 1998, 2004).

In a cultivar development program, assessment of genetic potential of breeding material and identification of superior genotype for broader or specific adaptation for release to farmers and progress from selection are routinely carried out in multilocation trials (Hill *et al*., 1998; Voltas *et al*., 2005). However, the relative performances of genotypes across environments complicates cultivar selection, cultivar recommendation and identification of superior genotype. Thus, the presence of GEI

reduces the relation between phenotypic and genotypic value, in that the phenotype becomes a poor indicator/predictor of genotype, making valid inferences more complicated. Hence, reducing selection efficiency in breeding program (Comstock and Moll, 1963; Signor *et al*., 2001; Annicchiarico, 2002; Yan and Kang, 2003). In addition, GEI affect the estimation of variance component (Hill *et al*., 1998), in that GEI has a negative effect on heritability. Heritability is a vital element in controlling genetic advance from selection (Yan and Kang, 2003).

2.6 Classification of Genotype-by-Environment Interaction

Evaluation of genetic potential of genotypes is a common practice and inevitable in plant breeding programs. The relative performance of genotypes across environment becomes important to the breeder when genotypes change ranks from one environment to the other (Kang, 2002). Changing environmental conditions has tremendous impact on plants' response to these conditions. The nature and magnitude of interaction influence the relative performances of genotypes depending on the degree of environmental variations. Allard and Bradshaw (1964) classified environmental variations into two categories, predictable and unpredictable environmental variations. The first class deals with environmental conditions that can be predicted with some level of certainty. Environmental variations characterized by cyclic or systemic fluctuations, unchanging and/or invariable features of the environment (climate and soil types) that can be controlled by the experimenter by will. On the other hand, environmental variations characterized by fluctuation in weather (such as temperature changes, distribution and amount of rainfall and relative humidity) such that it cannot be predicted with certainty or controlled artificially by the experimenter, can be described as unpredictable environmental variations (Xu, 2010). These classes of variations have the tendency to differential genotypes response to changing

environmental conditions that are predictable and unpredictable. The changes in ranks of genotypes grown across these environments are as a result of lack of perfect correlation across the environments. The differential response of the genotypes in this manner is referred to as crossover interaction. Crossover interactions are non-additive and non-separable. It is of practical importance to a plant breeder as, the presence of crossover interaction implies breeding for specific adaptation. This means that a breeder must develop cultivars suitable for specific agro-ecological zones depending on their adaptability and stability. Thus, cultivars and /or genotypes must be evaluated at multilocation or multiple environments in order to obtain reliable result for selection and recommendation for cultivar/varietal release. Hence, a lot of resources must be committed for establishment of sub-stations for multi-location trials. (Baker, 1988; Kang, 1998; Annichiarico, 2002). However, when the performances of genotypes remain unchanged when genotypes are evaluated across environments, this pose less difficult in selecting superior genotypes in a breeding program. In that, a breeder will only need to develop a cultivar and/or a genotype with wide adaptation for all the different environment, provided the rank order of genotypes across environments remains unchanged and genotypes that are superior in one environment maintain their superiority in other environments. This is particularly common when non-crossover interactions occur. (Kang, 2004). Various types of Genotype-by-Environment interactions have been described in literatures (Allard and Bradshaw, 1964; Yan and Kang, 2003). However, according to Allard and Bradshaw (1964) as the number of environments and the number of genotypes increase, the number of possible GE interaction (given by $\frac{GE!}{G!E!}$, where; !: factorial, G: number of genotypes, E: number of environments) also increases.

When two genotypes (G1 and G2) are grown in two different environments (E1 and E2), there are four possible types of response patterns of genotypes in the two environments. Type A occur, when there is no interaction between genotypes (G1, G2) and environments (E1, E2), resulting in no genotype-by-environment interaction because the two lines are parallel. For Type B, there is no change in ranks of genotype G1 and G2 in environment E1 and E2 resulting in noncrossover interaction. But, genotype (G1) is consistently performing better than the G2 across the environments. In contrast, Type C and D represent crossover interactions which shows the differential responses of genotype G1 and G2 in environments E1 and E2 resulting in changes in ranks across the environments. However, Type C shows that genotype G1 and G2 have their own favored environments whereas Type D shows that both genotypes are favored by E2.

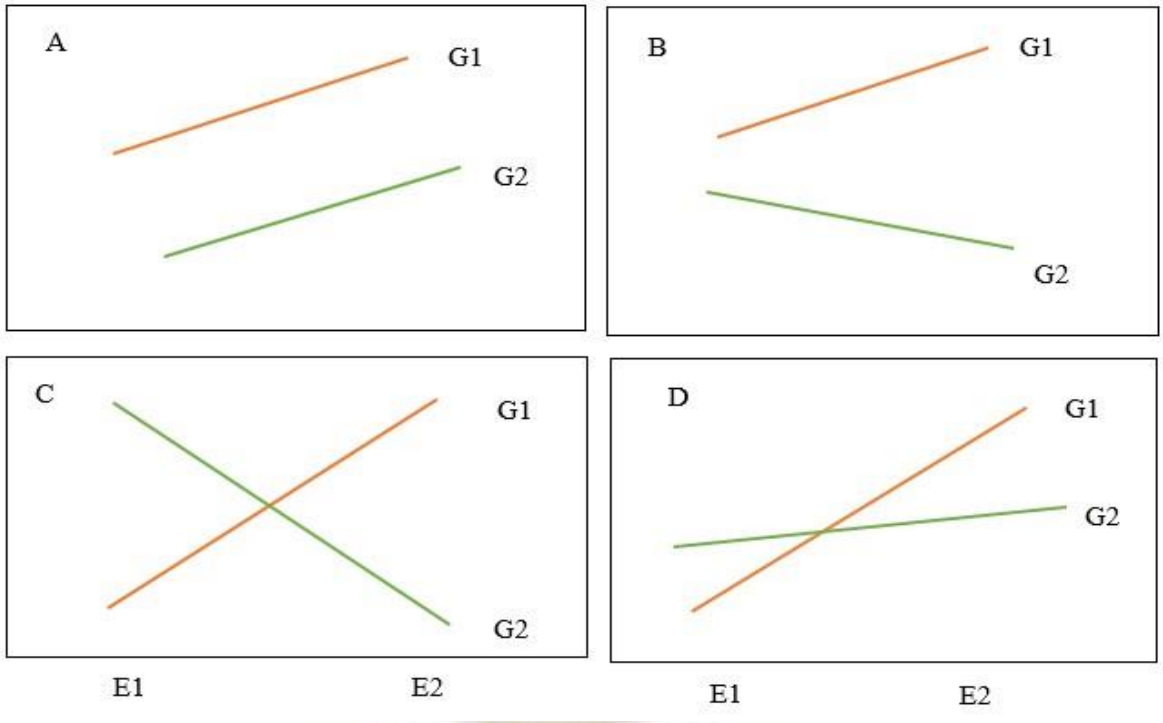

Figure 1: Graphical representations of Genotype-by-Environment interactions. (A) No interaction (B) non crossover interaction with no change in ranks of genotypes (C) crossover interactions with change in ranks of genotypes, G1 favored in E2. Whereas genotype G2 is favored in E1 (D) crossover interaction-change in ranks of genotypes G1 and G2 all favored in E2.

Furthermore, Ceccarelli (1989), described the implication of GEI to plant breeding given the mean performances of a genotype as well as the degree of interaction between genotype and environment. When the amount of GEI is high coupled with high mean performances of genotype, is said to be an indication that the genotype has the potential of local adaptation to specific environment. Similarly, high magnitude of GEI coupled with low mean performance also suggest that the genotype is suitable for local adaptation. However, low amount of GEI and low mean performances will suggest that the genotype is neither locally adaptable nor has the potential for wide adaptability, thus the genotype and/ or cultivar is undesirable. On the other hand, when the mean performance of a genotype is high relative to low amount of GEI, indicates that the genotypes performances remains unchanged across wide range of environment. Thus, has the potential for wide adaptability. To this end, three ways of dealing with GEI has been suggested in literature. These are : (1) ignore (2) Avoid (3) Exploit them in a breeding objective depending on the magnitude and nature of these interaction owning to the differences in interaction between genotype and environment. Crossover interaction are mostly preferred by plant breeders since the presence of crossover interaction are suitable for breeding for specific adaptation. Thus, exploitation of GEI are often highly advocated. On the other hand, when the interaction is noncrossover in nature, ignoring and avoidance becomes ideal (Eisemann *et al*., 1990; Cooper and Hammer, 1996).

2.7 Yield stability and Adaptation

The identification of genotypes that are high yielding whiles producing consistent performance across wide range of environment are of utmost importance in breeding programs. Adaptation is a characteristic of an organism, in which it has the ability to survive, reproduce and adapt to changing environmental conditions while producing

consistent performance by adjusting its physiology to suit the environment or ecology (Cooper and Byth, 1996; Hill *et al*., 1998; Annicchiarico, 2002). According to Cooper and Byth (1996), adaptation is a function of response to environments differing quantitatively in time and degree for a number of uncontrollable factors.

In plant breeding programs, adaptation, yield stability and adaptability are often used interchangeably as the terms describe consistency of performance and good yield response across environments (Simmonds, 1962; Hill *et al*., 1998; Annicchiarico, 2002; Kang, 2002). Several workers (Lin and Binns, 1988; Simmonds,1991; Evans, 1993) have used the concept of adaptation and the concept of yield stability to describe consistency in performance of a genotype in space and time respectively.

Adaptation concept can be viewed from two distinct levels, wide adaptation and specific adaptation. Breeding for genotypes that exhibit consistent performances well in nearly all environments are said to be widely adapted. Consequently, when selecting genotypes for wide adaptation, plant breeders look for a non-crossover genotype-by-environment interaction (Matus-Ca´diz *et al*., 2003). Hence, the estimation of stability of performance becomes important to identify consistentperforming and high-yielding genotypes whiles minimizing GEI (Xu, 2010). Genotypes which show consistent performances well in a definite or unique to a set of environmental conditions are said to be specifically adapted. Specific adaptation can be exploited to maximize yield when genotype-by-environment interaction are large and repeatable. Thus, large number of cultivar for a given crop are grown whiles maintaining high genetic diversity within that crop compared to wide adaptation (Ceccarelli, 1996; Cooper *et al*., 1996).

Yield and yield stability are often considered equally important in plant breeding program, in that after developing a variety or cultivar, a decision will have to be made as to whether a particular cultivar is stable and high yielding and whether the genotypes

are specifically adapted or widely adapted (Federer and Scully, 1993; Pingali and Rajaram, 1999; Cleveland, 2001).

The concept of yield stability is widely used in plant breeding and genetics. According to Cleveland (2001) yield stability is a measure of the differences in yield of a crop variety over different environments when compared with other varieties. Thus a stable genotype is one that is consistently well ranked (Kempton and Fox, 1997). Yield stability is often considered associated with wide adaptation. A variety can be considered stable when it performs relatively better across wide range of environment (Westcott, 1986). According to Kang and Gauch (1996), stability describes the behavior of a crop in varying environments. In general, the concept of stability can be categorized into two: the static concept and the dynamic concept

(Becker and León, 1988). The static concept also referred to as biological stability (Becker, 1981), explains when a genotype shows invariable performance across environments such that among environments variance is absolutely nonexistent and/or negligible. The most commonly used measure is based on variance of a genotype across environments when environmental range is small and the coefficient of variation is then plotted against genotype means according to Francis and Kannenberg (1978). Moreover, maximum stability or genotype stability reaches its plateau, in that genotypes respond to no high levels of inputs (Piepho, 1996). In contrast, dynamic concept also referred to as agronomic concept of stability, occurs when a genotype is considered stable if its performance in different environments is close to what can be expected from the potentials of those environments (Becker, 1981; Romagosa and

Fox 1993; Hill *et al*., 1998; Annicchiarico, 2002; Kang, 2002; Yan and Kang, 2003; Xu, 2010). For dynamic concept, Shukla's (1972) stability variance and Wricke's (1962) ecovalence are most commonly used parameters used to measure genotype

stability.

Consequently, Lin *et al*. (1986) classified stability statistics into four groups and assigned three classes of stability to each of the groups (Table 1)

Table 1: Groups of stability Statistics and their equivalent classes of Stability types

Stability Statistics	Classes of Stability
Group A	Type 1 Stability
Group B	Type 2 Stability
Group C	Type 2 Stability
Group D	Type 3 Stability

Source: (Yan and Kang, 2003)

The Group A stability statistics is considered departure from the mean genotypic effect. While Group B is based on Genotype by environment interaction. However, both Group A and B correspond to sum of squares, in that phenotypic sum of square of genotypic effects and environment effects are used as measure of genotypes stability of performance across the environment (Cooper *et al*., 1996). On the contrary, Group C and D depend on genotypic effect and genotype-by-environment interaction. Thus, they depend on regression coefficient or deviations from regression as a measure of genotype performance.

Stability analysis explores reaction of a genotype, relative to other genotypes, to different environments. With regards to the classes of stability, Type 1 stability is one in which a genotype is considered stable on the assumption that among-environment variance is small. In Type 2 stability, a genotype is considered stable granted that its response to environments and mean response of all genotypes under consideration are responding in the same direction. For Type 3 stability, a genotype is considered as stable with the condition that residual mean square from the regression model on the environmental index is small (Lin *et al.*, 1986). Predictable and unpredictable

nongenetic variations such as locations, seasons and years alike have been proposed as a basis of Type 4 stability concept (Lin and Binns, 1988). Thus, estimation of Type 4 stability is based on a genotype's years-within-locations mean square and independent of the regression analysis and the genotype means. Type 4 stability is related to static concept (Hill *et al*., 1998; Yan and Kang, 2003). Several stability parameters have been proposed to characterize yield stability when genotypes are tested across multiple environments. These stability parameters range from regression model, stability-variance statistic, ecovalence, rank-sum method, yield-stability statistic (Wricke, 1962; Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Shukla,

1972; Kang *et al*., 1987; Nassar and Huhn, 1987; Kang, 1993)

2.8 Statistical analysis of genotype-by-environment interaction

The variation between genotypes in their yield stability in multiple environment trials can be attributed to Genotype-by-Environment interaction. Several statistical tools, models, methodologies and strategies such as joint regression, pattern analysis, factorial regression, partial least squares regression; AMMI model and GGE Biplot and mixed models have been proposed, developed and used for analyzing, describing, exploring, understanding, and predicting GEI in multienvironment trials (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Cornelius *et al*., 1992; Crossa *et al*., 1993; Gauch, 1992; Dennis *et al*., 1997; Balzarini *et al*., 2002; Yan *et al*., 2002 Crossa *et al*., 2004; van Eeuwijk, 2006; Xu, 2010; Malosetti *el al*., 2013).

2.9 GGE biplot Analysis

There are two types of biplots, GE biplot and GGE biplot (Yan *et al*., 2000). The genotype-by-environment biplot appertain to graphically display of the genotype-byenvironment interaction obtained from the additive main effects and multiplicative

interactions (AMMI) model whereas the genotype plus genotype-by-environment biplot involves graphical display of two sources of variation based on SREG model of GGE biplot (Burgueno *et al*., 2001). It is a biplot that displays GGE of MET data. GGE biplot is a linear-bilinear model based on the Sites Regression (SREG) linearbilinear model partitioning GGE into multiplicative terms (Yan and Kang, 2003; Yan and Tinker, 2006). The GGE biplot model equation is expressed as:

$$y_{ij} - \beta_j = \lambda_1 \xi_{i1} + \lambda_2 \xi_{i2} \eta_{2j} + \varepsilon_{ij}$$

Where; y_{ij} is the yield of genotype i in environment j

;β_j is the mean yield in environment$j$;λ_1 and λ_2 represent the singular values of principal component one and principal component two, respectively;

ξ_{i1} and ξ_{i2} denote the eigenvectors of genotype i for principal component one and principal component two, respectively; η_{i1} and η_{i2} are the eigenvectors of environment for principal component one and principal component two, respectively; and ε_{ij} is the residual associated with genotype i and environment j. (Yan and Kang,

2003)

A GGE biplot is thus, constructed this way by subjecting the GGE matrix to singularvalue (SV) decomposition of environment-centered or environment-standardized to obtain the principal components. A single scatter plot can then be displayed by plotting the first two principal components (PC1=primary scores and PC2=secondary scores) scores of the genotypes and the environments (Yan *et al*., 2000; Yan, 2001).

The GGE biplot analysis are mostly used in multienvironment trials to evaluate the performances and stability of genotypes, determine the relationship among locations, relationship among traits, ranking of the cultivar performance as well as discriminating of genotypes and identification of representativeness of test locations (Yan, 2014).

GGE biplot analysis have been applied and utilized widely in multi environment trial analyses in winter wheat (*Triticum aestivum* L.) (Yan *et al*., 2000; Lee *et al.,* 2003; Fan *et al*. 2007), soybean (Yan and Rajcan, 2002), Rice (Samonte *et al*., 2005), cotton (Blanche and Myers, 2006), common bean (Kang *et al*., 2006), Maize (Fan *et al*., 2007; Setimela *et al*., 2007; Badu-Apraku *et al*., 2010). It has been used extensively in maize drought tolerant breeding program at CIMMYT and IITA to identify stable, high yielding and superior preforming inbred lines and hybrids. A study conducted by Badu-Apraku *et al.* (2011), identified four mega-environments for evaluating early maize cultivars in West Africa. In a similar study, Badu-Apraku *et al.* (2013) obtained information on the yield performance and stability of the single-cross hybrids under striga infestation, drought stress, and optimum growing environments.

2.10 AMMI model

AMMI model is a multiplicative statistical model based on another class of fixed effect linear-bilinear model with multiplicative terms (Cornelius *et al*., 1996; Cornelius and Seyedsadr, 1997; Crossa, 2012). Zobel *et al*. (1988) proposed the additive main effects and multiplicative interaction (AMMI) model, which combined the additive effect analysis of genotypes and environments using the standard analysis of variance (ANOVA) coupled with the multiplicative analysis of the residuals using principal component analysis (PCA) to identify any patterns in the data. Thus, a biplot graphically display information on main effects and interactions of genotypes and environments. Consequently, least square estimates of the parameters along with mean

values of genotypes and environments are interpreted to classify genotypes and environments for their stability (Crossa and Cornelius, 2002; Xu, 2010). The AMMI model equation is:

$$Y_{ij} = \mu + G_i + E_j + \sum_{n=1}^{N} \lambda_n \gamma_{in} \delta_{in} + \epsilon_{ij}$$

Where,

Y_{ij}=response variable

μ = the overall mean,

G_i= genotypic main effects,

E_j= environmental effects,

N = number of principal component axes used, λ_n denote singular value of the nth principal component axis,

γ_{in} and δ_{in} are scores for the i^{th} genotype and j^{th} environment on the n^{th} principal component axis ϵ_{ij} denote residual (Hayward *et al*., 1993).

A genotypes is considered generally adapted to a test environment if the first principal-component axis value is close to zero. Similarly, a large genotypic PCA1 score reflects more specific adaptation to environments with PCA1 scores of the same sign. (Kempton, 1984; Gauch and Zobel, 1996).

Gauch and Zobel (1988), proposed postdictive and predictive accuracy methodology for choosing an appropriate AMMI model for a GE data set. Postdictive procedure facilitate the selection of ideal model based on the variation explained by PCA axes

whereas the predictive procedure allows for random allocation of individual replicates each genotype x environment combination to either a data set for modelling or a set for cross validation of model. Thus, accurately estimate genotypic means the optimum number of interaction principal component axes required (Gauch *et al*., 2008). AMMI method has three (3) main advantages. These include (1) an analytical tool for diagnosing models and/or other models (2) summarizes pattern and relationship of genotypes and the environments and (3) improving the accuracy of yield estimates (4) imputing of missing data (5) increasing the flexibility and efficiency of experimental designs (Crossa *et al*., 1990; Gauch *et al*., 2008)

The AMMI techniques have been utilized in various plant breeding programs for identification of best performing, stable and adaptable, mega environment analysis and making cultivar recommendation. Samonte *et al*. (2005), used AMMI model analysis to identified mega environment for rice growing environment in Texas, USA. Maize breeding program at CIMMYT and IITA have extensively utilized AMMI model in the analysis of most multienvironment trials (Malosetti *et al*., 2013)

2.11 Mixed models

Conventional analytical methods are often used to estimate the contribution of genotype to the overall GEI effect based on a fixed effects model. These methods depend on the assumptions analysis of variance (Hu and Spike, 2011). Thus, requires homogenous variance-covariance of data. (Arnold, 2004). Thus, applicable only to complete and highly balanced data sets. However, multi-location trials are often characterized by heterogeneous mean variances and heterogeneity of within-site variance across environment since each genotype contribute differently to the GE interaction (Ye *et al*., 2001). This can be attributed to incomplete or unbalance data which may arise when genotypes are discarded in a selection experiment or long-term trials. Experimental

plots may be discarded due poor performance or when the number of replications are unequal for genotypes across environments (Kang and Magari, 1996; Yan and Kang, 2003). Thus, the fixed analysis of variance method to

MET does not utilize available information resulting in narrow inference on the performances of genotypes and in term of specific adaptation or widely adaptation to target environments. Application of mixed model analysis of variance procedure overcome this problem (Piepho, 1998; Balzarini, 2002). Mixed has become a method of choice in multi-environment trials and plant breeding in general due to a number of advantages afforded by linear mixed models compared with ordinary linear models (Standard ANOVA). The advantages include (1) can easily handle incomplete or unbalanced data (2) ability to properly model within-trial error variation (3) ability to model heterogeneous variance-covariance of MET data for accurate inferences of genotype performance across environment (4) Can elucidate data that do not conform to assumptions used in standard analysis of variances (Piepho, 1998; Smith *et al*., 2002, 2005; Balzarini, 2002; Yang *et al*., 2005).

Linear mixed models have become widely accepted and used for analyzing MET in plant breeding (Baker, 1996; Piepho, 1997a; 1997b; 1998; Piepho and Mohring, 2005; Smith *et al*., 2002, 2005; Crossa *et al*., 2004; 2006; Yang *et al*., 2005; Burgueño *et al*., 2007; 2008).

Mixed model is a statistical model which contains both fixed and random-model effects (Little *et al*., 2006). Fixed effects is one in which a breeder is interested in only the actual treatments used or where inferences are made on only specific treatments or when all of the levels in the population of parameters are present or when all levels of interest are in the experiment (Basford and Cooper, 1998). Whereas random effects are when treatments are a random sample from a large population about which we want to

make inferences (Lynch and Walsh, 1998; Ye *et al*., 2001; Piepho *et al*., 2003; Bradshaw, 2016).

The general form of a linear mixed model is expressed as:

$$\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Zu} + \mathbf{e}$$

Where:

$\mathbf{Y}$ is the column vector ($n \times 1$) denoting the phenotypic values of a traits (yield)

$\mathbf{X}$ and $\mathbf{Z}$ are design matrices of $\boldsymbol{n \times p \; and \; n \times q}$ respectively with elements of 1 or zero $\boldsymbol{\beta}$ is $\boldsymbol{p \times 1}$ column vector of fixed effects. $\mathbf{u}$ is $\boldsymbol{q \times 1}$ column vector of random effects.

$\mathbf{e}$ is $\boldsymbol{n \times 1}$ the column vector of residual error or random error.

Means and variances of the component vectors of the mixed model are based on fixed and random effects. Fixed effects are estimated as Best Linear Unbiased Estimators (BLUEs). Thus, obtain by subtracting overall means from treatment effects or genotypic effect or variety effect. BLUEs estimate the mean performance of a response variable using ordinary least squares. Random effects are predicted by Best Linear Unbiased Predictors (BLUPs), a technique for estimating random effects. Thus, BLUP can be estimated by adding variance proportion into the denominator which shrink the treatment effect or regression toward means. Shrinking increases accuracy (Henderson, 1975; Robinson, 1991).

BLUP is used for identification of individuals with maximum genetic merits in selection programs, predict breeding value, monitoring response to selection and can

be used to estimate genotypic value of genotypes or variety or cultivar (Bradshaw, 2016). According to Benardo (2002), BLUP methodology allows for the analysis of unbalanced data and exploits information on relatives.

$$\mathbf{BLUE}(\boldsymbol{\beta}) = (\mathbf{X}'\mathbf{V}^{-1}\mathbf{X})^{-1}\mathbf{X}'\mathbf{V}^{-1}\boldsymbol{y}$$

$$\mathbf{BLUP}(\mathbf{u}) = \mathbf{G}\mathbf{Z}'\mathbf{V}^{-1}(\boldsymbol{y} - \boldsymbol{X\beta})$$

Where $\mathbf{V} = \mathbf{ZGZ}' + \mathbf{R}$ (the $n \times n$ covariance matrix of y), $\mathbf{G}$ is the ($\mathbf{q} \times \mathbf{q}$) covariance matrix of $\mathbf{u}$, $\mathbf{R}$ is the ($\boldsymbol{n} \times \boldsymbol{n}$) covariance matrix of$\mathbf{e}$,

Statistically speaking, Best in both BLUE and BLUP because they minimize the sampling variance, Linear in that, they are linear functions of phenotype trait (e.g. yield),$\boldsymbol{y}$, Unbiased because they are expected (mean) values of fixed effects and random effects respectively. Predictors because they are estimators of random effects and Estimators because they are estimators of fixed effects (Robinson, 1991).

In MET, there have been considerable debate as to when to consider genotypes as fixed or random. At early stages of a selection or cultivar development, genotype maybe regarded as random because large number of genotypes or breeding materials are assembled and screened. At advance stages, genotypes might be regarded to be fixed because the experimenters are only interested in the particular set of genotypes but environmental and/or genotype-by- environment interaction (GEI) effects may be considered as random variables, since they represent a larger target population (Arnold, 2004; Piepho *et al.*, 2008).

On the contrary, others argue that genotype should be considered random in that when genotypes are regarded as random, it allows information to be borrowed across trials depending on the magnitude of the genetic correlations. Smith *et al*. (2005), believes that the purpose of analysis determines whether a variety/genotype/cultivar effects should be regarded as fixed or random. If the analysis is aimed at selection of the best

performing genotypes, when relying on genotype rankings, then genotype effects should be regarded as random. Calling for the use of BLUPs. But if the analysis is aimed at differentiating between set of genotypes, then genotype effects must be considered as fixed since the best linear unbiased prediction (BLUP) of a specific difference is biased (Cullis *et al*., 1998; Piepho, 1998; Smith *et al*., 2001; Smith *et al*., 2002; Smith *et al*., 2005; Yang *et al*., 2009).

However, there is a penalty to be paid if false claims are made if either genotypes or environments should be random but are treated as fixed. Based on mixed model analysis. Yang (2007), revealed that significant crossover interaction may be exaggerated when random GEI effects are considered as fixed. Thus, two approaches are currently available for detecting crossover interactions (COI), depending on whether a fixed-effect or a random-effect model is used (Yang, 2007).

Several workers (Piepho, 1997, 1998; Balzarini, 2002; Crossa *et al*., 2004; Piepho and Möhring, 2005; Cotes *et al*., 2006; Oakey *et al*., 2006, 2007; Burgueño *et al*., 2007; Kelly *et al*., 2007; Yang, 2007; Stefanova and Buirchell, 2010; Hu and Spike, 2011) applied mixed models in analysis of MET data in crops such as maize, barley, wheat, lentil and lupin to explore the heterogeneity of experimental error variance in field trials, used for efficient estimation of variety performance, to assess the genetic gain in historical variety/cultivar trials and selection of best performing varieties.

2.12 Genetic correlation and heritability Estimates

Genetic correlation can be used as invaluable techniques for studying the interaction between genotype and environment in multi-environment trials (Burdon, 1977, 1990). Thus, the effectiveness of a cultivar evaluation largely depends on the genetic correlation between genotype performance in METs (Xu, 2010). The study of

genotype-by-environment interaction can be treated as a case of indirect selection criterion. In that, selection applied in one environment can be used to achieve selection gain in another environment (Falconer,1952; Itoh and Yamada, 1990; Cooper and De Lacy, 1994; Cooper *et al*.,1996).

When the same genotype is measured for a particular trait in distinct environments, indirect selection can be utilized given information on the heritability and the genetic association for the trait in the two environments (Makumbi *et al*., 2015). Genetic association among locations can be used as a selection criterion to determine the magnitude of genetic variation between locations and how the locations are influenced by the same genes.

Genetic association can be used to assess the homogeneity between locations in multi-location trial to elucidate the degree of genotype-by-environment interaction (Atlin, 2003). Cooper *et al*. (1996), pointed out that lack of correlation of genotype performance across environment would substantially impact on selection if it led to change of ranking of performance in different environments. Generally speaking, high genetic correlation gives an indication of low or little genotype-by-environment variance between a pair environment and suggest that genotype ranks remain unchanged and thus traits are controlled by the same genes. Furthermore, the lower the genetic correlation between any two environments, the greater the degree of genotype-by-environment interaction and gives an indication that these environments are very different resulting in change of ranking of performance from one environment to the other. Moreover, low genetic correlation implies different genetic systems have become more important for adaptation in the two environments.

(Falconer, 1952; Eisen and Saxton, 1983).

Heritability of a trait is an important ingredient for determining genetic advance from selection and/or a critical component of selection response. (Kang, 2002). In multienvironment trials, broad heritability or repeatability is used to measure the ability of the trial(s) to discriminate genotypes. It is also a measure of the reliability or precision of a trial. (Yan, 2014). It can also be described as the expected correlation between cultivar or genotypes means estimated in different sets of trials in the same TPE (Atlin, 2003). Atlin *et al.* (2000a), pointed out that high heritability (broad sense), implies that the means of a set of genotypes and/or cultivars tested in different trials will be highly correlated. On the other hand, he explained that low heritability (broads sense) implies there is little association between means from different trials. Thus, the lower the heritability (broad sense), the lower the progress from selection or the lower selection gains from the trials.

Many researchers (Atlin *et al*., 2000b; Malla *et al*., 2010; Mandal *et al*., 2010; BaduApraku *et al*., 2011, 2012; Makumbi *et al*., 2015) have used these techniques to assess similarities between environment, quantify GEI, determine genetic structure and predict selection gains from genotypes evaluated cross environment.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Germplasm

A total of forty-eight three-way cross maize hybrid materials was used in the trials. This consisted of 36 white and yellow hybrids from IITA-DTMA breeding program bred for drought and *Striga spp* resistance, 11 commercial hybrids and a local check

(Appendix 1)

3.2 Experimental site

The field experiment was carried out at Savanna Agricultural Research Institute (SARI), substations in the Northern Ghana. The three-way hybrids were evaluated during the 2015 growing seasons at Nyankpala, Damongo, Yendi, Wa and Manga in five different agro-ecologies respectively (Table.2).

Table 2. Description of the test location of 48 three-way hybrids

Location	Code	Latitude	Longitude	Altitude (m)	AEZ	Rainfall
Nyankpala	NYP	9°25' N	0°58'E	340	NGS	899
Yendi	YD	9°26'N	0°10'E	157	SGS	815
Manga	MAN	11°01'N	0°16'E	270	SS	
Wa	WA	10°3'N	2°30'W	304	GS	996
Damongo	DAM	09°04'N	01°49'W	252	GSWL	765

NGS denote northern guinea savanna; SGS, Southern Guinea savanna; SS, Sudan savanna; GS, Guinea Savanna; GSWL, Guinea Savanna woodland, AZE, Agro Ecological Zone

3.3 Experimental Design and Management

The trial was laid out in incomplete block design as (8 x 6) alpha lattice design with three replications at each location. Each plot comprised two rows, 5.0 x 0.75 m. The spacing was 50 cm between hills and 75 cm between rows as well as two plants per hill. Serpentine pattern was used in plot arrangement. Three seeds per hill were at first sown and later thinned to two plants per stand two weeks after emergence, giving a final population density of 66,666 plants/ha.

The trials were conducted during the rainy (rain-fed) season at five locations (Damongo, Yendi, Nyanpkala, Manga and Wa) in 2015.

In all the trials, standard agronomic practices such as weed control were carried out; pre- and post-emergence herbicides (gramoxone and atrazine) application and manual hoeing were conducted to control weeds. A compound fertilizer was applied as basal application two weeks after planting at the rate of 60 Kilogram of nitrogen (N) per

hectare, 60 kilogram of phosphorus (P) per hectare, and 60 kilogram of potassium (K) per hectare was applied as 15–15–15 N.P.K. The plants were then top dressed at four (4) weeks after sowing with 60 kilogram of nitrogen (N) per hectare using Sulphate of ammonia.

3.4 Data Collection

Data were collected on yield and other important traits according to standard protocol of IITA (Badu-Apraku *et al*., 2012). The following specific data were collected:

3.4.1 **Plant Stand**: Total number of plants per plot obtained soon after thinning.

3.4.2 **Days to anthesis**: Mean number of days to anthesis was estimated from the number of days from planting to the day when fifty percent of the plants in plot have their tassels shedding pollen.

3.4.3 **Days to silking**: This was calculated from the number of days from planting to the day when fifty percent of the plants per plot have emerged silks.

3.4.4 **Anthesis-silking interval**: This was calculated by subtracting days to anthesis from days to silking.

3.4.5 **Plant height**: Mean height of ten randomly sampled plants per plot was measured from the base of the maize plant to the tip of the flag leaf using a long wooden meter ruler in centimeters.

3.4.6 **Ear height**: Mean ear height of ten randomly sampled plants per plot was measured from the base of the plant to the node bearing the ear in centimeters using a long wooden meter ruler. If a plant has more than one ear, the height considered is usually the one of the upper ear.

3.4.7 **Husk cover**: The husk cover was determined on a scale of 1-5, where1= ear with tightly arranged husk cover and extended beyond the ear tip and 5=ear tips exposed usually taken 1- 2 weeks before harvested.

3.4.8 **Plant aspect**: The plant aspect was determined on a scale of 1 to 5, in which 1=excellent overall phenotypic appeal and 5=poor overall phenotypic appeal.

3.4.9 **Ear aspect**: The ear aspect was determined on a scale of 1 to 5, where 1 = clean, uniform, large, and well-filled ears, and 5 = rotten, variable, small and partially filled ears.

3.4.10 **Grain moisture**: Grain moisture was measured by hand shelling ten random cobs per plot and taking the moisture of grains using a moisture tester at harvest.

3.4.11 **Grain weight**: The weight of grains per plot was obtained by hand shelling cobs per plot and weighing grains in kilograms using a weighing scale.

3.4.12 **Field Weight**: The weight of cobs per plot was measured in kilograms using a weighing scale.

3.4.13 **Grain yield** (kg/ha) was computed in kilograms per hectare, adjusted to 15% moisture (Badu Apraku *et al*., 2012). It was computed by using the following formula:

$$\text{Grain yield(kg/ha)} = \frac{\text{FW} \times (100 - \text{moisture \%}) \times \text{S} \times 10{,}000}{85 \times \text{Area harvested}}$$

Where: Area of plot harvested = 3.75 m^2

FW=Field weight

S= shelling percentage of 80 % (Magorokosho *et al*., 2009)

3.5 Data analysis

Analysis of variance was first carried out for each location for all measured traits. Bartlett's test to assess homogeneity of variances was also performed prior to combined analysis (McIntosh, 1983; Moore and Dixon, 2015). Combined analysis across

environment was based on the general linear model (where hybrids are considered fixed whiles environment, replication within environment and incomplete block within replication-by-environment were regarded as random) as implemented by the SAS PROC GLM in SAS software version 9.2 (SAS, 2009). Means were separated using the Least Significant Difference (LSD). The standard analysis of variance table (Table 3) and standard linear mixed model for the response variable was expressed as:

$$Y_{ijkb} = \mu + E_j + R(E)_{kj} + IB(RE)_{bkj} + G_i + GE_{ij} + e_{ijkb}$$

Where:

Y_{ijkb}=response variable (e.g. grain yield)

μ =the overall mean,

E_j = the effect of the j^{th} location,

$R(E)_{kj}$ = the effect of the k^{th} replicate within the i^{th} location,

$IB(RE)_{bkj}$=the effect of the incomplete block within the k^{th} replicate in the j^{th} environment.

G_i= the effect of the i^{th} genotype.

GE_{ij}= the interaction effect of the i^{th} genotype with the j^{th} location.

Table 3 Mixed model combined analysis of variance for g genotypes at e locations with r replications at each location

SV	DF	MS	EMS	F-ratios
Total	$erg-1$			
Environ (E)	$e-1$	MS1	$\sigma_e^2 + g\sigma_{R(E)}^2 + {}_E^2\, rg\sigma$	MS1/MS2
Rep./E		MS2	$\sigma_e^2 + g\sigma_{R(E)}^2$	MS2/MS5
Genotype(G)		MS3	$\sigma_e^2 + g\sigma_{GE}^2 + er\emptyset_G^2$	MS3/MS4
$G\ x\ E$			$r_e^2 + g\sigma_{GE}^2$	MS4/MS5
Error		MS5	r_e^2	

	$e(r-1)\ 1)^{-}$
	$g-1$
	$(e-1)(g$
	$e(g-1)(r-1)$

Source: (Hayward *et al*., 1993) Where SV: source of variation, DF: degree of freedom, MS: mean squares, EMS: expected mean squares, r: replication, g: genotype, e: environment

3.6 Biplot analysis of interaction between genotype and environment

GGE biplot methodology based on Sites Regression (SREG) Model was used to analyze genotype performance for each environment, genotype stability, relationship among locations, representative environment, and discriminating power of each environment. Information on the significance and magnitude of the GE interaction effect on grain yield, identification of high-yielding and best performing hybrids was obtained using GGE biplot. Plot mean values were subjected to GGE Biplot to partition the main effects of genotypes (G) plus the GE interaction using GGE Biplot GUI package in R (Frutos *et al*., 2013). The GGE biplot model equation was expressed as:

$$y_{ij} - \beta_j = \lambda_1\xi_{i1} + \lambda_2\xi_{i2}\eta_{2j} + \varepsilon_{ij}$$

Where; y_{ij} is the yield of genotype i in environment j ; β_j is the mean yield in environment j; λ_1 and λ_2 are the singular values of PC1 and PC2, respectively; ξ_{i1} and ξ_{i2} are the eigenvectors of genotype i for PC1 and PC2, respectively; η_{i1} and η_{i2} are the eigenvectors of environment for PC1 and PC2, respectively; and ε_{ij} is the residual associated with genotype i and environment j. (Yan and Kang, 2003).

3.7 Estimation of variance components and heritability

Variance components and their standard errors for estimates of genotypic variance ($\boldsymbol{\sigma_G^2}$), location variance ($\boldsymbol{\sigma_l^2}$), genotype-by-location variance ($\boldsymbol{\sigma_{GL}^2}$), and error variance ($\boldsymbol{\sigma_E^2}$) was computed using the PROC MIXED (option = REML) of SAS (SAS Institute, 2009). Broad-sense heritability ($\boldsymbol{H^2}$) or Repeatability for each trials were estimated by using variance components as follows:

$$H^2 = \frac{\sigma_G^2}{\left[\sigma_G^2 + \left(\frac{\sigma_E^2}{r}\right)\right]}$$

Where $\boldsymbol{\sigma}_{\boldsymbol{G}}^{\boldsymbol{2}}$ denote genotypic variance, $\boldsymbol{\sigma_E^2}$ denote error variance, and $\boldsymbol{r}$ denote the number of replications (Cooper *et al*., 1996; Holland *et al*., 2003; Hallauer *et al*., 2010)

$$H^2 = \frac{\sigma_G^2}{\left(\sigma_G^2 + \frac{\sigma_{GL}^2}{E} + \frac{\sigma_E^2}{Er}\right)}$$

Where: $\boldsymbol{\sigma_G^2}$denote genotype variance component

$\boldsymbol{\sigma_{GL}^2}$ denote genotype-by-location variance component

$\boldsymbol{\sigma}_{\boldsymbol{E}}^{\boldsymbol{2}}$**,** represent error variance,$\boldsymbol{E}$ denote the number of environments,

$\boldsymbol{r}$ represents the number of replications (Cooper *et al*.,1996; Holland *et al*., 2003; Hallauer *et al*. 2010). The standard error for heritability and variances were computed as the square root of heritability and variances respectively.

3.8 Estimation of genetic correlation between five locations

The genotypic correlations ($\boldsymbol{r}_{\boldsymbol{g}}$) between locations were computed as:

$$r_g = \frac{r_{p(X,Y)}}{\sqrt{(H_X * H_Y)}}$$

Where:

$r_{p(X,Y)}$ represent phenotypic correlation between locations X and Y of the traits measured.

H_X and H_Y represent broad-sense heritability in locations X and Y for the traits measured (Cooper *et al*., 1996). This was estimated following Holland (2006).

Pearson correlation were estimated for measured traits with PROC CORR in SAS version 9.2 (SAS Institute 2009).

CHAPTER FOUR

4.0 RESULTS

4.1 Analysis of variance and mean performances of hybrids

4.1.1 Mean plant stand

The differences observed were highly significant ($p<0.001$) among environments, genotypes and genotype-by-environment effects for plant stand (Table 4). The test environments, genotype and genotype-by-environment interaction effects accounted for 17.7 %, 1.3 % and 24 % of the total variation in the sum of squares for plant stand (Table 5).

Plant stand ranged from 29 to 40 with Hybrid 13 (M1428-4) having the lowest and hybrid 21 (AS1204-4) having the highest. The mean plant stand was 37 (Appendix 5). Among the checks, hybrid 37 (Oba Super 7) had the lowest plant stand of 37 whereas hybrid 48, a local check, had the highest plant stand of 34. High plant stand corresponded with high yield in most cases.

4.1.2 Mean plant height

The combined analysis of variance across the five locations showed significant difference ($p<0.001$) among genotypes for Plant height (Table 4). The environment and

genotype-by-environment interaction mean squares were highly significant and accounted for 79.8 % and 6 % of the total variations whereas the genotype mean square accounted for 3 % of the total variation.

The plant height ranged from 150 cm to 189 cm (Appendix 5). The mean plant height was 172 cm. Hybrid 14 (M1227-12) had the highest plant height (181 cm) whereas hybrid 22 (AS1205-2) recorded the lowest plant height of 150 cm. Similarly, among the checks, hybrid 44 (SC719) exhibited the highest plant height (189 cm) with lowest being hybrid 46 (11C87) with a plant height of 168 cm.

4.1.3 Mean days to anthesis

The analysis of variance revealed significant differences ($p<0.001$) among the hybrid genotypes for days to anthesis (Table 4). The environment main effect and genotypeby-environment interaction effects were also significant. The test environments contributed 85.3 % of the total variation in the sum of squares for days to anthesis, while hybrid genotype and genotype-by-environment sources of variation accounted for 1.4 % and 4.5 % of the total variation (Table 5)

The days to anthesis ranged from 53 to 56 days. The mean day to anthesis was 55 days (Appendix 5). Hybrids 32 (M1428-10) 15 (AS1204-1), 16 (AS1204-5), 32 (M1428-10) gave the highest days to anthesis (56 days) whereas hybrid 14 (M122712) exhibited the lowest days to anthesis (53 days).

4.1.4 Mean days to Silking

The combined analysis of variance revealed that there were significant differences ($p<0.01$) among the hybrids for days to silking (Table 4). The mean square for environment and genotype-by-environment interaction showed significant differences and accounted for 83.1 % and 5.2 % of the total variation in the sum of squares

respectively for numbers of days to silking. The genotype main effect contributed 1.6 % of the total variation (Table 5).

The days to silking among the hybrid genotypes ranged between 55 to 58 days (Appendix 5). The mean days to silking was 56 days. Hybrid 16 (AS1204-5) exhibited the highest number of days to silking (58 days) whereas hybrid 14 (M122712) recorded the lowest number of days to silking (55 days). Among the checks, hybrid 46 (11C87) recorded the highest days to silking (56 days) while hybrid 45 (SC643) recorded the lowest days to silking (55 days).

4.1.5 Mean anthesis-silking interval

The results of combined analysis of variances revealed no significant difference among the hybrid genotypes for anthesis-silking interval (Table 4). The test environments and genotype-by-environment interaction effects were significant and accounted for 28.2 and 23.2 % of the total variation in the sum of squares for interval between days to silking and days to anthesis (Table 5).

The interval between days to anthesis and days to silking ranged between 1 to 2 days. The mean anthesis-silking interval was 1.76 days (Appendix 5). Hybrids 12 (M14283), 24 (M1428-7), 34 (M1428-14) and 3 (M1124-9) recorded the highest interval between days to anthesis and days to silking of 2 days. The remaining hybrids recorded the lowest anthesis-silking interval of 1 day.

4.1.6 Mean ear height

The results from combined analysis of variance revealed that significant mean squares were detected for ear height for genotype main effect, environment and genotype by environment interaction effects (Table 4). The test environment accounted for 76.3 % of the total sum square variation whereas the genotype and genotype-by-environment

interaction mean square accounted for 2.6 % and 7. 6 % of the total variation in the sum of squares for ear height (Table 5).

Ear height ranged between 64 cm to 93 cm (Appendix 5). The mean ear height was 80 cm Hybrid 10 (M1326-3) gave the highest ear height (84 cm) whereas hybrid 22 (AS1205-2) recorded the lowest ear height (64 cm). Among the checks, hybrid 44 (SC719) exhibited the highest ear height (93 cm) whereas hybrid 40 (Oba Super I) recorded the lowest ear height (76 cm).

4.1.7 Mean husk cover

The results of the combined of variance showed that genotype main effect, environment main effect and genotype-by-environment effects were all highly significant (P<0·001) for husk cover (Table 4). The percentage sum of squares of the total variation for husk cover as a result of the test environments, contributed 17.9 %; genotypes accounted for 8.6 % while genotype-by-environment interaction explained 29.5 % of the total variation (Table 5).

The husk cover ranged between 1.3 to 2.1. The mean rating for husk cover was 1.7 (Appendix 5). Hybrids 15 (AS1204-1) and 21 (AS1204-46) recorded a good husk cover score of 1.3 whereas hybrids 5 (M1326-1) recorded a husk score of 2.1 (Appendix 5). Among the checks, hybrids 44 (SC719) and 48 (Local check) recorded a good husk cover rating of 1.4 compared to hybrids 39 (Oba Super I) and 45 (SC643), which recorded a husk cover rating of 1.9. The hybrids had similar or better husk cover compared to the checks.

4.1.8 Mean plant aspect

The combined analysis of variance showed highly significant (p<0.001) genotype, environment and genotype-by-environment effects for plant aspect (Table 4). The effect

of environment explained 26 % of the total variations while hybrid genotypes contributed 8.6 % and genotype-environment interaction contributed 30.4% to the total variation for plant aspect (Table 5).

The plant aspect ranged from 1.1 to 1.9. The mean rating of plant aspect was 1.6 (Appendix 5). Hybrids 6 (M1227-9) and 26 (M1124-7) recorded very good scores for plants aspect of 1.1 compared to hybrids 30 (M1428-5) which recorded a scores of 1.9 for plant aspect. Among the checks, hybrid 44 (SC719) recorded a good score of 1.3 while hybrid 47 (10C2897) had a score of 1.9 for plant aspect. Generally, the hybrids had similar or better overall phenotypic appeal plant compared to the checks.

4.1.9 Mean ear aspect

The combined analysis of variance revealed highly significant difference ($p<0.001$) among hybrid genotypes for ear aspect (Table 4). The mean squares for environment and genotype-by-environment were highly significant ($p<0.001$) for ear aspect. The test environments, genotype and genotype-by-environment interaction effects accounted for 23.9 %, 8.6 % and 29.5 % of the total variation in the sum of squares for ear aspect (Table 5).

The ear aspect ranged from 1.2 to 1.9. The mean ear aspect was 1.5. (Appendix 5). Hybrids 1 (M1124-3) and 14 (M1227-12) had a very good score of 1.2 whereas hybrids 15 (AS1204-1), 16 (AS1204-5) and 32 (M1428-10) recorded a score of 1.9 for ear aspect. Among the checks, hybrid 44 (SC719) recorded a very good score for ear aspect of 1.2 whereas hybrid 41 (Oba Super 2) recorded a score of 1.8.

4.1.10 Mean plant harvested

The combined analysis of variance revealed that environment, genotype and genotype-by-environment mean squares were significant ($p<0.01$) for plant harvested

(Table 4). The environment source of variation accounted for the largest proportion (28.6 %) of the total variation whereas the genotype-by-environment and hybrid genotype variation explained 23.5 % and 8.2 % of the total variation (Table 5).

Plant harvested was in the range of 31 to 39 in all the hybrid genotypes. The mean plant harvested was 36 (Appendix 5). The hybrid 13 (M1428-4) gave the lowest plant harvested whereas hybrids 30 (M1428-5), 6 (M1227-9 11), 11 (M1326-421) and 21 (AS1204-46) had the same number of plant harvested and exhibited the highest number of plant harvested. Among the checks, hybrid 44 (SC719) recorded the lowest number of plant harvested whereas hybrid 45 (SC643) gave the highest number of plant harvested (Appendix 5).

4.1.11 Mean ear harvested

The combined analysis for ear harvested showed that environment, genotype and genotype-by-environment interaction effects were significant ($p<0.001$) (Table 4). The proportion of the total variation due to environment, genotype and genotype-byenvironment interaction were 30.0 %, 6.6 % and 20.4 % respectively (Table 5).

Ear harvested ranged between 30 to 39 (Appendix 5). The mean ear harvested was 35. Hybrid 13 (M1428-4) had the lowest number of ear harvested of 30 whereas hybrid 21 (AS1204-46) gave the highest number of ear harvested of 39. Among the checks, hybrid 44 (SC719) gave the lowest number ear harvested (32) while hybrid 45 (SC643) recorded the highest number of ear harvested of 38. The number of ears harvested is often used to indicate the presence or absence of single eared, double eared and barren plant.

4.1.12 Mean grain moisture

The combined analysis of variance showed significant difference ($p<0.05$) among genotypes for grain moisture (Table 4). The mean square for environment main effects

were significant ($p<0.01$). No significant difference was detected for genotypeby-environment effect for grain moisture.

The effect of environment explained 58.6 % of the total variance while genotype contributed 4.0 % and genotype-by-environment interaction contributed 10 % to the total variation for grain moisture (Table 5).

The percentage grain moisture ranged from 10.82 % to 13.83 %. The mean grain moisture was 12.5 % (Appendix 5). Hybrid 15 (AS1204-1) recorded the lowest grain moisture of 11.58 % whereas hybrid 2 (M1124-4) recorded the highest grain moisture of 13.83 %. Among the checks, hybrid 41 (Oba Super 2) recorded the lowest grain moisture of 10.83 % whereas hybrid 44 (SC719) recorded the highest grain moisture of 13.68 %.

4.1.13 Mean grain weight

The combined analysis of variance revealed that genotype main effect, environment main effect and genotype-by-environment were all highly significant ($P<0{\cdot}001$) for grain weight (Table 4). The percentage sum of squares of the total variation for grain weight as a result of the test environments, contributed 4.4 %; genotypes accounted for 13.1 % while genotype-by-environment interaction explained 30.7 % of the total variation (Table 5).

The grain weight ranged between 2.4 kg/ha to 3.6 kg/ha. The mean grain weight was 3.0 kg/ha. Hybrids 15 (AS1204-1), 19 (AS1204-43), 20 (AS1204-44), 22 (AS1205-2) and 32 (M1428-10) had the lowest grain weight of 2.5 kg/ha whereas hybrid 14 (M1227-12) had the highest grain weight of 3.6 kg/ha. Among the checks, hybrid 37 (Oba Super 7) had the lowest grain weight of 2.7 kg/ha whereas hybrid 48, a local check, had the highest grain weight of 3 kg/ha.

4.1.14 Mean grain yield

The homogeneity of variance test performed using the Bartlett's test indicated unequal error variance for each environment (Appendix 3 and 4). This provides evidence of heterogeneity of location error variance. Weight analysis were performed thereafter to make location error variance homogeneous prior to combined analysis of variance.

The combined analysis of variance showed that genotype main effect (G), environment main effect (E) and interaction between genotype and environments (GE) were all highly significant ($P<0{\cdot}001$) for grain yield (Table 4). Similarly, analysis of variance for each location revealed that there were significant differences among the hybrids at Damongo, Nyankpala, Manga and Wa. Yendi location revealed non-significant genotype mean square for grain yield (Appendix 2).

The percentage sum of squares of the total variation for grain yield as a result of the test environments, contributed 70.1 %; genotypes accounted for 4.1 % while genotype-by-environment interaction explained 9.4 % of the total variation (Table 5). The significant genotype and genotype-by-environment interaction for yield allow the need for further decomposition of genotype and interaction between genotype and environment effects.

In this study, different hybrids produced varied yields levels in each environment (Table 6 and Appendix 6). Hybrid 13 (M1428-4) was the highest yielding hybrid whereas hybrid 12 (M1428-3) was the lowest yielding hybrid genotype in Damongo. The best hybrid (M1428-4) outperformed the best check (SC643) by 9 %. Similarly, at Manga, hybrid 21 (AS1204-46) was found to be the highest yielding genotype whereas hybrid 13 (M1428-4) was lowest yielding hybrid. The check, hybrid 45 (SC643) was the best yielding check. However, the best hybrid genotype (AS120446) was out yielded by the

best check by 7.5 %. Hybrids 30 (M1428-5), 21 (AS120446), and 30 (M1428-5) were the highest yielding genotypes in Nyankpala, Wa and

Yendi respectively. The lowest yielding hybrid in these environments were hybrid 22 (AS1205-2), hybrid 15 (AS1204-1) and hybrid 13 (M14 28-4) respectively. The best check in Nyankpala, Wa and Yendi were hybrid 46 (11C87), hybrid (SC627) and hybrid 44 (SC719) respectively. On the other hand, the best hybrid genotypes M14285 and AS1204-46 out yielded the best check, 11C87 and SC627 in Nyankpala and Wa by 0.5 and 9.7 percent respectively. At Yendi, the best hybrid genotype (M1428-5) was out yielded by the best check (SC719) by 5 percent.

Among the five environments, the mean yield varied from 4,113 kg/ha to 8784 kg/ha. Nyankpala recorded the highest average yield of 8,784 kg/ha followed by Damongo (8,377 kg/ha-1), Yendi (8,359 kg/ha) Wa (7,794 kg/ha) and Manga (4,113 kg/ha).

Across the five environments, the three-way hybrids bred for drought and striga produced mean grain yield varying from 6,055 kg/ha to 9,219 kg/ha whereas the commercial hybrid checks and the local check had mean yields ranging from 5,960 kg/ha to 8,335 kg/ha

Hybrid 14 (M1227-12) was identified as the highest yielding hybrid with mean yield of 9,219 kg /ha while the lowest yielding hybrid genotype was hybrid 22 (AS1205-2) with mean grain yield of 6,055 kg ha-1. The best highest yielding check was identified as hybrid 44 (SC719) while the lowest yielding check was identified as hybrid 39 (Oba Super I). This hybrid was also identified as the lowest yielding hybrid genotype among the 48 hybrids evaluated in the study. The best hybrid genotype, hybrid 14 (M1227-12) out yielded the best check (SC719) by 10 %.

On the basis of performances, the top 10 ranked best performing hybrids were identified as hybrid 14 (M1227-12)>30 (M1428-5)>27 (M1227-2)>21 (AS120446)>34 (M1428-14)>28 (M1227-4)>29 (M1124-10)>1(M1124-3)>36(M1428-17) and 9 (M1227-17). Whereas the lower 10 ranked hybrids were identified as hybrid 10 (M1326-3) > 13 (M1428-4) > 4 (M1227-3) > 19 (AS1204-43) > 16 (AS1204-5) > 3 (M1124-9) >20 (AS1204-44) > 15 (AS1204-1) > 32 (M1428-10) > 22 (AS1205-2). Among the top 10 hybrids, only six of the hybrids out yielded the best check. The six hybrids, hybrid 14 (M1227-12); 30 (M1428-5); 27 (M1227-2); 21 (AS1204-46); 34 (M1428-14) and 28 (M1227-4) outperformed the best commercial check (SC719) by 10, 5.0, 4.0, 3.3, 1.8 and 0.4 percent respectively.

Table 4 Combined analysis of variance for grain yield and other important traits of forty-eight three-way maize hybrids evaluated across environments.

Source of variation	DF	Grain yield(kg/ha)	Grain weight (kg)	Plant stand	Days to anthesis(days)	Days to silk(days)	Anthesis Silking interval	Plant height(cm)
Environment(E)	4	418763***	4.46***	1317.83***	3861.79***	3258.83***	26.81***	155752.30***
REP(E)	10	4375***	1.86***	53.43**	10.05***	10.0***	0.32NS	173.08NS
Block(E*REP)	105	1005***	0.49***	38.13***	3.69*	3.59*	0.35NS	282.73***
Genotype(G)	47	2107***	1.12***	86.02***	5.25**	5.22**	0.45NS	495.36***
G*E	188	1198***	0.66***	38.94***	4.33***	4.34***	0.47**	250.09***
Error	365	517	0.26	20.11	2.62	2.67	0.34	135.28
R^2		92.10	76.47	75.90	94.73	93.79	67.58	93.67

Source of variation	DF	Ear height(cm)	Husk cover	Plant aspect	Ear aspect	Plant harvested	Ear harvested	Grain moisture(%)
Environment(E)	4	80162.73***	8.39***	19.14***	16.6***	2463.21***	2629.05***	1044.14***
REP(E)	10	256.00**	0.38*	0.37NS	0.27NS	60.77**	142.43***	10.05*
Block(E*REP)	105	161.21***	0.17NS	0.13NS	0.20NS	38.45***	36.51**	5.95***
Genotype(G)	47	228.22***	0.41***	0.54***	0.51***	60.08***	49.38***	5.99*
G*E	188	169.63***	0.29***	0.48***	0.44***	42.92**	38.13***	3.80NS
Error	365	91.97	0.15	0.20	0.20	20.82	22.25	3.4
R^2		92.01	71.10	75.12	74.07	77.91	76.86	82.59

J * = P < 0.05., **= P < 0.01 and ***=P < 0.001.

ffiREP, replication; G, Genotype (Hybrid); E, Environment

Table 5 Percentage sum of squares from the combined analysis of variance for measured traits of 48 three-way hybrids across five location

Source of variation	DF	Grain yield(kg/ha)	Grain weight (kg)	Plant stand	Days to anthesis	Days to silk	Anthesis silking interval	Plant height
Environment(E)	4	70.1***	4.4***	17.3***	85.3***	83.1***	28.2***	79.8***
REP(E)	10	1.8***	4.6***	1.8**	0.6***	0.6***	0.8NS	0.2NS
Block(E*REP)	105	4.4***	12.9***	13.1***	2.1*	2.4*	9.7NS	3.8***
Genotype(G)	47	4.1****	13.1***	13.3***	1.4**	1.6***	5.6NS	3.0***
G*E	188	9.4***	30.7***	24.0***	4.5***	5.2***	23.2**	6.0***
Error	365	7.9	23.5	24.1	5.3	6.2	32.4	6.3
R^2		92.1	71.3	75.9	94.7	93.8	67.6	93.7

Source of variation	DF	Ear height	Husk cover	Plant aspect	Ear aspect	Plant harvested	Ear harvested	Grain moisture
Environment(E)	4	76.3***	17.9***	26.0***	23.9***	28.6***	30.0***	58.6**
REP(E)	10	0.6**	2.0*	1.3*	1.0NS	1.8**	4.1***	1.4*
Block(E*REP)	105	4.0***	9.6NS	4.6NS	7.6NS	11.7***	10.9**	8.8***
Genotype(G)	47	2.6***	10.2***	8.6***	8.6***	8.2***	6.6***	4.0*
G*E	188	7.6***	29.4***	30.4***	29.5***	23.5**	20.4***	10.0NS
Error	365	8.0	28.9	24.9	25.9	22.1	23.1	17.4
R^2		92.01	71.10	75.12	74.07	77.91	76.86	82.59

Ɉ * = P < 0.05., ** =P < 0.01 and ***=P < 0.001.

ffiREP, replication; G, Genotype (Hybrid); E, Environment

Table 6 Mean yield of 48 three-way hybrid maize evaluated across five environments.

Hybrid	NAMES	Damongo	Manga	Nyankpala	Wa	Yendi	Mean(Kg/ha)
1	M1124-3	8015	4083	11167	7803	9740	8162 2
	M1124-4	10070	3752	7452	7109	9058	7488 3
	M1124-9	7429	4039	5150	7064	9400	6616 4
	M1227-3	8578	3634	7112	7426	7122	6774 5
	M1326-1	6484	4371	9979	8024	9799	7731 6
	M1227-9	10801	4116	7588	7295	6083	7177 7
	M1227-11	7597	4606	9565	7610	8284	7532 8
	M1227-14	10253	3520	9855	8034	7868	7906 9
	M1227-17	10028	3600	7837	8725	10070	8052 10
	M1326-3	8092	4452	6733	8109	7343	6946 11
	M1326-4	7553	4359	10338	8061	9227	7908 12
	M1428-3	3699	4816	8940	8718	9809	7197 13
	M1428-4	11465	3505	5627	7858	5647	6821 14
	M1227-12	10962	4367	12377	8467	9924	9219 15
	AS1204-1	7389	3820	6829	6163	7007	6242 16
	AS1204-5	9435	3662	6088	7676	6622	6697 17
	AS1204-7	10022	3846	9057	7338	7074	7467 18
	AS1204-26	6809	4504	8743	7275	9852	7437 19
	AS1204-43	5864	4280	8895	7655	6990	6737 20
	AS1204-44	4273	4737	7496	7672	7612	6358 21
	AS1204-46	9465	5181	11900	9285	7262	8618 22
	AS1205-2	5219	3971	4584	7506	8998	6055 23
	M1227-5	9416	4049	10528	7547	8521	8012 24
	M1428-7	10282	4780	8111	8316	8459	7990 25
	M1124-6	8909	4212	10400	8210	7743	7895 26
	M1124-7	9515	4240	8385	9166	8718	8005 27
	M1227-2	10487	4976	10611	7858	9465	8679 28
	M1227-4	11265	4110	10686	7986	7802	8370 29
	M1124-10	6582	4369	12372	8146	10147	8323 30
	M1428-5	7721	4426	12788	8503	10354	8758 31
	M1428-8	10132	3749	6755	8344	8803	7556 32
	M1428-10	7147	3614	6756	6974	6098	6118 33
	M1428-11	9598	3648	7541	7584	8889	7452 34
	M1428-14	10441	4348	10350	8715	8570	8485 35
	M1428-15	5793	4308	9480	8063	9877	7504 36
	M1428-17	10219	3558	10694	8541	7700	8142 37
	Oba Super 7	7433	3614	5314	7171	8519	6410 38
	ObaSuper 9	7465	4116	8134	7695	7907	7063 39
	Oba Super I	4923	4114	7460	6039	7264	5960 40
	Oba Super I	8714	4151	8921	7826	8427	7608 41
	Oba Super 2	6289	3544	7400	6845	6934	6202 42
	SC627	9186	4358	6776	8426	8244	7398 43
	SC637	5354	4422	10326	6823	7960	6977 44
	SC719	10381	3621	9883	6919	10872	8335 45
	SC643	10496	5586	7831	8335	8012	8052 46
	11C87	7360	4101	12721	7725	6191	7620 47
	10C2897	8020	3926	12258	8169	8492	8173 48
	Local check	9461	3215	5816	7322	10491	7261
	Mean	8377	4133	8784	7794	8359	7489
	SE	284.49	69.29	311.01	98.91	186.97	114.71

4.2 Broad sense heritability/Repeatability of traits of each location

Broad sense heritability (repeatability) of traits for individual trial are presented in Table 7. Heritability(repeatability) of grain yield ranged from 31 % to 97 % for individual trial with Damongo recording heritability estimates as high as 97 %. followed by Nyankpala (69 %), Wa (44 %), Manga (33 %) and Yendi recording low heritability estimate of 31 %. Heritability estimate for all traits at Damongo ranged from 25 % to 99 %. Plant height, ear height, grain yield, grain weight, plant aspect, ear aspect,

plant stand, days to anthesis, husk cover, plant harvested and ear harvested recorded heritability estimates above 50 % whereas anthesis-silking interval, days to silk and grain moisture recorded heritability below 50 %. Similarly, at Manga, plant stand and plant harvested had heritability estimate above 50 % while the rest of the traits recorded estimates below fifty percent. Broad sense heritability for Grain yield was 33 %. Grain weight and grain moisture recorded zero percent. Broad sense heritability for grain moisture, plant stand, days to anthesis, days to silk, anthesissilking interval, plant height, ear height, husk cover, plant aspect, ear aspect, plant harvested and ear harvested are low and below 50 % except for grain yield (69 %) and grain weight (72 %) at Nyankpala.

In Wa, repeatability or heritability of grain yield, grain weight, grain moisture, days to anthesis, days to silk, anthesis-silking interval, ear height, husk cover, plant aspect and ear aspect were low, below 50 % except for plant stand, plant harvested and Ear harvested with considerably high estimate above 50 %. However, grain moisture, anthesis-silking interval, plant aspect and ear aspect had broad sense heritability of zero. A similar trend was observed for the Yendi location. Grain yield, grain weight, grain moisture, anthesis silking interval, plant height, ear height, husk cover, plant aspect, ear aspect, plant harvested and ear harvested recorded broad sense heritability below 50 % with anthesis silking interval and ear height recording zero heritability estimated. However, plant stand, days to anthesis and days to silk had moderately high heritability estimate of 59, 52 and 57 % respectively.

Traits	DAMONGO	MANGA	NYANKPALA	YENDI	WA
Grain yield	0.97±0.01	0.33±0.18	0.69±0.08	0.31±0.18	0.44±0.15
Grain weight	0.97±0.01	0.00±0.00	0.72±0.08	0.30±0.18	0.47±0.15

Grain moisture	0.28±0.18	0.00±0.00	0.11±0.22	0.41±0.17	0.00±0.00
Plant stand	0.83±0.04	0.60±0.11	0.19±0.21	0.59±0.11	0.70±0.08
Days to anthesis	0.63±0.09	0.19±0.23	0.15±0.23	0.52±0.13	0.22±0.20
Days to silk	0.25±0.19	0.10±0.23	0.07±0.26	0.57±0.12	0.22±0.20
Anthesis-silking interval	0.39±0.15	0.43±0.15	0.04±0.25	0.00±0.00	0.00±0.00
Plant height	0.99±0.00	0.25±0.19	0.21±0.23	0.41±0.15	0.67±0.10
Ear height	0.78±0.06	0.37±0.16	0.27±0.21	0.00±0.00	0.39±0.17
Husk cover	0.94±0.02	0.26±0.19	0.35±0.17	0.16±0.21	0.06±0.26
plant aspect	0.94±0.02	0.05±0.24	0.49±0.13	0.20±0.20	0.00±0.00
Ear aspect	0.96±0.01	0.33±0.17	0.15±0.22	0.10±0.23	0.00±0.00
plant harvested	0.82±0.04	0.61±0.11	0.23±0.20	0.16±0.23	0.67±0.09
Ear harvested	0.80±0.05	0.47±0.15	0.38±0.16	0.11±0.24	0.58±0.11

ǂ ± indicates standard error of heritability.

Table 7. Broad sense heritability (Repeatability), standard error of measured traits for each environment.

4.3 Variance Component and heritability (Repeatability) traits across environments

Estimates of genotype, environment, genotype-by-location variances across the environment is presented in Table 8. Variance component of environment was not significant for all the traits but had a larger magnitude than genotypic, genotype-byenvironment and residual variance for all traits except grain moisture and husk cover. For example, the ratio of environment variance to genotype-by-environment variance was fifteen times larger for grain yield across the environment. This implied that the hybrids were largely influenced by the environment. Genotypic variance was significant for all traits except days to anthesis, days to silk, ear height, husk cover, plant aspect, ear aspect, plant harvested and ear harvested. It is evident that traits that lack significant differences for genotypic variances reflected in their corresponding low heritability estimate across the environment. This implied that the hybrids lacked variability for those trait. This further suggests that the traits had similar response across

the environment. The residual and genotype-by-environment variance component were observed to positive and highly significant (P<0.001) the traits measured. The genotype-by-environment variance component was 5, 4, 2, 7, 11, 2, 6, 3, 11, 8 and 7 times larger than genotypic variance for grain yield, grain weight, plant stand, days to anthesis, days to silk, plant height, ear height, husk cover, plant aspect, plant harvested and ear harvested respectively.

Heritability estimates and variance component of measured traits are presented in Table 8. Heritability estimates across environment ranged from 0 to 60 %. Grain yield, grain weight, grain moisture, days to anthesis, days to silk, anthesis silking interval, ear height, husk cover, plant aspect, ear aspect, plant harvested and ear harvested had low heritability below 50 %. However, anthesis silking had zero heritability. In contrast, Plant stand and plant height had heritability estimates of 60 % and 40 % respectively. Grain yield and weight had moderate heritability estimates of
40 and 41 percent respectively.

Table 8 Variance component and Broad sense heritability of measured traits across the environment.

Trait	Environment (E)	Genotype	Genotype*E	Residual	*H* (%)	*H* Genotype
Grain yield	3.54±2.58NS	0.25±0.13*	1.23±0.20***	1.82±0.13***	40	0.40±0.14
Grain weight	0.01±0.02NS	0.04±0.02*	0.16±0.03***	0.26±0.02***	41	0.41±0.14
Grain moisture	7.18±5.13NS	0.14±0.08*	0.00±0.00	3.57±0.22***	36	0.36±0.14
Plant stand	8.64±6.47NS	4.16±1.50**	6.89±1.58***	20.54±1.50***	60	0.60±0.09
Days to anthesis	26.73±18.96NS	0.10±0.09NS	0.66±0.18***	2.64±0.19***	24	0.24±0.18
Days to silk	22.54±16.00NS	0.06±0.09NS	0.66±0.18***	2.70±0.19***	16	0.16±0.20
Anthesis-silking interval	0.18±0.13NS	0.00±0.00	0.04±0.02**	0.34±0.02***	0	0.00±0.00
Plant height	1078.71±764.85NS	17.31±7.51**	40.07±10.00***	139.33±10.22***	50	0.50±0.12
Ear height	554.34±393.64NS	4.36±3.62NS	27.43±6.7***	94.16±6.85***	27	0.27±0.17
Husk cover	0.05±0.04NS	0.00±0.01NS	0.06±0.01***	0.15±0.01***	17	0.17±0.19
plant aspect	0.13±0.09NS	0.01±0.01NS	0.11±0.02***	0.19±0.01***	22	0.22±0.18
Ear aspect	0.11±0.08NS	0.00±0.01NS	0.09±0.02***	0.20±0.01***	12	0.12±0.20
plant harvested	16.51±12.10NS	1.11±0.97NS	8.42±1.77***	21.32±1.56***	26	0.26±0.18
Ear harvested	17.14±12.92NS	0.94±0.85NS	6.29±1.58***	22.30±1.60***	25	0.25±0.18

ffi G, Genotype (Hybrid); E, Environment.

† *H*, heritability (Repeatability), *H* (%), heritability in percentage

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4.4 Phenotypic correlation of measured traits

Phenotypic correlation of measured traits are presented in Table 9. Positive and highly significant (P<0.001) correlation was observed among grain yield and plant stand (0.12), grain yield and days to anthesis (0.34), grain yield and days to silk (0.34), grain yield and plant height (0.63), grain yield and ear height (0.60), grain yield and plant harvested (0.16), grain yield and ear harvested (0.30) as well as grain yield and grain weight (0.78). Significant negative correlation was observed between grain yield and anthesis-silking interval (-0.17), grain yield and husk cover (-0.33), grain yield and ear aspect (-0.31), as well as grain yield and grain moisture (-0.32).

In contrast, the association between grain yield and plant aspect (0.02) were nonsignificant. Similarly, positive and highly significant (P<0.001) correlation was noted between days to anthesis and days to silk (0.99). However, days to anthesis and days to silk were observed to be highly significant (P<0.001) but negatively correlated with anthesis silking interval (-0.53 and -0.42 respectively). Days to anthesis was also negatively correlated with husk cover (-0.35), plant aspect (-0.17), ear aspect (-0.08), grain moisture (-0.48), plant stand (-0.22), plant harvested (-0.08) and ear harvested (-0.18) except for grain weight (0.01). A similar trend was observed for days to silk.

Anthesis-silking interval presented a significant correlation for all traits except for ear aspect (0.00), ear harvested (0.06) and grain weight (-002). The correlation between anthesis-silking interval and ear aspect was equal to zero. Highly significant phenotypic correlation was found between plant and ear height (0.93), plants harvested and plant stand (0.86) as well as ear harvested and plant stand (0.76).

However, there was low but significant correlations between plant height and days to anthesis (0.24), plant height and days to silk (0.24), ear height and days to anthesis

(0.28), ear height and days to silk (0.28), plant aspect and anthesis silking interval (0.11), plant aspect and plant height (0.33), plant aspect and ear height (0.29), plant aspect and husk cover (0.14), ear aspect and plant aspect (0.43), ear aspect and husk cover (0.11), ear aspect and plant height (0.22),ear aspect and ear height (0.22), and plant height (0.25), grain weight and ear height (0.22),grain moisture and anthesis silking interval (0.28) as well as grain moisture and husk cover (0.22).

Furthermore, negative phenotypic correlation was realized between plant height and husk cover (-0.35), husk cover and grain weight (-0.15), ear height and husk cover (-0.35), plant aspect and grain weight (-0.10), plant harvested and grain moisture (0.17), ear harvested and grain moisture (-0.27), ear aspect and grain weight (-0.31) as well as ear aspect and grain moisture (-0.15) while negative but non-significant phenotypic correlation existed between plant stand and plant aspect (-0.01), plant stand and ear aspect (-0.02) and husk cover and ear harvested (-0.02).

Table 9. Phenotypic correlation of traits measured across five environment

Trait	PSD	DA	DS	ASI	PH	EH	HC	PASP	PHV	EHV	EASP	GYLD	Gwt	GM
PSD														
DA	-0.22***													
DS	-0.22***	0.99***												
ASI	0.11**	-0.53***	-0.42***											
PH	0.05NS	0.24***	0.24***	-0.12**										
EH	0.04NS	0.28***	0.28***	-0.18***	0.93***									
HC	0.06NS	-0.35***	-0.34***	0.23***	-0.35***	-0.35***								
PASP	-0.01NS	-0.17***	-0.16***	0.11**	0.33***	0.29***	0.14***							
PHV	0.86***	-0.18***	-0.17***	0.12**	0.10**	0.09*	0.06NS	-0.02NS						
EHV	0.76***	-0.08*	-0.07*	0.06NS	0.21***	0.20***	-0.02NS	0.00NS	0.90***					
EASP	-0.02NS	-0.08*	-0.08*	0.00NS	0.22***	0.22***	0.11**	0.43***	0.04NS	0.04NS				
GYLD	0.12***	0.34***	0.34***	-0.17***	0.63***	0.60***	-0.33***	0.02NS	0.16***	0.30***	-0.13**			
Gwt	0.11**	0.01NS	0.02NS	-0.002NS	0.25***	0.22***	-0.15***	-0.10**	0.10**	0.16***	-0.31***	0.78***		
GM	-0.09*	-0.49***	-0.48***	0.28***	-0.20***	-0.21***	0.22***	0.07NS	-0.17***	-0.27***	-0.15***	-0.32***	0.07NS	

ffi*=P < 0.05., ** Significant=P < 0.01 and ***=P < 0.001.

†PSD, plant stand; DA, days to anthesis; DS, days to silk; ASI, anthesis silking interval; PH, plant height; EH, ear height; HC, husk cover; PASP, plant aspect; PHV, plant harvested; EHV, ear harvested; EASP, ear aspect; GYLD, grain yield; Gwt, grain weight; GM, grain moisture.

4.5 Genetic correlation among five locations

Genetic correlation among five locations for grain yield is presented in Table 10. Genetic correlation for grain yield among location ranged from -0.3107 to 0.9999 for all the five environment. Manga and Wa (rG=0.9999) were observed to be positively correlated at 0.1 percent probability. This could be due to the fact that, the two locations have similar climatic and soil characteristics. However, there was a nonsignificant but positive genetic correlation between Yendi and Nyankpala (rG=0.5151), Wa and Nyankpala (rG=0.7194), Manga and Nyankpala (rG=0.7375), Wa and Yendi (rG=0.6242), Wa and Damongo (rG=0.4701) as well as Manga and Yendi (rG=0.3726), while a negative but non-significant genetic correlation was observed for Yendi and Damongo (rG=-0.1055), and Manga and Damongo (rG=-0.3107).

Table 10 Genetic correlation for grain yield among five environment

Environment	Nyankpala	Damongo	Yendi	Wa	Manga
Nyankpala		0.0881NS	0.5151NS	0.7194NS	0.7375NS
Damongo	-0.1055NS		0.4701NS	-0.3107NS	
Yendi	0.6242NS	0.3725NS			
Wa	0.9999***				
Manga					

ffi* =P < 0.05., ** =P < 0.01 and ***=P < 0.001.
ffiNS, indicates not significant.

4.6 Genotype plus genotype × environment biplots analysis

4.6.1 Which-won-where pattern of 48 three-way hybrid maize

The GGE biplots for grain yield of 48 three-way hybrid maize cultivars evaluated under rain fed conditions across five locations is shown in figure 2. The polygon view of the GGE biplot based on grain yield revealed that PC 1 (45.81 %) and PC 2 (35.40 %) explained 81.2 % of the total variation across the environments.

The polygon in figure 2 is drawn by joining hybrid genotypes located farthest from the biplot origin such that all other genotypes are contained in the polygon. Genotypes at the vertices of the polygon are called vertex genotypes. The vertex genotypes have the longest vector in their respective direction and are either the best or the poorest in one or more environments. The lines that are perpendicular to the sides of the polygon are the equality lines. These equality lines are drawn to divide the biplot into sectors, which enhance visual comparison of them (Yan and Tinker, 2006). The equality lines divide the biplot into six sectors. Each sector has its own winning genotype. Thus, the polygon view divided the environments into three groups: These suggest the existences of three mega environments. DAM is located at the upper-right region of the polygon, WA below the upper-right region of the polygon while NYAN was located at lower-right region of the polygon with MAN and YEN. However, environment, MAN and YEN fell in none of sector except on the line.

A polygon was formed with hybrid 13 (M1428-4), 22 (AS1205-2), 12 (M1428-3), 29 (M1124-10), 30 (M1428-5) and 14 (AS1204-46) as vertex genotypes (hybrids). Vertex genotypes are usually the most responsive genotypes and can be either the best or the poorest genotypes in a few or all of the environments (Yan and Kang, 2003;

Yan *et al*., 2007). Thus, 13 (M1428-4) was the winning genotype for DAM., 14 (AS1204-46) was the winner genotype for WA while 29 (M1124-10) and 30 (M14285) were the winning genotype for MAN, YEN and NYAN. This indicates that the vertex genotypes were the highest yielding hybrids in all the locations that share the sector with it. Thus, had a positive response to the environments. In contrast, vertex genotypes 22(AS1205-2) and 12 (M1428-3) had no environment to share or no environment within its sectors. This suggest that the hybrids were the poorest in terms of their response in all or some of the environment.

In contrast, 42 hybrids out of the 48 hybrids were located in the polygon, showing that the hybrids were less responsive than the vertex hybrids (13, 22, 12, 29, 30 and 14).

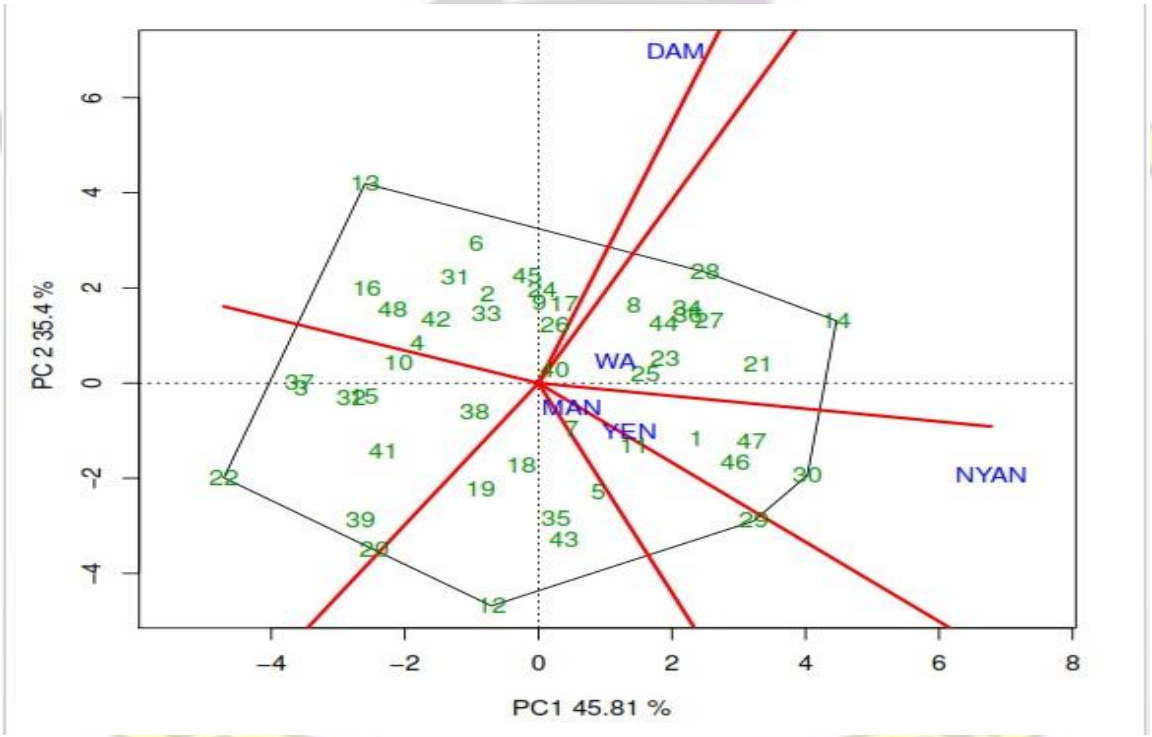

Figure 2: The who-won-where view of GGE biplot of the 48 three-way hybrid genotypes evaluated under rain fed conditions in five locations.

Environments' codes: WA, Wa; MAN, Manga; YEN, Yendi; DAM, Damongo; NYAN, Nyankpala. Hybrids' codes:1=M1124-3; 2=M1124-4; 3=M1124-9; 4= M1227-3; 5= M1326-1; 6= M1227-9; 7= M1227-11; 8= M122714; 9= M1227-17; 10= M1326-3;11= M1326-4; 12 = M1428-3; 13= M1428-4; 14= M1227-12; 15= AS1204-1; 16= AS1204-5; 17= AS1204-7; 18= AS1204-26; 19= AS1204-43; 20= AS1204-44; 21= AS1204-46; 22= AS12052; 23= M1227-5; 24= M1428-7; 25= M1124-6; 26 = M1124-7; 27 = M1227-2; 28 = M1227-4; 29 = M1124-10; 30 = M1428-5; 31 = M1428-8; 32 = M1428-10; 33 = M1428-11; 34 = M1428-14; 35 = M1428-15; 36 = M1428-17; 37 = Oba Super 7; 38 = ObaSuper 9; 39 = Oba Super I; 40 = Oba Super I; 41 = Oba Super 2; 42 = SC627; 43 = SC637; 44 = SC719; 45 = SC643; 46 = 11C87;47 = 10C2897 and 48=Local check

4.6.2 Hybrid performance and Stability of Yield of 48 Three-way hybrids

The mean performance and stability of 48 three-way hybrids across five environments is shown in figure 3. The mean grain yield performances and stability of 48 hybrid maize were virtualized by genotype-focused GGE biplot. It is made up of two lines; the average environment coordinate (AEC) abscissa and average environment coordinate (AEC) ordinate. The average environment coordinate (AEC) abscissa is a line that pass through the GGE biplot origin described as the average environment axis. The average environment coordinate (AEC) abscissa (average environment axis) is represented by a small circle with the pointer in the direction with highest mean performances across the environments. The contribution of each hybrid to the overall effects of hybrids are approximated by the average environment axis. Projections of the hybrids onto the average environment axis, gives an indication of the relative mean yield of the hybrid. Similarly, the axis of the AEC ordinate is the line that pass through the biplot origin at an angle of 90° to the AEC abscissa. It points to the directions with greater variability and/ or poor stability. It explains each genotypes' contributions .to GEI.

In the present study, eighteen (18) hybrids with two commercial checks were ranked with higher mean performances above the grand mean because they were ranked along the AEC abscissa, with the pointer in the direction of superior mean performance. The list includes 14 (M1227-12), 21 (AS1204-46), 30 (M1428-5), 28 (M1227-4), 27 (M1227-2), 34 (M1428-14), 47 (10C2897), 29 (M1124-10), 23 (M1227-5), 1 (M1124-3), 25 (M1124-6), 11 (M1326-4), 24 (M1428-7), 26 (M11247), 45 (SC643), 9 (M1227-17), 7 (M1227-11) and 5 (M1326-1) in order of ranks. On the other hand, hybrid 14 (M1227-12), 23 (M1227-5), 25 (M1124-6) and hybrid 40 (Oba Super I) were the very stable because of their small projection and/or their near zero projection onto the ACE ordinate (Yan *et al*., 2001; Yan *et al*., 2006). Hybrids 21 (AS1204-

46), 24 (M1428-7), 27 (M1227-2) and 34 (M1428-14) were moderately stable. On the other hand, hybrids with high mean performances but unstable were 30 (M1428-5), 47 (10C2897), 29 (M1124-10), 45 (SC643) and 5 (M1326-1) due to their long projection onto the AEC ordinate.

In contrast, hybrids 38 (ObaSuper 9), a commercial check and 22 (AS1205-2) were highly stable for grain yield but low-yielding hybrid genotypes while hybrids 41 (Oba Super 2), 31 (M1428-8), 25 (M1124-6) and 10 (M1326-3) were moderately stable and low-yielding but produced mean grain yield greater than the grand mean except hybrid 41 (Oba Super 2) which produced the least mean grain yield below the grain mean among all the hybrid genotypes across the environment.

A total of eight hybrid genotypes were found to be unstable and low-yielding. The list includes hybrids 12 (M1428-3); 13 (M1428-4); 43 (SC637), 35 (M1428-15), 20 (AS1204-44), 39 (Oba Super I) 16 (AS1204-5) and 31 (M1428-8). However, hybrids 35 (M1428-15) and 31 (M1428-8) produced mean grain yield higher than the grand mean but were classified as unstable and low-yielding.

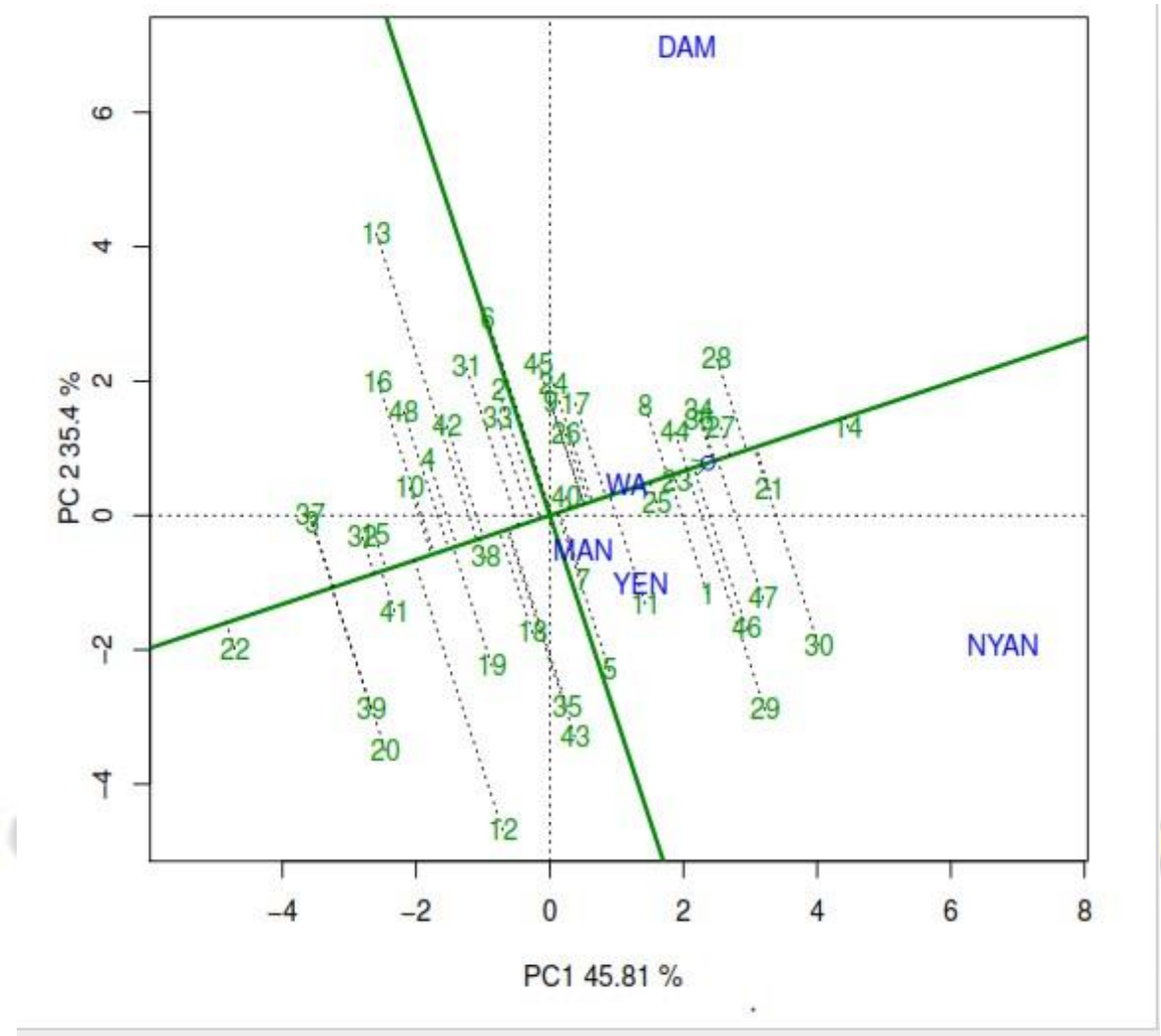

Figure 3. GGE biplot view of mean performance and stability of 48 three-way hybrids across five locations.

Environments' codes: WA: Wa; MAN: Manga; YEN: Yendi; DAM: Damongo; NYAN: Nyankpala. Hybrids' codes:1=M1124-3; 2=M1124-4; 3=M1124-9; 4= M1227-3; 5= M1326-1; 6= M1227-9; 7= M1227-11; 8= M1227-14; 9= M1227-17; 10= M1326-3;11= M1326-4; 12 = M1428-3; 13= M1428-4; 14= M1227-12; 15= AS1204-1; 16= AS1204-5; 17= AS1204-7; 18= AS1204-26; 19= AS1204-43; 20= AS1204-44; 21= AS1204-46; 22= AS1205-2; 23= M1227-5; 24= M1428-7; 25= M1124-6; 26 = M1124-7; 27 = M1227-2; 28 = M1227-4; 29 = M1124-10; 30 = M1428-5; 31 = M1428-8; 32 = M1428-10; 33 = M1428-11; 34 = M1428-14; 35 = M1428-15; 36 = M1428-17; 37 = Oba Super 7; 38 = ObaSuper 9; 39 = Oba Super I; 40 = Oba Super I; 41 = Oba Super 2; 42 = SC627; 43 = SC637; 44 = SC719; 45 = SC643; 46 = 11C87;47 = 10C2897 and 48=Local check

4.6.3 Discrimitiveness and representativeness of test locations

The GGE biplot view showing the discriminating ability and representativeness of 48 three-way maize hybrids evaluated across five environments is shown in figure 4. Testing environment performance in multi-environment helps to identify ideal environment that can distinguish between genotypes and simultaneously be representative of the intended environment. This is achieved by a biplot constructed with concentric circles, proportional to the standard deviation of the environments under consideration. The concentric circles are useful in assessing the discriminating ability of a particular environment. An axis called Average environment axis, is a line drawn such that it passes through average environment and the biplot origin with the average coordinates of all test environments. The small circle is the averageenvironment axis (AEA), and the arrow pointing to it, is used to indicate the direction of the AEA (Yan, 2014). The length of an environment vector is a measure of the discriminating ability. Thus, the longer the environment vector, the more discriminative the environment. The shorter the length of the environment vector, the nondiscriminative the test environment. Environment with short-vector length shown in GGE biplot view were: WA, MAN and YEN. These environments are considered less informative and less discriminating among the hybrids as such environments will give little or no information about the hybrid performances. On the other hand, DAM and NYAN had long vector and are considered very discriminating. Such

environments are useful in selecting best performing hybrid genotypes.

The angle between the vector of an environment and the AEC axis is a measure of the representativeness of the environment (Yan and Kang, 2003). As a rule, the smaller the angle between the environment vector and AEA axis, the more representative of the target environment. On the other hand, the larger the angle between the environment

vector and the AEA axis, the less representative of the target environment. In the present study, the most representative environments are WA,

MAN and YEN because they formed smaller angles with AEA axis. In contrast, DAM and NYAN formed larger angle with AEA axis. Therefore, they are less representative of the target environment.

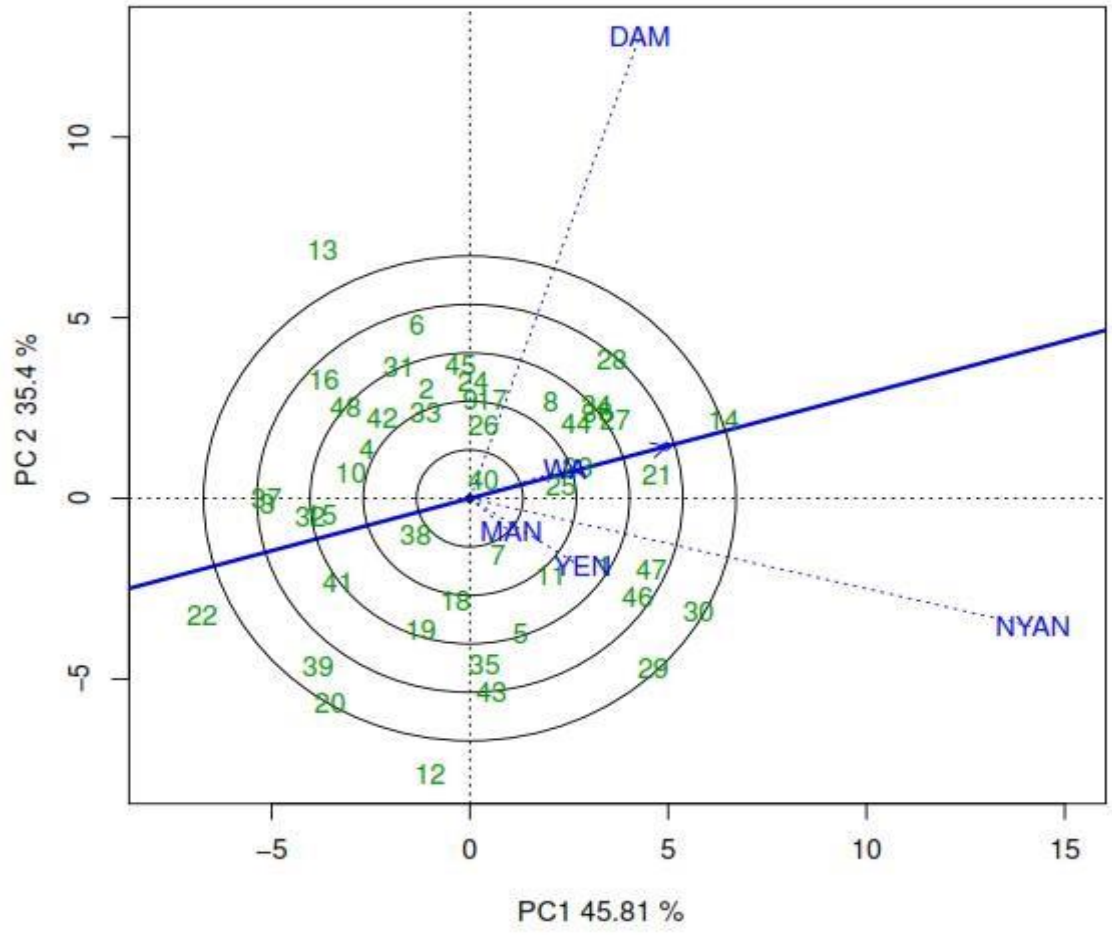

Figure 4. GGE biplot view showing the discriminating ability and representativeness of 48 three-way maize hybrid evaluated across five environments.

Environments' codes: WA, Wa; MAN, Manga; YEN, Yendi; DAM, Damongo; NYAN, Nyankpala. Hybrids' codes:1=M1124-3; 2=M1124-4; 3=M1124-9; 4= M1227-3; 5= M1326-1; 6= M1227-9; 7= M1227-11; 8= M1227-14; 9= M1227-17; 10= M1326-3;11= M1326-4; 12 = M1428-3; 13= M1428-4; 14= M1227-12; 15= AS1204-1; 16= AS1204-5; 17= AS1204-7; 18= AS1204-26; 19= AS1204-43; 20= AS1204-44; 21= AS1204-46; 22= AS1205-2; 23= M1227-5; 24= M1428-7; 25= M1124-6; 26 = M1124-7; 27 = M1227-2; 28 = M1227-4; 29 = M1124-10; 30 = M1428-5; 31 = M1428-8; 32 = M1428-10; 33 = M1428-11; 34 = M1428-14; 35 = M1428-15; 36 = M1428-17; 37 = Oba Super 7; 38 = ObaSuper 9; 39 = Oba Super I; 40 = Oba Super I; 41 = Oba Super 2; 42 = SC627; 43 = SC637; 44 = SC719; 45 = SC643; 46 = 11C87;47 = 10C2897 and 48=Local check.

4.6.4 Relationships among five test locations

The GGE biplot vector view showing the relationship among the five environments is presented in figure 5. The GGE biplot explained 81.21 % of the total variation of grain yield in the environments. The GGE biplot is achieved by environment centering and concentric circles drawn to approximate standard deviation of the environment. The lines that connected each environment to the biplot origin are known as vectors. The ratio of length of the adjacent side to the length of the hypotenuse side between the vectors of any two environments approximates the correlation coefficient, the magnitude and direction of correlation among them (Yan and kang, 2003; Yan and Tinker, 2006). Hence, small angle formed between the vectors of any two environments suggests a positive correlation whereas an angle formed between any two environments vector more than 90° but less than 180 suggests negative correlations. An angle of 90° indicates no correlation.

The angle formed between DAM and WA, WA and NYAN, WA and YEN, MAN and WA NYAN and YEN, NYAN and MAN were small angles less than 90 . The correlation between them are 0.601, 0.843, 0.610, 0.488, 0.940 and 0.881 respectively (Table 11). This suggests that the environments were positive and closely related. On the other hand, the angle formed between DAM and MAN, DAM and YEN were larger than 90 and are said to be an obtuse angle. Thus, the correlation between them are -0.403 and -0.266 respectively. This gives an indication that the environments were negatively correlated. In contrast, the angle between DAM and NYAN were at right angle. This implies that the two environments were not correlated and should be treated as independent environments.

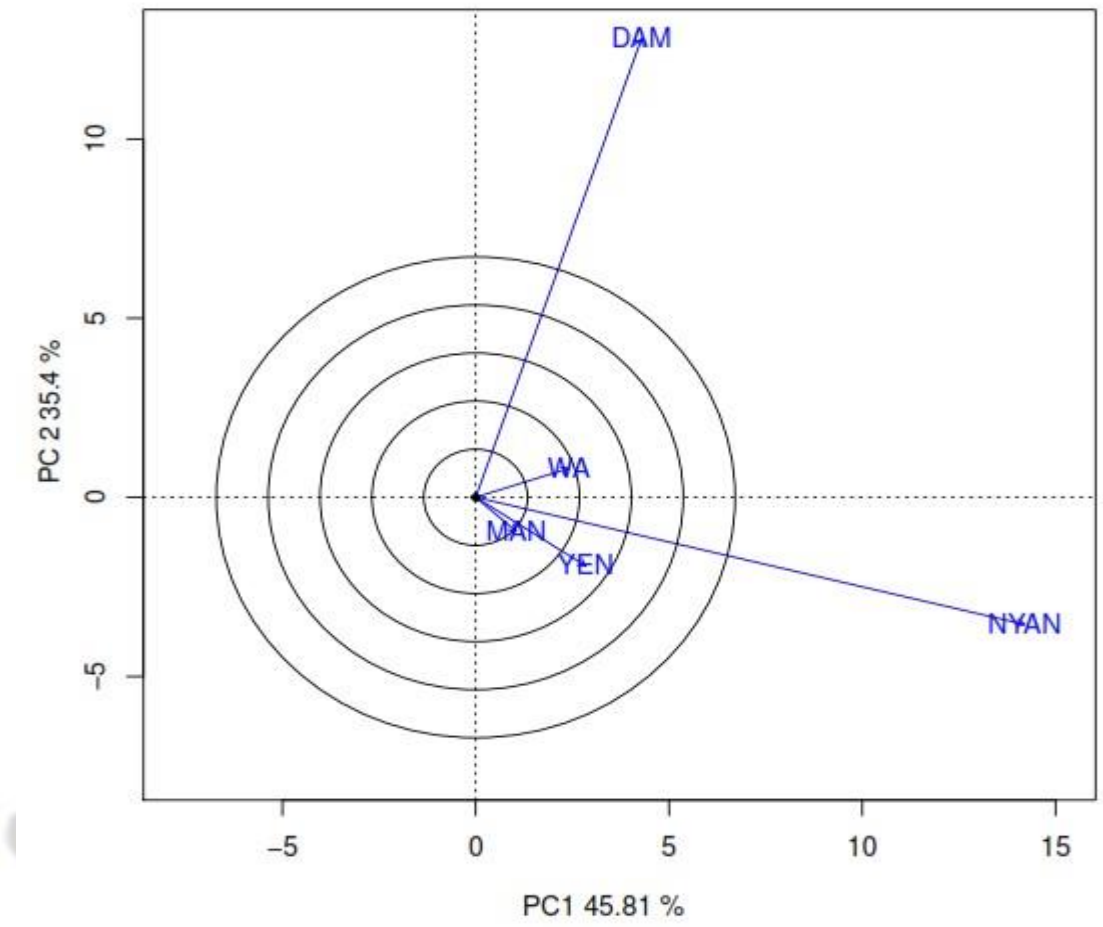

Figure 5. GGE biplot view showing the relationship among five test environments. Environments' codes: WA, Wa; MAN, Manga; YEN, Yendi; DAM, Damongo; NYAN, Nyankpala.

Table 11 Correlation coefficients among five tests environments

ENVIRONMENTS	DAM	MAN	NYAN	WA	YEN
DAM					
MAN	-0.403				
NYAN	0.078	0.881			
WA	0.602	0.488	0.843		
YEN	-0.266	0.989	0.940	0.610	

ffiEnvironments' codes: WA: Wa; MAN: Manga; YEN: Yendi; DAM: Damongo; NYAN: Nyankpala.

CHAPTER FIVE

5.0 DISCUSSION

5.1 Analysis of variance

The results of the study revealed very significant environment mean squares for grain yield, grain weight and other traits at 0.1 percent probability The environment main effect contributed 70.1 % of the total variation for grain yield. This implied that the test environments were distinct and highlight the need for testing the three-way hybrids over wide range of environment over years before recommendation can be made for release (Badu-Apraku *et al*., 2013). The very significant genotype (hybrids) mean square at 0.1 percent probability was observed for grain yield, grain weight, plant stand, ear height, husk cover, plant aspect, ear aspect, plant harvested, ear harvested, days to anthesis ($P<0.01$), days to silking ($P<0.01$) and grain moisture ($P<0.05$) except for anthesis-silking interval (Sabaghnia *et al*., 2008) This implied that the hybrids exhibit differential responses in the test locations. It is therefore imperative to identify hybrids that are high yielding and hybrids that are stable across the test locations or environment. This further suggests that selection gains can be achieved under the different environments for grain yield as well as the possibility of genetic improvement through selection (Badu-Apraku *et al*., 2003).

However, lack of significant genotype mean square for anthesis-silking interval suggests that anthesis-silking interval were consistent or had similar performance across the test environment. Similarly, the presence of a highly significant genotypeby-environment effect for grain yield, anthesis-silking interval, plant harvested, grain weight, plant stand, days to silking, days to anthesis, plant height, ear height, husk cover, plant aspect, ear aspect and ear harvested necessitate a widespread testing of

hybrid genotypes in multiple environments. The implication is that the three-way hybrids performed differently in the individual environments. Therefore, the presence of large variation due to GE interactions is evidence for the existence of distinct testing environments. In contrast, lack of significant genotype-by-environment mean square for grain moisture implies that percentage grain moistures were stable and consistent across the testing environment (Badu Apraku *et al*., 2012).

Environment contributed large sum of squares of 70.1 % relative to the genotype (9.4 %) contribution for grain yield. Thus, environment effect was more pronounced on the genotype performance. These may be attributed to the differences in the amount of rainfall each environment received during growing season as well as other climatic factors. These results are in-line with most multi environment trials, where, percentage contribution of overall effect of the environment are high coupled with low percentage of the genotype main effects to the total sum of squares for grain yield and other agronomic traits (DeLacy *et al*., 1996; Cooper *et al*., 1996; Badu Apraku *et al*., 2003, 2010, 2011, 2013).

5.2 Hybrid mean performances of 48 three-way hybrids

Hybrid selection in breeding programs are based on proven performances for grain yield and other agronomic characteristics useful in assessing yield potential, stability and other useful characteristics well suited for the farmer and the final consumer (Ransom *et al*.,1997). Assessment of mean performance is a useful way for evaluating the potential value of a hybrid (Kaya *et al*., 2006). The differences among the hybrids for grain yield and other agronomic traits indicated the potential inherent genetic diversity in the hybrids. These further implied the existences of large variation in yield potential of hybrid genotypes. According to Kang (1996), genotypes evaluated in different

locations often show inconsistency in their yield performance due to the reaction of genotypes to environmental agents including rainfall, soil fertility, temperatures, biotic, and abiotic stresses.

Among the top 10 ranked hybrids, six hybrids, hybrids 14 (M1227-12); 30 (M14285); 27 (M1227-2); 21 (AS1204-46); 34 (M1428-14) and 28 (M1227-4) outperformed the best commercial check (SC719) by 10, 5.0, 4.0, 3.3, 1.8 and 0.4 percent respectively. These hybrids exhibited high superior mean performance over the best check and have high potential for utilization in hybrid development programme (Meseka *et al*., 2016).

The top ranked hybrids had similar or better agronomic performances and characteristics for husk cover, plant aspect and ear aspect as well as anthesis-silking interval compared to the checks. The husk cover rating for the hybrids including the checks had a mean rating of 1.7 with a range of 1.3 to 2.1, indicating that most of the ears were tightly covered with husk tightly arranged beyond the ear tip. A good husk cover protects the ear from pest, diseases and adverse weather conditions. According to Demissie *et al*. (2008), a good husk cover confers resistance to maize ears against the maize weevil (*Sitophylus zeamais*) in the field. Whereas a poor husk cover exposes the ear to pest damage.

Plant aspect was rated based on visual assessment of plants architecture on plot basis. The mean rating of the hybrids was 1.6 with a range of 1.1 to 1.9, suggesting that the hybrids had very good overall phenotypic appeal. Similarly, ear aspect was rated based on visual assessment of ear by taking into consideration the ear size, uniformity of size, colour and texture, grain filling, and insect or disease damage (Badu-Apraku *et al*., 2011). The mean ear aspect of 1.5 with a range of 1.2 to 1.9, implies that the ears were in most of the cases clean, uniform and well-filled with desirable

characteristics.

Plant and ear aspect are important traits because it has been reportedly used in drought research as part of a base index to select drought tolerant genotypes at the flowering and grain-filling periods (Banziger and Lafitte, 1997; Banziger *et al*., 1999; BaduApraku *et al*., 2011).

The mean number of days to anthesis of 55 days with a range of 53 to 56 days and the mean number of days to silking of 56 days with a range of 55 to 58 days, implies that the hybrids used in the study were early maturing genotypes. Early maturing genotypes are suitable for regions with low rainfall by allowing the genotypes to escape the effects of drought. These results are similar to finding of Bello *et al*. (2012). The interval between the number of days to anthesis and number of days to silking was 1-2 days. This implied that the anthesis-silking interval for was short. Short anthesis-silking interval is a useful selection trait for successful pollination. The short interval between pollen shed and silk intrusion observed in the hybrid is useful for selection because it has been reported that short anthesis-silking is useful for breeding for drought tolerances during flowering and ensures good grain filling under stress (Banziger *et al*., 1999; Badu-Apraku *et al*., 2013).

Plant and ear height are very important agronomic trait in plant breeding. Hybrid 14 (M1227-12), identified as the highest yielding hybrid, had ear height below average (80 cm) and plant height above average (172 cm), indicating that the hybrid had short ear height and tall plant height. Tall plant and ear height could be prone to root and stalk lodging, therefore, some breeders select for short plant height and lower ear height because short ear and plant height are important for improving root and stalk lodging

and facilitate mechanised harvesting. These results are similar to the finding of Nazir *et al.* (2010) and Bello *et al.* (2012).

On the other hand, hybrids 1 (M1124-3); 36 (M1428-17); 9 (M1227-17); 23 (M12275); 26 (M1124-7); 24 (M1428-7); 11 (M1326-4); 8 (M1227-14) 25 (M1124-6); 5 (M1326-1); 31(M1428-8); 7 (M1227-11) and 35(M1428-15) gave mean performances greater than grand mean performance. Hybrids expressed superior mean performances over the local check. These hybrids also exhibited fairly uniform days to anthesis and days to silking. They showed similar performances for plant aspect, ear aspect and husk cover. This indicated that the hybrids had good genetic potential for further testing for stability (Badu Apraku *et al*., 2012).

5.3 Heritability/Repeatability

The effectiveness of selection for grain yield and other traits depends on genetic variability and heritability. Heritability is the proportion of the total phenotypic variation manifested among genotypes that can be attributed to the differences between them. However, the results of the estimation depend on the population under consideration. Heritability estimates is the property of the population, not a property of the traits (Holland *et al*., 2003; Hallauer *et al*., 2010).

In multi-environment trials, heritability is the measure of the efficiency or accuracy of the cultivar trials in cultivar evaluation (Atlin, 2003). In this study, estimates of heritability ranged from low to very high in each environment. Traits with moderate to high heritability estimates observed in the study indicated high genetic potential and low environment influence on the traits and that the results are highly repeatable in the test environment. Therefore, selection would be effective for those traits under the test environments. On the other hand, low heritability for some traits indicated low genetic

potential and high effects of environment in determining these traits under the test environment, thus, results for traits were not repeatable. Grain yield recorded a high heritability estimate at Damongo (97 %) and Nyankpala (69 %) whereas Wa (44 %), Manga (33 %) and Yendi (31 %) recorded low heritability estimates. Similarly, grain weight recorded high heritability estimates at Damongo and Mango while the rest of locations had low estimates. Grain moisture and anthesis-silking interval recorded low heritability at all the location or environment. Some traits recorded zero heritability estimates at various environments. Zero heritability estimates were observed for grain weight and grain moisture at Manga and Wa. Anthesis-silking interval at Yendi and Wa while ear height at Yendi. Plant aspect and ear aspect had zero heritability estimate at Wa. This shows that these traits were highly influenced by the test environment. The implication is that selection gains will be low under those environments. According to Yan (2014), low trial heritability could be as a result of large field spatial variations or human errors.

Across environments, heritability estimates for all traits were below 50 % across the test environment except for plant stand (60 %) and plant height (50 %). High heritability for plant stand and plant height implied that the traits were less influenced by the environment coupled with low interaction of genotype and environment effects for those traits across the environment. Heritability in the broad sense were low for grain yield (40 %) and moderate for grain weight (41%). Low heritability of grain yield can be attributed to strong genotype-by-environment interaction. Thus, limiting progress from selection. These findings are in consonance with earlier studies by (Saleh *et al*., 2002; Abady *et al*., 2013). Heritability in the broad sense as reported by

Tazeen *et al.* (2009), performs a prognostic role when selections are conducted.

Anthesis-silking interval gave zero heritability estimates and suggest that the traits were highly influenced by environmental factors as well as large genotype-byenvironment interaction effect. Similarly, low heritability estimates for ear height, husk cover, plant aspect, ear aspect, plant harvested, ear harvested, grain moisture, plant stand, days to anthesis, days to silk and anthesis-silking interval indicated that the traits were largely influenced by the environment. This further suggests that the hybrids had low genetic variability and that little progress could be made in improvement of those trait. Anthesis-silking interval however, had zero heritability because genetic variance was zero. Similar findings by Maphumulo *et al*. (2015), revealed no genetic variation for anthesis-silking interval.

5.4 Correlation between grain yield and other essential traits of 48 hybrids.

The interrelationship among traits is of utmost importance for effective selection in cultivar development. The significant and positive association of grain yield with plant stand, days to anthesis, days to silk, plant height, ear height, plant harvested, ear harvested as well as grain weight implied that selection for increase plant stand, plant harvested; days to anthesis, plant height, ear height, days to silk, ear harvested and grain weight could simultaneously increase grain yield. Thus, could be utilized in direct selection program. Similar finding relating to this study (Mostafavi *et al*., 2013; Maphumulo *et al*.,2015; Oyekunle *et al*., 2015), revealed that positive association of grain yield with plant heights and ear height demonstrated that hybrids with height advantage are more likely to produce higher grain yields relative to short ones. These further suggested that increase in ear height and plant height may contributed to an increase in grain yield. However, hybrids that exhibit very high plant height and ear height could be prone to root and stalk lodging (Bello *et al*., 2012).

Days to anthesis and days to silk were positively correlated with yield. This implies that such traits can be improved together with grain yield during selection for superior yield performance. It shows that the three-way hybrids are able to flower and mature early (earliness) without compromising on higher grain yield. These further suggest that the hybrids possess some attributes for drought escape and adaptability. The findings of the present study is in line with previous studies. Cairns *et al*. (2013), revealed that grain yield was directly correlated with days to anthesis. Bello *et al.* (2012), made a similar finding and explained that superior individuals that flowered and matured earlier with high yield could be used to escape the prolonged moisture stress during the later part of the cropping season.

The interval between anthesis and silking was found to be negatively correlated with grain yield. This implied that an inverse relationship exists between grain yield and anthesis-silking interval such that an increase in grain yield resulted in reduced anthesis-silking interval (Bello *et al*., 2012). These results confirm previous studies where anthesis–silking interval was negatively correlated with grain yield under drought conditions (Bolanos and Edmeades, 1993; Edmeades *et al*., 1995). The shorter anthesis–silking interval is preferable under drought conditions because prolonged period between days to anthesis and days to silk causes lower grain filling ability of a genotype resulting in decreased grain yields.

The genetic correlation among locations is an essential element controlling indirect selection among locations (Cooper *et al*., 1996). Genetic correlations could be used to assess the homogeneity of test locations as the efficiency in selection depends on similarity of test locations in discriminating among the genotypes. Selection is effective when the testing locations are similar. In this study, the presence of highly significant

and strong positive genetic correlation between environment (for example Manga and Wa) for grain yield suggested that genotype-by-environment interaction had little influence on the environment for grain yield. This implied the environments were similar. This further suggest that the same genetic systems were operating between the two environments for grain yield. Hence, the same information regarding the grain yield of the hybrids can be obtained in both environments because the hybrids have identical ranking (Falconer, 1952; Eisen and Saxton, 1983; Makumbi *et al.*, 2015; Sserumaga *et al*., 2016)

However, several locations showed statistically non-significant genetic correlation. For example, Yendi and Nyankpala, Wa and Nyankpala, Manga and Nyankpala, Wa and Yendi, Wa and Damongo as well as Manga and Yendi were positively correlated but non-significant whereas Yendi and Damongo and Manga and Damongo were negatively correlated but non-significant.

5.5 Hybrid performances and Stability of 48 three-way hybrids

The utilization of GGE biplot analysis in the present study, provided relevant information on hybrid performance and stability. A genotype is considered ideal provided it has high mean grain yield coupled with high stability across environments (Yan and Tinker, 2006). Based on this selection criteria, hybrids 14 (M1227-12), 23 (M1227-5) and 25 (M1124-6) were best high yielding and most stable. Similarly, hybrids 21 (AS1204-46), 24 (M1428-7), 27 (M1227-2) and 34 (M1428-14) were also picked out as high yielding and moderately stable. This implied that, the hybrids showed consistent rank performance across the environment with less genotype-byenvironment effects (Setimela *et al*., 2005). Consistent rank performance could be an indicator of broad adaptation. Plant breeders often prefer cultivar with broad adaptation because it helps to save scarce resources required for multi-location testing due to GEI effects and

such cultivars provide reliable and consistent performance season after season (Yan and Hunt, 2002; Kaya *et al*., 2006)

On the other hand, some hybrids were high yielding, but unstable whereas others exhibited high stability but low yielding. Hybrids that are high yielding but unstable is an indicator of specific adaptation because the high yielding ability of the hybrids are limited to a particular location due to their inherent instability across the environment. Such hybrids may be well suited for specific adaptations and can be promoted and approved for specific locations for utilization by farmers. These hybrids include 30 (M1428-5), 47 (10C2897), 29 (M1124-10), 45 (SC643) and 5 (M1326-1).

The which-won-where pattern of GGE biplot is vital for identification of best hybrids for each test environment and for determining the existence of divergent megaenvironments (Yan and Rajcan, 2002; Gauch *et al*., 2008). The polygon view of the GGE biplot revealed six sectors with three environment groups. An attractive characteristic of the polygon view of a GGE biplot is that the vertex genotype for each sector serve as the best or higher yielding genotype relative to the rest of the genotypes in all the environments that fall in the sector (Yan, 2002). Hybrid 13 (M1428-4) was found as the winning genotype for Damongo (DAM.). Hybrid 14 (AS1204-46) winner genotype for Wa (WA) while hybrids 29 (M1124-10) and 30 (M1428-5) were the best genotypes for Manga (MAN), Yendi (YEN) and Nyankpala (NYAN). However, some vertex genotypes like hybrid 22 (AS1205-2) and 12 (M1428-3) had no environment within its sectors, suggesting that those hybrids were not outstanding in any of the environments. These also implied those hybrids responded poorly in part of or all of the environments under consideration (Badu

Apraku *et al*., 2011, 2012). The results of the present study are in line with the findings of Yan *et al*. (2010), who observed that the vertex genotype in each megaenvironment represents the highest-yielding genotype in the locations that fall within the polygon.

5.6 Ideal hybrids and environment

According to Yan and Hunt (2002), mega environment can be identified provided different test environments have different winning genotypes. Based on this principle, three mega environments were identified.

The first mega environment was Damongo (DAM) followed by Wa (WA). Then Manga (MAN), Yendi (YEN) and Nyankpala (NYAN) constituted a single mega environment. However, Manga, Yendi and Nyankpala belonged to different agroecological zone but have been grouped under the same mega environment suggesting that they share some common similarity. According to Yan *et al.* (2000), grouping of locations into mega environment, in most of the cases do not correspond to the local subdivisions or zones due to unpredictable of crossover type of GEI. The results of the present are consistent with the findings of Badu Apraku *et al.* (2012), who observed that differences in the grouping of the locations into mega environments could be attributed to the large environmental variations.

5.7 Discriminating and representativeness of five test locations

The discrimitiveness versus representativeness view of the GGE biplot of test locations was used to identify locations that can be used to effectively select superior genotypes for mega-environment (figure 4). The main reason for assessment of test environment is to find environments that efficiently and adequately identify good performing genotypes in a test environment (Yan *et al*., 2007)

According to Yan (2014), an environment is considered ideal if ultimately it is very discriminating and representative of the test environments. However, in the present study, none of the test environments qualified as an ideal environment for selecting superior hybrids. This implied that the environments were not useful for selecting superior hybrids. Environments identified as very discriminating but nonrepresentative of the test location (such as DAM and NYAN locations) are useful in culling unstable hybrids and also for genetic differentiation of the hybrid genotypes. These could also be useful for selecting specifically adapted hybrids if mega environments exist (Yan *et al*., 2007, 2010). Furthermore, environments identified as less discriminating but most representative of test environment may be marked as separate, unique and indispensable test environment because selected hybrids are expected to have the desired adaptation (Badu Apraku *et al*., 2011).

The following locations, WA, MAN and YEN were identified as the most representative of the test environments whereas, DAM and NYAN were the highly discriminating locations. On the other hand, WA, MAN and YEN were identified as less discriminating whereas DAM and NYAN were identified as less representative of the target environment.

5.8 Relationship among five locations of 48 three-way hybrid maize

The vector view of the GGE biplot in figure 5 display the relationship between the environments. The cosine of the angle between the vectors of any two environments closely relate to correlation between the environment (Yan *et al*., 2007). The presence of positive associations between DAM and WA; WA and NYAN; WA and YEN; NYAN and YEN as well as NYAN and MAN in which the angles between them were less than 90° suggested that indirect selection can be utilized over the test environments

such that similar information about the hybrid can be obtained in just a few test environments. Kaya *et al*. (2006) reported similar results. Plant breeders will prefer to use only few locations in order to save resources, thereby reducing cost of multi-location testing. According Yan *et al*., (2003) correct choice of test locations can minimize test cost and boost breeding efficiency. In contrast, the presence of negative correlation among test environment in which the angle among them is large than 90° implied that there is a crossover type interaction between the hybrid genotypes and the test environment (Yan and Tinker, 2006).

CHAPTER SIX

6.0 CNCLUSION AND RECOMMENDATION

6.1 CONCLUSION

Combined analysis of variance was useful in estimating the magnitude of genotype-byenvironment interaction as well as the percentage sum of squares attributed to hybrid genotypes, environments and interaction between genotype and environment effects.

Among the 48 three-way hybrids evaluated, hybrids 14 (M1227-12); 30 (M1428-5); 27 (M1227-2); 21 (AS1204-46); 34 (M1428-14) and 28 (M1227-4) outperformed the best check hybrid (SC719) by 10, 5.0, 4.0, 3.3, 1.8 and 0.4 percent respectively. The hybrid 14 (M122712); was found to be the highest yielding, with yield advantage of 10% over the commercial check SC719. However, thirteen hybrids with high mean performances and better agronomic performance over all the local check hybrid were also identified. These promising hybrids demonstrated that three-way hybrid maize productivity can be improved in the Savannas of Ghana. The study identified Damongo and Nyankpala as individual environments with high repeatability for grain yield. This implied those trials were less influenced by the environment and exhibited high progress from selection. However, across environment, progress from selection for grain yield and other measured traits were small due to low heritability estimates attributable to strong genotype-by-environment interaction.

The results revealed strong phenotypic correlation between grain yield and the other measured traits, which demonstrated that selection for those traits can simultaneously be improved with grain yield. The computation of genetic correlation was a useful measure of homogeneity of test environments in their ranking of the hybrids. A strong genetic correlation between Manga and Wa demonstrated that the pair of environment are very similar and correlated with little influence of GEI. The implication is that similar information about the hybrids ranking can be

obtained in either of the environments. Therefore, one of the environment should be dropped to ensure judicious use of resources, useful for increasing breeding efficiency.

Genotype plus Genotype × Environment Biplots analysis demonstrated the presence of crossover type of genotype-by-environment interaction for the three-way hybrids studied. This led to differential response of the hybrids across the Savanna environments. The biplot analysis allowed for the identification of stable and unstable three-way hybrids and their adaptation to the Savanna environment. Hybrids 14 (M1227-12), 23 (M1227-5) and 25 (M1124-6) were found to be the best high yielding and most stable hybrids. Similarly, hybrids 21 (AS1204-46), 24 (M1428-7), 27 (M1227-2) and 34 (M1428-14) were also high yielding and moderately stable. These hybrids exhibit broad adaptation potential. On other hand, hybrids 30 (M1428-5), 47 (10C2897), 29 (M1124-10), 45 (SC643) and 5 (M1326-1) exhibited specific adaptation potential. The polygon view of the GGE biplot was useful in displaying which hybrid is best for which environment, and this information will be useful for making hybrid recommendations and release. Hybrids 13 (M1428-4) and 14 (AS1204-46) were the best hybrids in Damongo and Wa respectively. Manga, Yendi and Nyankpala had hybrid 29 (M1124-10) and 30 (M1428-5) as their best hybrid performers.

6.1 RECOMMENDATION

Promising and outstanding hybrids should further be tested largely in multiple location and on-farm for testing the distinctness, uniformity and stability of the hybrids as well as their value for cultivation and use (VCU) before release. The outstanding hybrids should be promoted for adoption by farmers and seed companies and possible commercialization in the Savanna zones of Ghana. Multiyear data should be generated to validate the existence of mega-environments for evaluating these three-way hybrids. Researchers should focus on increasing the number of test location to increase heritability estimate and genetic advance in selection.

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APPENDICES

Appendix 1 List of 48 three-way cross hybrids used in the study

ENTRY	NAME	PEDIGREE	SOURCE
1	M1124-3	ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37- 5-BBB//IWD-SYN-STR-C3--4 7-1-BB	13A11748B
2	M1124-4	ZDiploBC4-19-4-1-#-3-1-B-1-B*4/TZLCompIC4S 1-37 -1- B*4/IWD-SYN-STR-C3—52-1-BB	13A11750B
3	M1124-9	ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37-1- B*4/IWD-SYN-STR-C3--55-3-BB	13A11762B
4	M1227-3	ZdiploBC4-472-2-2-1-2-3-B*6/TZLCompIC4S 1-37-5- BBB/IWD-SYN-STR-C3—55-3-BB	13A11764B
5	M1326-1	ZDiploBC4-4 72-2-2-1-2-3-B-1-B*5/TZLCompIC4S 1-37-5- BBB/IWD-SYN-STR-C3--55-3-BB	13A11770B
6	M1227-9	ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37-5-BBB/IWD-SYN-STR-C3-32-2-BB	13A11778B
7	M1227-11	ZDiploBC4-19-4-1-#-3-1-B-1-B*4/TZLCompl C4S 1-37-5·BBB/IWD-SYN-STR-C3--502-BB	13A11782B
8	M1227-14	ZdiploBC4-4 72-2-2-1-2-3-B*6/TZLCompIC4S 1-37-5-BBB/IWD-SYN-STR-C3--52-4BB	13A11786B
9	M1227-17	ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37 -1-B*4/IWD-SYN-STR-C3--52-3-BB	13A11790B
10	M1326-3	((ZDiploBC4-472-2-2-1-2-3-B-1-B*5/ZDiplo8C4-19-4-1-#-3-1-B-1-B*4)-25-1-BB /(ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37 -1-B*4)-36-B*4)/IITATZISTR1133	13A11794B
11	M1326-4	((ZDiploBC4-472-2-2-1-2-3-8-1-B*5/ZDiploBC4-19-4-1-#-3-1-B-1-B*4)-43-1-BB /(ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37 -5-BBB)-3-B*4/IITATZISTR1133	13A11796B
12	M1428-3	(ZDiploBC4-472-2-2-1-2-3-B-1-B*5/ZDiploBC4-19-4-1-#-3-1-8-1-8*4)-25-1-BB /(ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37 -5-BBB)-38-1-1-BB/IITATZISTR1134	13A11800B

Continued on the next page

		(1393/ZDiploBC4-19-4-1-#-3-1-B-1-B*4)-40-BB	
13	M1428-4	/IWD-SYN-STR-C3--50-2-BBB/TZLCompIC4S 1-37-1-B*6	13C20048B
		ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37 -1-	
14	M1227-12	B*4/IWD-SYN-STR-C3--52-1-BB	14A19479B
		ZDiploBC4-19-4-1-#-3-1-B-1-B*4	
15	AS1204-1	/(ACRSYN-W-S2-173-S*4/TZLCompIC4S1-37-1-B*4)-16-B/(IITATZI1872	14A19551B
		ZdiploBC4-472-2-2-1-2-3-B*6	
16	AS1204-5	/(ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37 -5-BBB) -4-B/(IITATZI1872	14A19553B
		ZeADiploBC4- WC3-29-3-1-B*4	
17	AS1204-7	/(AC RSYN- W-S2-173-B*4/TZLCompl C4S1-37-5-BBB)-27-B/IITATZISTR 1129	14A19555B
		(1393/Z.Diplo.BC4-19-4-1-#-3-1-B-1-B* 4)-46-B-B-B-B	
		/(ACRSYN-W-S2-173-B-B-B-B/TZL Compo. IC4 S1- 375-B-B-B)-31-1-1-B-B/1IT	
18	AS1204-26	ATZI STR 1129	14A19557B
		ACRSYN-W-S2-173-	
19	AS1204-43	B*6/TZLCompIC4S 1-37 -5-BBB/TZISTR1128	14A19559B
		ZdiploBC4-4 72 -2 -2 -1-2 -3-	
20	AS1204-44	B*8/TZLCompIC4S 1-37-5-B*5/TZISTR 1128	14A19561B
21	AS1204-46	ACRSYN-W-S2-173-B*6/TZLCompIC4S1-37 -5-BBB/TZISTR1132	14A19563B
		ZdiploBC4-376-1-1-#-3-1-B-2-BBB/ACR97TZL-CCOMP1-Y -S3-34-3-	
22	AS1205-2	BBB/ACR97SYN-Y -S 1-76-B-B-B-B	14A19565B
		ZDiploBC4-4 72-2-2-1-2-3-B-1-	
23	M1227-5	B*5/TZLCompIC4S 1-37-5-BBB/IWD-SYN-STR-C3--67-1-BB	14C30052B
		ZDiploBC4-19-4-1-#-3-1-B-1-B*4/(ACRSYN-W-S2-173-	
24	M1428-7	B*4/TZLCompIC4S1-37-1-B*4)-32-B/IWD-SYN-STR-C3--70-2-B	14C30054B
		ZDiploBC4-19-4-1-#-3-1-B-1-B*4/TZLCompIC4S-1-37-1-	
25	M1124-6	B*4/IWD-SYN-STR-C3--53-2-BB	14C30056B

Continued on the next page

26	M1124-7	ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37-1-B*4/IWD-SYN-STR-C3--53-2-BB 14C30058B
27	M1227-2	ZDiploBC4-4 72-2-2-1-2-3-B-1-B*5/TZLCompIC4S 1-37-5-BBB/IWD-SYN-STR-C3--53-2-BB 14C30060B
28	M1227-4	ZDiploBC4-19-4-1-#-3-1-B-1-B*4/TZLCompIC4S1-37 -5-BBB/IWD-SYN-STR-C3--55-3-BB 14C30062B
29	M1124-10	ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37-5-BBB/IWD-SYN-STR-C3--55-3-BB 14C30064B
30	M1428-5	(ZDiploBC4-472-2-2-1-2-3-B-1-B*5/ZDiploBC4-19-4-1-#-3-1-B-1-B*4)-2-1-BB/(ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37 -5-BBB)-4-B*4/IITATZISTR1134 14C30070B
31	M1428-8	ZdiploBC4-472-2-2-1-2-3-B*6/(ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37 -1-B*4)-57 –B/IWD-SYN-STR-C3--70-2-B 14C30078B
32	M1428-10	ZdiploBC4-472-2-2-1-2-3-B*6/(ACRSYN-W-S2-173-B*4/TZLComplC4S 1-37 -5-BBB)-4-B/IWD-SYN-STR-C3--70-2-B 14C30082B
33	M1428-11	ZeaDiploBC4-WC3-29-3-1-B*4/(ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37 -5-BBB)-27 –B/IWD-SYN-STR-C3--32-2-BB 14C30084B
34	M1428-14	(ZDiploBC4-472-2-2-1-2-3-B-1-B*5/ZiploBC4-19-4-1-#-3-1-B-1-B*4)-26-1-BB/(ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37 -1-B*4)-50-B*4/IWD-SYN-STR-C3--47-1-B*5 14C30088B
35	M1428-15	(ZDiploBC4-472-2-2-1-2-3-B-1-B*5/ZDiploBC4-19-4-1- #-3-1-B-1-B*4)-2-1-BB/(ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37-5-BBB)-4-B*4/IITATZISTR1134 14C30090B
36	M1428-17	(ZDiploBC4-472-2-2-1-2-3-B-1-B*5/ZDiploBC4-19-4-1-#-3-1-B-1-B*4)-25-1-BB/(ACRSYN-W-S2-173-B*4/TZLCompIC4S 1-37 -5-BBB)-56-B*4/IITATZISTR1134 14C30094B
37	Oba Super 7	H05-01STR 13A18800B

38	Oba Super 9	H05-02STR	13A18802B

Continued the on the next page

39	Oba Super I	Oba Super 1	Premier
40	Oba Super I	Oba Super 1	Premier
41	Oba Super 2	Oba Super 2	Premier
42	SC627	SC627	SEEDCO
43	SC637	SC637	SEEDCO
44	SC719	SC719	SEEDCO
45	SC643	SC643	SEEDCO
46	11C87	11C87	SEEDCO
47	10C2897	10C2897	SEEDCO
48	Localcheck	Localcheck	SARI

Appendix 2 Analysis of variance per location for grain yield and other important traits.

Damongo

SOV	DF	GYLD	PSD	DA	DS	ASI	PH	EH
REP	2	1312.51*	89.06***	2.63NS	3.80NS	0.27NS	43.36***	70.51NS
BLK(REP)	21	419.35NS	6.41NS	1.02NS	0.79NS	0.38NS	5.27NS	111.48NS
GEN	47	8798.97***	38.69***	2.51***	1.69NS	0.79NS	369.87***	385.46***
ERROR	73	341.63	542.6	0.97	1.31	0.55NS	4.23	96.73
CV		6.98	6.88	2.01	50.7	33.28	0.99	9.68
R^2 %		95.76	81.15	68.02	2.24	54.05	98.51	76.71

SOV	DF	PASP	EASP	EHV	PHV	HC	Gwt	GM
REP	2	0.02NS	0.05NS	140.34***	114.06***	0.09NS	0.14NS	0.19NS
BLK(REP)	21	0.1NS	0.05NS	8.20NS	6.96NS	0.04NS	0.06NS	1.89NS
GEN	47	1.41***	1.12***	40.06***	39.86NS	0.65NS	1.26***	2.20*
ERROR	73	0.11	0.06724	8.54	7.92	0.05	0.05	1.33
CV (%)		15.08	13.43	7.49	7.14	13.13	7.16	8.38
R^2(%)		91.35	93.12	79.87	80.73	91.4	95.64	57.89

Manga

SOV	DF	GYLD	PSD	DA	DS	ASI	PH	EH
REP	2	6297.91***	23.01NS	0.22NS	0.02NS	0.22NS	8.55NS	9.81NS
BLK(REP)	21	693.56*	91.22*	2.56*	1.89NS	0.57NS	257.85NS	102.95NS
GEN	47	645.03*	112.72***	1.61NS	1.92NS	0.75*	302.76NS	139.13NS
ERROR	73	410.54	44.96	1.3	1.62	0.44	250.71	96.25
CV(%)		15.5	18.31	2.32	2.48	30.32	13.21	23.41
R^2 %		66.07	70.36	59.45	51.55	60.86	53.32	57.16

SOV	DF	PASP	EASP	EHV	PHV	HC	Gwt	GM
REP	2	0.03NS	0.028NS	477.80***	31.09NS	0.03NS	2.14***	31.99*
BLK(REP)	21	0.08NS	0.21NS	100.51*	93.31*	0.05NS	0.36*	12.88*
GEN	47	0.22NS	0.31**	77.87**	110.23***	0.06NS	0.19NS	7.62*
ERROR	73	0.24NS	0.12	43.008	43.58	0.04	0.19	7.66NS
CV(%)		38.12	31.95	20.53	19.05	9.85	15.51	17.63
R^2 %		40.28	57.89	70.68	71.03	55.4	61.93	55.32

Nyankpala

SOV	DF	GYLD	PSD	DA	DS	ASI	PH	EH
REP	2	7571.31NS	76.40*	17.55***	19.15***	0.30NS	749.31*	792.29**
BLK(REP)	21	10522.32**	24.16NS	1.99NS	2.78*	0.24NS	777.38***	363.70***
GEN	47	12441.98***	25.38NS	1.48NS	1.77*	0.20NS	304.67NS	213.23*
ERROR	73	4205.72	21.71	1.25	1.56	0.18	214.09	135.17
CV(%)		23.35	12.52	1.89	2.07	33.48	7.94	12.73
R^2 %		75.6	55.11	63.17	62.49	53.27	68.99	66.31

SOV	DF	PASP	EASP	EHV	PHV	HC	Gwt	GM
REP	2	1.6875***	0.56NS	15.15NS	84.05*	0.92*	1.2NS	2.30NS
BLK(REP)	21	0.13NS	0.45NS	13.87NS	24.43NS	0.27NS	1.30***	2.13NS
GEN	47	0.28*	0.41NS	35.35NS	26.95NS	0.30*	1.56***	2.41NS
ERROR	73	0.18	0.33	29.55	22.22	0.19	0.48	2.19
CV(%)		30.01	30.9486	14.6174	12.62	30.06	22.45	14.97
R^2 %		62.31	55.4331	51.4392	55.85	61.04	77.11	50.79

Wa

SOV	DF	GYLD	PSD	DA	DS	ASI	PH	EH
REP	2	2127.92NS	3.56NS	7.13*	4.72NS	0.30NS	55.15NS	397.19*
BLK(REP)	21	2422.10***	38.21***	1.81NS	2.02NS	0.21NS	304.01**	174.71**
GEN	47	1294.55*	33.14***	1.85NS	1.85NS	0.22NS	387.26***	111.86*
ERROR	73	749.63	11.64	1.6	1.59	0.24	118.26	66.38
CV(%)		11.11	8.82	2.22	2.15	30.07	6.61	11.2
R^2 %		70.31	77.61	56.35	56.58	46.64	73.42	67.49

SOV	DF	PASP	EASP	EHV	PHV	HC	Gwt	GM
REP	2	0.03NS	0.08NS	17.69NS	6.25NS	0.81*	0.28NS	0.45NS
BLK(REP)	21	0.10NS	0.17NS	32.15**	33.30***	0.34*	0.30***	1.78NS
GEN	47	0.23NS	0.25NS	27.62**	30.47***	0.28NS	0.17*	1.08NS
ERROR	73	0.27	0.27	13.38	11.91	0.2	0.09	1.6
CV(%)		39.47	37.77	9.46	8.87	27.7959	11.07	13.26
R^2 %		36.75	41.67	71.38	75.29	57.85	70.84	42.24

Yendi

SOV	DF	GYLD	PSD	DA	DS	ASI	PH	EH
REP	2	39406.63*	75.13*	22.72NS	22.30NS	0.51NS	9.03NS	10.19NS
BLK(REP)	21	3232.38NS	30.67*	11.05NS	10.48NS	0.36NS	69.13NS	53.24NS
GEN	47	4238.44NS	31.86*	15.11*	15.36*	0.38NS	131.14NS	57.06NS
ERROR	73	3472.63	14.81	7.96196	7.25	0.2744	89.09	65.34
CV(%)		22.29	12.0943	4.78028	4.45	35.2484	5.03	8.86
R^2 (%)		60.19	72.3029	65.57	67.57	52.2753	55.52	45.46

SOV	DF	PASP	EASP	EHV	PHV	HC	Gwt	GM
REP	2	0.09NS	0.63*	61.19*	68.38*	0.03NS	5.51***	15.30*
BLK(REP)	21	0.23NS	0.14NS	27.82NS	34.23*	0.16NS	0.45ns	11.09**
GEN	47	0.30NS	0.16NS	20.98NS	24.25NS	0.29NS	0.58ns	7.90**

ERROR	73	0.21	0.15	16.77	18.47	0.26	0.48	4.21
CV(%)		27.29	32.53	13.86	14.67	34.89	22.39	14.91
R^2 (%)		53.68	51.87	58.05	59.99	46.34	60.02	67.19

ffi GLYD=Grain yield; PSD=Plant stand; DA=Days to anthesis; DS=Days to silking; ASI=Anthesis-silking interval; PH=Plant height; EH=Ear height; HC=Husk cover; PASP=Plant aspect; EASP=Ear aspect; PHV=Plant harvested; EHV=Ear harvested; GM=Grain moisture; Gwt=Grain weight

Appendix 3 Error variance for each location

Cov Parameter	Group	Estimate	standard error
Residual	Damongo	341632	56547
Residual	Manga	410536	67952
Residual	Nyankpala	4205726	696137
Residual	Wa	749632	124080
Residual	Yendi	3472635	574795

Appendix 4 Bartlett's Test for Homogeneity of grain yield variance

Source	DF	Chi-Square	Pr > ChiSq
Environment	4	269.7	<.0001

Levene's Test for Homogeneity of grain yield variance

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Environment	4	5.955E+15	1.49E+15	44.74	<.0001
Error	715	2.38E+16	3.33E+13		

Appendix 5 Mean grain yield and other important traits of 48 three-way hybrids evaluated across five locations

ENTRY	NAMES	GLYD	PSD	DA	DS	ASI	PH	EH	HC	PASP	EASP	PHV	EHV	GM	Gwt
1	M1124-3	8,162	37	55	56	1.7	177	84	1.7	1.4	1.2	35	35	12.89	3.4 2	M1124-4	7,488
33	55 56	1.6	169	78	1.6	1.4	1.3	34	34	13.83	3.0 3	M1124-9		6,616	38	55 57	2.2
170	78 1.8	1.7	1.8	37	37	12.07	2.7										
4	M1227-3	6,774	36	54	56	1.7	172	82	1.5	1.3	1.5	35	34	13.56	2.7 5	M1326-1	7,731
33	54 56	1.9	177	83	2.1	1.8	1.8	34	33	11.94	3.0 6	M1227-9		7,177	40	54 56	1.9
163	77 1.7	1.1	1.4	39	38	12.45	2.8										
7	M1227-11	7,532	38	55	56	1.9	174	81	1.7	1.7	1.6	36	36	12.52	3.1 8	M1227-14	7,906
35	55 57	1.7	170	76	1.9	1.5	1.5	35	34	12.91	3.2 9	M1227-17		8,052	38	54 56	1.9
170	76 1.9	1.7	1.6	38	36	12.79	3.2 10	M1326-3		6,946	39	54	56	1.9	174	84 1.7	1.6
1.7	38 37	11.82	2.7														
11	M1326-4	7,908	38	55	57	1.7	176	82	1.6	1.5	1.3	39	37	12.3	3.1		
12	M1428-3	7,197	38	54	56	2	175	80	1.5	1.5	1.5	36	37	12.23	3.0		
13	M1428-4	6,821	29	55	57	1.9	166	80	1.7	1.6	1.6	31	30	13.06	2.8		
14	M1227-12	9,219	38	53	55	1.9	181	79	1.4	1.3	1.2	36	36	13.17	3.6 15	AS1204-1	6,242
	38	56	57	1.7	172	82	1.3	1.8	1.9	36	36	11.58	2.5 16	AS1204-5		6,697 34	56
	58	1.7	172	79	1.7	1.7	1.9	34	32	12.57	2.8 17	AS1204-7		7,467	40	55 57	1.6
	177	82	1.6	1.5	1.5	38	37	12.43	3.0								
18	AS1204-26	7,437	39	55	56	1.7	172	82	1.8	1.8	1.7	37	37	12.29	2.9 19	AS1204-43	6,737
38	54 56	1.8	168	77	1.7	1.7	1.4	35	35	11.82	2.5 20	AS1204-44		6,358	35	55 56	1.7
166	77 1.7	1.7	1.6	34	33	13.05	2.5 21	AS1204-46		8,618	41	54	56	1.9	179	82 1.3	1.2
1.3	39 39	12.82	3.3														
22	AS1205-2	6,055	33	54	56	1.6	150	64	1.7	1.7	1.7	34	34	11.62	2.5		
23	M1227-5	8,012	38	55	56	1.6	175	80	1.7	1.3	1.5	35	35	12.79	3.2		
24	M1428-7	7,990	37	54	56	2	171	78	1.7	1.7	1.8	35	34	12.96	3.1		
25	M1124-6	7,895	39	54	56	1.8	170	75	1.5	1.6	1.3	38	37	12.67	3.0		

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26	M1124-7	8,005	38	54	56	1.9	174	80	1.5	1.1	1.3	37	38	12.07	3.2	
27	M1227-2	8,679	39	54	56	1.7	171	80	1.4	1.2	1.3	38	38	12.43	3.5	
28	M1227-4	8,370	39	55	56	1.6	171	76	1.8	1.3	1.5	37	37	13.03	3.3	
29	M1124-10	8,323	37	54	56	1.7	179	80	1.7	1.6	1.5	35	35	12.76	3.2	
30	M1428-5	8,758	40	55	56	1.7	170	80	1.5	1.9	1.5	39	38	12.73	3.5	
31	M1428-8	7,556	37	55	57	1.7	172	76	1.7	1.4	1.5	37	36	12.79	3.0	
32	M1428-10	6,118	32	56	57	1.5	177	81	1.6	1.7	1.9	33	34	12.19	2.5	
33	M1428-11	7,452	33	55	57	1.8	162	75	1.6	1.7	1.7	33	33	13.29	2.9	
34	M1428-14	8,485	38	55	57	2.1	174	80	1.6	1.4	1.7	37	36	12.28	3.3	
35	M1428-15	7,504	37	54	56	1.8	167	79	1.7	1.5	1.3	37	35	13.25	3.0	
36	M1428-17	8,142	34	55	56	1.6	172	80	1.9	1.7	1.3	34	34	13.34	3.1	
37	Oba Super 7	6,410	37	55	57	1.5	175	86	1.7	1.4	1.5	36	36	12.97	2.7	
38	ObaSuper 9	7,063	38	54	56	1.9	183	86	1.6	1.4	1.6	38	37	12.39	2.9	
39	Oba Super I	5,960	37	55	56	1.8	173	79	1.9	1.4	1.6	36	34	12.02	2.4	
40	Oba Super I	7,608	40	55	56	1.4	172	76	1.7	1.8	1.5	39	37	11.39	2.9	
41	Oba Super 2	6,202	36	55	57	1.9	169	79	1.6	1.8	1.8	34	34	10.82	2.4	
42	SC627	7,398	33	55	57	2	173	83	1.7	1.4	1.5	33	33	12.53	2.8	
43	SC637	6,977	39	55	57	1.8	180	86	1.7	1.7	1.5	37	36	11.92	2.9	
44	SC719	8,335	32	56	57	1.6	189	93	1.4	1.3	1.2	32	32	13.68	3.4	
45	SC643	8,052	41	54	55	1.8	176	82	1.9	1.8	1.5	39	38	12.79	3.1	
46	11C87	7,620	40	56	57	1.5	168	79	1.5	1.8	1.5	37	37	11.85	3.0	
47	10C2897	8,173	35	53	55	1.8	174	79	1.7	1.9	1.5	34	33	12.33	3.1	
48	Localcheck	7,261	34	54	56	1.7	169	77	1.4	1.7	1.5	33	32	12.73	3.0	
	Grand Mean	7489	37	55	56	1.8	172	80	1.7	1.6	1.5	36	35	12.5	3.0	

LSD(0.05) 669.5 3.2 1.2 1.2 0.4 8.4 6.9 0.3 0.3 0.3 3.3 3.4 1.3 0.4 CV (%) 10.61 12.19 2.96 2.89 32.98 6.74 12.02 23.33 28.55 0.32 12.7 13.37 14.7 17.13

ffi GLYD=Grain yield; PSD=Plant stand; DA=Days to anthesis; DS=Days to silking; ASI=Anthesis-silking interval; PH=Plant height; EH=Ear height; HC=Husk cover; PASP=Plant aspect; EASP=Ear aspect; PHV=Plant harvested; EHV=Ear harvested; GM=Grain moisture; Gwt=Grain weight

Appendix 6 Ranking of 48 hybrids based on mean grain yield across five environment

Hybrid	NAMES	Mean	Ranks	Hybrid	NAMES	Mean	Ranks
6945.58	27 30	M1428-5	8758	2	13	M1428-4	6820.5
6774.36	29 21	AS1204-46	8618	4	19	AS1204-43	6736.98
AS1204-5	6696.54	31 28	M1227-4	8370	6	3	M1124-9
20	AS1204-44	6358.12	33 1	M1124-3	8162	8	15
9	32	M1428-10	6117.8	35 9	M1227-17	8052	10
11	44	SC719	8334.92	1 26	M1124-7	8005	12
13	45	SC643	8052.08	3 11	M1326-4	7908	14
40	Oba Super I	7607.82	5 25	M1124-6	7895	16	42
48	Localcheck	7260.78	7 31	M1428-8	7556	18	38
19	43	SC637	6977.08	9 35	M1428-15	7504	20
21	41	Oba Super 2	6202.3	11 17	AS1204-7	7467	22
23 18	AS1204-26	7437	24 12	M1428-3	7197	25 6	M1227-9

14	M1227-12	9219	1	10	M1326-3		
28 27	M1227-2	8679	3	4	M1227-3		
30 34	M1428-14	8485	5	16			
32 29	M1124-10	8323	7				
AS1204-1	6241.62	34 36	M1428-17	8142			
AS1205-2	6055.46	36 23	M1227-5	8012			
10C2897	8172.88	2 24	M1428-7	7990			
11C87	7619.68	4 8	M1227-14	7906	15		
SC627	7397.84	6 5	M1326-1	7731	17		
ObaSuper 9	7063.34	8 7	M1227-11	7532			
Oba Super 7	6410.24	10 2	M1124-4	7488			
Oba Super I	5960.02	12 33	M1428-11	7452			
42	39	26					