

KWAME NKRUMAH UNIVERSITY OF SCIENCE AND TECHNOLOGY (KNUST)

KUMASI, GHANA

SCHOOL OF GRADUATE STUDIES

DEPARTMENT OF CROP AND SOIL SCIENCES

**COMBINING ABILITY AND STABILITY OF EXTRA-EARLY YELLOW INBRED
LINES OF MAIZE (*Zea mays* L.) FOR GRAIN YIELD IN THREE AGRO-
ECOLOGICAL ZONES OF GHANA**

BY

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AUGUST, 2016.

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AGRO-ECOLOGICAL ZONES OF GHANA

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FACULTY OF AGRICULTURE

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AUGUST, 2016.

KNUST



DECLARATION

I hereby declare that, except for references to works of other researchers which have duly been acknowledged, this work is the outcome of my own research and that neither part nor whole of this document has been presented for a degree at any other University.

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We declare that we have supervised the student to undertake the study submitted herein and verify that he has our permission to submit.

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ABSTRACT

Maize (*Zea mays* L.) is an important cereal crop in Ghana with a wide adaptation to all agroecological zones. In Ghana, maize yield in farmers' field is far less than the world's average yield, producing just about 1.7 t/ha. This low yield could be attributed to a larger extent the effect of continuous use of traditional/unimproved and open-pollinated varieties (OPVs), climate change, low soil fertility etc. Thus, development of superior extra-early hybrid varieties with wide adaptation to the effects of climate change on the environment is important to alleviate this constraint and improve maize production. However, there is scanty information on combining abilities and mode of inheritance of grain yield (GY) of extra-early maturing yellow inbred lines of maize in Ghana for a successful hybrid development programme. The objectives of this research were (i) to determine the combining ability, genetic control and heritability of GY of 10 extra-early inbred lines of maize and (ii) to assess the stability of hybrids of the 10 extra-early inbred lines in three agro-ecological zones of Ghana. 45 single-cross hybrids were developed using 10×10 half-diallel approach. The single-cross hybrids were evaluated at three environments, Fumesua (Forest zone), Ejura (Forest-Transition zone) and Kpeve (CoastalSavannah zone). The experiment was laid-out in a Randomized Complete Block Design (RCBD) with three replications. Data were collected on GY, days to 50% silking (DS), days to 50% tasseling (DTAS), anthesis-silking interval (ASI), plant height (PHT), ear height (EHT), stalk lodging (STLG), root lodging (RTLG), husk cover (HUSK) and grain moisture (MO). Analyses of data showed that, effects of General combining ability (GCA) and Specific combining ability (SCA) were important in modulating the inheritance of GY and other agronomic traits of the inbred lines. Mean squares of GCA and SCA effects showed preponderance of GCA over SCA for GY and other agronomic traits across environments. This suggested that the additive gene effect was more important than the non-

additive gene effect in the inheritance of GY and other relevant agronomic traits. Significant mean squares of GCA×E interaction observed for GY and some relevant traits suggested variation in the combining abilities of inbred lines at different environments. However, significant mean squares of SCA×E interaction for GY and other traits also suggested variations in the expression of traits of the single-cross hybrids across the three research environments. The moderately high narrow-sense heritability (h^2) and genetic advance (GA) for GY indicated the important role of the additive gene action, thus, selection of the trait would be feasible. Single-cross hybrids 28 (TZEEI 78×TZEEI 66), 2 (TZEEI 64×TZEEI 61) and 41 (TZEEI 94×TZEEI 76) were observed as high yielding and most stable across the three environments and out-yielded the local check variety, ‘Abontem’ by 28%, 20% and 18%, respectively. Kpeve (Coastal-Savannah zone) was the most discriminative and representative environment for the hybrids, hence, represented an ideal environment for the hybrid genotypes. It is recommended that the high yielding and most stable hybrids should be extensively tested in on-farm trials before release to farmers.

DEDICATION

This work is dedicated to Dr K. Obeng-Antwi for his immeasurable fatherly support, contribution and advice towards the success of this research.



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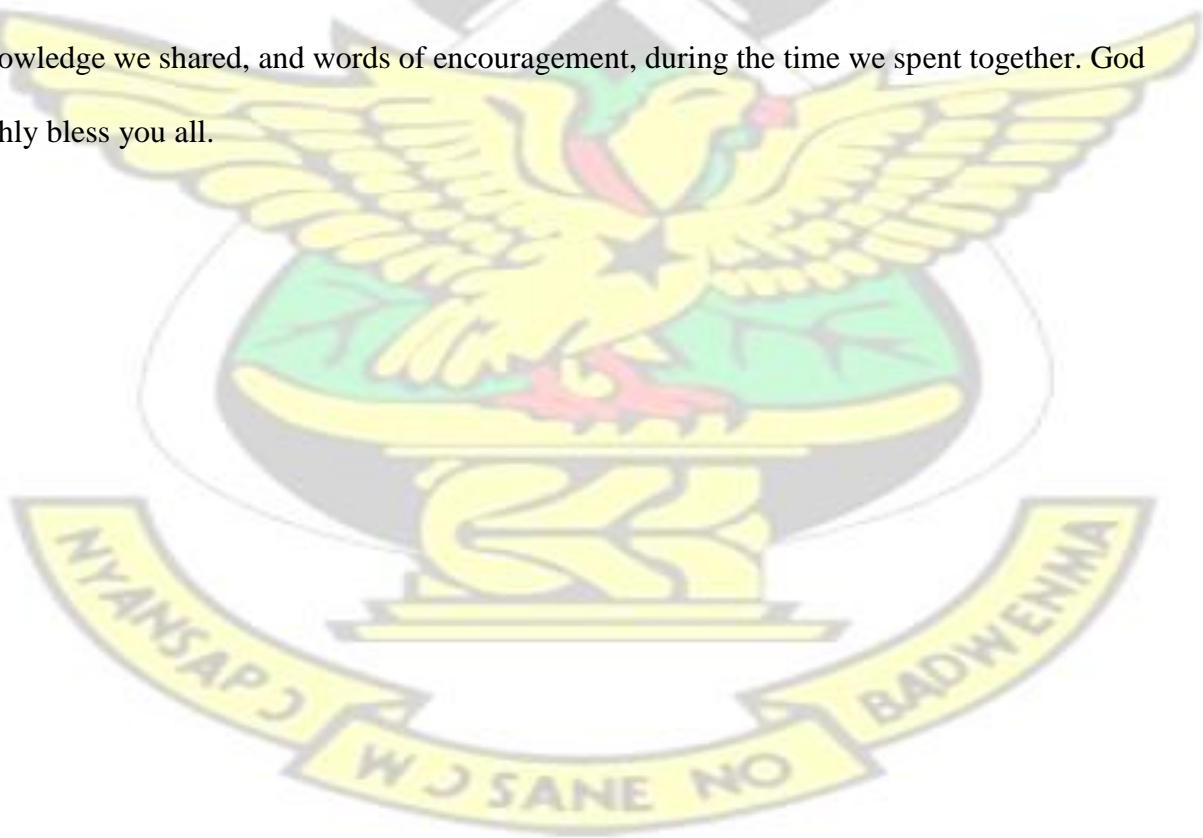


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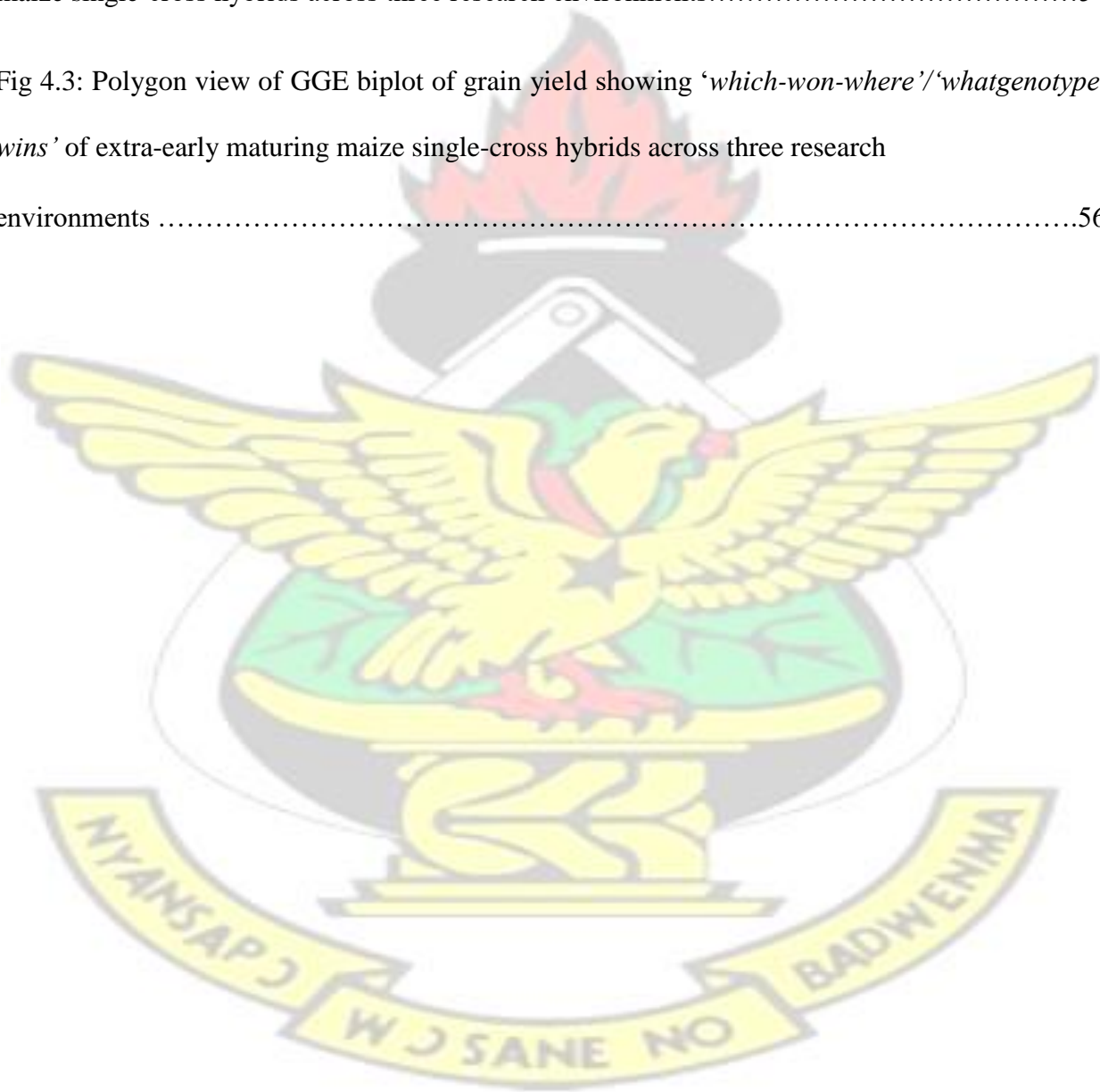
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CHAPTER ONE

1.0 INTRODUCTION

Maize (*Zea mays* L.) is an important cereal which serves as food for a large population of the world and as a primary source of feed for livestock and poultry (Prasanna, 2012). Maize plays key role in the agricultural economy of Ghana, ranking as the primary cereal commodity crop for food, feed and industrial applications (MoFA, 2010). It has a wider adaptability to variations among environments and grown across agro-ecological zones of West and Central Africa. In Ghana, maize is cultivated in all agro-ecological zones (Fening *et al.*, 2011).

Despite the enormous potential of maize, grain yield in the main producing areas in the developing parts of the world is still lower than the global average, producing just about 3.1 tons/hectare (t/ha) (Pixley *et al.*, 2009). In Ghana, maize yield is around 1.7t/ha in farmers' fields (Edgerton, 2009; MoFA, 2011; Oppong *et al.*, 2014). The discrepancy in yield is among the lowest globally especially in comparison with countries such as U.S.A. (10.73t/ha), China (5.81t/ha), and South Africa (3.49 t/ha) in 2014/2015 cropping year (USDA/FAS, 2016). MoFA (2011), however, reported possible yield increase of up to 6 t/ha in evaluation trials. This value is 70% more than what is obtained on farmers' fields. The variation in yields may be attributable to some extent the continuous use of open-pollinated maize varieties (OPVs) as well as unimproved varieties, low rates of inputs and poor management of soil by farmers (Edgerton, 2009). Hence, researches that contribute to improve yields are necessary to alleviate this constraint. One of the main approaches to increase yield is the introduction and adoption of improved varieties, especially hybrid maize varieties.

In the quest to improve maize production in the sub-region, breeders over the years have dedicated a lot of time and effort to develop superior hybrid genotypes with improved yields and adaptation to various stresses. Badu-Apraku *et al.* (2013) indicated that most of these hybrids produced are intermediate and late maturing, although several extra-early maturing inbred lines are available for hybrid seed programme.

Badu-Apraku *et al.* (2011a) has reported that global warming and its consequential effects have resulted in climate change in Sub-Saharan Africa liable to the sudden unpredictable change in rainfall pattern causing perennial drought. The occurrence of drought is liable to cause as much as 90% reduction in maize yield especially when it occurs at the most sensitive stages of the crop, that is, some few days before anthesis through to start of grain filling (NeSmith and Ritchie, 1992). Thus, breeding for extra-early varieties with tolerance to environmental stresses is important to adapt to effects of climate change and improve maize productivity and stability across environments since farmers cannot predict the weather.

Low nitrogen coupled with drought are reported to be the most important stresses that often limit the productivity of maize, food security, as well as economic growth in the sub-region (Bänziger *et al.*, 2006). It has been reported by Weber *et al.* (2012) that, there is a complex interaction among environmental stresses such as the incidence of drought which hinders nutrient uptake. Research attention should thus be directed towards breeding hybrids that can withstand moisture stress ecologies.

To identify potential hybrids for commercial hybrid seed programme, there is the need to obtain information on combining ability as well as the mode of inheritance among inbreds. Several research efforts has been made to understand combining ability and mode of inheritance of GY

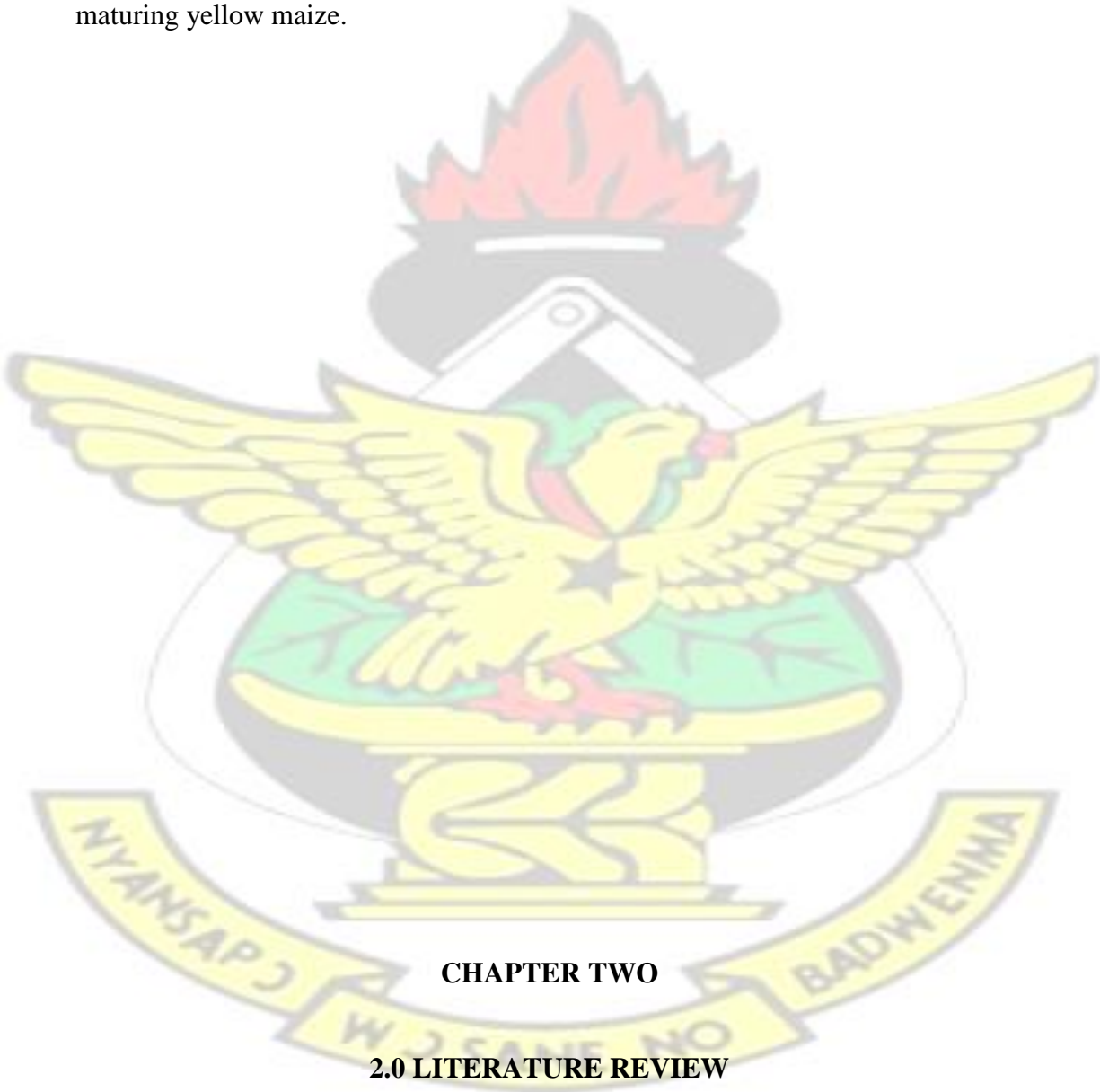
and other agronomic traits (Badu-Apraku and Oyekunle, 2012). Several of these studies contradict each other on gene effects contributing to inheritance of GY and environment has a major effect on general combining ability and inheritance of GY (Vasal *et al.*, 1993a; Bhatnagar *et al.*, 2004; Musila *et al.*, 2010; Wegary *et al.*, 2013). The effects of environment interaction with genotypes is expected in maize production due to wide range of environmental differences. It is thus, important to identify genotypes that do not only produce high yields but able to express consistent performances across environments. The concept of stability is important for plant breeders in analyzing data involving G×E interactions (Fan *et al.*, 2007). This has prompted the need to a greater extent investigate the genetic potential and gene action contributing to inheritance of GY and other agronomic traits in extra-early maturing maize inbred lines across different environments.

Good understanding of information regarding gene action, combining abilities, heritability and genetic gain in grain yield is essential for selection of suitable parents for hybridization and identification of promising hybrids for the development of improved hybrid varieties for a diverse agroecology in Ghana. The overall goal of this study was to determine the inheritance and estimate GCA, SCA and stability of 10 extra-early maturing maize inbred lines and singlecross hybrids across three agro-ecological zones of Ghana.

The specific objectives were to:

1. Evaluate the breeding value of introduced inbred lines for the development of varieties adapted to contrasting environments,
2. Determine the genetic control of GY and other agronomic traits in extra-early maturing maize,

3. Determine heritability and genetic advance of GY and other agronomic traits in extraearly maturing maize,
4. Assess the stability and yield performance of the single-crosses under contrasting environments and,
5. Estimate the better and mid-parent heterosis of GY and other agronomic traits in extraearly maturing yellow maize.



CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 The origin of maize

Maize (*Zea mays* L.) belongs to the family of Gramineae (*Poaceae*). It is an ancient cultivated crop which served as the main food crop for the American Indians during the arrival of Columbus. It thus, have been the main cereal crop in Central America, Mexico, as well as most countries in sub-Saharan Africa and South America. There have been suggestions about two places as possible centers of origin of maize: Central America and Southern Mexico and the highlands of Peru, Ecuador, and Bolivia. Several maize types have been identified at the two locations.

Theories of various kinds have been devised to precisely explain its origin but the relationship between the early-pod maize and the Teosinte, *Tripsacum*, identified in archeological dilapidations have not fully been settled yet (Poehlman, 1987). Now, there is wide adaptation of maize and cultivated across several areas of the globe under several environmental variations between latitude 50° N and S of the equator. It thrives in over 3000m above sea-level (Dowswell *et al.*, 1996). Maize was first introduced into Africa via Ghana and the Sao Tome islands by traders from Portugal in the 16th century (Shepherd *et al.*, 2010).

2.2 Uses of maize

Maize serves as the main food crop cultivated all over the globe serving as food source for many homes (FAO, 2011). Maize serves as source of animal feed in the developed parts of the world; whiles, in Africa and other developing parts of the globe, it serves as main food source for millions of its population and a major venture for generating income. In Ghana, maize is the most important cereal, accounting for more than 50% of the total cereal production. Maize cultivation remains the main source of livelihood for most Ghanaians, providing employment to more than 60% of the population and contributes about 30% to GDP (Browne Klutse *et al.*, 2013). Over 20% of the

income earned by small-holder farmers in Ghana comes from maize cultivation (Acquaah and Kyei, 2012). In Africa, the per capita consumption of maize ranges from 52g to 328g per person per day (FAOSTAT, 2012). The per capita consumption of maize in Ghana in 2007 and 2009 was estimated as 53g per person per day (FAOSTAT, 2012).

2.3 Maize production trends

Maize production in sub-Saharan Africa, where it is an important staple food crop, yields are still below 1 t/ha, while many countries record only 1-2 t/ha due mainly to climate change, poor soil fertility, frequent occurrence of droughts, high incidence of insect-pests, diseases and weeds, farmers' limited access to fertilizer, and lack of access to improved maize seed (Adu *et al.*, 2013). The average yield of maize in Ghana for instance is about 1.7 t/ha (MoFA, 2011; Adu *et al.*, 2013) though potential yield of 4-6 t/ha were achieved in on-station trials (Ragasa *et al.*, 2014).

Maize, among other cereal crops, is the third after wheat and rice and has the highest average yield per production area (FAOSTAT, 2012). The average maize production area across the globe is reported to as 144,376,477 ha, producing an estimated GY of 4.82 t/ha (FAO, 2011). Maize production in the United States alone is about half the average world production. Maize production area in Sub-Saharan Africa is estimated around 26,117,628 ha with average GY production of 1.77 t/ha. Maize production area in East Africa is also estimated 11,734,616 ha with an average yield production of 1.48 t/ha. The largest proportion of maize production in Africa is cultivated by resource-limited farmers who are often constrained by cash shortage and low inputs use, hence, producing low yields (Dawit *et al.*, 2008). The continual demand for maize has resulted in production in marginal land areas prone to the risk of biotic and abiotic stresses liable to minimal

production. To meet the increasing demand of maize in the sub-region, there is the need to increase production and reduce yield losses resulting from various environmental stress components including pests and diseases (Dagne *et al.*, 2004).

The continuous increase in population, urbanization, and growing poultry and fish sectors in Ghana, it is expected that the demand for maize will rise steadily at a projected compound annual growth rate of over 1.83% (FAO, 2013). The projected maize import in Ghana was estimated to be 267,000 metric tons (MT) in 2015 alone (FAO, 2013). Interventions are thus, needed to increase the productivity of maize in Ghana on limited land resources.

2.4 Development of inbred lines

Inbred lines are pure lines which are produced by cycles of continuous selfing of selected heterozygous plants till homozygosity is attained. Inbred lines are the products from inbreeding of heterozygous plants from open-pollinated populations till homozygosity is reached or products from inbreeding of populations following segregating cross between two inbred lines. The latter is similar to the hybridization procedure in breeding self-pollinated species. In developing inbred lines in maize, Sleper and Poehlman (2006) reported that pollination should be controlled. The choice of potential inbred lines that possess a certain measurable traits could be drawn out from populations from recurrent selection to increase frequency of gene action through continuous cycles of selection and inter-breeding (Sleper and Poehlman, 2006). Sleper and Poehlman (2006) reported that the success of developing an inbred line is enclosed in manipulation and characteristics of the original germplasm for the intended purpose.

2.5 Methods of maize breeding

Improvement in maize breeding programmes could be achievable through several methods of breeding depending on the start-up amount and type of materials available, end product, and the heritability of traits to be measured (Bänziger *et al.*, 2006). There are two main breeding methods commonly adopted in breeding for improved grain yield. First breeding method referred to as selection breeding, is a common method for generating OPVs and usually linked with high heritability of traits. This method incorporates recurrent selection as a breeding criteria. The second method also refers to inbreeding and hybrid development.

2.5.1 Recurrent selection method

This method adopts continuous breeding intended for improvement in the average performance of genotypes under a certain selection intensity. The method is achieved through simultaneous maintenance of genetic variability with a systematic increase in the frequency of favourable alleles (Bänziger *et al.*, 2006).

The method has effectively been used in a systematic improvement of performance of populations and increased stability of varieties (Tollenaar and Lee, 2002). This process like other methods, demands attention in selecting the appropriate germplasms that possess accurate information of its pedigree (Tollenaar and Lee, 2002). However, recurrent selection is highly effective and simpler for improved breeding of highly heritable traits such as ear heights, lodging resistance, and disease resistance in maize. The population to be developed could be landraces or inter-mated inbred lines superior for the measurable trait to be developed. Several selection methods have been developed for maize. However, effectiveness of these methods mainly depends on the kind of maize

population to be improved, objectives and state of breeding programme, and traits to be determined (Pratt *et al.*, 2003).

2.5.2 Inbreeding and hybrid development

The method of inbreeding and hybrid development in maize development programme involves manipulating the genetic make-up in order to improve the trait. The purpose of endogamy involves producing homozygous inbred lines for developing future crosses with high heterosis. Crossing inbred lines in hybrid combinations play an important role in improving maize production (Falconer and Mackay, 1996). In addition, they reported achieving hybrid vigour, prospective inbred lines in crossbreeding should be sourced from divergent populations. The vigour in the hybrids is dependent on the relative performance of inbred lines in the hybrid combinations and effects of the environment (Pandey and Gardener, 1992). It is thus, more important to characterize certain hybrid combinations with increased vigour in GY in a specific environment or across range of environments (Poehlman, 1987). Several benefits other than improved hybrid development programmes have been achieved through inbreeding. Falconer and Mackay (1996) reported elimination of deleterious and lethal genes during inbreeding due to the added improvements crosses over the original population.

2.6 Hybrid maize

A hybrid maize variety is the progeny of first-generation from a cross between inbred lines or a hybrid among them. The single-cross hybrid has replaced the modified single-cross hybrids, double-cross hybrids, and three-way hybrid combinations. This replacement has been attributed to the cultivation of F_1 progenies of crosses of homozygous parent lines (Sleper and Poehlman, 2006).

2.6.1 Trends in hybrid maize development

The double-cross hybrid, proposed in (1918) by D.F. Jones, became the tool for developing hybrid maize till its replacement in 1960s by single-crosses. During the 1920s and 1930s, major attention in breeding hybrid maize were geared towards developing inbred lines from OPVs and fitting the lines into productive single, double cross and three-way cross hybrid combinations adaptable to the Corn Belts of the United States. This effort, led by F.D. Richey for the United States Department of Agriculture, H.K. Hayes in Minnesota, M.T. Jenkins and G.F. Sprague in Iowa, and many other scientists, was dedicated to finding the most efficient procedures for breeding hybrids. By the 1940s, hybrid maize had replaced most of the open – pollinated maize throughout the United States Corn Belt and was being introduced to other major maize producing areas of the world (Sleper and Poehlman, 2006).

The 1950s and 1960s brought innovations that shifted hybrid maize seed development practices by introducing cytoplasmic male-sterility (cms) to avoid detasseling in seed production fields and replaced double-cross hybrids with productive single-cross hybrids.

Until the concept of hybrid maize, there was no breeding method by which every plant within a field of maize would be a high-yielding genotype. Additionally, the breeder's ability to identify high-yielding plants was limited because procedures for field-plot testing and data analyses available at that time did not permit separation of genetic and environmental effects on yield. For hybrid maize to be widely grown, it was also necessary that the hybrid seed be available at prices that the farmer could afford. To meet this need, private seed companies emerged to produce and market hybrid seed. Most of the seed companies developed extensive breeding and research

programs, and, over time, the breeding of hybrid cultivars of maize passed from publicly supported breeding programs to the private breeding programs (Sleper and Poehlman, 2006).

2.7 Heterosis and Combining ability

2.7.1 Heterosis

Heterosis is defined as the phenomenon whereby the progeny of a cross between inbred lines produces enhanced agronomic performance relative to both parents. However, some hypotheses that explain the heterosis phenomenon have been revised (Reif *et al.*, 2005b). Many hypotheses although have been suggested but the physiology, genetic and biochemical basis of heterosis concept still have not been explained. The overdominance, dominance (complementation) and the epistasis hypotheses are often raised.

According to the overdominance hypothesis, the amelioration of the F1 hybrid relative to its parent line is as a result of well-disposed allelic interaction at the loci of the heterozygote that outperforms either homozygote.

However, dominance theory also states that, deleterious alleles at different loci in the genomes of the two homozygous parents complement each other in the F1 heterozygote hybrid while the epistatic hypothesis assigns heterosis to interactions between non-allelic genes (Reif *et al.*, 2005b).

In situations when two or more genes produce the same phenotype, then they are referred to as non – allelic. In the broader sense, depending on the parents, there are two major means of estimating heterosis: namely, mid-parent heterosis (MPH), which is a measure of increased vigour of the F1 hybrid over the average performance of the parents; and better

(BPH) or high parent (HPH), which also is an estimation of the increased vigour of the F1 hybrid over the better or high performed parent (Sinha and Khana, 1975). However, heterosis is not only

dependent on the combinations of the parents but also affected by various environmental conditions and the trait involved in the study. Betrán *et al.* (2003a) reported a heterotic gain in grain yield with an increased intensity of stress of drought. Welcker *et al.* (2005) also reported a significantly higher mid – parent heterosis in terms of yield in acidic soils (32%) than non-acidic soils (20%). This was however concluded that, developing a variety of hybrids between populations tolerating acidic soils could be used to increase the yields of maize in acidic-soil cropping systems.

2.7.2 Combining ability and Gene action

The future usefulness of inbred lines for a successful hybrid development programme depends on the combining abilities of inbred (Hallauer and Miranda, 1988). Sprague and Tatum (1942) defined GCA as the mean performance of an inbred line in hybrid combinations and SCA as the case where some cross hybrids express poorer or better performance than the expected average performance of the parent inbred lines used. GCA and SCA effects have been emphasized to be relatively dependent on the genetic diversity of the inbred lines used in hybrid combinations, a highly significant principle that is often left. In maize breeding programme, introduction of new germplasm demands testing for effect of GCA and effect SCA (Hallauer and Miranda, 1988). However, different quantitative genetic protocols including line by tester analysis procedure provides some genetic information. Kempthorne (1957) proposed the usefulness of this method in breeding cross and self-pollinated plants, as well as providing estimates for favouring parents, crosses, and their GCA and SCA effects.

In choosing an efficient and effective breeding method for any trait to a larger extent depends on irremissible study of the gene action controlling the inheritance of traits. The effect of dominant

gene is favourable in hybrid production whereas additive gene effect indicates that procedure for standard selection would be feasible to cause significant changes in expression of traits. Wolf and Hallauer (1997) reported that, information on genetic variances, levels of dominance, and the importance of genetic effects have resulted to better understanding of the gene action modulating the expression of heterosis in the progenies. They emphasized that variation due to GCA indicates the effect of additive gene action, whereas SCA is a measure of the effect of non-additive gene action in the inheritance of traits.

In determining the mode of inheritance of a trait, it must be noted that environment plays an important role in modulating the inheritance of traits. Betrán *et al.* (2003b) evaluated a 17x17 diallel of white-grained tropical maize inbred lines under optimal, drought and low-N stress conditions, indicating the gene action in modulating the inheritance of traits were different under drought from that under low N, and further suggested that additive gene effect was more important under drought while dominant gene effect was also more important under low N. Some earlier authors (Derera *et al.*, 2008; Meseka *et al.*, 2013), reported preponderance of the additive gene effect over non-additive gene effect conditioning GY of maize under different environment conditions. In contrast, Guei and Wassom (1992) also reported that effect of nonadditive action in the inheritance of GY under environmental drought stress condition. Thus, understanding the gene action involved in hybrid performance under different environmental conditions is important in designing an effective and appropriate breeding strategy.

2.8 Heritability

Heritability as described by Falconer (1989) has two types of definitions with reference to the genotypic value or the breeding value. Narrow-sense heritability (h^2) or the breeding value is

defined as the ratio of the additive variance to the phenotypic variance. It determines the extent to which an expression of the phenotype of a trait are transmitted genes from parents to the progenies. It also determines the extent of genotypic variance in a population, mainly modulating the change in genetic composition of the population through selection.

On the other hand, broad-sense heritability (H^2) is the ratio of the genetic variance to the phenotypic variance. Also, it determines the extent at which the phenotype is expressed by the genotype. Stress factors within an environment affect the magnitude of heritability for GY and other associated traits. In general, heritability for yield is low under stressed environments since the genetic variance for yield decreases more rapidly than the environmental variance. Secondary traits whose genetic variance increases under stress conditions or are reduced less than that of yield, have relatively high heritability (Blum, 1988; Edmeades *et al.*, 1989; Ludlow and Muchow, 1990). The differences that exist within environments also reduce the proportion of heritability characters while more uniform environment conditions increases it (Blum, 1988).

The estimate of heritability is such that more closely related individuals are likely to show resemblance with each other more than distantly related ones (Falconer and Mackay, 1996). Heritability estimates help breeders to effectively allocate resources to improve selection of important traits with little effort and time investment (Ogunniyan and Olakojo, 2014). The estimate of genetic advance determines the extent of gain in a particular trait under a particular selection intensity. It has been emphasized that selection based on heritability estimates alone is not an effective criteria for genetic improvement unless associated with substantial estimate of genetic advance. However, heritability increases with the estimation of genetic advance to reveal the degree of gain of a trait under a certain selection intensity. Hence, determination of genetic advance

is an important procedure which assists breeders in selection program (Ogunniyan and Olakojo, 2014).

2.9 Mating designs

The success associated with breeding for improved trait in maize involves adequate knowledge of how many genes are associated in expressing the trait and actions of the respective genes. To achieve this technique, a specific genetic or mating design is used. Several genetic or mating designs have been proposed in maize populations where genetic variances have been estimated (Hallauer and Miranda, 1988). In maize breeding, mating designs commonly employed are North Carolina (NC) design I (NC I), North Carolina design II (NC II), North Carolina design III (NC III), and diallel cross. Jensen (1970) reported that the choice of appropriate design demands verifying assumptions of random mating, avoiding epistasis, behaviour of a diploid chromosome, absence of maternal gene effects, as well as linkage equilibrium of genes during results interpretation from studies involving genetics.

Diallel mating design is used most extensively to study type of gene action associated with the inheritance of traits quantitatively. Singulas *et al.* (1988) reported that diallel mating design permits an estimate of GCA and SCA of a genotype. A complete diallel scheme estimate variances resulting from parent genotypes, crosses, as well as reciprocal effects (Falconer and Mackay, 1996). This design is more convenient for ease of management when few parents are used (Hallauer and Miranda, 1988).

On the contrary, NC I mating design allows breeders to put some plants in a population to test. It is highly appropriate to use an unequal number of parents as either female or male. Again, it allows an easier means to estimate dominance variance (VD) and additive genetic variance (VA). The

exceptional attribute associated with NC I design allow components to be nested in one another other than factorial design crossing fashion. The NC I is mostly adopted in maize breeding than other mating designs, especially diallel mating design (Hallauer and Miranda, 1988).

With NC II, progenies are produced by crossing males to females. This method enables estimating component variances plus GCA and SCA. It has a major advantage to handle a large number of parents (Singulas *et al.*, 1988). The design allows estimation of mean squares of GCA and SCA of females and males while the interaction between males and females is equal to that of SCA of diallel design (Hallauer and Miranda, 1988). Furthermore, Falconer and Mackay (1996) reported that the dominance genetic variance could be estimated directly from mean square estimates of SCA effect.

2.10 Effect of Genotype \times Environment interactions

The performance of a genotype is also determined by the interaction between the genotype and environment (G \times E) (differential response of genotypes to changes in environment), aside its genotype (G) and environment (E) main effects (Vargas *et al.*, 2001). The common types of G \times E interaction include, genotype \times environment interaction, genotype \times year interaction, and genotype \times environment \times year interaction effects (Crossa, 1990). Seasonal variations as well as soil properties among others influences G \times E interactions. For instance, Troyer (1996) reported that genotype \times year interaction was larger than genotype \times environment interaction as a result of different soil moisture present during flowering. G \times E interaction that changes the order of rank of performance of a genotype is referred to as cross-over interaction. Mostly, the order of rank of G \times E remains static except for absolute differences of the performances of genotypes in the variable environments. Interactions resulting from cross-over creates challenges in breeding as it obstructs

progress of selection due to changes in the composition of genotypes selected at other environments (Cooper and Delacy, 1994; Crossa *et al.*, 1995).

Sallah *et al.* (2004) reported that, the phenotype of a crop can be determined by G×E interactions other than its genotype, accounting for a greater portion of yields attainable in improved varieties. Ewool (2004) reported a high G×E interaction effect on yield of crops due to soil fertility status, season and location, as well as dates of sowing in Ghana.

2.10.1 Stability of yield and yield components

Tollenaar and Lee (2002) reported that, varieties that are stable have little interaction with environments. There are two types of stability as defined by Becker and Leon (1988). These were dynamic and static. In dynamic stability, yield of the genotype varies predictably and the genotype stability is influenced by the genotype sets being evaluated (Becker and Leon, 1988; Tollenaar and Lee, 2002). However, dynamic stability is a relative measure while static stability is an absolute measure. In selection of a genotype, the best genotype should effectively exploit a higher input levels under optimum growth regimes and express appreciable grain yield under comparatively lower input regimes.

Improvement in stability of grain yield could be achieved through selection since it is contributed by additive gene action and highly heritable (Lee *et al.*, 2003). However, the stability of genotypes could be achieved from multi-environment trials (Troyer, 1996). The yield performance and stability of hybrids in USA were as a result of an extensive multiple environment trials (Duvick and Cassman, 1999). This provides a tentative evidence to evaluate important genotypes under several environments to assess consistencies in yield and stability for commercial production.

Sleper and Poehlman (2006) also reported that, like yield, adaptability is a complex objective in hybrid breeding that is directly affected by cultivar maturity, response to soil fertility level and conservation tillage practices as well as resistance to heat and drought. Adaptation is also indirectly affected by other plant characters such as husk covering, root and stalk quality, disease and insect resistance and endosperm properties that affect seed storage.

Generally, maize hybrids that will effectively utilize the full growing season and still safely mature will be the most productive hybrids to grow in a region limited by length of the production season. Nevertheless, early-maturing hybrids have significant attributes that combine certain characters, such as early harvest before damage from rain at the time of harvest or enhance sowing of the successive crop in a cyclical fashion in terms of maturity to fit the area of production.

2.10.2 Genotype and genotype by environment (GGE) biplot analysis

Gabriel (1971), initiated the method of biplot analysis of data and the use of the method was subsequently expanded by Kempton (1984), and Zobel *et al.* (1988). The broad practical use of the GGE biplot, where G refers to the effect of the Genotype, and the GE refers to the effect of the Genotype \times Environment, until recently been enlightened (Yan *et al.*, 2000). The approach in the use of the GGE biplot has immensely attracted the attention of breeders as well as agronomists. It is a multifarious tool for plant breeding and quantitative genetic analyses.

Moreover, the GGE biplot facilitates analyzing data on diallel crosses, genotype \times marker, and genotype \times trait (Yan *et al.*, 2000, 2001; Yan, 2001; Yan and Hunt, 2001, 2002; Yan and Rajcan, 2002). From the above perspective, the GGE biplot has become the most comprehensive tool in plant breeding and quantitative genetics.

Butran *et al.* (2004) and Samonte *et al.* (2005) reported that the GGE biplot analysis has increasingly been used in genotype×environment inheritance in plant breeding research.

Visualizing “which-genotype-won-which-environment” pattern of multi-environment trial (MET) is essential to study the presence of different mega-environments (Gauch and Zobel, 1997; Yan *et al.*, 2000; Yan, 2001).

The GGE biplot view in the form of a polygon provides a better approach to observe the patterns of interaction between genotypes and environments (Yan and Kang, 2003). However, the presence or absence of cross-over G×E interaction is significant in determining the possible existence of different mega-environments (Yan and Rajcan, 2002; Yan and Tinker, 2006). The polygon of the GGE biplot is formed by connecting genotype markers from the origin of the biplot such that all genotypes that are farther away could be contained in the polygon (Kaya *et al.*, 2006). The genotypes located on vertices of the polygon view are either the best or poorest in one or more environments (Yan *et al.*, 2000; Yan and Rajcan, 2002; Yan and Tinker, 2006). The genotypes located at the vertex of the polygon in each sector is referred to as the best genotype for sites whose markers fell into respective sectors so that sites within the same sector share the same winning genotype (Yan *et al.*, 2000; Yan, 2002). On the biplot, the polygon is divided into sectors by drawn perpendicular lines to the sides.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Planting materials

Ten yellow endosperm maize inbred lines were obtained from the International Institute of Tropical Agriculture (IITA), Ibadan-Nigeria. The inbred lines were developed from two broadbased populations, TZEE-Y Pop STR C₀ and TZEF-Y SR BC₁ × 9450 STR identified to be resistant to *Striga* and maize streak virus (Table 3.1). The source populations were formed from exotic and local germplasm identified through several years of extensive evaluation in West and Central Africa (Badu-Apraku *et al.*, 2007a). The inbred lines used for this study were chosen in an effort to alleviate the major production and productivity constraints in maize associated with low grain yield, low soil productivity and *Striga* infestation within certain environments.

Table 3.1: Description of the 10 extra-early maturing yellow maize inbred lines used for the study.

Inbred line	Pedigree	Reaction to low-N	Reaction to <i>Striga</i> - infestation
TZEEI 61	TZEE-Y SR BC ₁ × 9450 STR S6 Inb 4B	Tolerant	Tolerant
TZEEI 63	TZEE-Y SR BC ₁ × 9450 STR S6 Inb 7B	Tolerant	Tolerant
TZEEI 64	TZEE-Y SR BC ₁ × 9450 STR S6 Inb 8A	Tolerant	Tolerant
TZEEI 66	TZEE-Y SR BC ₁ × 9450 STR S6 Inb 9A	Susceptible	Resistant
TZEEI 67	TZEE-Y SR BC ₁ × 9450 STR S6 Inb 10B	Tolerant	Resistant

Table 3.1 continued

Inbred line	Pedigree	Reaction to Low-N	Reaction to <i>Striga</i> infestation
TZEEI 71	TZEE-Y SR BC ₁ × 9450 STR S6 Inb 2B	Tolerant	Tolerant
TZEEI 76	TZEF-Y SR BC ₁ × 9450 STR S6 Inb 8B	Tolerant	Tolerant

TZEEI 78	TZEE-Y SR BC1 × 9450 STR S6 Inb 9A	Susceptible	Resistant
TZEEI 94	TZEE-Y Pop Co S6 Inb 47-2-4B	Susceptible	Resistant
TZEEI 96	TZEE-Y Pop Co S6 Inb 78	Susceptible	Tolerant

Source: Badu-Apraku *et al.* (2009)

3.2 Generation of single-crosses

The 10 yellow-endosperm maize inbred lines were planted during the minor season (September - December) of 2014 at the breeding nursery of the Council for Scientific and Industrial Research Crops Research Institute (CSIR-CRI), Fumesua, Ghana. All possible crosses were made among the inbred lines using 10×10 half-diallel mating design to generate 45 single-crosses. One local variety, 'Abontem', was included as local check.

3.3 Site selection for hybrid trial

The single-crosses were evaluated across three locations (Fumesua, Ejura and Kpeve) in Ghana. Fumesua is located in the Forest zone on latitude $06^{\circ} 41'N$ and longitude $01^{\circ} 28'W$. Ejura and Kpeve are Forest-Guinea savannah Transition and Coastal Savannah zones located on latitude $07^{\circ} 23'N$ and longitude $01^{\circ} 21'W$ and latitude $06^{\circ} 41'N$; longitude $00^{\circ} 20'E$, respectively. All trials were carried out in the major season (May – September, 2015).

3.4 Experimental design, planting procedure and crop management practices

The experiment was laid out in a Randomised Complete Block Design (RCBD) with 45 treatments replicated three times.

Treatments were randomly assigned to $5\text{m} \times 0.75\text{m}$ plots. Seeds (three per hill) were manually planted at a spacing of $0.75\text{m} \times 0.45\text{m}$ giving plant population of 44 per plot (equivalent to 59260 plants ha^{-1}). Stands were thinned to two plants per hill two weeks after planting.

Fertilizer equivalent to 90:60:30 kg ha^{-1} of N- P_2O_5 - K_2O plus sulphate of ammonia (125 kg/ha) was applied at 21 days after planting and at ear emergence. Pre-emergence weeds were chemically controlled with pre-emergence herbicide, Isoxaflutole + Aclonifene (50+330 g/l) at a rate of 0.5 liters/hectare (l/ha). Hand hoeing of post-emergence weeds were also done on all fields as and when necessary to keep the plots free from weeds. All agro-chemicals were applied using a knapsack sprayer.

3.5 Data Collection

3.5.1 Days to Tasseling (DTAS)

This was collected as the number of days from time of seed sowing to the date when 50% of the plants had visible tassels.

3.5.2 Anthesis Date (AD)

This was determined per plot as the number of days from time of planting to when 50% of plants were shedding pollen.

3.5.3 Silking Date (DS)

This was the number of days from planting to the day 50% of the plants had visible silks.

3.5.4 Anthesis – Silking interval (ASI)

ASI was calculated as the difference between the number of days when 50% of the plants had produced silks and the number of days when 50% of plants were shedding pollen (DS – AD).

3.5.5 Ear height (EHT)

This was the average height from soil level to upper ear insertion node (cm) on five randomly selected plants per plot at milk stage.

3.5.6 Plant Height (PHT)

This was the average height (cm) from the base of five randomly selected plants to where tassel begins branching.

3.5.7 Husk Cover (HUSK)

This data was scored when ears were fully developed and leaf husks were drying out (physiological maturity) using a score rating of 1 to 5, where 1= husk tightly arranged and protracted beyond the tip of the ear and 5= ear tips were fully exposed.

3.5.8 Rust (RUST)

This recording on rust (*Puccinia polysora*), was carried out during the 2nd to 4th week period after 50% of plants had emerged silks. A scale of 1 to 5 was applied, where 1 = no rust, and 5 = severe rust.

3.5.9 Maize Blight (BLT)

The data recoded on leaf blight, *Helminthosporium maydis* was done during the 2nd to 4th -weeks after silking. Disease incidence (plants showing symptoms) and infection severity were subjectively estimated using a scale of 1 to 5 following the procedure by Badu-Apraku *et al.* (2012).

1 = slight infection	observed as few lesions on leaves, mostly found only on the lower leaves.
2 = light infection	observed as few to moderate lesions observed on leaves below the top ear. No lesions observed on the leaves above the top ear.
3 = moderate infection	observed moderate to large visible lesions on leaves below the top ear. On the other hand such lesions can be observed on leaves above the top ear.
4 = heavy infection	observed as large number of lesions on leaves below the top ear, moderate to large number of lesions on leaves above the top ear.
5 = very heavy infection	observed on all leaves with large number of lesions leading to premature death of the plant and light ears.

3.5.10 Streak (ST)

This data was also taken by scoring on the basis of the percentage number of ear (cob) leaves covered with lesions. Disease incidence (plants that show symptoms) and infection severity were subjectively estimated using a scale of 1 to 5 following the procedure by Badu-Apraku *et al.* (2012).

1 = slight infection	less than 10% of the ear-leaf covered by lesions.
2 = light infection	10-25% of the ear-leaf covered by lesions.
3 = moderate infection	26-50% of the ear-leaf covered by lesions.
4 = heavy infection	51-75% of the ear-leaf covered by lesions, leading to premature death of the plant and light cobs.
5 = very heavy infection	76-100% of the ear-leaf covered by lesions, which leads to premature death of the plants and produces light cobs.

3.6 Harvest Data

3.6.1 Root Lodging (RTLG)

This was scored as the number of plants leaning more than 45° from the standing position of 90°.

3.6.2 Stalk Lodging (STLG)

This was scored a week before harvest as the number of plant stalks broken below the ear.

3.6.3 Plant Stand at Harvest (PHARV)

The total number of plants standing per plot at harvest was counted and recorded.

3.6.4 Ears Harvested (EHARV)

This was recorded as the total number of ears harvested per plot that bore kernels.

3.6.5 Cob Aspect (CASP)

A scale of 1 to 5 was used on the basis of the general appearance of harvested cobs in each plot, where 1= best, 3= average, and 5= poorest ear aspect. Certain factors such as ear size, insect

damage, grain filling, and uniformity of cob size, grain colour and texture were all considered in the scoring.

3.6.6 Grain moisture (MO)

This was recorded with a moisture meter at harvest. Five randomly selected ears were shelled in a half-way from sampling rows at the centre of each ear harvested and grains used to determine the moisture content.

3.6.7 Field Weight (FWT)

This was the weight (kg) of all dehusked ears per plot.

3.6.8 Grain Yield (GY)

This was recorded on plot basis of all shelled ears (cobs) by hand to the nearest tenth of a kg using the weighing balance. The grain yield was standardized to 12.5% moisture as:

$$\text{Grain yield (12.5\% MO)} = \frac{\text{grain yield} \times (100 - \text{grain moisture})}{87.5}$$

3.6.9 Ear Rot (EROT)

This was counted on the basis of the number of ears showing rot by considering the number of ears rotten and the extent of rot in each plot harvested.

3.7 Data Analyses

The analysis of variance (ANOVA) for each trait under study was obtained for and across research environments using Statistical Analysis System software. The 10×10 half-diallel analyses, excluding the check used was performed using Griffing's method IV, fixed model (Griffing, 1956)

developed by Zhang *et al.* (2005) DIALLEL-SAS program adapted to SAS software version 9.2 (SAS, 2001), where component GCA and SCA effects were estimated. Mean squares of parents were estimated from the GCA effects, while that of single-crosses were obtained from the SCA effects of the diallel analysis where the mean squares were used to estimate GCA: SCA ratios (Beil and Atkins, 1967; Haussmann *et al.* 1999).

3.7.1 Estimates of genetic components

The relative contributory effects of the genetic components were determined to obtain the estimates of GCA variance component as VAR_{gca} (additive variance) and SCA variance component as VAR_{sca} (dominance) for each trait across environments. Variances, heritability and genetic ratio were estimated as:

$$VAR_{gca} = \frac{MS_{gca} + MS_{scaenv}}{MS_{sca} + MS_{gcaenv}} \dots \dots \dots (1)$$

$$VAR_{sca} = \frac{MS_{sca}}{MS_{scaenv}} \dots \dots \dots (2)$$

$$VAR_{gcaenv} = \frac{MS_{gcaenv}}{MS_{scaenv}} \dots \dots \dots (3)$$

$$VAR_{scaenv} = \frac{MS_{sca}}{MSe} \dots \dots \dots (4)$$

$$H^2 = \frac{2VAR_{gca} + VAR_{sca}}{2VAR_{gca} + VAR_{sca} + \frac{2VAR_{gca}}{Env} + \frac{VAR_{sca}}{Env} + \frac{VARE}{REnv}} \dots \dots \dots (5)$$

$$h^2 = \frac{2VAR_{gca}}{2VAR_{gca} + VAR_{sca} + \frac{2VAR_{gca}}{Env} + \frac{VAR_{sca}}{Env} + \frac{VARE}{REnv}} \dots \dots \dots (6)$$

$$Genetic\ ratio = \frac{2MS_{gca}}{2MS_{gca} + MS_{sca}} \dots \dots \dots (7)$$

where MS_{gca} = mean square of GCA, MS_{sca} = mean square of SCA, MS_{gcaenv} = mean square of GCA×Env interaction, MS_{scaenv} = mean square of SCA×Env interaction, MSe = error mean

square, and $REnv$ = Number of replications \times Environment, H^2 = broad-sense heritability, h^2 = narrow sense heritability.

Genetic advance (GA) for traits were determined following Allard (1964) procedure as; $GA = ih^2V_p$, where $i = 1.76$ (10% selection intensity), V_p = phenotypic variance, and h^2 = narrow sense heritability. The GGE biplots were generated using Genstat Statistical Package (12th Edition) across location for the single-cross hybrid genotypes. The SCA effects of the GGE biplot analysis was also used to identify outstanding hybrids for GY and stability as well as helping to select the ideal genotype (s) across research environments.

Estimates of heterosis were calculated from the mean values of grain yield across research environments using the formulae;

$$\text{Better - parent heterosis (BPH)} = \frac{F1 - BP}{BP} \times 100$$

$$\text{mid - parent heterosis (BPH)} = \frac{F1 - MP}{MP} \times 100$$

Following Cochran and Cox (1960), and Singh and Chaudhary (1985) criteria, the error mean squares (Ems) for each trait and degree of freedom (DF) in the analysis of variance from the randomized complete block design procedure were used. The t -test was then employed to ascertain whether the hybrid means of the $F1$ single-cross hybrids were statistically different from better-parent (BP) and mid-parent (MP) means according to the relationship earlier established by Wynne *et al.* (1970) as;

$$t - \text{test (MPH)} = \frac{F1 - MP}{\sqrt{3/2r(EMs)}}$$

$$t - \text{test (BPH)} = \frac{F1 - BP}{\sqrt{2/r(EMs)}}$$

where FI is the mean performance of the single-cross hybrids, BP is the performance of better parent and MP is the average of two parents, and r is the number of replications. Mean estimates of the single-cross hybrids were analyzed using Statistical Tool for Agricultural Research (STAR, 2014) software, version 2.0.1.



CHAPTER FOUR

4.0 RESULTS

4.1 Analysis of Variance, Estimates of GCA and SCA across Research Environments

Combined analysis of variance (ANOVA) of the diallel cross showed that estimated mean square for environment (E) were significant ($p < 0.01$) for most traits and significant ($p < 0.05$) for ASI (Table 4.1). Mean square estimates for Entry (G) were significant ($p < 0.01$) for GY, DS, DTAS, PHT, EHT, HUSK, STLG, and MO, and significant ($p < 0.05$) for RTLG (Table 4.1). However, entry mean square estimate for ASI was not significant (Table 4.1).

Mean square estimates for $G \times E$ were significant ($p < 0.01$) for GY, DS, DTAS, PHT, HUSK, and MO and significant ($p < 0.05$) for EHT and STLG (Table 4.1). Mean square value for $G \times E$ for ASI was not significant (Table 4.1).

Partitioning G into component GCA and SCA showed that, mean squares of GCA were significant ($p < 0.01$) for GY, ASI, PHT, EHT, HUSK, STLG, and MO, and significant ($p < 0.05$) for DS, DTAS, and RTLG (Table 4.1). On the other hand, mean square estimates of SCA were significant ($p < 0.01$) for GY, DTAS, EHT, HUSK, and MO, and significant ($p < 0.05$) for PHT (Table 4.1). In addition, SCA mean squares for DS, ASI, RTLG, and STLG were observed as not significant (Table 4.1). In all cases, mean square estimates of GCA were relatively greater than SCA for all measured traits (Table 4.1).

Mean square estimates of $GCA \times E$ were significant ($p < 0.01$) for all traits except ASI, EHT, HUSK, and RTLG (Table 4.1). On the hand, mean square estimates of $SCA \times E$ were significant

($p < 0.01$) for GY, DS, PHT, HUSK, RTLG, STLG and MO, and significant ($p < 0.05$) for DTAS and EHT (Table 4.1). In addition, SCA \times E mean square estimate for ASI was not significant (Table 4.1). The estimated ratios of GCA: SCA for all traits were observed to range from 1.19 for EHT to 4.08 for DS (Table 4.1). In all cases, the estimated ratios were relatively higher than a unit ratio for all measured traits (Table 4.1).

4.2 GCA effects for grain yield and other related traits

Significant ($p < 0.01$) positive GCA effects for GY were observed for inbred lines TZEEI 61, and TZEEI 66 (Table 4.2). In addition, significant ($p < 0.05$) positive GCA effects for the same trait was observed for inbred line TZEEI 78 (Table 4.2). However, significant ($p < 0.01$) negative GCA effects for GY were also observed for inbred lines TZEEI 63, and TZEEI 96 (Table 4.2). GCA effects for GY for inbred lines TZEEI 64, TZEEI 67, TZEEI 71, TZEEI 76, and TZEEI 94 were not significant ($p > 0.05$) (Table 4.2).

Significant ($p < 0.01$) positive GCA effect for DS was observed for inbred lines TZEEI 63 and TZEEI 64 (Table 4.2). On the contrary, significant ($p < 0.01$) negative effects were also observed for inbred lines TZEEI 61 and TZEEI 66 (Table 4.2). GCA effect of DS for inbred lines TZEEI 67, TZEEI 71, TZEEI 76, TZEEI 78, TZEEI 94, and TZEEI 96 was observed as not significant for DS ($p > 0.05$) (Table 4.2).

Estimates of GCA effect for DTAS showed significant ($p < 0.01$) positive values for inbred lines TZEEI 63, and TZEEI 64 (Table 4.2). However, significant ($p < 0.01$) negative effect was also observed for TZEEI 61 (Table 4.2). Moreover, significant ($p < 0.05$) negative GCA effect was observed for inbred line TZEEI 66 (Table 4.2). However, estimated GCA effect for inbred lines TZEEI 67, TZEEI 71, TZEEI 76, TZEEI 78, TZEEI 94, and TZEEI 96 was observed not

significant ($p>0.05$) (Table 4.2).

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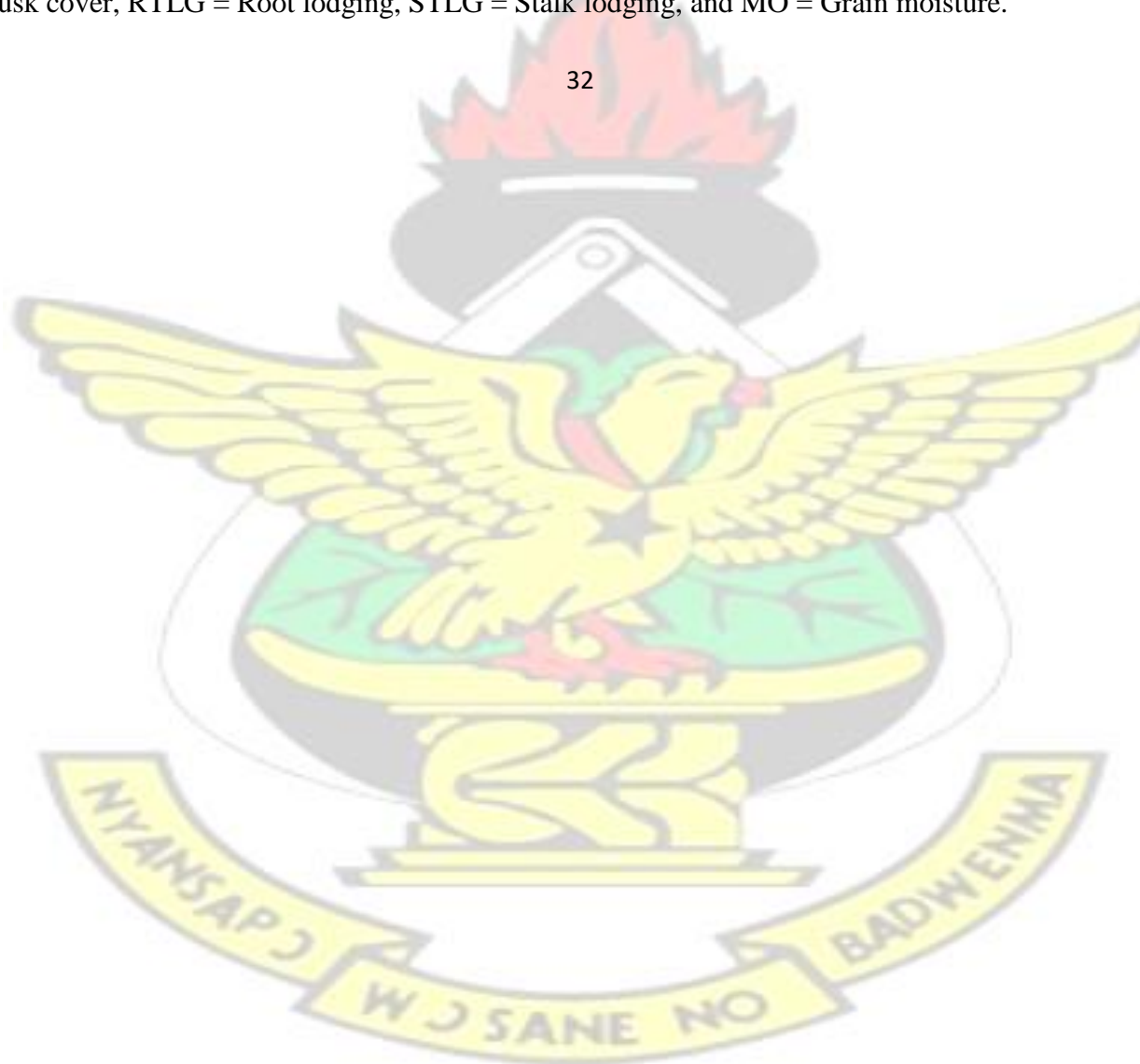
Table 4.1: Mean squares from the combined ANOVA of grain yield and related traits of extra-early maturing yellow single-cross hybrids evaluated across research environments

Source	DF	Mean squares									
		GY (t/ha)	DS (days)	DTAS (days)	ASI	PHT (cm)	EHT (cm)	HUSK	RTLГ	STLG	MO (%)
Env. (E)	2	66.03**	116.31**	71.87**	0.36*	10367.00**	752.72**	2.19**	1.70**	2.87**	47.49**
Rep (E)	6	0.99**	2.10*	1.35*	0.04*	65.85	30.22	0.09*	0.03	0.09*	0.85
Entry (G)	44	3.19**	4.51**	3.75**	0.03	636.07**	75.73**	0.10**	0.05*	0.06**	1.75**
G×E	88	0.82**	2.11**	1.47**	0.02	250.05**	36.81*	0.06**	0.05**	0.06*	1.57**
GCA	9	5.37**	11.30*	7.45*	0.06**	1341.36**	87.02**	0.23**	0.05*	0.12**	2.34**
SCA	35	2.63**	2.77	2.79**	0.02	454.71*	72.83**	0.07**	0.04	0.04	1.59**
GCA×E	18	0.84**	3.30**	2.95**	0.02	299.31**	34.25	0.06	0.05	0.10**	1.95**
SCA×E	70	0.82**	1.81**	1.09*	0.03	237.38**	37.47*	0.07**	0.05**	0.05**	1.47**
Error		0.28	0.54	0.55	0.02	84.50	25.45	0.04	0.03	0.03	0.61

GCA:SCA	2.04	4.08	2.67	3.97	2.95	1.19	3.25	1.25	2.79	1.47
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*, and **, represent significant levels at 0.05, and 0.01 probability levels.

GY = Grain yield, DS = Days to silking, DTAS = Days to tasseling, ASI = Anthesis-Silking Interval, PHT = Plant height, EHT = Ear height, HUSK = Husk cover, RTLG = Root lodging, STLG = Stalk lodging, and MO = Grain moisture.



Estimates of GCA effect for ASI showed significant ($p<0.01$) positive value for inbred line TZEEI 64 (Table 4.2). Significant ($p<0.05$) negative GCA effect for ASI was also observed for inbred line TZEEI 67 (Table 4.2). However, GCA effect for inbred lines TZEEI 61, TZEEI 63, TZEEI 66, TZEEI 71, TZEEI 76, TZEEI 78, TZEEI 94, and TZEEI 96 were not significant ($p>0.05$) (Table 4.2).

For PHT, significant ($p<0.01$) positive estimates of GCA effects were observed for inbred line TZEEI 78 (Table 4.2). In addition, significant ($p<0.05$) positive GCA effect was observed for inbred lines TZEEI 71 and TZEEI 76 (Table 4.2). However, significant ($p<0.05$) negative estimates of GCA effect was also observed for inbred lines TZEEI 61, TZEEI 63, and TZEEI (Table 4.2).

Estimates of GCA effects for EHT showed significant ($p<0.05$) positive values for inbred line TZEEI 78 (Table 4.2). However, significant ($p<0.05$) negative effects were also observed for inbred lines TZEEI 61 and TZEEI 63 (Table 4.2).

The estimates of GCA effects for HUSK showed significant ($p<0.05$) positive values for inbred line TZEEI 63 (Table 4.2). Significant ($p<0.05$) negative effects were also observed for inbred line TZEEI 78 (Table 4.2). Estimates of GCA effects for RTLG and STLG showed significant ($p<0.05$) positive and negative values for TZEEI 64 and TZEEI 66, respectively (Table 4.2).

Table 4.2: GCA effects of extra-early yellow inbred lines of maize for grain yield and other related traits across three environments

	GY	DS	DTAS		PHT	EHT				MO
	(t/ha)	(days)	(days)	ASI	(cm)	(cm)	HUSK	RTLG	STLG	(%)
Inbred line										
TZEEI 61	0.43**	-0.50**	-0.51**	0.01	-6.60**	-1.32*	0.04	-0.02	0.03	-0.41**
TZEEI 63	-0.39**	0.60**	0.50**	0.02	-7.11**	-2.07**	0.10**	0.03	0.04	0.17
TZEEI 64	-0.04	0.75**	0.49**	0.07**	-0.50**	0.65	0.00	0.05*	0.01	0.03
TZEEI 66	0.31**	-0.40**	-0.30*	-0.03	-2.54	0.09	-0.01	-0.04	-0.06*	-0.11
TZEEI 67	-0.04	-0.11	0.04	-0.04*	2.67	0.36	0.01	0.03	0.03	0.20
TZEEI 71	-0.17	0.00	0.07	-0.02	3.29*	0.47	0.02	-0.03	0.05	-0.07
TZEEI 76	-0.12	-0.21	-0.22	0.00	3.26*	0.98	-0.01	0.01	-0.04	0.06
TZEEI 78	0.25*	-0.09	-0.08	0.00	6.10**	1.59*	-0.11**	-0.05	-0.03	0.10
TZEEI 94	0.10	-0.11	-0.11	0.00	0.53	-0.74	-0.11	0.00	-0.04	-0.09
TZEEI 96	-0.35**	0.06	0.11	-0.01	0.90	-0.02	0.02	0.02	0.02	0.12
SE (Gi-Gj)	0.09	0.12	0.12	0.02	1.53	-0.74	0.03	0.02	0.04	0.16

*, and **, represent significant differences at 0.05, and 0.01 probability levels; GY = Grain yield, DS = Days to silking, DTAS = Days to tasseling, ASI = Anthesis-Silking Interval, PHT = Plant height, EHT = Ear height, HUSK = Husk cover, RTLG = Root lodging, STLG = Stalk lodging, and MO = Grain moisture.



4.3 SCA effects for grain yield and other related traits

The estimate of SCA effects for GY and other related traits across research environments is presented in Table 4.3. Significant ($p<0.01$) positive SCA effects for GY were observed for the single-cross hybrids, TZEEI 64×TZEEI 61, TZEEI 78×TZEEI 66, TZEEI 96×TZEEI 71, and TZEEI 94×TZEEI 76 (Table 4.3). In addition, significant ($p<0.05$) positive effects for the same trait were observed for TZEEI 76×TZEEI 63, and TZEEI 66×TZEEI 64 (Table 4.3). However, significant ($p<0.01$) negative effect of SCA for GY was observed for TZEEI 96×TZEEI 76, and TZEEI 94×TZEEI 78, as well as significant ($p<0.05$) negative effects for TZEEI 71×TZEEI 64, TZEEI 94×TZEEI 66, and TZEEI 78×TZEEI 76 (Table 4.3).

Significant ($p<0.05$) positive SCA effect for DS was observed for the single-cross hybrid TZEEI 94×TZEEI 64, whereas significant ($p<0.05$) negative SCA effect of the same trait were observed for TZEEI 63×TZEEI 61, TZEEI 96×TZEEI 71, and TZEEI 96×TZEEI 76 (Table 4.3). Significant ($p<0.05$) positive SCA effects for DTAS were observed for the single-cross hybrids, TZEEI 94×TZEEI 64, TZEEI 96×TZEEI 64, and TZEEI 76×TZEEI 66 (Table 4.3). However, significant ($p<0.05$) negative SCA effects for DTAS were observed for TZEEI 63×TZEEI 61, TZEEI 96×TZEEI 71, TZEEI 94×TZEEI 76, and TZEEI 96×TZEEI 76 (Table 4.3). Significant ($p<0.05$) positive SCA effect for ASI was observed for the single-cross hybrid TZEEI 96×TZEEI 61 (Table 4.3).

Significant ($p<0.05$) positive SCA effect for PHT were observed for the single-cross hybrids, TZEEI 71×TZEEI 61, TZEEI 96×TZEEI 63, TZEEI 78×TZEEI 64, TZEEI 94×TZEEI 64, and TZEEI 96×TZEEI 71 (Table 4.3). In contrast, significant ($p<0.05$) negative SCA effects were observed for, TZEEI 67×TZEEI 61, TZEEI 71×TZEEI 64, and TZEEI 67×TZEEI 66 (Table 4.3).

Significant ($p < 0.05$) positive SCA effects for EHT were observed for the single-cross hybrids TZEEI 96×TZEEI 63, TZEEI 78×TZEEI 64, TZEEI 76×TZEEI 66, TZEEI 94×TZEEI 71, and TZEEI 96×TZEEI 71 (Table 4.3). Moreover, significant ($p < 0.05$) negative SCA effects for EHT were observed for TZEEI 66×TZEEI 63, TZEEI 96×TZEEI 64, and TZEEI 67×TZEEI 66 (Table 4.3). Significant ($p < 0.05$) negative SCA effects for HUSK were observed for single-cross hybrids TZEEI 67×TZEEI 64, TZEEI 78×TZEEI 66, and TZEEI 76×TZEEI 61 (Table 4.3).

Significant ($p < 0.01$) positive SCA effect for RTLG was observed for single-cross hybrid, TZEEI 96×TZEEI 61 (Table 4.3). Significant ($p < 0.05$) negative SCA effect for STLG was also observed for the single-cross hybrid, TZEEI 64×TZEEI 61 (Table 4.3). Significant ($p < 0.05$) positive SCA effects for MO were observed for single-cross hybrids, TZEEI 67×TZEEI 63, and TZEEI 96×TZEEI 67, whereas significant ($p < 0.05$) negative SCA effect for TZEEI 96×TZEEI 63, and TZEEI 67×TZEEI 66 were also observed (Table 4.3).



Table 4.3: SCA effects of extra-early maturing single-cross hybrids for grain yield and other related traits across research environments

	GY	DS	DTAS	ASI	PHT	EHT	HUSK	RTL	STL	MO
Single-crosses	(t/ha)	(days)	(days)		(cm)	(cm)				(%)
TZEEI 63×TZEEI 61	-0.05	-0.88*	-0.75*	-0.03	6.28	2.68	0.03	-0.12	0.12	0.29
TZEEI 64×TZEEI 61	0.70**	-0.70	-0.52	-0.05	7.11	1.40	-0.07	0.00	-0.16*	-0.30
TZEEI 66×TZEEI 61	-0.06	0.34	0.27	0.02	4.71	0.73	0.13	-0.01	-0.01	0.09
TZEEI 67×TZEEI 61	-0.37	0.16	0.26	-0.02	-9.06*	1.80	0.06	-0.05	-0.05	-0.20
TZEEI 71×TZEEI 61	-0.22	0.27	0.23	0.01	8.43*	-2.20	0.01	-0.06	0.02	0.31
TZEEI 76×TZEEI 61	0.09	0.15	0.08	0.02	-2.54	1.62	-0.20**	0.01	0.03	-0.24
TZEEI 78×TZEEI 61	-0.50	-0.07	-0.06	0.00	-6.27	-2.88	-0.03	0.02	0.03	-0.30
TZEEI 94×TZEEI 61	0.16	-0.07	0.30	-0.04	-5.36	-2.88	0.01	0.03	0.02	0.10
TZEEI 96×TZEEI 61	0.27	0.55	0.19	0.09*	-3.29	-0.27	0.07	0.18**	-0.01	0.25
TZEEI 64×TZEEI 63	-0.48	-0.57	-0.53	-0.01	1.29	-1.30	0.04	-0.02	-0.08	0.25
TZEEI 66×TZEEI 63	-0.50	-0.20	-0.30	0.03	-7.78	-4.19*	0.04	0.08	0.08	-0.13

TZEEI 67×TZEEI 63 -0.42 0.07 -0.09 0.04 3.35 1.88 0.04 0.04 -0.02 0.75*

Table 4.3: continued

	GY	DS	DTAS	ASI	PHT	EHT	HUSK	RTL	STL	MO
Single-crosses	(t/ha)	(days)	(days)		(cm)	(cm)				(%)
TZEEI 71×TZEEI 63	0.16	0.62	0.44	0.05	-1.83	-1.67	-0.05	-0.07	-0.06	-0.07
TZEEI 76×TZEEI 63	0.59*	0.50	0.62	-0.05	-5.58	-2.52	-0.09	0.10	-0.04	0.09
TZEEI 78×TZEEI 63	-0.02	0.61	0.59	0.01	-4.42	-1.69	0.06	-0.06	0.05	-0.09
TZEEI 94×TZEEI 63	0.34	-0.38	-0.38	0.00	-0.40	0.87	0.01	-0.03	-0.07	-0.32
TZEEI 96×TZEEI 63	0.38	0.23	0.40	-0.04	9.11*	5.93*	-0.06	0.09	0.03	-0.77*
TZEEI 66×TZEEI 64	0.55*	-0.24	-0.39	0.04	-0.50	2.98	-0.03	0.00	0.05	0.22
TZEEI 67×TZEEI 64	0.22	0.14	0.26	-0.03	3.18	0.50	-0.21*	0.00	0.04	-0.05
TZEEI 71×TZEEI 64	-0.63*	-0.53	-0.44	-0.02	-19.33**	-2.17	0.02	0.04	0.03	-0.23
TZEEI 76×TZEEI 64	-0.02	-0.21	-0.14	-0.01	-6.97	-2.02	0.08	0.01	-0.01	0.02
TZEEI 78×TZEEI 64	0.21	0.68	0.38	0.07	11.19**	3.81*	0.05	-0.01	-0.07	0.51

TZEEI 94×TZEEI 64	-0.29	0.91*	0.75*	0.03	8.87*	0.37	0.08	0.05	0.11	-0.28
TZEEI 96×TZEEI 64	-0.25	0.52	0.63*	-0.03	-4.83	-3.57*	0.06	-0.06	0.09	-0.14
TZEEI 67×TZEEI 66	-0.42	0.18	-0.06	0.06	-8.56*	-5.50**	0.06	-0.07	0.04	-1.01**

Table 4.3: continued

	GY	DS	DTAS	ASI	PHT	EHT	HUSK	RTL	STLG	MO
Single-crosses	(t/ha)	(days)	(days)		(cm)	(cm)				(%)
TZEEI 71×TZEEI 66	-0.36	0.29	0.47	-0.05	-1.29	-0.06	-0.04	0.07	0.04	0.46
TZEEI 76×TZEEI 66	-0.16	0.61	0.76**	-0.04	5.51	3.54*	0.03	0.05	0.07	0.55
TZEEI 78×TZEEI 66	1.28**	-0.73	-0.60	-0.03	4.01	1.81	-0.16*	-0.07	-0.10	0.13
TZEEI 94×TZEEI 66	-0.56*	-0.27	-0.35	0.02	2.03	0.04	-0.11	-0.04	-0.10	-0.16
TZEEI 96×TZEEI 66	0.24	0.01	0.20	-0.05	1.87	0.65	0.07	-0.02	-0.06	-0.14
TZEEI 71×TZEEI 67	0.14	0.55	0.56	-0.03	3.39	-1.32	0.04	0.01	0.01	-0.32
TZEEI 76×TZEEI 67	0.39	-0.46	-0.59	0.04	6.75	2.27	0.08	-0.01	-0.01	-0.19
TZEEI 78×TZEEI 67	0.33	-0.57	-0.50	-0.01	3.80	1.77	-0.02	0.09	-0.01	-0.48

TZEEI 94×TZEEI 67	0.49	0.22	0.52	-0.08	0.37	1.22	-0.03	0.03	0.03	0.87
TZEEI 96×TZEEI 67	-0.37	-0.28	-0.37	0.02	-5.22	-2.62	-0.03	-0.05	-0.04	0.63*
TZEEI 76×TZEEI 71	-0.35	0.65	0.61	0.02	-5.65	-2.62	0.10	-0.05	0.05	0.03
TZEEI 78×TZEEI 71	0.22	-0.57	-0.42	-0.04	1.62	1.55	-0.05	0.00	-0.02	0.45
TZEEI 94×TZEEI 71	0.17	-0.34	-0.39	0.02	6.75	4.00*	0.09	0.09	-0.02	-0.48

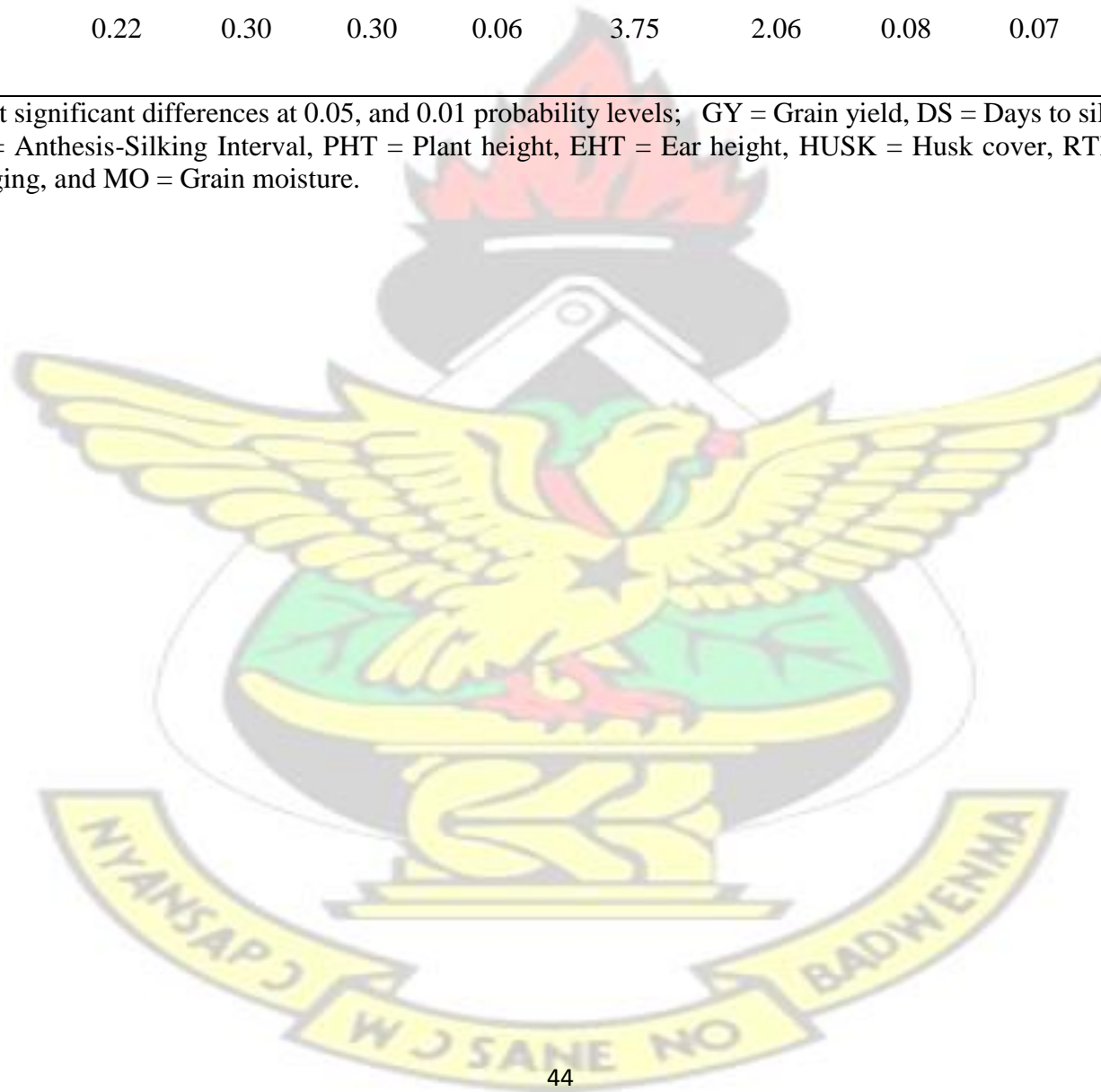
Table 4.3: continued

	GY	DS	DTAS	ASI	PHT	EHT	HUSK	RTL	STLG	MO
Single-crosses	(t/ha)	(days)	(days)		(cm)	(cm)				(%)
TZEEI 96×TZEEI 71	0.87**	-0.95*	-1.06**	0.03	7.93*	4.50**	-0.12	-0.07	-0.05	-0.16
TZEEI 78×TZEEI 76	-0.65*	0.30	0.31	0.00	3.21	1.04	0.10	-0.05	0.07	-0.10
TZEEI 94×TZEEI 76	0.95**	-0.68	-0.66*	0.00	-0.67	0.37	-0.01	-0.06	-0.04	-0.03
TZEEI 96×TZEEI 76	-0.86**	-0.85*	-0.99**	0.04	5.96	-1.69	-0.09	-0.04	-0.11	-0.13
TZEEI 94×TZEEI 78	-0.93**	-0.02	-0.24	0.05	-7.61	-3.24	-0.04	0.01	-0.01	-0.13
TZEEI 96×TZEEI 78	0.07	0.37	0.54	-0.04	-5.54	-2.19	-0.04	0.07	0.06	0.03
TZEEI 96×TZEEI 94	-0.34	0.39	0.45	-0.02	-5.97	-0.74	0.00	-0.10	0.08	0.43

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SE (Sij-Sik)	0.23	0.32	0.33	0.06	4.05	2.22	0.08	0.08	0.08	0.35
SE (Sij-Skl)	0.22	0.30	0.30	0.06	3.75	2.06	0.08	0.07	0.07	0.32

*, and **, represent significant differences at 0.05, and 0.01 probability levels; GY = Grain yield, DS = Days to silking, DTAS = Days to tasseling, ASI = Anthesis-Silking Interval, PHT = Plant height, EHT = Ear height, HUSK = Husk cover, RTLG = Root lodging, STLG = Stalk lodging, and MO = Grain moisture.



4.4 Genetic variances, Heritability, and Genetic Advance

Estimates of variance components of GCA and SCA showed that, variances of GCA (VAR_{gca}) were higher than variance of SCA (VAR_{sca}) for all measured traits except GY, DTAS, EHT, and MO (Table 4.4). Variance estimates of SCA×E (VAR_{scaenv}) were relatively higher than GCA×E (VAR_{gcaenv}) for all measured traits except STLG (Table 4.4). In all cases, estimates of environmental variance for all traits were higher than the total genetic variance ($VAR_{gca}+VAR_{sca}$) (Table 4.4). It was deduced from the estimated variance components in Table 4.4 that, $VAR_{gca}+VAR_{sca}$ for all measured traits contributed 33.4% to the total phenotypic variance (VAR_p) for GY, 34.7% for DS, 34.2% for DTAS, 70.3% for ASI, 37.7% for PHT, 45.1% for EHT, 54.8% for HUSK, 48.2% for RTLG, 37.9% for STLG, and 35.6% for MO. In addition, $VAR_{gcaenv}+VAR_{scaenv}$ considerably contributed 66.6% to the total VAR_p for GY, 65.3% for DS, 65.8% for DTAS, 29.7% for ASI, 62.3% for PHT, 54.8% for EHT, 45.2% for HUSK, 51.6% for RTLG, 62.3% for STLG, and 64.5% for MO (Table 4.4).

Estimates of heritability showed that narrow sense heritability (h^2) for all measured traits ranged from 24% (low) for PHT to 67% (high) for ASI (Table 4.4). Similarly, broad sense heritability estimates for all measured traits ranged from 35% (moderate) for PHT to 75% (high) for GY, ASI, HUSK, RTLG, and STLG (Table 4.4). Estimates of genetic advance (GA) for all measured traits ranged from 3.31 for EHT to 10.41 for GY (Table 4.4).

The estimated genetic ratios of GCA: SCA effects for all traits measured were observed as closer to unity and ranged from 0.71 for EHT, and RTLG to 0.89 for DS (Table 4.4).



Table 4.4: Estimates of Genetic Variances, Heritability, and Genetic advance for GY and other related traits.

	GY	DS	DTAS	ASI	PHT	EHT	HUSK	RTLG	STLG	MO
	(t/ha)	(days)	(days)		(cm)	(cm)				(%)
<i>VAR_{gca}</i>	1.78	2.16	1.49	2.83	2.09	1.16	2.37	1.19	1.20	1.08
<i>VAR_{sca}</i>	3.21	1.53	2.56	0.63	1.92	1.94	1.06	0.78	0.83	1.09
<i>VAR_{gcaenv}</i>	1.02	1.82	2.71	0.61	1.26	0.91	0.82	0.87	1.93	1.33
<i>VAR_{scaenv}</i>	9.39	5.13	5.07	0.85	5.38	2.86	2.01	1.24	1.41	2.60
<i>VAR_p</i>	15.41	10.64	11.83	4.92	10.65	6.88	6.26	4.09	5.36	6.09
<i>H₂</i>	0.75	0.74	0.74	0.75	0.35	0.50	0.75	0.75	0.75	0.74
<i>h₂</i>	0.39	0.55	0.40	0.67	0.24	0.27	0.61	0.56	0.56	0.49
GA	10.67	10.29	8.32	5.84	4.48	3.31	6.75	4.06	5.26	5.26
Baker's ratio	0.80	0.89	0.84	0.89	0.86	0.71	0.87	0.71	0.85	0.75

VAR_{gca} = Variance of GCA, *VAR_{sca}* = Variance of SCA, *VAR_{gcaenv}* = Variance of GCA and environment interaction, *VAR_{scaenv}* = Variance of SCA and environment interaction, *H²* = Broad sense heritability, *h²* = Narrow sense heritability, GA = Genetic advance. GY = Grain yield, DS = Days to silking, DTAS = Days to tasseling, ASI = Anthesis-Silking-Interval, PHT = Plant height, EHT = Ear height, HUSK = Husk cover, RTLG = Root lodging, STLG = Stalk lodging, and MO = Grain moisture.

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4.5 Estimate of heterosis

Estimates of heterosis for GY, DS, PHT, and EHT is presented in Table 4.5. Significant ($p<0.01$) positive mid-parent heterosis (MPH) estimates for GY were observed for most single-cross hybrids (Table 4.5). In addition, significant ($p<0.05$) positive MPH estimates for GY were observed for singlecross hybrids, TZEEI 96×TZEEI 67 and TZEEI 96×TZEEI 76 (Table 4.5). MPH values for GY for all single-cross hybrids were observed to range from 238% (TZEEI 96×TZEEI 76) to 539% (TZEEI 94×TZEEI 76) (Table 4.5). Estimates of MPH for GY for all the single-cross hybrids were observed as greater than the average of parents used for generating the single-cross hybrids (Table 4.5). The top five MPH estimates for GY were observed for single-cross hybrids, TZEEI 94×TZEEI 76 (539%), TZEEI 66×TZEEI 64 (514%), TZEEI 78×TZEEI 66 (497%), TZEEI 76×TZEEI 63 (494%), and TZEEI 64×TZEEI 61 (488%) (Table 4.5).

Significant ($p<0.01$) positive better-parent heterosis (BPH) for GY were observed for most singlecross hybrid (Table 4.5). Significant ($p<0.05$) positive BPH estimates were also observed for singlecross hybrids TZEEI 67×TZEEI 63, TZEEI 78×TZEEI 63, TZEEI 96×TZEEI 63, TZEEI 71×TZEEI 64, TZEEI 96×TZEEI 64, TZEEI 96×TZEEI 67, TZEEI 76×TZEEI 71, TZEEI 78×TZEEI 76, TZEEI 94×TZEEI 78, and TZEEI 96×TZEEI 94 (Table 4.5). In addition, BPH estimates for GY were observed to range from 165% (TZEEI 96×TZEEI 76) to 496 % (TZEEI 66×TZEEI 64) (Table 4.5). In general, estimates of BPH for GY for all single-cross hybrids were greater than the mean of the parents (Table

4.5). The best five single-cross hybrids with high BPH values were observed for singlecross hybrids TZEEI 66×TZEEI 64 (496%), TZEEI 94×TZEEI 76 (474%), TZEEI 76×TZEEI 63 (463%), TZEEI 64×TZEEI 61 (462%), and TZEEI 76×TZEEI 66 (452%) (Table 4.5).

Significant ($p<0.01$) negative estimates of MPH and BPH for DS were observed for all single-cross hybrids (Table 4.5). Significant ($p<0.01$) positive MPH and BPH values for PHT and EHT were observed for all single-cross hybrids (Table 4.5). The highest significant ($p<0.01$) positive MPH value for PHT was observed for single-cross hybrid TZEEI 78×TZEEI 64 (51%) (Table 4.5). Similarly, the highest significant ($p<0.01$) positive BPH value was observed for TZEEI 78×TZEEI 64 (51%) (Table 4.5). The highest significant ($p<0.01$) positive MPH observed for EHT was 63% for TZEEI 78×TZEEI 64, and TZEEI 96×TZEEI 63 (Table 4.5). In addition, the highest significant ($p<0.01$) positive BPH value observed for EHT was 61% for single-cross hybrids TZEEI 96×TZEEI 63, TZEEI 78×TZEEI 64, and TZEEI 78×TZEEI 64 (Table 4.5).

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Table 4.5: Mean performances and estimates of heterosis for GY and other related traits across research environments

Entries	GY			DS			PHT			EHT		
	(t/ha)			(days)			(cm)			(cm)		
	Mean	MPH	BPH	Mean	MPH	BPH	Mean	MPH	BPH	Mean	MPH	BPH
TZEEI 61	1.13			54.89			115.28			54.14		
TZEEI 63	0.95			55.11			124.04			53.63		
TZEEI 64	1.02			54.89			118.82			55.64		
TZEEI 66	0.96			54.56			131.89			55.27		
TZEEI 67	1.11			55.00			129.79			54.76		
TZEEI 71	1.00			55.11			123.72			55.13		
TZEEI 76	0.85			55.89			123.29			56.28		
TZEEI 78	1.41			55.33			118.92			56.89		
TZEEI 94	1.08			55.78			123.62			57.64		
TZEEI 96	1.49			55.22			119.13			56.39		
TZEEI 63×TZEEI 61	5.25	4.05**	3.65**	50.00	-0.09**	-0.09**	155.33	0.30**	0.25**	84.89	0.58**	0.57**
TZEEI 64×TZEEI 61	6.35	4.88**	4.62**	50.33	-0.08**	-0.08**	162.78	0.39**	0.37**	86.33	0.57**	0.55**

Table 4.5 continued

	GY			DS			PHT			EHT		
	(t/ha)			(days)			(cm)			(cm)		
TZEEI 66×TZEEI 61 Entries	5.94 Mean	4.66** MPH	4.26** BPH	50.22 Mean	-0.08** MPH	-0.09** BPH	158.33 Mean	0.28** MPH	0.20** BPH	85.11 Mean	0.56** MPH	0.54** BPH
TZEEI 67×TZEEI 61	5.29	3.72**	3.68**	50.33	-0.08**	-0.08**	149.78	0.22**	0.15**	86.44	0.59**	0.58**
TZEEI 71×TZEEI 61	5.31	3.96**	3.70**	50.56	-0.08**	-0.08**	167.89	0.40**	0.36**	82.56	0.51**	0.50**
TZEEI 76×TZEEI 61	5.67	4.73**	4.02**	50.22	-0.09**	-0.10**	156.89	0.32**	0.27**	86.89	0.57**	0.54**
TZEEI 78×TZEEI 61	5.45	3.29**	2.87**	50.11	-0.09**	-0.09**	156.00	0.33**	0.31**	83.00	0.50**	0.46**
TZEEI 94×TZEEI 61	5.96	4.37**	4.27**	50.33	-0.09**	-0.10**	151.33	0.27**	0.22**	80.67	0.44**	0.40**
TZEEI 96×TZEEI 61	5.62	3.29**	2.77**	50.89	-0.08**	-0.08**	153.78	0.31**	0.29**	84.00	0.52**	0.49**
TZEEI 64×TZEEI 63	4.35	3.39**	3.26*	51.56	-0.06**	-0.06**	156.44	0.29**	0.26**	82.89	0.52**	0.49**
TZEEI 66×TZEEI 63	4.68	3.88**	3.88**	50.78	-0.07**	-0.08**	145.33	0.14**	0.10**	79.44	0.46**	0.44**
TZEEI 67×TZEEI 63	4.42	3.29**	2.98*	51.33	-0.07**	-0.07**	161.67	0.27**	0.25**	85.78	0.58**	0.57**
TZEEI 71×TZEEI 63	4.86	3.96**	3.86**	52.00	-0.06**	-0.06**	157.11	0.27**	0.27**	82.33	0.51**	0.49**
TZEEI 76×TZEEI 63	5.35	4.94**	4.63**	51.67	-0.07**	-0.08**	153.33	0.24**	0.24**	82.00	0.49**	0.46**
TZEEI 78×TZEEI 63 Entries	5.10 Mean	3.32** MPH	2.62* BPH	51.89 Mean	-0.06** MPH	-0.06** BPH	157.33 Mean	0.30** MPH	0.27** BPH	83.44 Mean	0.51** MPH	0.47** BPH

Table 4.5 continued

	GY			DS			PHT			EHT		
	(t/ha)			(days)			(cm)			(cm)		
TZEEI 94×TZEEI 63	5.32	4.22**	3.93**	50.89	-0.08**	-0.09**	155.78	0.26**	0.26**	83.67	0.50**	0.45**
TZEEI 96×TZEEI 63	4.90	3.02**	2.29*	51.67	-0.06**	-0.06**	165.67	0.36**	0.34**	89.44	0.63**	0.59**
TZEEI 66×TZEEI 64	6.08	5.14**	4.96*	50.89	-0.07**	-0.07**	159.22	0.27**	0.21**	89.33	0.61**	0.61**
TZEEI 67×TZEEI 64	5.41	4.06**	3.87**	51.56	-0.06**	-0.06**	168.11	0.35**	0.30**	87.11	0.58**	0.57**
TZEEI 71×TZEEI 64	4.43	3.39**	3.34*	51.00	-0.07**	-0.07**	146.22	0.21**	0.19**	84.56	0.53**	0.52**
TZEEI 76×TZEEI 64	5.09	4.41**	3.99**	51.11	-0.08**	-0.09**	158.56	0.31**	0.29**	85.22	0.52**	0.51**
TZEEI 78×TZEEI 64	5.68	3.66**	3.03**	52.11	-0.05**	-0.06**	179.56	0.51**	0.51**	91.67	0.63**	0.61**
TZEEI 94×TZEEI 64	5.04	3.8**	3.67**	52.33	-0.05**	-0.06**	171.67	0.42**	0.39**	85.89	0.52**	0.49**
TZEEI 96×TZEEI 64	4.63	2.67**	2.11*	52.11	-0.05**	-0.06**	158.33	0.33**	0.33**	82.67	0.48**	0.47**
TZEEI 67×TZEEI 66	5.12	3.92**	3.61**	50.44	-0.08**	-0.08**	154.33	0.18**	0.17**	80.56	0.46**	0.46**
TZEEI 71×TZEEI 66	5.05	4.15**	4.05**	50.67	-0.08**	-0.08**	162.22	0.27**	0.23**	86.11	0.56**	0.56**
TZEEI 76×TZEEI 66	5.30	4.82**	4.52**	50.78	-0.08**	-0.09**	169.00	0.32**	0.28**	90.22	0.62**	0.60**
Entries	Mean MPH		BPH	Mean	MPH	BPH	Mean	MPH	BPH	Mean MPH		BPH

Table 4.5 continued

	GY			DS			PHT			EHT		
	(t/ha)			(days)			(cm)			(cm)		
TZEEI 78×TZEEI 66	7.10	4.97**	4.04**	49.56	-0.10**	-0.10**	170.33	0.36**	0.29**	89.11	0.59**	0.57**
TZEEI 94×TZEEI 66	5.12	4.02**	3.74**	50.00	-0.09**	-0.10**	162.78	0.27**	0.23**	85.00	0.51**	0.47**
TZEEI 96×TZEEI 66	5.46	3.44**	2.66**	50.44	-0.08**	-0.09**	163.00	0.30**	0.24**	86.33	0.55**	0.53**
TZEEI 71×TZEEI 67	5.20	3.91**	3.68**	51.22	-0.07**	-0.07**	172.11	0.36**	0.33**	85.11	0.55**	0.54**
TZEEI 76×TZEEI 67	5.50	4.61**	3.95**	50.00	-0.10**	-0.11**	175.44	0.39**	0.35**	89.22	0.61**	0.59**
TZEEI 78×TZEEI 67	5.80	3.6**	3.11**	50.00	-0.09**	-0.09**	175.33	0.41**	0.35**	89.33	0.60**	0.57**
TZEEI 94×TZEEI 67	5.82	4.29**	4.24**	50.78	-0.08**	-0.09**	168.33	0.33**	0.30**	86.44	0.54**	0.50**
TZEEI 96×TZEEI 67	4.52	2.48*	2.03*	50.44	-0.08**	-0.09**	161.11	0.29**	0.24**	83.33	0.50**	0.48**
TZEEI 76×TZEEI 71	4.63	3.98**	3.63*	51.22	-0.08**	-0.08**	163.67	0.33**	0.32**	84.44	0.52**	0.50**
TZEEI 78×TZEEI 71	5.57	3.6**	2.95**	50.11	-0.09**	-0.09**	173.78	0.43**	0.40**	89.22	0.59**	0.57**
TZEEI 94×TZEEI 71	5.37	4.16**	3.97**	50.33	-0.09**	-0.10**	173.33	0.40**	0.40**	89.33	0.58**	0.55**
TZEEI 96×TZEEI 71	5.62	3.5**	2.77**	49.89	-0.10**	-0.10**	174.89	0.44**	0.41**	90.56	0.62**	0.61**

Table 4.5 continued

Entries	GY			DS			PHT			EHT		
	(t/ha)			(days)			(cm)			(cm)		
	MPH		BPH	MPH		BPH	MPH	BPH		Mean	MPH	BPH
	Mean			Mean								
TZEEI 78×TZEEI 76	4.75	3.2**	2.37*	50.78	-0.09**	-0.09**	175.33	0.45**	0.42**	89.22	0.58**	0.57**
TZEEI 94×TZEEI 76	6.20	5.39**	4.74**	49.78	-0.11**	-0.11**	165.89	0.34**	0.34**	86.22	0.51**	0.50**
TZEEI 96×TZEEI 76	3.95	2.38*	1.65	49.78	-0.10**	-0.11**	172.89	0.43**	0.40**	84.89	0.51**	0.51**
TZEEI 94×TZEEI 78	4.69	2.75**	2.33*	50.56	-0.09**	-0.09**	161.78	0.33**	0.31**	83.22	0.45**	0.44**
TZEEI 96×TZEEI 78	5.23	2.61**	2.51**	51.11	-0.08**	-0.08**	164.22	0.38**	0.38**	85.00	0.50**	0.49**
TZEEI 96×TZEEI 94	4.68	2.63**	2.14*	51.11	-0.07**	-0.08**	158.22	0.30**	0.28**	84.11	0.48**	0.46**

*, and **, represent significant differences at 0.05, and 0.01 probability levels; GY = Grain yield, DS = Days to silking, PHT = Plant height, EHT = Ear height, MPH = mid-parent heterosis; BPH = better-parent heterosis.

4.6 Discriminating and representative powers of the research environments

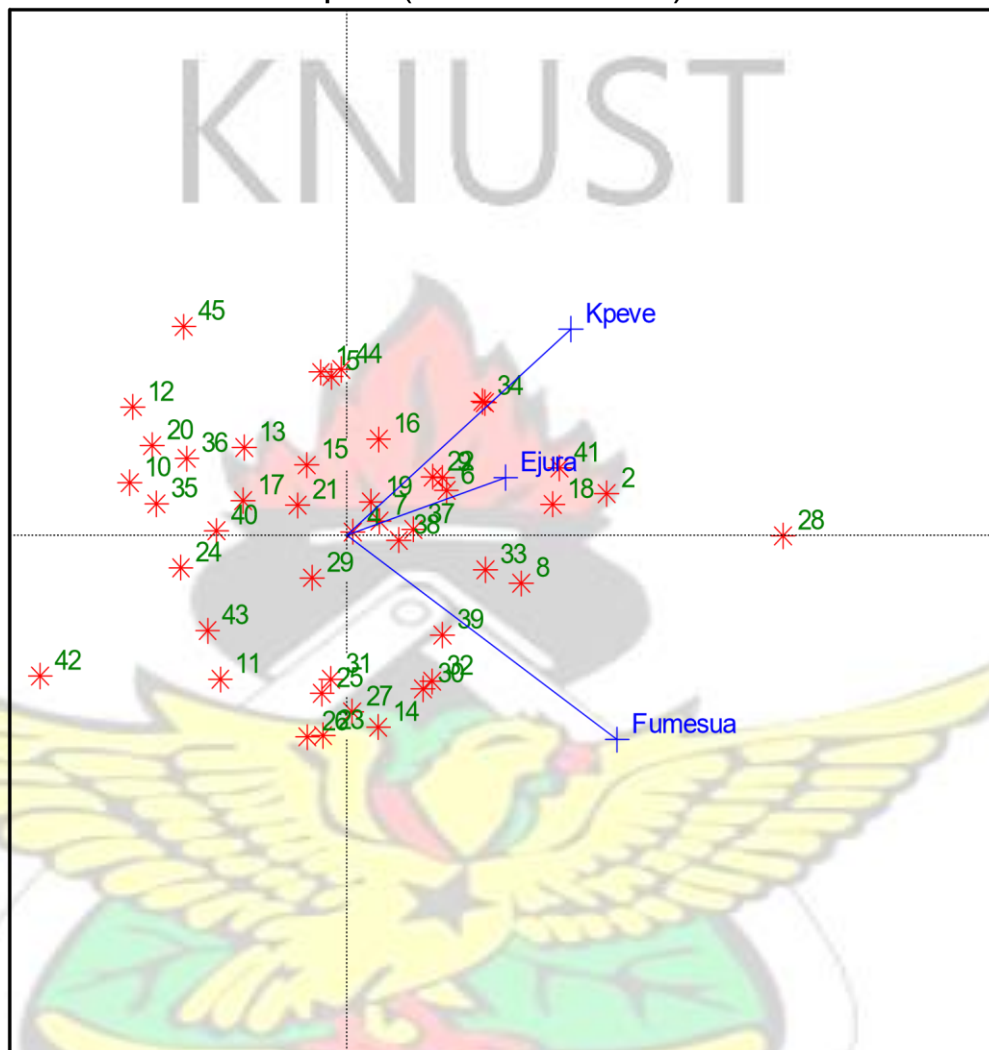
GGE biplot showing discriminating and representative powers of the three research environments is presented in Figure 4.1. Principal Component 1 (PC1) explained 68.23% while Principal Component 2 (PC2) also explained 19.02% and the two components together accounted for 87.26% of the total variation for the SCA effects of the single-cross hybrids across research environments. The length of the vector of the three environments from AEA (average environment axis) showed that, Fumesua had the longest vector, followed by Kpeve, and then Ejura, the least environment vector (Figure 4.1). It was observed that, Ejura had the smallest angle to the AEA, followed by Kpeve, and then Fumesua had the largest angle to the AEA (Figure 4.1). The length of projections of the marker of an environment from AEA shows that Fumesua had the longest projection, followed by Kpeve, and then Ejura had the shortest projection from the AEA (Figure 4.1).

4.7 Mean performance and stability analysis of the single-cross hybrids across research environments

From the GGE biplot of the mean performance and stability analysis of the single-cross hybrids, the genotypes were ranked along the average-environment coordinate (AEC abscissa); with an arrow pointing to a greater value based on their mean performance across all research environments. The long perpendicular blue line to the AEC separates the single-cross hybrids below-average performance from the above-average performances (Figure 4.2). The average yield performance of each single-cross hybrid was determined by projections of their markers onto the AEC. The stability of the single-cross hybrids across environments were determined following the assumptions of Yan *et al.* (2000; 2010), where projected lines perpendicular to

AEC measures the genotypes' stability in either direction.

Scatter plot (Total - 87.26%)



PC1 - 68.23%

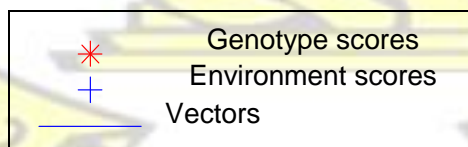
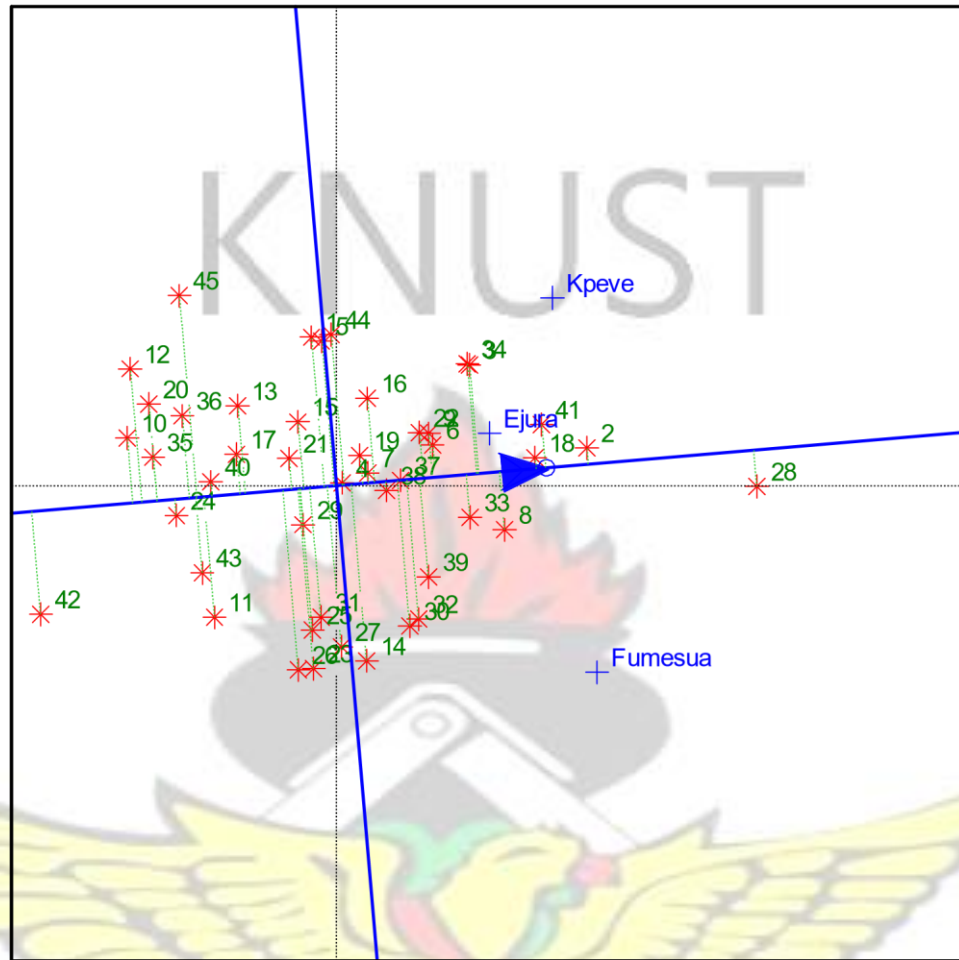


Figure 4.1: Vector view of GGE biplot showing discriminating and representative powers across three research environments.

Yan *et al.* (2000; 2010) further emphasized that, genotypes with shortest perpendicular line and close to AEC are stable genotypes. Thus, the single-cross hybrids, 18 (TZEEI 66×TZEEI 64), 2 (TZEEI 64×TZEEI 61), 28 (TZEEI 78×TZEEI 66), 8 (TZEEI 94×TZEEI 61), 33 (TZEEI 78×TZEEI 67) and 41 (TZEEI 94×TZEEI 76) were most stable and had above-average yield performance across the three environments (Figure 4.2). In contrast, the greater the absolute length of projection of a genotype from AEC, the less stable that genotype. Thus, single-cross hybrids, 42 (TZEEI 96×TZEEI 76), 10 (TZEEI 64×TZEEI 63) and 20 (TZEEI 71×TZEEI 64) were least stable with below-average yield performance across the three environments (Figure 4.2). The high yielding and most stable single-cross hybrids 28 (TZEEI 78×TZEEI 66) and 2 (TZEEI 64×TZEEI 61) across the three environments out-yielded one of the best extra-early varieties ‘Abontem’ by 28% and 20%, respectively.

Ranking biplot (Total - 87.26%)



PC1 - 68.23%

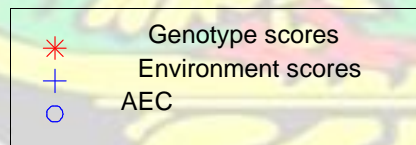


Figure 4.2: GGE biplot analysis view of the mean performance and stability of extra-early maturing maize single-cross hybrids across three research environments.

4.8 The ‘which-won-where’ pattern analysis of the single-cross hybrids

The polygon view of the GGE biplot showing ‘which-won-where’ or ‘what-genotype-wins’ across research environments revealed best performing genotypes at each research environment and across environments by connecting all the genotypes that are farther apart (Figure 4.3). The

polygon has perpendicular lines dividing it into sectors which help visualize mega environments for winning genotypes for each sector of an environment located at the vertex of the polygon view. The single-cross hybrid genotype, 28 which is a cross between TZEEI 78 and TZEEI 66 is located at a vertex of the polygon to qualify it as winning genotype within and across the specific (Figure 4.3). Similarly, 34 (TZEEI 94×TZEEI 67), located at another vertex of the polygon was also a winning genotype across environments whereas 45 (TZEEI 96×TZEEI 94), 12 (TZEEI 67×TZEEI 63), 42 (TZEEI 96×TZEEI 76), 26 (TZEEI 71×TZEEI 66), and 14 (TZEEI 76×TZEEI 63) located at other vertices of the polygon fell outside the range of the three research environments though seen as winning genotypes (Figure 4.3).

The hybrid, 42 (TZEEI 96×TZEEI 76) was observed as least winning single-cross hybrid genotype across research environments (Figure 4.3). All the single-cross hybrid genotypes located within the polygon, especially those located close to the origin of the biplot were not only less responsive than those located at other vertices but also did not provide any winning pattern for the three environments (Figure 4.3).

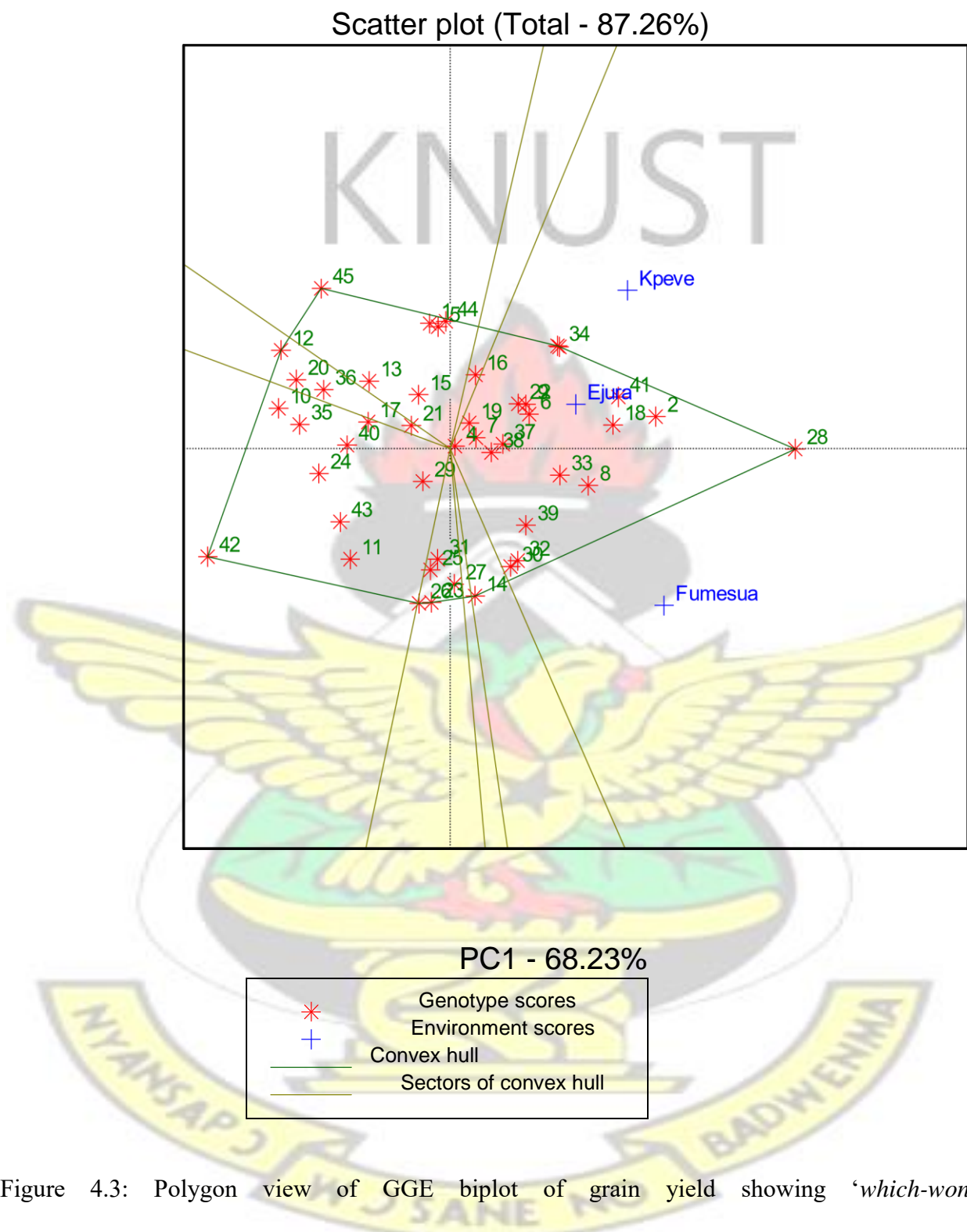


Figure 4.3: Polygon view of GGE biplot of grain yield showing ‘which-won-where’/‘whatgenotype-wins’ of extra-early maturing maize single-cross hybrids across three research environments.

CHAPTER FIVE

5.0 DISCUSSIONS 5.1 Analysis of variance, component GCA and SCA effects for GY and other agronomic traits.

The observed significant mean squares of E and G for GY and other traits indicate that the three environments were distinct and that there is genetic variations among the single-cross hybrids, suggesting that selection of such traits for further improvement could be feasible. This results corroborate with the findings of Badu-Apraku *et al.* (2011) who reported that significant mean squares of E and G observed for all traits in a related study involving early-maturing white maize inbred lines under contrasting test environments suggested that the test environments were unique and further indicated genetic variations among the inbred lines to allow effective selection of all traits for genetic improvement. The non-significant mean square estimate observed for ASI indicate that the expression of the trait was consistent across the three environments to allow good selection of trait for further improvement.

The significant G×E interaction for GY and other traits except ASI suggest differences in expression of traits of the set of hybrid genotypes across the three environments. That is, the hybrid genotypes were inconsistent in the expression of traits across the three research environments. Aside the differences in genetic composition of the single-cross hybrids evaluated, the expression of all traits except ASI was influenced by the environmental differences. This further suggest the need to develop specific varieties for specific environments to take into account the high influence of the environment on the expression of traits of the set of hybrid genotypes evaluated. This observations corroborate with the findings of Badu-Apraku *et al.* (2008) that significant G×E interaction for GY and other related traits suggest impact of environmental variances. However,

the lack of significant mean square estimates for $G \times E$ interaction for ASI suggest that the expression of the trait was consistent across the research environments. Thus, good selection progress of the trait for further genetic improvement could be feasible especially when breeding for reduced number of days to ASI in drought tolerant varieties. The significant mean squares of G, and $G \times E$ interaction for GY suggest the need to use GGE biplots to decompose the G, and GEI for GY and to assess mean performance and stability of GY for the single-cross hybrids across the three environments.

The significant mean square estimates of GCA observed for all measured traits indicated the important role of additive genes in the inheritance of such traits. On the other hand, the significant mean squares of SCA for GY and some traits indicated that the non-additive gene effect also contributed to the inheritance of such traits. Thus, selection of such traits for further improvement could be achieved through hybridization, recurrent selection, and backcrossing methods. This result corroborates the findings of Badu-Apraku *et al.* (2015) who observed significant mean square of GCA and SCA for GY and other relevant traits to suggest presence of additive and non-additive gene actions and further argued that improvement of those traits could be achieved through hybridization, backcrossing and recurrent selection methods to develop synthetics, populations and hybrid varieties.

In all cases, GCA effect was more important than SCA effect for GY and other measured traits across environments, suggesting that the additive gene action was more important than the nonadditive gene action in the inheritance of GY and other measured traits, hence, GCA played the predominant role to account for expression of such traits in hybrid evaluated. The preponderance

GCA effect over SCA effect for GY and other agronomic traits suggested that early generation testing could be feasible and that selection of potential hybrids could base solely on predictions from GCA effects. In a related study involving combining of extra-early yellow-endosperm inbreds, Badu-Apraku *et al.* (2013) observed preponderance of GCA effect over SCA effect and further suggested that the additive gene action was more important than the non-additive gene action in modulating the expression of GY and other agronomic traits. Again, the present results corroborate with the findings of Bhatnagar *et al.* (2004) in a related study who reported that the additive gene action was more important than the non-additive gene action in the inheritance of root lodging (RTL_G) and stalk lodging (STL_G). Moreover, Badu-Apraku and Oyekunle (2012) also reported that the additive gene effect was more important than the non-additive gene effect in controlling the inheritance of GY and other related traits under different environmental conditions.

The observed significant mean square of GCA×E interaction for most traits indicated variations in the combining abilities of the inbred lines and further emphasize the need for testing the inbred lines under different environments with the view to assess performance and yield stability.

The present finding is consistent with earlier observation of Menkir *et al.* (2003) and Badu-Apraku *et al.* (2007a) in a related study.

On the other hand, the significant mean squares of SCA×E interaction for GY and most traits implies that expression of such traits among the single-cross hybrids were not consistent in the three environments. This further suggest the need to use different inbred lines to develop sitespecific hybrid varieties for the three environments and justifies our strategy of evaluating the single-cross hybrids across the three environments to assess hybrids with stable performances.

This results corroborate with the findings of Akinwale *et al.* (2014) who observed significant

SCA×E interaction for GY and other related traits and attributed this effect to inconsistent expression of traits across environments, suggesting the need to identify and select different inbred lines as parent seed for developing hybrids for each environment. Again, this findings agrees with Badu-Apraku *et al.* (2013) who justified the need to evaluate the single-cross hybrids across different growing environments with the view to identifying high yielding and consistent genotypes across environments. The lack of significant mean square estimates of SCA×E interaction for some traits suggested that, expressions of such traits among the single-cross hybrids were consistent across environments. That is, good selection progress for improvement of the trait could be feasible.

5.2 Effects of GCA and SCA on grain yield and other related traits

The observed significant positive and negative GCA effects for GY for the inbred lines TZEEI 61, TZEEI 66, and TZEEI 78 indicates possibility of transmitting favourable alleles from the parental lines to their hybrid combinations for improved GY.

The significant positive effects of GCA for DS observed for inbred lines TZEEI 63 and TZEEI 64 implies that these inbred lines may transmit favourable alleles towards breeding to improve DS. However, the significant negative GCA effect for DS for inbred lines TZEEI 61 and TZEEI 66 suggests that these lines could be useful for breeding to improve silking date. The significant negative GCA effect for DTAS, ASI and HUSK as well as those with significant positive GCA effect for PHT and EHT for the inbred lines implies possibility of transmitting favourable alleles for improving these traits across research environments. This result corroborates the findings of Badu-Apraku *et al.* (2013) who suggested that significant negative effects of GCA for DS, DTAS, and ASI as well as inbred lines with significant positive GCA effect for PHT and EHT would make

positive contributions towards breeding for improved DS, DTAS, ASI, PHT and EHT for the research environments. Moreover, significant negative GCA effect for STLG observed for inbred line TZEEI 66 suggested possibility of transmitting favourable alleles capable of developing resistance to stalk lodging. Also, significant negative effect of GCA for MO observed for inbred line TZEEI 61 also suggest possibility of transmitting favourable alleles towards breeding for reduced grain moisture.

The significant positive effect of SCA for GY for single-cross hybrids TZEEI 78×TZEEI 66, TZEEI 64×TZEEI 61, TZEEI 96×TZEEI 71, TZEEI 76×TZEEI 63, TZEEI 66×TZEEI 64, TZEEI 94×TZEEI 76, and TZEEI 96×TZEEI 71 across research environments could contribute favourable alleles from parent inbred lines to these single-cross hybrid offsprings. Evidently, these single-cross hybrids were observed as high yielding with significant SCA effects across research environments.

Even though GCA effects for GY of some inbred lines were low and negative but resulted in increased SCA effect, it is feasible to identify such inbred lines to develop hybrids with high yielding abilities, test and select based on increased SCA effects, even if GCA is more important in identifying potential inbred lines (Hallauer and Miranda, 1988). The hybrid TZEEI 78×TZEEI 66 showing a good SCA effect for GY was identified as single-cross tester based on assumptions earlier described by Pswarayi and Vivek (2008). They argue that a single-cross tester should demonstrate good effect of GCA of parent inbreds, as well as possess good yielding abilities of promising single-cross hybrid tester. This implies that, the tester could be used as seed parent in a double-cross and three-way hybrid seed production programme. The hybrid TZEEI 78×TZEEI 66 expressed the highest mean yield performance of 7.10 t/ha across environments with its parent

inbred lines, TZEEI 78 and TZEEI 66, characterized with high significant positive GCA effect. Thus, the hybrid (TZEEI 78×TZEEI 66) was the best single-cross tester for the two parent inbred lines.

5.3 Genetic variances, heritability and genetic advance

The variance estimates of GCA and SCA effects and heritability for GY and other traits were observed to vary due to the different genetic composition of the set of inbred lines, environment effect, as well as Genotype×Environment interactions. The high estimates of environmental variance over the total genetic variances for GY and other traits indicated that the environment played a major role in the inheritance of such traits. The variations across the three environments were characterized by intermittent and poor distribution of rainfall as well as increase in atmospheric temperatures relative to crop growth and development. Perhaps, the observed variations in the environment during the evaluation stage of this research could have resulted in the high environmental variance over the total genotypic (additive and dominance) variances for GY and other related traits.

The observed genetic ratios of GCA: SCA suggested a greater predictability of the performance all traits of the single-cross hybrids across environments based solely on GCA effects as a result of the close relationships of the estimated ratios to unity (Baker, 1978). The closer relationships of estimated ratios to unity for GY and other traits suggested that GCA effects were more important than SCA indicating preponderance of additive gene effects, hence, possibility for genetic improvement of these traits. Notwithstanding, DS, ASI, PHT, HUSK, RTLG, and STLG had variances of GCA greater than SCA. The closer to unity of their genetic ratios suggested that the traits were highly heritable and under the control of additive gene action.

The high broad sense heritability (H^2) estimates for GY and other agronomic traits suggest possibility of selection of these traits for genetic improvement. The present results corroborates the findings of earlier authors (Nelson and Somers, 1992; Rafique *et al.*, 2004; Kashiani *et al.*, 2008; Wannows *et al.*, 2010). The high broad sense heritability and moderately high genetic advance estimates for GY and DS suggest that expression of the phenotypic expression of these traits were controlled mainly by the additive gene action. These results provide evidence of the greater magnitude of the phenotypic variance attributable to the genotypic variance, thus, selection based on phenotypic expression of these traits could be feasible. This results agree with the findings of earlier authors (Akbar *et al.*, 2008; Kashiani *et al.*, 2010) who reported greater proportion of broad sense heritability and genetic advance in the inheritance of GY and DS traits. The authors further suggested that expression of these traits were predominantly influenced by action of additive gene. Other authors (Sumathi *et al.*, 2005) also suggested possible manipulation of these traits and sufficiently valuable genetic improvement could be possible through selection at early generations for superior hybrids. These traits were though observed as highly heritable, careful attention should also be taken in breeding for improved GY and DS since these traits are complex polygenic traits considerably influenced by environment factors. Thus, selection for improved yield and silking date could be achieved through indirect selection of other related traits.

The high broad sense heritability and low genetic advance estimates observed for DTAS, ASI, HUSK, RTLG, STLG, and MO could be attributed to the effect of non-additive gene action in the inheritance of these traits. This results partly agrees with the findings of Sumathi *et al.* (2005) who reported high broad sense heritability and low genetic advance estimates for DTAS and ASI. Though, these traits were observed to be highly heritable, selection for improvement through early generation may not produce the desired results. It is thus, suggested that improvement in

these traits could be achieved through hybridization and heterosis breeding. Low broad sense heritability and low genetic advance observed for PHT indicated the effect of nonadditive gene action in the inheritance of the trait.

However, moderately high narrow sense heritability observed for GY and some agronomic traits suggested possibility of selection of such traits. The moderately high narrow sense heritability observed for all traits except low estimated values for PHT and EHT suggested the effect of the additive gene action in the inheritance of such traits. The results from this study provided evidence for some chances of selection of the traits for further improvement. However, the observed moderately high narrow sense heritability and genetic advance for GY was particularly not surprising since GY is a complex polygenic trait considerably influenced by certain environmental factors. Thus, care must be taken when breeding for this complex trait due to the influence of environmental factors. The present results corroborate earlier findings of Bello *et al.* (2012) that GY is a product of many complex traits and that, direct selection of the trait may not be desirable since the trait is influenced to a greater extent by environmental factors. They argued that indirect selection of other yield related traits for further improvement could be feasible. Other authors Blum (1988), Edmeades *et al.* (1989), and Ludlow and Muchow (1990) argue that the genetic variances for GY decrease rapidly than the environmental variance in environments with increasing stress, while other yield related traits whose genetic variance increases under stress or are reduced less than that of GY, have relatively high heritability. Therefore, selection of other yield related traits with high heritability estimates such as DS and

ASI observed in this study could be beneficial towards breeding for improved yield of maize.

The moderately high narrow sense heritability coupled with low genetic advance estimates for DTAS, ASI, HUSK, RTLG, STLG, and MO indicated the effect of non-additive gene action in

expression of these traits. This present result agrees with the findings of Bello *et al.* (2012) that genetic improvement of traits associated with high heritability and low genetic advance is attributable to non-additive gene action and that further improvement of such traits could be achieved through hybridization and heterosis.

The low narrow sense heritability and low genetic advance estimates observed for PHT and EHT also indicated action of non-additive gene action in modulating these traits, and that selection on for further improvement may not be possible but indirect selection of other yield related traits may be feasible.

5.4 Estimates of heterosis

The significant positive MPH estimates for GY for all the single-cross hybrids indicates expression of bidirectional dominance deviation. Literature asserts that in addition to some degree of dominance, expression of heterosis depends on divergence between parents since differences in allelic frequencies at different loci are required for the expression of the trait. In view of this, a number of key genes in the parental zygote combines dominant genes in expression of the high vigour in the progenies (Moll *et al.*, 1962; Hallauer and Miranda, 1981; and Falconer and Mackay, 1996). On the other hand, it is reported that parental divergence does not necessarily produce high heterosis values since heterosis is not only dependent on differences in allelic frequencies but also epistasis interactions which was not considered in this study.

It has been emphasized that the desired levels for use of heterosis involving crosses of maize is at least 20% (Gutiérrez *et al.*, 2002). The estimated values of MPH for GY for all the single-crosses had values which were greater than 20%. Notwithstanding, the observed MPH and BPH values greater than 20% indicated the presence of genetic diversity among parental inbred lines and that

expression of vigour in the single-cross hybrids were dependent on degree of fit and genetic diversity. This finding corroborates earlier findings of Sprague and Tatum (1942) who emphasized that using maize inbred lines in combining ability studies does not only depend on the genetic composition of parents but also the diversity of their origin.

The observed significant negative estimates of MPH and BPH for DS for all the single-cross hybrids indicated the presence of bidirectional dominance deviations. Breeding for reduction in silking date is a desirable trait, hence, selection of the single-cross hybrids on the basis of significant negative heterosis for DS could be considered for breeding for reduced silking date. The high significant positive MPH and BPH values for PHT and EHT over the average of midparent and better-parents for the single-cross hybrids could be attributable to overdominance, accumulation of dominant alleles at different loci or epistasis. This results corroborates the findings of Hallauer and Miranda (1981).

5.5 Discriminative and representativeness of the research environments

The GGE biplot of the environment vector analysis revealed that, the longer projection of an environment from the AEA, the more discriminative that environment. This means that, Fumesua was the most discriminative, followed by Kpeve, and then Ejura, the least discriminative environment. In contrast, the shorter the projection of an environment, the more representative that environment is. This implies that the Ejura was the most representative, followed by Kpeve, and then Fumesua, the least representative environment. It was observed that, Kpeve represented an ideal research environment based on the assumption that, an ideal environment should effectively discriminate genotypes and represent the environments (Yan and Rajcan, 2002). This further implies that among the three research environments, Kpeve (Coastal savanna zone) represents an

ideal research environment for the single-cross hybrids, hence, will aid in selection of superior hybrid genotypes.

5.6 Yield performance and stability analysis of single-cross hybrids across environments

Stability of maize genotypes in an environment was determined by the ability of the genotypes to interact with factors within the environment. The shorter length of projections from AEA and close to the AEC observed for the single-cross hybrids, 2 (TZEEI 64×TZEEI 61) and 28 (TZEEI 78×TZEEI 66), indicated above-average performance and was most stable across the three environments. The single-cross hybrids 28 (TZEEI 78×TZEEI 66) and 2 (TZEEI 64×TZEEI 61) represented ideal and most stable across the three research environments since these genotypes had an above-average performance. This therefore, suggest that selection for broad adaptation could be feasible. This result further suggest that these ideal hybrids were consistent in performances with high mean performance as well as environmental stability across the three research environments. This results corroborate the findings of Badu-Apraku *et al.* (2011a) that, selection for broad adaptation in maize production, the ideal genotype should display high yielding performance and most stable.

5.7 The ‘which-won-where’ patterns for the single-cross hybrids

The polygon view of the “which-won-where” GGE biplot identified all winning genotypes within and across environments. The single-cross genotype 28 (TZEEI 78×TZEEI 66) located at a vertex of the polygon within an environment sector of the GGE biplot did not only express above-average yield performance but also won across all research environments. The present findings is in agreement with Yan *et al.* (2010) who indicated that presenting two or more environments in a sector gives an indication that a single genotype displays the highest yield performance in those

environments and if any environment is found within different sectors, it implies that different genotypes are winning at different environments. In contrast, the singlecross hybrids 42 (TZEEI 96×TZEEI 76), 12 (TZEEI 67×TZEEI 63), 45 (TZEEI 96×TZEEI 94), 26 (TZEEI 71×TZEEI 66), 23 (TZEEI 94×TZEEI 64), 14 (TZEEI 76×TZEEI 63) that fell out of the domain of the three research environments but located at other vertices implies that these genotypes expressed low yield performances across environments. Similarly, other genotypes located within the polygon, for example, 2 (TZEEI 64×TZEEI 61) as well as 39 (TZEEI 96×TZEEI 71) means that those genotypes were less responsive than the ideal hybrid genotype.



CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATIONS

6.1 CONCLUSION

The results of this study showed that additive and non-additive gene effects were important in the inheritance of GY and other traits of the extra-early maturing maize single-cross hybrids evaluated. The mean squares of GCA for GY and other related traits were greater than mean squares of SCA across the three environments. This suggested the preponderance of the additive gene action in the inheritance of GY and other traits among the single-cross hybrids. The observed significant mean squares of GCA×E interaction for GY and most traits indicated that the combining ability of inbred lines varied in different environments, suggesting the need to test the inbred lines in the different environments to identify lines with stable performances across environments. The observed significant mean squares of SCA×E interaction for GY and other traits across environments indicated inconsistencies in the expression of such traits across environments suggesting the need to develop hybrid varieties for the different environments.

The ratio of GCA: SCA effects for GY and other agronomic traits were observed to be close to unity, indicating predominant role of the additive gene action over non-additive gene action in controlling the inheritance of these traits across the three environments.

The high broad sense heritability for GY and other traits suggested that the phenotypic variance of such traits was greatly influenced by additive gene action indicating that selection of such traits for improvement could be feasible. The observed moderately high narrow sense heritability and high genetic advance estimate for GY indicated the important role of additive gene in the inheritance of the trait to buttress the feasibility of selection of the trait for improvement. Notwithstanding, it should be noted that GY is a complex polygenic trait considerably influenced by environmental variances, thus, care should be taken when breeding for this complex trait.

Mean performance and heterosis estimates for GY and other measured traits showed that hybrid 28 (TZEEI 78×TZEEI 66) was the best and most stable across the three environments with mean performance of 7.10 t/ha. The results showed that the most stable hybrid, 28 (TZEEI 78×TZEEI 66), had MPH and BHP estimated values of 497% and 404% respectively, indicating 28% increase in vigour over one of the best extra-early maturing OPV (Abontem) in Ghana.

Inbred lines TZEEI 61, TZEEI 66 and TZEEI 78 were identified as the best combiners based on good display of significant positive GCA for GY suggesting that these parental lines could be used as base populations for breeding for improved yield through hybridization. Based on a good display of significant positive SCA for GY for the single-cross hybrid, 28 (TZEEI 78×TZEEI 66), the hybrid could be used as seed parent for developing double-cross or three-way cross for high seed production. Also, the hybrid was observed as the winning genotype across the three environments. Kpeve (Coastal-Savannah zone) was identified as the most discriminative and representative environment for the single-cross hybrids, hence, represented the ideal environment for the set of hybrid genotypes evaluated.

6.2 RECOMMENDATION

It is recommended that the most stable and high yielding hybrids identified in this study should be tested in on-farm trials at different growing seasons to assess stable performance before release to farmers for commercialization to improve food security and income in Ghana.

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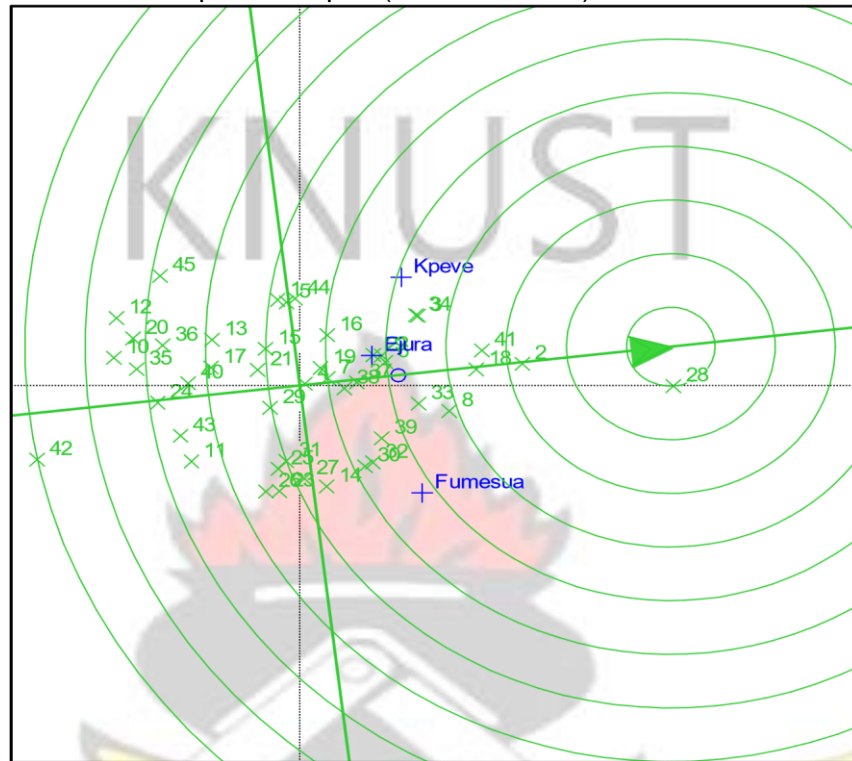


APPENDICES

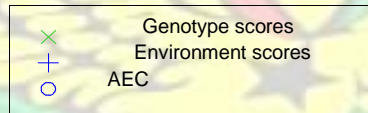
Single-cross hybrids and their representations

Symbols	Representation	Symbols	Representation
1	TZEEI 63×TZEEI 61	24	TZEEI 96×TZEEI 64
2	TZEEI 64×TZEEI 61	25	TZEEI 67×TZEEI 66
3	TZEEI 66×TZEEI 61	26	TZEEI 71×TZEEI 66
4	TZEEI 67×TZEEI 61	27	TZEEI 76×TZEEI 66
5	TZEEI 71×TZEEI 61	28	TZEEI 78×TZEEI 66
6	TZEEI 76×TZEEI 61	29	TZEEI 94×TZEEI 66
7	TZEEI 78×TZEEI 61	30	TZEEI 96×TZEEI 66
8	TZEEI 94×TZEEI 61	31	TZEEI 71×TZEEI 67
9	TZEEI 96×TZEEI 61	32	TZEEI 76×TZEEI 67
10	TZEEI 64×TZEEI 63	33	TZEEI 78×TZEEI 67
11	TZEEI 66×TZEEI 63	34	TZEEI 94×TZEEI 67
12	TZEEI 67×TZEEI 63	35	TZEEI 96×TZEEI 67
13	TZEEI 71×TZEEI 63	36	TZEEI 76×TZEEI 71
14	TZEEI 76×TZEEI 63	37	TZEEI 78×TZEEI 71
15	TZEEI 78×TZEEI 63	38	TZEEI 94×TZEEI 71
16	TZEEI 94×TZEEI 63	39	TZEEI 96×TZEEI 71
17	TZEEI 96×TZEEI 63	40	TZEEI 78×TZEEI 76
18	TZEEI 66×TZEEI 64	41	TZEEI 94×TZEEI 76
19	TZEEI 67×TZEEI 64	42	TZEEI 96×TZEEI 76
20	TZEEI 71×TZEEI 64	43	TZEEI 94×TZEEI 78
21	TZEEI 76×TZEEI 64	44	TZEEI 96×TZEEI 78
22	TZEEI 78×TZEEI 64	45	TZEEI 96×TZEEI 94
23	TZEEI 94×TZEEI 64		

Comparison biplot (Total - 87.26%)



PC1 - 68.23%



A vector view of GGE biplot showing the ranking of single-cross based on their discriminating ability and representatives across three research environments.

b

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