EVALUATION OF HYBRID MAIZE VARIETIES IN THREE AGRO-ECOLOGICAL ZONES IN GHANA

AMOS RUTHERFORD AZINU

(10240901)

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DECLARATION

This is to certify that this is the result of research undertaken by Amos Rutherford Azinu towards the award of the Master of Philosophy Degree in the Department of Crop Science, University of Ghana.

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Amos Rutherford Azinu (Student)

………………………………………………………….

Professor E.Y Danquah (Supervisor)

…………………………………………………………..

Professor Kwadwo Ofori (Supervisor)

ABSTRACT

Maize (*Zea mays* L.) is an important food crop in Ghana, but its productivity in farmers' fields throughout the country is generally low. The low grain yields can be attributed partly to the use of traditional low-yielding maize varieties. Farmers' adoption of hybrid varieties would reduce deficit of demand and supply of maize in the country. A study was undertaken to assess the relative yielding abilities and stability of 20 hybrids selected from the breeding programme of the West Africa Centre for Crop Improvement maize breeding program together with three locally released varieties. The trial was conducted in the coastal, savannah and transitional forest zones over major and minor seasons in 2012 and 2013. A randomized complete block design with three replications was used in each experiment. The relationship between yield and its components were also determined. Significant differences ($p<0.05$) were observed among the genotypes for days to anthesis, days to silking, ear height, plant height, field weight and grain yield. Highly significant ($P<0.01$) differences were observed among the three trial locations for all the traits studied. Grain yield showed highly significant differences ($p<0.01$) among the genotypes across the three locations. Significant differences among locations were observed for the 23 genotypes for grain yield, days to tasseling, days to silking, plant height, field weight, ear height. For genotypes, variations were highly significant for grain yield, field weight, plant height, days to anthesis and silking. However, there were no significant differences among the genotypes for ear height, ear harvest and plant stand. Apart from grain yield and field weight, differences due to the interaction (genotype x location) were not significant for all the other traits studied. The magnitude and nature of genotype by environment (GE) effect was significant using additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield. The main effects also were highly significant. Further analysis showed that the genotypes significantly contributed more than the environments in these effects. The significant genotype - environment interaction revealed by AMMI suggests that the relative performance of the genotypes changed for grain yield across all environments. The study also identified Wenchi as the location for the best grain yield performance and Tamale as an environment yielded low grain yield in both seasons. GGE biplot analysis revealed that varieties “wacci-m-1212”, “wacci-m-1204”, “wacci-m-1208”, “wacci-m-1209”, “wacci-m-1206”, “wacci-m-1220”, “wacci-m-1205” and “wacci-m-1207” were the high yielding and very stable hybrids. This supports the general opinion held by many stakeholders that use of hybrids holds the future of maize production in Ghana’s agriculture and that serious efforts must be made to encourage the adoption and use of superior hybrid maize varieties in Ghana as a means of increasing maize productivity and production in the country.

DEDICATION

To the memory of late Dr. Charles Thè.

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LIST OF ABBREVIATIONS

AMMI	Additive Main Effects and Multiplicative Interaction
ANOVA	Analysis of Variance
Cm	Centimeter
COV_G	Genetic Covariance
COV_P	Phenotypic Covariance
CRI	Crops Research Institute
d.f.	Degrees of Freedom
DA	Days to anthesis
DS	Days to silking
EH	Ear height
EMS	Expected Means Squares
FAO	Food and Agriculture Organization of the United Nations
GEI	Genotype by Environment Interaction
GY	Grain Yield
Ha	Hectare
kg/ha	Kilogram per Hectare
L	Location
MiDA	Millennium Development Authority
MoFA	Ministry of Food and Agriculture
OPV’s	Open-Pollinated Varieties
PC	Principal Component
PC1	Principal Component One
PC2	Principal Component Two
PCA	Principal Component Analysis
PH	Plant height

r_P	Phenotypic Correlations
TAMALE 1	Major season at Tamale
TAMALE 2	Minor season 2
V_E	Variance due to Error
V_G	Genotypic Variance
V_{GL}	Variance due to Genotype by Location Interaction
V_{GLR}	Variance due to Genotype, Location and Replication
Vp	Phenotypic variance
WACCI	West Africa Center for Crop Improvement
WACCI 1	Major season at Legon
WACCI 2	Minor seasons at Legon
WENCHI 1	Major season at Wenchi
WENCHI 2	Minor seasons at Wenchi

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CHAPTER ONE

1.0. INTRODUCTION

Maize (*Zea mays* L.) is the second most important food crop after cassava on the African continent (De Vries and Toenniessen, 2001). It is the most important grain crop in West Africa in terms of quantity produced and consumed (Tweneboah, 2000). According to FAO (2009), the area in West Africa countries planted to maize increased from 3.2 million ha in 1961 to 8.9 million ha in 2005. Between 1987 and 2007, this area increased from 7,958,927 ha to 11,752,136 ha (FAO 2010). This phenomenal expansion of the land area devoted to maize resulted in increased production from 2.4 million tonnes in 1961 to 10.6 million tonnes in 2005. However, although the average yield in the developed countries is up to 8.6 t/ha, production in several areas of West Africa is still very low 1.3 t/ha (FAO, 2010). Maize currently covers 25 million hectares in Sub-Saharan Africa, largely in smallholder systems that produced 38 million metric tons in 2005-2008 primarily for food (Melinda *et al.,* 2011).

Maize is used as human food, livestock feed, and as raw material for industry (FAO, 1992). Average annual per capita human consumption of maize is 20 kg in developing countries, but in Latin America and the Caribbean, it approaches 80 kg and, in Sub-Saharan Africa, it is estimated 60 kg (CGIAR, 2002).

Between 2004 and 2006, over 700 million tonnes of maize were annually produced on 145 million ha; of which 380 million tonnes on 100 million ha were in the developing world. By 2020 maize production in industrialized and developing countries will have surpassed that of wheat and rice and will have increased since 1997 by 45% at the global level and by 72% in developing countries (Rosegrant *et al.,* 2001). Within the developing world, the demand for food maize will be the greatest in sub-Saharan Africa (40 million t), followed by Latin America (30 million t), and then South and Southeast Asia (25 million t).The World maize yield averaged 4.9 t/ha in 2009 (Edgerton, 2009). However, yields in major maize growing areas in the developing world still lag behind the world average, producing only about 2.8 t /ha (Pixley *et al.*, 2009). Yields in the United States for example have increased remarkably from an average of 1.6 t/ha in the early 1930's to the current approximately yield of 10 t/ha (Edgerton, 2009) as a result of adoption of hybrid seed maize, whereas yields presently obtainable in Ghana hover around 1.7 t/ha. This large discrepancy in yield has been ascribed partly to the use of unimproved or open pollinated varieties instead of hybrid maize, traditional farming practices, the use of low-yielding varieties, poor soil fertility and limited use of fertilizers, low plant population, inappropriate weed and inadequate disease control. MoFA (2011), reported that achievable yields of about 6 t/ha have been obtained in maize yield evaluation yield. This therefore indicates that the average maize yield of 1.7 t/ha currently obtained in Ghana, is about 70% less than what is usually achieved in maize yield trial by researchers. However, yields as high as 5.0-5.5 t/ha have been realized by farmers using hybrid seeds, under fertilizer, mechanization and irrigation (MiDA, 2010). Maize is grown in all of agro-ecological zones of Ghana. However, the main areas are in the middle parts of Ghana or the transitional forest zone (FAO, 2010). The area includes Brong Ahafo and parts of Ashanti and Eastern regions. In Ghana, maize is mostly grown by peasant farmers and on small scale with low yielding cultivars and therefore leading to low output.

There is low use of improved maize hybrid seed in the country. The rate of adoption of improved maize seeds in Ghana is 1 percent (Langyintuo *et al.*, 2010). Most of the maize varieties used in Ghana are open pollinated varieties (OPVs) with low yields, and degenerate after many years of cultivation without seed renewal. In order to meet the growing needs of farmers in Ghana, nine

(9) hybrid maize varieties have been released by CSIR – CRI (MoFA, 2011). Maize farmers throughout the country, though yields are still low have adopted these released varieties and small holder farmers continue to meet difficulties in accessing improved hybrid seed maize. At present, there is growing demand for the use of hybrid seed maize and this is thriving the emergency of a number of seed companies in Ghana.

Farmers and breeders want successful new maize hybrids that show high performance for yield and other essential agronomic traits. Their superiority should be reliable over a wide range of environmental conditions. The basic cause of difference between genotypes in their yield stability is the occurrence of genotype-environment interaction (GEI). Genotype – environment interaction may be expected to be high when environmental differences are high as in Ghana. Hence, it is important to assess the importance of interactions in the selection of genotypes across several environments besides calculating the average performance of the genotypes under evaluation (Fehr, 1991; Gauch and Zobel, 1997).

Various studies have been conducted to analyze effects of GEI on Ghanaian maize varieties and in Sub-Saharan Africa (Badu-Apraku *et al*., 1995, 2003; Fakorede and Adeyemo, 1986, Abdulai *et al*., 2007). However, the changing conditions, the introduction of maize to new agro-ecologies as a result of inadequate maize varieties available for the different environments necessitates a rigorous and continuous study of GEI for a dynamic crop improvement program. The West Africa Center for Crop Improvement (WACCI), University of Ghana, maize breeding program has produced a number of high yielding hybrids. These materials are yet to be tested on farmers' fields. Hence, the study was conducted of twenty hybrid maize from West Africa Center for Crop improvement, maize breeding program and three locally released hybrid maize to identify stable and high yielding hybrids with superior agronomic performance for commercial production in Ghana.

The specific objectives of this study were to:

I. assess grain yield of hybrid maize varieties in three agro –ecological zones of Ghana

II. Determine relationship among grain yield and its components within and across the three agro –ecological zones.

III. Assess stability of grain yield of these hybrids

CHAPTER TWO

2.0. LITERATURE REVIEW

2.1. Maize production and distribution

The origin of maize has long been a controversial ethno-botanical problem because the origin of maize remains uncertain, although it is generally agreed that its evolution into modern forms took place primarily in Central America. There are several theories about the specific origin of maize in Mesoamerica. These theories include; one, it is a direct domestication of a Mexican annual teosinte, *Zea mays, parviglums,* native to the Balsas River valley of Southern Mexico, with up to 12% of its genetic material obtained from *Zea mays* spp. mexicana through introgression (Jugendheimer, 1958). Second, it derives from hybridization between small-domesticated maize (a slightly changed form of wild maize) and a teosinte of section *Luxuriantes*, either *Zea luxurians* or *Zea diploperennis* (Collins, 1912). Third, it underwent two or more domestications either of wild maize or of a teosinte, and fourth, it evolved from a hybridization of *Zea diploperennis* by *Trispacum dactyloides* (Collins, 1912).

In the late 1930s, Paul Mangelsdorf suggested that domesticated maize was the result of a hybridization event between unknown wild maize and a species of *Trispacum*, a related genus. However, modern genetics has refuted the proposed role of tripsacum (gamma grass) in the origins of maize testing, refuting Mangelsdorf's model and the fourth listed above (Mangelsdorf and Reeves, 1945). Nobel Prize winner George Beadle proposed the first model in 1939. Though it has experimental support, it has not explained a number of problems, among them include, how the immense diversity of the species of sect. *Zea* originated how the tiny archaeological specimen of 3,500 – 2,700 BCE (uncorrected) could have been selected from a teosinte, and how domestication could have proceeded without leaving remains of teosinte or maize with teosintoid traits 1100 BCE. The theory that suggests that maize is descended from the wild plant 'teosinte' is the oldest of four widely considered hypotheses and the most likely and widely accepted at present. Cultivated maize *Zea mays* L. subsp. *mays* (IItis and Doebley, 1980) is most likely the product of a single domestication event through human selection on annual teosinte *Zea mays* L. subsp. *parviglums* according to Doebley *et al*., (1987), and to Matsuoka *et al*., (2002). This conclusion was reached after studying isozyme variation of maize and teosinte (Doebley *et al*., 1987) and through phylogenetic analysis based on genotyping a comprehensive sample of maize and teosinte from the American continent (Matsuoka *et al*., 2002). Additional evidence supporting the teosinte ancestry of maize is provided by the discovery of a number of genetic loci coding for basic phenotypic differences between maize and teosinte (Doebley, 1992; Wang *et al.*, 1999; Whitt *et al.*, 2002).

The process of domestication of maize is of particular interest to researchers. The process of maize development is thought to have started from 7,500 to 12,000 years ago. It is unknown what precipitated its domestication since the cultivated varieties of maize differ considerably from the wild plants which researchers regard as the cereal's ancestors, this is because the edible portion of the wild plant is too small to be worth cultivating. It would have taken many generations of selective breeding in order to produce a plant with cobs large enough to eat. McClintock's research (1959) on chromosome knob positions in maize from south America, Mexico, and Central America led her to the multiple- origins proposal that was further developed by Kato (1976 and 1984), McClintock (1978 and 1981). These authors proposed five independent centers of maize domestication; four were in Mexico; two in Oaxaca – Chiapas region, one in the central highlands and other one in the mid –highlands of Morelos-Northern

Guerrero and one in the highlands of Guatemala. Furthermore, Matsuoka and co-workers (2002) proposed the central Balsas River Valley in Michoacan and Guerrero states of Mexico as possible cradle of maize domestication.

Research by Matsuoka *et al*., (2002) led them to the seemingly conflicting conclusions that the cradle of domestication lies at an altitude of 800 to 1,200 meters above sea level, while the first diversification of maize occurred at a higher elevation more than 1,800 meters. Three cobs of fossil maize were excavated at the Guila Naquitz cave in Oaxaca, Mexico, at 1926 meters above the sea level and were directly dated by the accelerator mass spectrometry 6250 calendar years before present (Piperno and Flannery, 2001). The second oldest fossil maize was found at the San Marcos Cave near Tehuacan, Puebla, and was directly dated by accelerator mass spectrometry to be seven centuries younger (Long *et al*., 1989).

Benz (2001) reports that Guila Naquitz fossil maize, in contrast with its teosinte ancestor, had non-disarticulating rachis, reduced rachis length, spikelet reoriented perpendicular to the rachis and opened cupulate fruit cases exposed the grain. However, these characters had not yet reached fixation to the maize- like phenotype with paired spikelets. Comparing these specimens with those excavated in San Marcos cave led the author to infer that domestication efforts in the 700 year interim were focused on stabilizing the distichously, non – disarticulating, naked- grain phenotype and on increasing the number of grain bearing spikelets per node from one to two. Maize relics from two caves bearing more recent dates are the Romero and Valenzuela caves near Ocampo, Tamaulips (Smith, 1998) and south western United States (Smith, 2001).

The dispersal of maize from its proposed origin, Mexico, throughout the world is believed to have taken two routes; the southward route and northward route. The southward route of maize dispersion took the Central America hybridized maize to South America some 4,000 years ago, where agricultural, ceramic- using cultures had already developed (Grobman *et al*., 1961). Maize spread first into lowlands of South America and finally into the Andes Mountains (Matsuoka *et al*., 2002). The northward route of dispersal from Mexico probably included two parallel corridors flanking the Sierra Madre Occidental into the South Western United States (Carter, 1945; Hernandez-Xolocotzi and Alanis – Flores, 1970). The first maize race to reach the south western United States was Chapalote, some 3,000 to 3,500 years ago (Fagan, 1995). Chapalote is a relic; an ancient, indigenous maize race that has a low yield potential. Maize remained as a supplement to regular foraging for a millennium or so after its initial introduction to the region. Further maize germplasm introductions from the south brought other races such as Oloton de Chiapas, Oloton and Sierra de Guatemala into the south western United States (Hernandez-Xolocotiz, 1985). Maize spread into the eastern woodlands of North America and appeared as a food in what now are New England and eastern New York during the twelfth century A.D (Fagan, 1995).

Furthermore, archaeological and biological evidence regarding origin and distribution shapes a northward path of dispersal of early maize. The study by Matsuoka et al., 2002 suggests one path that starts in Mexico's highlands and traces through western and northern Mexico into the southwestern United States and then into the eastern United States and Canada. A second path goes from the Mexico highlands to the Western and southern lowlands of Mexico into Guatemala, the Caribbean Islands, the lowlands of South America and Andes mountains. In accordance with this study, maize diversified first in Mexico's highlands and dispersed to lowlands at a later stage. Some archaeological studies support this assertion (Smith, 1998, 2001).

However, there is also an alternative archaeological position: diversification in the lowlands of Mexico and dispersal to the highlands at a later stage (Piperno and Perasall, 1998).

Taba (1997), quoting several authors, report that Coloumbus found maize in Cuba and introduced into Europe (Mangelsdorf,1938) and that maize spread into the Asian continent via three routes in the sixteen century; the Mediterranean trade route, the Atlantic and Indian Ocean route and, after Magellan's voyage, to the Philippines and eastern Indonesia (Taba,1997). He also mentions that maize was introduced to Africa from Spain and Italy and that a later introduction of maize spread into Africa from the lowlands of Brazil and Guyanas, the southern United States and Northern Mexico.

According to Tweneboah (2000), maize reached West Africa through the early European traders in the sixteen century and by the end of seventeeth century, it became an entrenched staple in West Africa as it replaced the local rice, *Oryza glabberima* by its high yielding capabilities. Today maize has become one of the most important grain crops in West Africa and the world at large in terms of quantity produced and consumed.

2.2. Utilization and economic importance

Maize is the most widely distributed cereal occupying two times the area occupied by any single crop in the world (Acquah, 2007). It is ranked the third highest most important produced cereal crop in the world after rice and wheat (Al-Swailem *et al.*, 2005). It is the most important grain crop in West Africa in terms of quantity produced and consumed (Tweneboah, 2000). Its importance has increased as it replaced other staples, particularly sorghum and millet (Smith *et al.*, 1994) and has become a major source of cash for smallholder farmers (Smith *et al.*, 1997). In view of this, the Grain and Legume Development Board under the national seed support produced 55 tons of foundation seed maize and processed 500 tons of certified maize seed to address the issue of low productivity in maize (ISSER, 2007). Higher yielding maize will increase the income of farmers and reduce the poverty rate in Ghana.

There are a number of industries that are involved in the production and utilization of the maize. They come in as input supplier, processors and marketing channels. All these industries create employment for people in the country and as such provide them with a source of income for their livelihood. The overall effect is improvement in the standard of living of the citizens in the country.

In 2006, Ghana produced a total of 1,188,000 tons of maize on a total of 793,000 hectares of land. This gave a corresponding yield of 1.5 ton per hectare (ISSER, 2007). Rice (paddy), millet and sorghum were produced on 125,000, 20,000 and 32,000 hectares of land respectively. These figures show how much maize is important to the economy of Ghana and therefore more much area is dedicated to its production.

Principally the use of maize can be grouped into three. These are for human consumption, industrial use and as feed for livestock. For human consumption, maize forms a major staple for most people especially in Africa. In Ghana, it is prepared into banku, porridge, kenkey and other traditional foods. In large parts of Eastern and Southern Africa, maize is the principal staple food, produced and consumed by most farming households. Maize still provides a major source of calories, especially in parts of Ghana, Nigeria, Benin, Mali and Cote d'lvoire. The cob is eaten fresh or allowed to mature and dried before it is used to prepare various dishes according to the locality. Upon maturity, the dried grain also has many industrial uses. It is used in the manufacture of beer, starch and other pharmaceutical products. The matured grain is also used as concentrates especially in the temperature regions to feed poultry, pigs and ruminants as supplements. The immature plant can also be harvested and fed to livestock in the form of fodder, hay or silage.

2.3. Maize production in Ghana

Maize cropping systems and production technologies vary between the four agro-ecological zones in which significant amounts of maize are cultivated. Farmers in these zones grow maize and cassava, often intercropped, as their principal staples. Annual rainfall, which is bi-modally distributed except the north, totals only 800mm, so most maize is planted following the onset of the major rains that begin in March or April (Oteng, 1998).

Maize in forest zone is grown in scattered plots, usually intercropped with cassava, plantain and or cocoyam. The technology used on most farms is rudimentary with very little purchased inputs. The hoe and the cutlasses are still major farm implements for cultivation (Asenso- Okyere, 2001). Although some is consumed in the forest zone, is not leading staple food and much of the crop is sold. Maize in the transitional zone is planted in both major and minor seasons, usually as a mono-crop or in associate with yam and or cassava. Maize is grown in permanently cultivated fields located close to homesteads, as well as in more distant plots under shifting cultivation (Morris *et al.,* 1999). Most of the maize grown in Ghana is cultivated in association with other crops, particularly in coastal savannah and forest zones, so planting densities are generally low. Total annual maize production is currently estimated at just over one million tons. Both of the two key determinants of production (area planted and yield) have increased over long term, although the upward trends have been characterized by high year-to-year variability typical of rain fed crops (Morris *et al*., 1999). The transition zone has become increasingly important for maize production (Smith *et al*., 1994). The rising importance of the transition zone as a source of maize supply can be attributed to a combination of factors, including the presence of favorable agro-ecological conditions, availability of improved production technology, a relative abundance of under-utilized land, and a well-developed road transport system. The relative abundance of arable land in the transition zone has attracted many migrant farmers, particularly from the north of the country, who have moved to the zone to commercial food farming. The forest and transition zone with 70 percent of production provides the best conditions. Smallholder farmers grow most of the maize under rain-fed conditions, but few progressive farmers and companies cultivate farms of 20-30 hectares usually with degree of modernization. The districts of Nkoranza, Techiman, Kintampo, Ejura- Sekyeremase, Afram plains-Northern Volta region and Damango are high maize production areas.

Ghana is self-sufficient in maize production in years of adequate rainfall; however, there is a cycle of drought. Weak storage, inadequate preservation, and marketing or distribution system cause substantial price fluctuation: often two or three times more than that of harvested period. The bulk of the maize produced is consumed within Ghana, but there is growing trade in maize grain and secondary maize products to our neighboring countries. There are opportunities for processing into secondary industrial products such as animal feed, industrial starch and composite baking flour (GAINS, 2003).

Plant configuration and recommendation were developed in Ghana based on extensive on-station and on-farm trials. The results of these experiments were then used to formulate crop management recommendations that could be communicated easily to farmers. The recommendations emphasized planting in row to help farmers calibrate plant population densities to stressing the importance of row planting, the recommendations also focused on reducing the distance between holes and reducing the number of seeds planted per holes (GGDP, 1991).

2.4. Maize improvement research in Ghana

2.4.1. Open pollinated varieties

The single most important research efforts on maize was implemented by the Ghana Grain Development Project (GGDP), funded by the Government of Ghana and Canadian government through CIDA (Mercer-Quashie *et al*., 1993). The project was initiated in 1979 to champion research for the improvement of maize and legumes, with a multiplicity of objectives including improvement in grain yields and resistance to diseases, pests and lodging. There were additional objectives to target different growing conditions and to improve nutritional quality (Dankyi, 1999). The most important technologies developed and promoted by the project are 15 improved maize varieties, fertilizer recommendations, plant configuration recommendations (Dankyi, 1999). Quality protein maize (QPM) development program was started in 1989 at the Crops Research Institute and this initially led to the release of an open-pollinated variety, obataapa, this has been widely adopted in Ghana and elsewhere in Africa and beyond (Twumasi-Afriyie *et al*., 1992). Alongside the development of obataapa, a QPM hybrid maize development program was initiated in 1991. Three 3-ways QPM hybrids, namely, GH110-5 (Mamaba), GH132-28 (Dadaba), and GH2328-88 (CIDA-ba) developed in this program were very productive, yielding among 6.3 and 7.3 t/ha on experimental station, representing an increase of 19 to 38 percent over obataapa. The QPM hybrids were, therefore, released for production in 1997 (Morris *et al*., 1999).

2.4.2. Synthetic Varieties

In 2010, four quality protein maize (QPM) varieties tolerant to drought and *Striga hermontica* were also released to boost maize production in drought and *Striga* endemic areas. The Crops Research Institute (CRI) and the Savanna Agricultural Research Institute (SARI) of the council for Scientific and Industrial Research (CSIR) of Ghana released the varieties, which are early and extra-early maturing, jointly. Of the four varieties, three were developed by IITA in the earliness program and have the IITA designation, EV DT-W 99 STR QPM Co; TZE-W Pop STR QPM C0; and TZEE-W Pop STR QPM C0 (an extra-early maturing variety). The fourth, an intermediate maturing drought-tolerant QPM hybrid, was developed in the national maize program of Ghana Table 1).

Table 1: Characteristics of the open pollinated maize varieties promoted by GGDP and CSIR-CRI

Name	Year	Origin	Yield (t/ha)	Maturity	Streak Resistance	Grain texture
Mex 17	1961	CIMMYT	-	90 -105	No	Dent
Comp 4	1972	CIMMYT	-	120	No	Dent
Comp W	1972	CIMMYT	-	120	No	Dent
Golden crystal	1972	CRI/CIMMYT	4.6	110-120	No	Dent
Laposta	1972	CIMMYT	-	120	No	Dent
Aburotia	1983	CRI/CIMMYT	3.5	105 -120	No	Dent
Dobidi	1984	CIMMYT	5.5	120	No	Dent
Kawanzie	1984	CIMMYT	4.6	90 -95	No	Flint
Safita -2	1984	CIMMYT	3.5	90 -95	No	Dent
Okomasa	1988	IITA/CIMMYT	5.5	120	Yes	Dent
Abeleehi	1990	IITA/CIMMYT	4.6	105-110	Yes	Dent
Dorke SR	1992	IITA/CIMMYT	3.8	95	Yes	Dent
Obatanpa	1992	IITA/CIMMYT	4.6	105	Yes	Dent
Dodzi	1997	IITA	3.5	80 -85	No	Dent
Aziga (yellow)	2007	CIMMYT	4.7	110	No	Dent
Akposoe	2007	IITA/CIMMYT	3.5	80 - 85	No	Flint
Golden Jubilee	2007	CIMMYT	5.0	105 - 110	No	Dent
Aburohemaa	2010	IITA	5.0	90	No	Dent
Abontem	2010	IITA	5.0	75 - 80	No	Dent
Omankwa	2010	IITA	4.7	90	No	Dent
Honampa	2012	IITA	5.2	105 -110	No	Dent

Source: Morrison *et al.*, 1999, pp6, GGDP, 1999, GNA, 2007, MOFA/CRI/SARI, (2012).

2.4.3. Hybrid maize varieties

Four varieties were released in 1997: three of them were high-yield, QPM hybrids (Mamaba, Cida-ba, and Dada-ba), and the other was an extra-early-maturing OPV (Dodzi). Four varieties were again released in 2007: two were high-yield, QPM, open-pollinated yellow maize varieties (Aziga and Golden Jubilee); one was an extra-early maturing, QPM, drought- tolerant variety (Akposoe); and the other was a QPM, drought-tolerant hybrid variety (Etubi). In 2010, another set of four varieties was released: three drought-tolerant, Striga-tolerant, QPM OPVs and one drought-tolerant, QPM hybrid (Enibi). In total, five hybrid varieties were developed and released by CRI and SARI, namely, Mamaba, Cida-ba, Dada-ba, Etubi, and Enibi. In 2012, six varieties were officially released: five hybrids and one OPV with pro-vitamin A. Private Companies have also begun promoting hybrid maize varieties in Ghana. Wienco has been promoting Pannar varieties (MoFA, 2012).

Table 2—Improved hybrid maize varieties promoted by CRI and SARI

Name	Year	Origin	Yield(t/ha)	Maturity	Streak resistance	Gain Texture
Mamaba	1996	CIMMYT	6.5	105	No	Dent
Cida-ba	1997	CIMMYT	6.5	110	No	Dent
Dada-ba	1997	CIMMYT	6.5	110	No	Dent
Etubi Pibi	2007	CIMMYT	6.5	105-110	No	Dent
Aseda	2012	IITA	6.7	110 -115	No	Dent
Opeaburoo	2012	IITA	7.5	110 -115	No	Dent
Tintim	2012	IITA	7.9	110 -115	No	Dent
Nwanwa (yellow)	2012	IITA	7.9	110 - 115	No	Dent
Odomfo (yellow)	2012	IITA	6.5	110 - 115	No	Dent

Source: Morrison *et al.*, 1999, pp6, GGDP, 1999, GNA, 2007, MOFA/CRI/SARI, (2012).

2.5. Genotype - environment interaction in hybrid maize development

Stability for yield of a variety is important because farmers cultivate the same variety under different management systems. Drought and low N cause different levels of stresses to plants in an area because many other factors (e.g. soil type) also affect them. It is, therefore, important that yield stability is developed in cultivars targeting such environments. Grain yield is quantitative and exhibits Genotype x environment interactions (GEI). This necessitates genotype evaluation in multi-environment trials (METs) in the advanced stages of selection (Fan *et al.*, 2007, Kang *et al.*, 2004, Badu-Apraku et al., 2003). In order to identify stable genotypes, genotype x environment must be partitioned into stability statistics that are assignable to each genotype evaluated across a range of environments (Fernandez, 1991).

At least two fundamentally different concepts of stability exist, the static and dynamic (Becker and Leon, 1988). Their application depends on the trait considered. Under the static concept, a stable genotype is defined as one having an unchanged performance regardless of any variation in the environmental conditions. This concept is particularly useful for quality characteristics where the level of performance has to be maintained at all cost. For grain yield dynamic concept of stability has been proposed, under which performance may change from environment to environment, but in a predictable way. Several methods are available for measuring the dynamic concept of phenotypic stability. All have one feature in common: they derive their estimates of stability from an analysis of genotype-environment interactions. They include regression analysis (Gauch, 1988), multivariate analysis (Westcoff, 1987), variance analysis (Perkins and Jinks, 1968) etc. The basic model for stability analysis is the same as that used for the analysis of genotype-environment interactions (Hill et al., 1998).

$Yij = \mu + gi + ej + geij + \bar{e}ijk$

Where μ: general mean

gi: effects of genotypes

ej: effects of environments

geij: effects of genotype x environment interactions

$\bar{e}ijk$: random error associated with observation of kth replication of ith genotype in jth environment.

The most widely used method for analyzing stability is the linear regression approach using

Eberhart and Russell, (1966) formula

$Yij = \mu 1 + \text{ß}1Ij + \delta ij$

Yij: Variety mean of the ith variety at the jth environment

µ1: ith variety mean over all environments

ß1 is the regression coefficient

δij: is the deviation from regression of the ith var at jth environment,

Ij: environmental index.

Lin et al., (1986) presented 10 stability statistics and categorized them into three types of stability statistics: Type 1 statistics, include standard deviation and coefficient of variation (Francis and Kannenberg, 1978), and are based on deviation from average genotype effect. A genotype is regarded as stable if its among-environment variance is small. Type 2 statistics are based on Genotype*Environment interaction. Ecovalence (Wricke, 1962), as well as the stability parameters (Plaised, 1960, Shuka, 1972) are examples of type 2. The ecovalence measures the contribution of the ith genotype to the genotype* environment interaction, low values signify stability. Type 3 statistics are based on deviation from regression. A genotype is regarded as stable if the residual mean square from the regression model on the environment index is small (Eberhart and Russel, 1966). Lin and Binns (1986, 1991) have added a fourth type of stability, which can be used in multi-environment trials encompassing both seasons and locations. Stability types 2 and 3 are relative to the other genotypes included in the trial and come within the scope of the dynamic concept; type 1 and 4 are static measures which do not depend on the remaining genotypes in the trial.

According to Langer et al., (1979) the regression coefficient (b) is a measure of response to varying environments and the mean square deviation from the linear regression is a measure of production stability. A genotype with $b = 1$ is adapted to all environment whereas a genotype with $b> 1$ is adapted to high yielding environment while the one with $b < 1$ is adapted to low yielding environments.

The GGE-bi-plot where G = genotype effect and GE = genotype-by-environment effect is a powerful technique that allows visual examination of the GE interaction pattern of MET data. The bi-plot method originated with Gabriel, (1971), and its use was subsequently expanded by Kempton, (1984) and Zobel et al., (1988). The extensive usefulness of GGE bi-plot, has only recently been elucidated (Yan et al., 2000). The GGE-bi-plot methodology has been reported in maize (Fan et al., 2007, Badu-Apraku and Oyekunle., 2012) in GE interaction evaluation and mega-environment investigation. Bi-plots can be used for analyzing diallel crosses; Yan, (2001). The GGE bi-plot model equation is:

$$\hat{Y}ij - \mu - \beta j = \lambda 1\xi i1\eta 1j + \lambda 2\xi i2\eta 2j + \xi ij$$

$\lambda 1$ and $\lambda 2$ are the singular values of first and second largest principal components, PC1 and PC2, respectively; the square of the singular value of a PC is the sum of squares explained by the PC; $\xi i1$ and $\xi i2$ are the eigenvectors of genotype I for PC1 and PC2, respectively; and $\eta 1j$ and $\eta 2j$ are the eigenvectors of environment j for PC1 and PC2, respectively.

2.6. Role of stability analysis

Factors that are of economic relevance may be related to complex or polygenic characteristics, and show a high influence of the environment. Because of this, in breeding programs, various experiments are conducted in several locations to evaluate grain yield. In these experiments, changes in the relative performance of the genotype in different environments are usually observed (Kandus *et al*., 2010). The genotype by environment interaction is an important aspect in both, plant breeding programs and the introduction of new maize hybrids. Deitos *et al*., (2006), indicated that genotype x environment interaction is important for plant breeding because it affects the genetic gain and recommendation and selection of cultivars with wide adaptability. On the other hand, different genotypes may have different performance in each region that can be capitalized to maximize productivity (Souza *et al*., 2008). Kang and Gorman (1989) indicated that, a significant GEI for a quantitative trait such as seed yield can seriously limit the efforts on selecting superior genotypes for improved cultivar development. For variety trials, which are tested in the same locations (L) and genotypes (G) and over years (Y), G x E analysis of variance may be partitioned into components due to G x L, G x Y and G x L x Y. Significance of mean square for G x L generally suggests that the region for which genotypes are being bred comprise of a number of special environments. In such circumstances, the geographic region could be subdivided into sub regions, which are relatively homogeneous. Varieties, which are specifically adapted to these ecotypes, should be bred. Implication of G x Y interaction is very different from G x L interaction. This is so because year-to-year fluctuations in the weather conditions cannot be predicted in advance and breeders can hardly aim their programmes to develop varieties suited to particular years (Dabholkar, 1999).

In some situations, environmental variation is predictable but can also be corrected. For example, saline soils can be corrected by certain agronomic practices or by addition of some amendments. This is easier and quicker than developing varieties suitable for such situations. However, breeding of varieties suitable for saline or acidic soils is low cost input and also a relatively permanent solution to the problem. Genotype by environment interactions can be an outcome of genotype rank changes from one environment to another, a difference in scale among environments, or a combination of these phenomena. According to Becker and Léon (1988), cultivar rank changes are of greater importance than scale change interactions in cultivar trials conducted over a series of environments. Hence, GEI is critical only if it involves significant crossover interactions (significant reversal in genotypic rank across environments). Kang and Gorman (1989) noted that GEI reduce the correlation between the genotype and the phenotype hindering the evaluation of the genetic potential of the cultivars.

2.6.1. Types of analysis

In maize breeding programs, the search for genotypes with high grain yield adapted in the most varied environments is one of the most important objectives for breeders. For that, the choice of populations that show good genetic homeostasis is essential for yield increases. Souza *et al*.,(2009) stated that, GEI is important for plant breeding because it affects the genetic gain and recommendation and selection of cultivars with wide adaptability. On the other hand, different genotypes have different performance in each region that can be capitalized to maximize productivity (Souza *et al*., 2008).

In attempts to provide a definition, Byth (1981) and Clements *et al*. (1983) argued that the term adaptation applied to both a 'condition' and a 'process'. The interpretation of their definition requires further consideration. The 'condition' or level of adaptation possessed by individuals or populations (hereafter referred to collectively as genotype) refers to the genetic constitution of a genotype and how this matches the plant to the environment it occupies.

Ultimately this is a function of the genes possessed by the plant, the regulation of biochemical and physiological processes by these genes during growth and development and how well these are matched with the available environmental resources and possible hazards (Bidinger *et al*., 1987). Therefore, a difference in the 'condition' of adaptation between individual's results from a genetic difference which influences the matching of their growth and development processes with the environment. Following this, the 'process' of adaptation is viewed as a change in the genetic constitution of individuals as they accumulate genes or a change in gene frequencies within populations which better match growth and development with the environment. From an evolutionary perspective, adaptation is evaluated in terms of reproductive capacity of the individual or Darwinian fitness. Under a particular set of environmental conditions, individuals with better adaptation will produce more offspring.

Thus, over time the process of improving adaptation through natural selection will unfold and the level of adaptation of individuals within the population will improve. The adaptability of a variety over diverse environments is usually tested by its degree of interaction with different growing environments. A variety or genotype is considered to be more adaptive or stable if it has a high mean yield but low degree of fluctuation in yielding ability when grown over diverse environments (Falconer, 1981). According to Simmonds (1962) adaptation has four separable aspects; these are:

1. Specific genotypic adaptation: it is close to adaptation of the corresponding genotypes to a limited environment.

2. General genotypic adaptation: is the capacity of a genotype to produce a range of phenotypes adapted to a variety of environments.

3. Specific population adaptation: is analogous to (1) and is the aspect of specific adaptation of heterogeneous population that is attributable to interaction between components rather than to the adaptations of components themselves.

4. General population adaptation: is analogous to general genotypic adaptation and is the capacity of a heterogeneous population to adapt to a variety of environments. The concepts of broad and specific adaptation are often used to describe the relative performance of genotypes when adaptation is evaluated in more than one environment. Broad adaptation describes the response of a genotype where superior performance is expressed across the majority of, or all environments, and specific adaptation describes a response where a higher level of performance is expressed in specific environments. In general, the genetic and physiological basis of the distinction between broad and specific adaptation are poorly understood and the concepts are generally statistically defined. Specific adaptation is often associated with the occurrence of G x E interactions. The incidence of these interactions is of particular concern to the plant breeder as they complicate the process of selection for broad adaptation and bring into question the overall effectiveness of such a strategy (Ceccarelli, 1989). A genotype is also considered to be stable if its environment variance is small. This is called stability statistic, or a biological concept of stability. A stable genotype possesses an unchanged or least changed performance regardless of

any variation of the environmental conditions. This concept of stability is useful for quality traits, disease resistance and for stress characters (Baker and Leon, 1988).

Stability analysis provides a general solution for the response of the genotypes to environmental change. In this way, Yates and Cochran (1938) proposed linear regression analysis, which has been widely used and revised by a number of authors (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Lin and Thompson, 1975; Becker and Leon, 1988; Crossa, 1990). Abdulai *et al*. (2007) worked on the GEI of four open pollinated varieties and eight experimental hybrids, which were late maturing lowland maize varieties. They concluded that, seven out of the 12 genotypes were stable, when b-values alone were considered. When the b-values and the deviations from regression (s2d) were considered, (GH24 x 1368) x 5012 and (GH22 x 1368) x 5012, were the most stable, but when the coefficient of determination was added to the b-value and s2d, GH132 - 28 was the most stable genotype. This analysis, which involves regressing the average of the genotypes on an environmental index (the average yield of all the genotypes evaluated in each environment), provides a stability index. However, the analysis has several limitations and criticisms from both the biological and statistical points of view. The main biological problem appears when only a few very low and very high yielding sites are included in the analysis, and the fit is determined by the genotype behaviour in a few extreme environments (Crossa, 1990). The main statistical problem is that the average of all genotypes evaluated in each environment is not independent of the average of each genotype in a particular environment (Freeman and Perkins, 1971). Another statistical limitation is that the errors associated with the slopes of the genotypes are not statistically independent. The last problem is the assumption of a linear relationship between interaction and environmental means, when the actual responses of the genotypes to the environments are intrinsically multi-variated (Crossa, 1990). Multivariate analysis has three main purposes: (i) to eliminate "noise" in the data set (for example, to distinguish systematic and non-systematic variation); (ii) to summarize the information and (iii) to reveal a structure in the data (Crossa *et al*., 1990; Gauch, 1992).

However, other methods for identifying cultivars with adaptability and stability have been developed and many multivariate techniques are available such as GGE (Genotype main effects and Genotype x Environment interaction) and AMMI (Additive Main effects and Multiplicative interaction) with new information for cultivars, environmental stratification and genotype x environment interaction (Miranda *et al*., 2009; Yan *et al*., 2000).

2.6.2. Interpretation of results of stability analyses

There are many statistical methods available to analyse GEI: for example, combined ANOVA, stability analysis and multivariate methods. Combined ANOVA is more often used to identify the existence of G x E interactions in multi-environmental experiments. However, the main limitation of this analysis is the assumption of homogeneity of variance among environments required to determine genotype differences. Although this analysis allows the determination of the components of variance arising from different factors (genotype, environment and the GEI), it does not allow exploring the response of the genotypes in the non-additive term: the GEI (Zobel *et al*., 1998). There are other methods for evaluating the performance of hybrids and their genotypic interactions with the environment (Cornelius *et al*., 1996; Crossa, 1990 and Crossa and Cornelius, 1997). These methods differ in the parameters used in the assessment, the biometric procedures employed, and the analysis. The sites regression (SREG) (Crossa and Cornelius, 1997) has been suggested as the appropriate model for analyzing multi-environmental trials when large yield variation is due to environments (Yan *et al*., 2000). The SREG method supplies a graphical display called genotype plus genotype by environment interaction (GGE) bi-plot that identifies cultivars that are superior in different environments.

Finlay and Wilkinson (1963) also indicated that for dealing with GEI, regression on the environmental means can be used. Pattern analysis methods (Byth *et al*., 1976.), principal coordinate analysis (Eisemann, 1981), canonical variate analysis and principal component analysis (Zobel et al., 1988) with each proving successful in the analysis of uni-variate GEI data in certain situations. The usual analysis of variance (ANOVA), having a merely additive model, identifies the GEI as a source but does not analyse it; PCA analysis, on the other hand, is a multiplicative model and hence contains no sources for additive, genotype or environment main effects; and linear regression (LR) analysis is able to effectively analyse interaction terms only where the pattern fits a specific regression model. The consequence of fitting inappropriate statistical models to yield trial data is that the interaction may be declared insignificant, although a more appropriate analysis would find agronomically important and statistically significant patterns in the interaction. Since ANOVA, PCA, and LR are sub-cases of the more complete AMMI model, AMMI offers a more appropriate first statistical analysis of yield trials that may have a GEI. Among the statistical analyses proposed for the interpretation of the GEI based on the use of bi-plots, the AMMI (additive main effect and multiplicative interaction) model stands out due to the largest group of technical interpretations available (Duarte and Vencovsky, 1999).

AMMI analysis interprets the effect of the genotype (G) and sites (E) as additive effects plus the GEI as a multiplicative component and submits it to principal component analysis. Its bi-plot was identified as GE bi-plot by Yan *et al*. (2000). Yan *et al*. (2000) proposed a modification of the conventional AMMI analysis called GGE (genotype main effect and genotype-environment interaction) that has been used for GEI analysis. The GGE analysis pools genotype effect (G) with GE (multiplicative effect) and submits these effects to principal component analysis. According to Yan *et al.* (2000), this bi-plot is identified as a GGE bi-plot. The GGE bi-plot has been recognized as an innovative methodology in bi-plot graphic analysis to be applied in plant breeding.

In the last years, the AMMI and GGE analyses were debated in relation to graph accuracy. Gauch *et al*. (2008) questioned GGE analysis about the proportion of G + GE retained in the bi-plot. In other words, these authors claimed that GGE bi-plot always explained less G + GE than did the AMMI 2 mega-environment analysis, and sometimes, when GGE2 is suppressed in noise, the GGE bi-plot is even less accurate than AMMI 1 analysis. On the other hand, Yan *et al.*, (2007) stated that GGE2 always explained more G + GE than AMMI 1 display resulting in a larger graph accuracy. In addition, GGE2 is a direct bi-plot product, while the AMMI 2 mega-environment analysis cannot be considered a true bi-plot because it makes use of a predicted table for “which-won-where” pattern discovery.

AMMI analysis can then be used to diagnose whether or not a specific sub-case provides a more appropriate analysis. AMMI has no specific experimental design requirements, except for a two-way data structure." Although the AMMI analysis of yield trials does not use the data on environmental factors, these factors themselves, such as precipitation, average daily, maximum and minimum temperatures, as well as, their height and amplitudes, nitrogen fertilizers, irrigation and the clay content, very often correlate with the data of the AMMI statistics (Gauch, 1992; Romagosa *et al*., 1993). Crossa *et al.* (1990) indicated that the AMMI model can be used to analyze the GEI and to identify the superior hybrid maize genotypes. Also, he pointed out that it can be used in the selection of the best test environments for hybrid maize genotype evaluation.

Fan *et al.*,(2007) showed that the GGE bi-plot methodology was a useful tool for identifying locations that optimized hybrid genotypes performance and for making better use of limited resources available for the maize testing programs.

Annicchiarico (1997) stated that AMMI analysis appears particularly useful for depicting adaptive responses of small grain cereals tested over a wide range of environments. At the same time, the researcher explained that joint regression and AMMI analysis are more likely to perform alike, and provide similar results, for small grain cereals over areas where cold stress is limited. The vast number of methods proposed to evaluate stability and adaptability are based on phenotypic analyses, where the treatments and or progenies are considered as a fixed effect of the model. However, when the objective is the choice of genotype based on progeny performance, the breeding values can be predicted through mixed models and not just estimated based on phenotypic means (White and Hodge, 1989). Smith et al. (2001a) stated that when genotypes and environments are assumed as random and fixed effects, respectively, in mixed models analysis, more realistic results are obtained. In mixed model context, few alternatives for stability and adaptability study have been available. Van Eeuwijk et al. (1995) suggested the singular value decomposition analysis of GE as random effects in the AMMI approach. Similarly, Smith et al. (2001b) and Resende and Thompson (2003) presented the factor analytic multiplicative mixed model for GEI analysis considering G and GEI as random effects.

CHAPTER THREE

3.0. MATERIALS AND METHODS

3.1. Experimental location

The experiment was carried out at transition forest, Guinea savannah and the coastal savannah zones. In the forest zone, the experiment was carried out at the Wenchi (8^o 45N, 2^o 6W, 339 ASL) tomato factory farm site popularly known as “Tomakan”, which is 400 meters away from Methodist University College, Faculty of Agriculture Science within Wenchi Municipality in the Brong- Ahafo Region of Ghana. The study in the Guinea Savannah was located at Tamale (9^o 25 N, 0^o53W, 183 ASL) in the Boltanga irrigation site within Tolon/ Kumbungu district of the Northern Region of Ghana. In the coastal savannah, it was located at the WACCI demonstration farm site in the University of Ghana (5^o 36N, 0^o 10W, and 68 ASL), Legon.

Table 3: Average monthly rainfall, sunshine, relative humidity, temperature and rain days at Legon experimental site for the period

Month	Year	Rainfall (mm)	Rain days	Relative humidity (%)	Sunshine (hours)	Temperature(^{O}C) Max.	Min.
Nov	2012	30	3	80	250	31	23
Dec	2012	20	2	80	250	29	23
Jan	2013	10	1	78	210	32	23
Feb	2013	20	2	79	200	32	24
May	2013	130	9	80	240	31	23
June	2013	210	10	82	145	29	23
July	2013	50	4	85	150	28	22
August	2013	30	3	85	152	28	22

Source: Ghana Meteorological Service, 2014.

Table 4: Average monthly rainfall, sunshine, relative humidity, temperature and rain days at Tamale experimental site for the period

Month	Year	Rainfall (mm)	Rain days	Relative humidity (%)	Sunshine (hours)	Temperature(^{o}C) Max.	Min.
Nov	2012	15	3	40	295	35	22
Dec	2012	10	2	28	286	35	18
Jan	2013	15	2	19	280	35	20
Feb	2013	15	2	20	270	37	23
May	2013	120	10	57	275	35	25
June	2013	100	12	62	250	34	24
July	2013	160	13	65	200	30	23
August	2013	200	15	66	140	32	23

Source: Ghana Meteorological Service, 2014.

Table 5: Average monthly rainfall, sunshine, relative humidity, temperature and rain days at Wenchi experimental site for the period

Month	Year	Rainfall (mm)	Rain days	Relative humidity (%)	Sunshine (hours)	Temperature(°C) Max.	Min.
Nov	2012	41	1	93	278	29	21
Dec	2012	15	1	86	291	29	20
Jan	2013	4	-	71	276	32	20
Feb	2013	29	1	82	298	33	21
May	2013	161	3	91	289	31	21
June	2013	164	3	96	256	28	21
July	2013	129	4	94	286	27	21
August	2013	97	4	95	292	26	20

Source: Ghana Meteorological Service, 2014

3.2. Experimental materials

Twenty-three genotypes made up of 20 hybrids from WACCI and three locally released hybrids were evaluated.

Table 6: Hybrids and check varieties used in the study

Entry	Genotypes	Source	Entry	Genotypes	Source
1	WACCI-M-1201	WACCI	12	WACCI-M-1212	WACCI
2	WACCI-M-1202	WACCI	13	MAMABA	CRI
3	WACCI-M-1203	WACCI	14	WACCI-M-1204	WACCI
4	WACCI-M-1205	WACCI	15	WACCI-M-1206	WACCI
5	ETUBI PIBI	CRI	16	WACCI-M-1209	WACCI
6	WACCI-M-1207	WACCI	17	WACCI-M-1210	WACCI
7	WACCI-M-1208	WACCI	18	WACCI-M-1213	WACCI
8	WACCI-M-1211	WACCI	19	WACCI-M-1215	WACCI
9	WACCI-M-1214	WACCI	20	WACCI-M-1216	WACCI
10	WACCI-M-1217	WACCI	21	WACCI-M-1218	WACCI
11	WACCI-M-1220	WACCI	22	WACCI-M-1219	WACCI
23	PANNAR	WIENCO			

3.3. Experimental design and field layout

A randomized complete block design was used with 3 replications. Genotypes were sown in two rows per plot on 5 m long row and at inter-row spacing of 0.75 m and within row spacing of 0.5 m.

3.4. Cultural practices

Three seeds per hill were initially sown but later thinned to two at 1 week after sowing. NPK 15-15-15 fertilizer was applied at the rate of 30 kg N/ ha and 60 kg of P_2O_5/ha as basal fertilizer at two weeks after sowing and top dressed with additional N at 60 kg/ha at four weeks after sowing.

The trial was conducted during the dry season at the locations (Wenchi, Tamale and Legon) under irrigation in the dry season in November 20, 2012, November 24, 2012 and November 29, 2012 respectively. During rain-fed season, planting was done May 23, 2013, May 21, 2013 and June 2, 2013 respectively.

Post emergence herbicide with trade name Roundup was used to control weeds after ploughing and harrowing before sowing the seed maize. Hand weeding was also done when necessary to control weeds during the growing period and other management practices were done according to the recommendations of the specific areas.

3.5. Data collection

- Days to Anthesis: The number of days from planting to the time when 50% of plants have tassels and shedding pollen.
- Days to silking: The number of days from planting to the time when 50% of plants have emerged silks.
- Plant height: The height of twenty-two (22) plants were randomly selected and measured with a graduated measuring stick from the ground level to the node bearing the flag leaf.
- Ear height: The height of the ear from ground level to the node bearing the uppermost ear from the same plants from which plant heights were recorded were also measured.
- Husk cover: data were taken when ears were fully developed and husk leaves were drying out 3 weeks before harvest. Use a 1 to 5 rating scale where 1 = husks tightly arranged and extend beyond the ear tip and 5 = ear tips exposed. The husk leaves above the ear tip was held by hand to determine how far they extend beyond the ear. Plants with ears that were not well developed were avoided, since the husk leaves on small ears will tend to extend further than those on well-filled ears (Badu-Apraku *et al*., 2012)

The following parameters were measured during harvesting;

- Plants Harvested: Total number of plants harvested per row.
- Ears Harvested: Total number of ears harvested per row.
- Moisture: Grain moisture taken by moisture tester on the day of harvesting in percentage.
- Field Weight: The weight of cobs per row measured in kilograms.

The following data were calculated before the data analysis was done;

- The anthesis-silking interval was computed as the difference between days to anthesis and days to silking.

The grain yield in kilograms per plot recorded was converted to grain yield in tons per hectare at 15% grain moisture using the formula below (Badu-Apraku *et al*., 2003).

- Grain yield(t/ha) at 15% moisture content was analyzed by using formular:

$$\text{Grain Yield (t/ha)} = \frac{\text{FW X (100} - \text{MC) x 0.83 x 10,000}}{\text{85 x 75}}$$

Where:

FW = field weight
0.83= shelling coefficient
MC = percentage moisture content (Rahman *et al*., 2007).

3.6. Data Analysis

Analyses of variance (ANOVA) per location and across location or environments for agronomic traits were carried out using Genstat 12th edition (Rahman *et al*., 2007).

Genotypes were considered as fixed effects, whilst environments and replication were considered as random effects. For each agronomic and morphological trait, an individual ANOVA was conducted to determine the statistical significance of the genotypes at each environment and across environments (Table 7).

Table 7: Format for analysis of variance on plot means basis across location

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

Genotypic and phenotypic variances were calculated according to Obilana and Fakorede, (1981) using values from ANOVA table.

Table 8: Computing estimates of variance components

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

Where,

VG = Genotypic variance

VP= Phenotypic variance

VGL= Variance due to genotype X location

VGLR = Variance due to genotype, location and replication

r = Replication

l = Location

VE= Variance due to error

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

3.7 Correlation coefficient

Estimates of correlation coefficients were determined to show the degree of association of the between yield and its components, and among yield components. The genetic (r_G) and phenotypic correlations (r_P) between two characters, X and Y, were estimated according to Akhtar *et al.* (2011). $r_G = \frac{COV_{G(XY)}}{\sqrt{V_{G(X)} \cdot V_{G(Y)}}}$

Where,

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

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

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

Where,

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

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

3.8 Stability of the Genotypes

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

CHAPTER FOUR

4.0. RESULTS

4.1. Performance genotypes across three locations in two seasons

4.1.1. Days to anthesis (DA)

The analysis of variance revealed significant differences ($p<0.05$) among the genotypes (Table 9). The days to anthesis ranged between 57 to 65 days. There were no significant differences among genotypes over major and minor for Legon farm (Table 9). However, there were significant differences among genotypes in Wenchi and Tamale. Varieties "wacci-m-1201, "wacci-m-1202", "wacci-m-1210", "wacci-m-1213" and wacci-m-1216" tasseled at the highest mean days to anthesis. Varieties "wacci-m-1206" and "wacci-m-1217" has the lowest tasseling days in both seasons (Table 9).

Among the check varieties, Etubi Pibi has lowest tasseling days in both seasons. It was observed that Legon has the relatively lower tasseling days compared to Wenchi and Tamale (Table 9), suggesting prevailing uniform condition in both seasons because the trial was under irrigation in both seasons. Across the locations, Tamale exhibited the highest mean days to anthesis. Location showed significant difference for days to anthesis (Table 22). Interaction between genotypes and locations were also significant (Table 22).

Table 9: Days to anthesis at three locations over major and minor seasons

Genotypes	Legon		Wenchi		Tamale	
	Major	Minor	Major	Minor	Major	Minor
Wacci-m-1215	62	62	61	60	64	63
Wacci-m-1209	61	61	61	59	62	61
Wacci-m-1214	61	61	61	60	62	62
Wacci-m-1219	60	60	60	60	64	60
Wacci-m-1203	59	59	61	59	62	61
Wacci-m-1204	59	59	61	60	63	61
Wacci-m-1205	59	59	61	59	62	60
Wacci-m-1207	59	59	59	58	64	60
Wacci-m-1212	59	59	60	59	64	62
Wacci-m-1213	59	59	60	59	65	63
Wacci-m-1201	58	58	59	57	65	61
Wacci-m-1202	58	58	60	60	65	61
Wacci-m-1208	58	58	59	60	64	61
Wacci-m-1211	58	58	60	59	64	61
Wacc-m-1206	57	57	60	60	62	60
Wacci-m-1210	57	57	58	58	65	61
Wacci-m-1216	57	57	60	60	65	61
Wacci-m-1217	57	57	59	59	63	60
Wacci-m-1218	57	57	56	56	61	61
Wacci-m-1220	57	57	59	59	63	61
checks						
mamaba	58	58	58	57	63	59
Pannar	58	58	60	58	64	60
Etubi Pibi	57	57	59	56	63	60
LSD (p<0.05)	0.5	0.6	0.6	0.3	0.6	0.5
CV (%)	3.9	3.9	3.3	3.7	1.9	2.6

4.1.2. Days to silking (DS)

The analysis of variance revealed that there were significant differences ($p<0.05$) for number of days to silking (Appendix 4). Days to silking ranged between 60 days to 70 days. The variety "wacci-m-1202" silked at the highest mean days in minor season and the same variety silked in 65 days in major (Table 10). This suggests that at Tamale where the highest silking was observed may have experienced some level of drought resulting in delay of female inflorescence. Among the check varieties, "Pannar" silked at 65 days in major season (Table 10). The lowest mean days to silking was exhibited by variety "Mamaba" in 60 days. Across the locations, Tamale has the highest days to silking in both major and minor seasons (Table 10). There were significant differences among locations for days to silking and interaction between locations and genotypes were significant (Table 22).

Table 10: Days to silking across three locations over major and minor seasons

Genotypes	Legon		Wenchi		Tamale	
	Major	Minor	Major	Minor	Major	Minor
Wacci-m-1214	65	65	64	66	66	67
Wacci-m-1215	65	65	63	64	62	64
Wacci-m-1209	64	64	64	65	66	68
Wacci-m-1219	64	64	64	64	65	69
Wacci-m-1203	63	63	62	64	65	66
Wacci-m-1204	63	63	64	65	65	69
Wacci-m-1211	63	63	64	63	66	69
Wacci-m-1212	63	63	62	64	66	69
Wacci-m-1213	63	63	63	64	67	69
Wacci-m-1201	62	62	62	63	64	69
Wacci-m-1205	62	62	63	64	64	66
Wacci-m-1208	62	62	63	63	65	69
Wacci-m-1216	62	62	64	64	65	70
Wacci-m-1220	62	62	62	64	65	69
Wacci-m-1202	61	61	62	65	65	70
Wacci-m-1210	61	61	62	63	65	68
Wacci-m- 1218	61	61	61	63	66	66
Wacci-m-1206	60	60	63	63	65	67
Wacci-m-1217	60	60	62	64	64	68
Wacci-m-1207	59	59	62	65	65	69
Checks						
Mamaba	62	62	60	62	64	69
Pannar	61	61	63	63	65	69
Etubi Pibi	61	61	61	63	64	68
LSD ($p<0.05$)	0.6	0.4	0.3	0.4	0.5	0.6
CV (%)	3.8	3.8	2.5	2.3	1.7	3.2

4.1.3. Plant height (PH)

The plant height ranged between 125 cm to 235 cm. The highest height was given by variety “wacci-m-1203” in both seasons and lowest was “wacci-m-1201” (Table 11). Among the checks, “Pannar” exhibited the highest plant height (228 cm) with lowest being Etubi Pibi (188 cm). Across the locations, Legon has the highest plant height and Tamale given the lowest (Table 11). Analysis of variance revealed significant difference ($p<0.05$) among genotypes for plant height (Appendix 7).

Table 11: Plant height (PH) across three locations over major and minor seasons

	Legon		Wenchi		Tamale	
Genotypes	Major	Minor	Major	Minor	Major	Minor
Wacci-m-1203	235	235	192	196	177	167
Wacci-m-1212	232	232	195.3	195.3	187.3	182.3
Wacci-m-1220	230	230	188	186	192	178
Wacci-m-1205	228.3	228	199	199	187	180
Wacci-m-1208	227	227	174	176.3	190	162
Wacci-m-1215	227	227	187	187	192	182
Wacci-m-1204	223.3	223	197	190	182	183
Wacci-m-1211	223.3	223	198.3	178.3	189.3	176
Wacci-m-1207	223	222	186	182	186	172.3
Wacci-m-1213	222	222	171.3	173	175.3	168
Wacci-m-1202	222	221	162	163	162	149
Wacci-m-1216	213.3	213	187	187	193	187.3
Wacci-m-1209	213	198	188	188	188	157.3
Wacci-m-1210	212	212	194	192.3	171	168.3
Wacci-m-1219	208	208.3	171.3	171.3	202.3	198
Wacci-m-1201	201	201	161	161	160	125
Wacci-m-1214	200	200	189	189	180	173
Wacci-m-1206	199.3	199	176.3	177	184	166
Wacci-m-1218	198	196	175	175	173.3	165
Wacci-m-1217	197	197	184	184	194.3	187.3
Checks						
Mamaba	196	196	190	190	189.3	185.3
Pannar	228	228	190	189	193.3	188
Etubi Pibi	198	198	190	189.3	188	182
LSD(p<0.05)	4.4	4.3		3.7		4.3
CV (%)	7.1	7.1		10.3		11.0

4.1.4. Ear height (EH)

Ear height ranged between 94.3 cm to 147 cm (Table 12). The variety “wacci-m-1205” in both seasons. “Mamaba” gave the lowest ear height in both seasons. Among the check varieties, “Pannar” exhibited the highest ear height (128.3 cm) in both seasons and there were significant differences among the checks. Across the locations, Legon has the highest ear height in both seasons (Table 12).

Table 12: Ear height across three locations over major and minor seasons

Genotypes	Legon		Wenchi		Tamale	
	Major	Minor	Major	Minor	Major	Minor
Wacci-m-1205	147	147	109.3	104	86	90
Wacci-m-1203	145	145	112	133	87	77
Wacci-m-1213	142	142	115	118	101	95
Wacci-m-1212	135	135	115	115	102	99
Wacci-m-1220	134	137	132	128	106	103
Wacci-m-1202	133.3	133	115.3	115	81	77
Wacci-m-1216	132	132	122	122	118.3	108
Wacci-m-1219	132	132	119	119	106.3	103.3
Wacci-m-1206	130	130	131	131	86	83
Wacci-m-1211	130	130	104	107	102	99.3
Wacci-m-1204	128.3	128	110.3	112.3	96	101
Wacci-m-1207	128	129	118	121	96	85.3
Wacci-m-1208	127	127	104	104	85.3	88
Wacci-m-1214	124.3	124	125.3	126	94	86.3
Wacci-m-1215	122	122	105	105	98	91.3
Wacci-m-1209	117	117	108.3	108	96.3	77.3
Wacci-m-1217	117	117	122	122	105	102.3
Wacci-m-1201	112	112	103.3	104	80.3	83
Wacci-m-1210	112	112	118	118	86	87
Wacci-m-1218	126	130	118	122	99	93.3
Checks						
Mamaba	94.3	94	122	107	98	91
Pannar	128.3	128	118	118	110	106
Etubi Pibi	112	112	103	103	105	102
LSD(p<0.05)	2.8	4.0	2.6	2.4	4.8	4.1
CV (%)	11.3	11.3	14.0	14.4	13.4	17.9

4.1.5. Ears Harvested

The combined revealed significant difference ($p<0.05$) among hybrids for ears harvested (Appendix 6). The highest mean ears harvested were 44 and these mean ears harvested were exhibited in both seasons across all locations. However, Wenchi gave the highest ear harvested in both seasons compared to Legon and Tamale. There were significant differences among the genotypes over major and minor seasons (Table 13).

Table 13: Ears harvested across three locations over major and minor seasons

	Legon		Wenchi		Tamale	
Genotypes	Major	Minor	Major	Minor	Major	Minor
Wacci-m-1209	44	44	43	40	43	41
Wacci-m-1217	44	44	39	40	40	40
Wacci-m-1207	43	43	44	40	41	42
Wacci-m-1212	43	43	44	40	42	40
Wacci-m-1214	43	43	43	44	40	38
Wacci-m-1203	41	40	38	39	40	40
Wacci-m-1204	41	42	44	41	43	39
Wacci-m-1205	41	40	43	40	44	43
Wacci-m-1206	41	41	44	43	43	42
Wacci-m-1208	41	41	38	40	44	44
Wacci-m-1210	41	41	43	42	40	40
Wacci-m-1213	41	41	42	43	39	40
Wacci-m-1215	41	41	43	36	43	38
Wacci-m-1216	41	41	39	42	44	39
Wacci-m-1220	41	41	41	39	39	41
Wacci-m-1218	40	40	38	37	40	39
Wacci-m-1219	40	40	40	40	40	40
Wacci-m-1211	39	39	43	41	40	43
Wacci-m-1202	38	38	44	43	41	40
Wacci-m-1201	34	36	38	40	39	38
Checks						
Mamaba	43	43	42	41	39	38
Pannar	42	42	41	41	43	37
Etubi Pibi	41	41	39	38	40	40
LSD (p<0.05)	0.7	0.8	1.0	1.6	0.8	1.1
CV(%)	8.6	8.4	7.5	8.4	10.7	9.2

4.1.6. Field weight (FW)

The combined analysis of variance showed significant difference ($p<0.05$) among genotypes for field weight (Appendix 2). The field weight ranged between 19.1 kg/ha to 5.3 kg/ha (Table 14). The highest mean field weight was given by variety “wacci-m-1212” in major season and “Mamaba” gave the lowest field weight. Among the check varieties, “Pannar” exhibited the highest mean field weight of 10.3 kg/ha and the lowest was exhibited by variety “mamaba” of 5.3 kg/ha. The highest mean field weight was recorded in Wenchi followed by Legon farm and

Tamale recorded the lowest mean field weight (Table 14). The interaction between genotypes and locations for field weight was significant (Table 21).

Table 14: Field weight (kg/ha) across three locations over major and minor seasons

	Legon		Wenchi		Tamale	
Genotypes	Major	Minor	Major	Minor	Major	Minor
Wacci-m-1204	16.2	15.3	12.4	10.7	10.6	6.6
Wacci-m-1207	15.6	14.9	13.5	10.9	10.4	4.9
Wacci-m-1205	14.4	13.6	13.0	8.6	11.4	5.2
Wacci-m-1209	14.2	13.5	12.6	10.2	8.8	6.7
Wacci-m-1212	12.9	12.2	19.1	13.9	10.3	5.5
Wacci-m-1206	12.2	11.5	15.2	13.2	11.8	6.5
Wacci-m-1220	11.2	12.5	13.6	9.0	7.5	5.1
Wacci-m-1203	10.5	11.1	6.4	6.6	6.2	4.7
Wacci-m-1208	10.4	9.5	10.4	8.3	8.4	5.8
Wacci-m-1210	10.4	10.6	15.8	11.4	8.1	6.3
Wacci-m-1211	10.4	10.6	15.8	11.4	8.1	6.3
Wacci-m-1213	10.4	10.0	7.7	6.3	5.9	5.1
Wacci-m-1202	9.3	8.9	6.8	4.6	6.3	5.3
Wacci-m-1219	9.2	8.0	7.4	8.5	5.7	5.0
Wacci-m-1215	9.1	8.7	7.5	5.2	6.5	6.2
Wacci-m-1218	8.6	8.7		4.4	5.9	5.6
Wacci-m-1216	8.4	7.9	7.6	5.0	6.3	5.1
Wacci-m-1214	7.8	7.3	7.8	6.2	6.3	5.4
Wacci-m-1201	7.5	6.8	7.8	7.3	6.4	5.4
Wacci-m-1217	6.6	6.2	6.3	6.3	5.8	5.0
Checks						
Mamaba	5.9	5.3	6.0	6.2	6.4	6.1
Pannar	10.3	9.9	7.8	5.9	7.2	5.3
Etubi Pibi	7.9	9.0	7.3	5.4	5.9	5.9
LSD(p<0.05)	1.0	0.8	0.5	0.7	0.3	0.8
CV(%)	20.7	21.2	18.5	21.8	11.2	17.1

4.1.7. Grain Yield (t/ha)

The combined analysis of variance revealed that there were significant differences among varieties for yield (Appendix 1). The grain yield ranged from 13.7 t/ha to 3.3 t/ha and grand mean of 6.3 t/ha. The highest mean grain yield was given by variety “wacci-m-1212”. Among the checks, variety “Pannar” exhibited the highest mean grain yield of 7.1 t/ha and 6.8 t/ha in major and minor seasons respectively (Table 15). In addition, the lowest mean grain yield was exhibited by variety “Mamaba” of 4.5 t/ha and 3.7 t/ha in major and minor seasons respectively. There were also significant differences among the checks and the twenty-hybrid maize selected from WACCI maize breeding program. Across the locations, Wenchi recorded the highest mean grain yield in major and Legon in minor season. Tamale recorded the lowest mean grain yield of the performance of the genotypes (Table 15). Across the three locations in two seasons, the analysis of ranked sum for grain yield suggests that eight hybrids, “ wacci-m-1212”, “wacci-m-1204”, “wacci-m-1207”, “wacci-m-1206”, “wacci-m-1205”, “wacci-m-1209”, “wacci-m-1210” and “wacci-m-1220” gave mean grain yield ranged between 7.1 t/ha to 9.0 t/ha above the yield of the best performing check varieties “Pannar” which gave 5.6 t/ha (Table 16). The performance of genotypes for grain yield is significant across location (Table 24). This is because there is great variation within these three location (Table 3). Wenchi showed high amount of rainfall and humidity resulting in conducive environment for grain production (Table 4). Rainfall and humidity volume in Tamale is relatively low and could not support grain production throughout entire crop production unless there is supplementary water through irrigation (Table 5)

Table 15: Grain yield (t/ha) across three locations over major and minor seasons

Genotypes	Legon		Wenchi		Tamale	
	Major	Minor	Major	Minor	Major	Minor
Wacci-m-1207	11.6	10.9	10.4	7.9	7.6	4.0
Wacci-m-1204	11.4	10.4	9.2	7.8	7.9	5.3
Wacci-m-1205	10.7	9.6	9.1	6.3	8.4	4.1
Wacci-m-1209	10.1	9.5	9.2	7.5	6.6	5.3
Wacci-m-1212	9.1	8.4	13.7	10.4	7.7	4.4
Wacci-m-1206	9.0	8.5	10.6	9.8	8.8	5.1
Wacci-m-1220	8.0	8.8	9.9	6.6	5.6	4.0
Wacci-m-1213	7.7	7.3	5.6	4.7	4.4	4.1
Wacci-m-1208	7.6	6.8	7.5	6.0	6.4	4.6
Wacci-m-1210	7.6	7.5	11.3	9.7	6.0	5.0
Wacci-m-1203	7.5	7.9	4.6	4.7	4.6	3.6
Wacci-m-1218	6.8	6.4	4.2	3.3	4.4	4.3
Wacci-m-1202	6.6	6.3	5.0	3.4	4.8	4.2
Wacci-m-1211	6.5	6.0	6.0	6.0	5.8	3.7
Wacci-m-1215	6.5	6.1	5.4	3.9	4.8	5.0
Wacci-m-1216	6.5	6.0	5.5	3.7	4.7	4.1
Wacci-m-1219	6.3	5.8	5.3	6.2	4.2	3.9
Wacci-m-1201	6.1	5.8	6.0	5.8	4.8	4.2
Wacci-m-1217	6.1	5.3	4.6	4.6	4.4	3.9
Wacci-m-1214	5.9	5.6	5.6	4.7	4.6	4.3
Checks						
Mamaba	5.8	3.7	4.5	4.7	4.6	4.8
Pannar	7.1	6.8	5.6	4.5	5.4	4.2
Etubi Pibi	5.8	5.1	5.2	4.0	4.9	4.6
LSD(p<0.05)	0.7	0.5	0.4	0.6	0.2	0.5
CV(%)	20.2	20.6	18.7	22.7	10.9	17.2

Table 16: Ranked sum of grain yield 23 genotypes of maize hybrid

GENOTYPES	YIELD (t/ha)	RANKED
Wacci-m-1212	9.0	1st
Wacci-m-1204	8.7	2nd
Wacci-m-1207	8.7	2nd
Wacci-m-1206	8.6	4th
Wacci-m-1205	8.0	5th
Wacci-m-1209	8.0	5th
Wacci-m-1210	7.8	7th
Wacci-m-1220	7.1	8th
Wacci-m-1208	6.5	9th
Wacci-m-1211	5.7	10th
Pannar	5.6	11th
Wacci-m-1213	5.6	11th
Wacci-m-1201	5.5	13th
Wacci-m-1203	5.5	13th
Wacci-m-1215	5.3	15th
Wacci-m-1219	5.3	15th
Wacci-m-1214	5.1	17th
Wacci-m-1216	5.1	17th
Wacci-m-1202	5.0	19th
Etubi Pibi	4.9	20th
Wacci-m-1218	4.9	20th
Wacci-m-1217	4.8	22nd
Mamaba	4.4	23rd
LSD ($p<0.05$)	1.2	

4.2. Phenotypic correlation of important agronomic traits

4.2.1. Correlation of agronomic traits

Strong positive and significant correlation ($p<0.05$) was observed among days to silking and anthesis (Table 17). Also highly positive correlation was observed between ear height and plant height (Table 20). Significant negative correlation was observed between ear height and plant stand but significant positive correlation was observed between ear height and grain yield (Table 18).

Highly positive correlation among number of ears harvested, numbers of plants harvested, plants stand and negative significant correlation between yield and field weight (Table 20). Strong positive correlation among field weight, plant height and grain yield was recorded.

Table 17: Phenotypic Correlation matrix of measured traits at Legon

Traits	DA	DS	EH	EHA	FW	PH	PHA	PS
DS	0.844**							
EH	0.112*	-0.073						
EHA	0.010	0.047	-0.036					
FW	0.108	-0.095	-0.264*	-0.027*				
PH	-0.088	0.118	0.664**	0.054	0.386**			
PHA	0.025	-0.077	0.016	0.964**	0.027*	-0.033		
PS	0.063	-0.111*	-0.082*	0.148**	0.000	-0.103*	0.301**	
YIELD	-0.067	0.047	0.270*	0.045*	0.992**	-0.357	-0.040*	0.005

*significant level (p<0.05) ** highly significant (p<0.01)

Table 18: Phenotypic Correlation matrix of measured traits at Wenchi

Traits	DA	DS	EH	EHA	FW	PH	PHA	PS
DS	0.737**							
EH	-0.129	0.106						
EHA	0.049	-0.043	-0.179					
FW	0.123	-0.007	0.107	-0.148*				
PH	0.072	0.026	0.321*	0.042	-0.057*			
PHA	-0.020	0.038	0.156	0.948**	0.137*	-0.038		
PS	-0.036	-0.022	0.166*	-0.195**	-0.043	-0.069	0.341**	
YIELD	-0.125	-0.001	-0.089	0.168*	0.990**	0.075*	-0.139*	0.030

*indicates significant level (p<0.05) ** highly significant level (p<0.01)

Table 19: Phenotypic Correlation matrix of measured traits at Tamale

Traits	DA	DS	EH	EHA	FW	PH	PHA	PS
DS	0.800**							
EH	-0.038*	0.065						
EHA	-0.019*	-0.009*	-0.204					
FW	-0.055**	-0.082**	0.285	0.352				
PH	-0.061*	-0.055*	0.675**	0.165	-0.210*			
PHA	0.033*	0.028*	0.206	0.977**	-0.409	0-.157		
PS	-0.016	-0.064	0.074	-0.135**	0.117	-0.020	0.255**	
YIELD	0.039*	0.067*	-0.291	-0.337*	0.991**	0.219*	0.401*	-0.112*

*indicates significant level (p<0.05) ** highly significant level (p<0.01)

Table 20: Phenotypic Correlation matrix of measured traits at all the three locations

Traits	DA	DS	EH	EHA	FW	PH	PHA	PS
DS	0.8711**							
EH	-0.3625**	-0.4129**						
EHA	-0.0156	-0.0861	0.0937					
FW	-0.2919**	-0.4044**	0.3971**	0.2743**				
PH	-0.2942**	-0.3585**	0.6765**	0.0902	0.40557**			
PHA	-0.0115	-0.0790	0.1059*	0.9755**	0.2547**	0.0874		
PS	-.00522	-0.0883	0.0601	0.5347**	0.1079*	0.0067	0.5784**	
YIELD	-0.2744**	-0.3793**	0.3687**	0.2873**	0.9921**	0.3789**	0.2670**	0.1128*

*indicates significant level ($p<0.05$) ** highly significant level ($p<0.01$)

Table 21: Variance components of 5 quantitative traits studied among 23 hybrids

Sources of variation	Df	Grain yield	Field weight	Plant height	Ear height	Ear harvested
Block	2	6.07	13.35	1081.4	951.25	6.75
Location	5	101.24*	244.53*	22812.17*	18593.56*	91.40
Genotypes	22	42.71*	81.56*	1355.28*	3187.86	43.19
Genotypes * location	110	4.02*	7.61*	275.60	2134.16	23.62

*indicates significant level ($p<0.05$)

Table 22: Variance components of 4 qualitative traits studied among 23 hybrids

Source of variation	Df	Days to anthesis	Days to silking	Plant stand
Block	2	1.04	0.88	8.86
Location	5	254.66*	414.07*	5.88
Genotypes	22	13.52*	11.63*	11.26
Genotypes * location	110	2.84	2.79	9.22

*indicates significant level ($p<0.05$).

4.3. Grain Yield Stability using AMMI

The magnitude and nature of genotype by environment (GE) effect was significant according to additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield (Table 23). The main effects also were highly significant. Further analysis showed that the genotypes significantly contributed more than the environments in these effects (Table 23).

Table 23: AMMI Analysis of grain yield

Source	Df	Ss	Ms	F	F_prob	Total SS (%)
Total	413	2361	5.72		0.00013*	
Treatments	137	1887.4	13.78	9.1	0.0001*	
Genotypes	22	939.6	42.71	28.22	0.0000*	39.79
Environment	5	506.2	101.24	16.38	0.0013*	21.43
Block	12	74.1	6.18	4.08	0.0064*	
Interaction	110	441.7	4.02	2.65	0.0008*	
IPCA1	26	244.4	9.4	6.23	0.0002*	
IPCA2	24	147.1	6.13	4.05	0.0009*	
Residual	60	50.2	0.84	0.55	0.99658	
Error	264	399.5	1.51			

*Indicates significant level ($p<0.05$)

Table 24: Variance components for yield at the three locations

Source of variation	Df	Legon		Wenchi		Tamale	
		MS	%SS	MS	%SS	MS	%SS
Location	2	6.79	0.98	50.77	4.99	58.44	22.12
Genotypes	22	20.79*	66.30	32.92*	71.21	4.33*	36.05
Error	114	1.98	32.69	2.12	23.79	0.9690	41.82
CV (%)		4.3		13.1			18.3

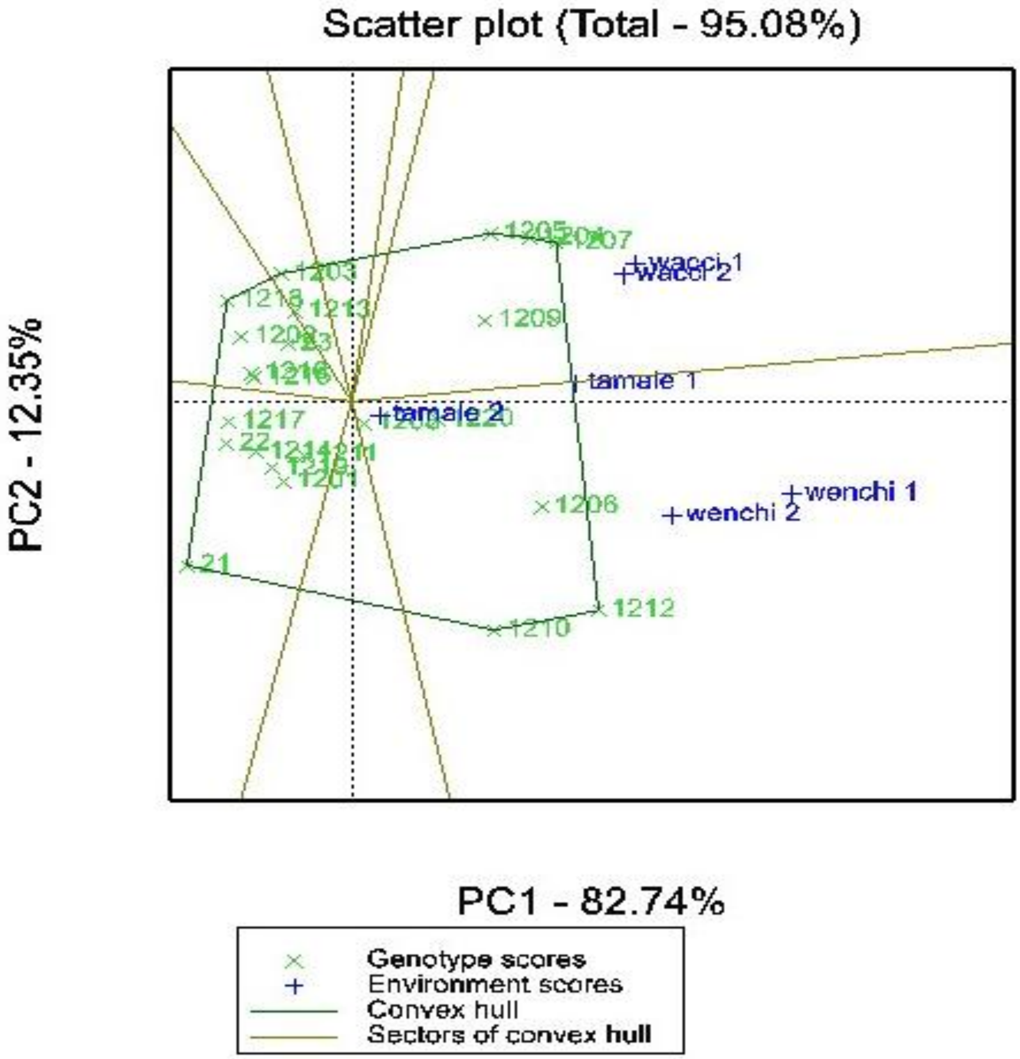
*indicates significant level ($p<0.05$)

4.4. Mean performance and stability of genotypes in test locations using GGE biplot

The GGE biplot data analysis conducted in this study showed the "which won where" pattern (fig 1), mean performance and stability of tested genotypes and rankings as well as the discriminating ability and representativeness of the genotypes (Yan 2002). The GGE biplot is an invaluable statistical tool for examining the performance of genotypes tested in different environments. The polygon view of the GGE biplot indicated the best genotype in each environment. The "which-won-where" view of the GGE biplot is an effective visual tool in mega-environment analysis (Yan *et al*., 2007).

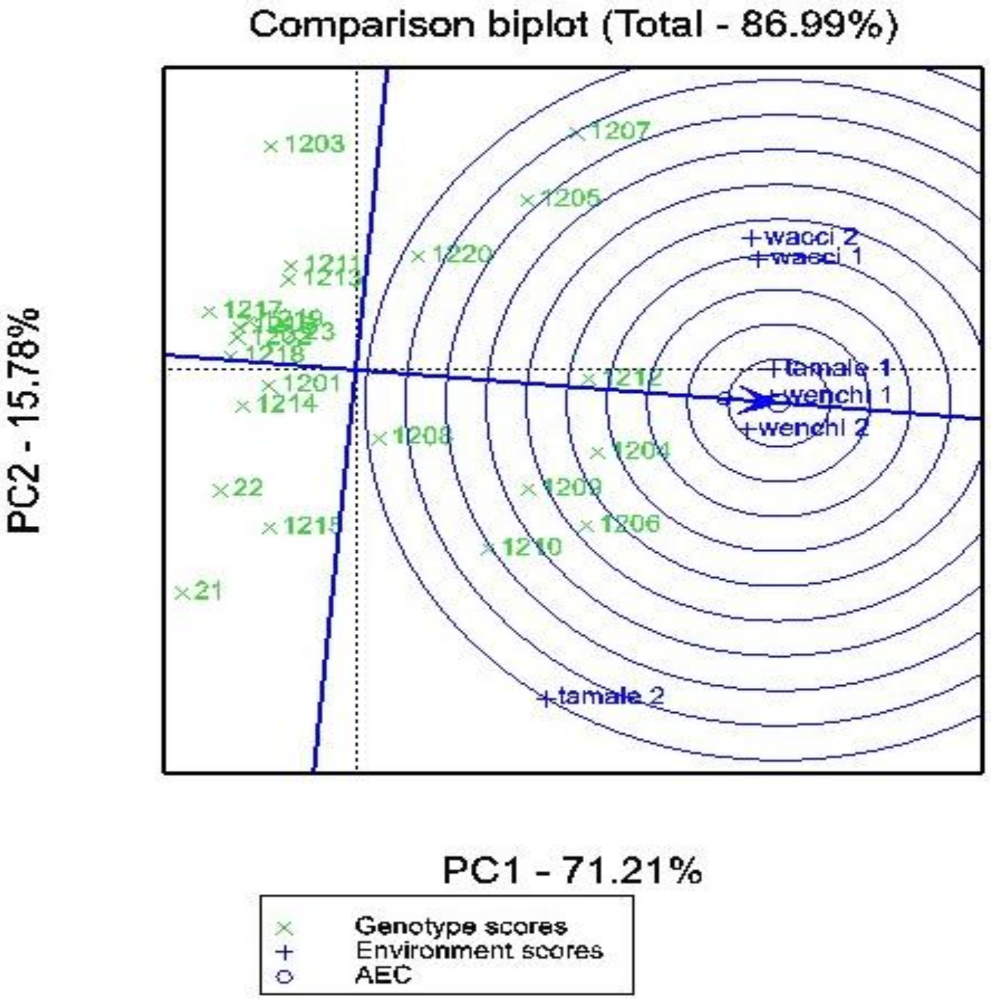
Principal components 1 and 2 (PC 1 and PC 2) together explained 95% of variation in yield (fig 1). Thus 95% of the variation in yield was due to genotypes and genotype – environment interaction (fig 1). According to biplot shown in fig 1, corner genotypes are most responsive ones, and can be visually determined. These genotypes were "wcci-m-1212" and "wacci-m-1207", were not significantly different from "wacci-m-1204" and "wacci-m-1205" (fig 1). Locations were divided in 3 sectors. The first sector represents wacci 1, wacci 2 (major and minor season respectively) with genotypes "wacci-m-1204", "wacci-m-1205" and "wacci-m-

1207" be the most favorable, second sector represents Wenchi 1, 2 and Tamale 2 with genotypes "wacci-m-1212" and "wacci-m-1210" were most favorable and the third sector was Tamale 1 (fig 1). The other two corner genotypes "wacci-m-1218" and 21(Mamaba) were the poorest yielding genotypes. They were located far away from all the testing locations, reflecting the fact that they performed poorly at each location. In addition, genotypes within the polygon ('wacci-m-1209", "wacci-m-1206", "wacci-m-1208" and "wacci-m-1220") were less responsive to location than the corner genotypes (fig 1). Fig 1 indicates the existence of the 3 mega-environments for maize in Ghana, "wacci-m-1207", "wacci-m-1204" and "wacci-m-1205" winning niche in coastal savannah and "wacci-m-1208" and "wacci-m-1220" winning niche in Guinea savannah zone.



Which wins where or which is best for what

Fig 1: GGE biplot identification of winning genotypes and their related mega-environment.



Ranking entries based on both mean and stability

Fig 2: GGE biplot of ideal genotype and comparison of the genotypes with the ideal genotype

The center of the concentric circles is where an ideal genotype (high mean yield and most stable variety) is located (fig 2). In other words, projection on the ATC vertical axis is obviously zero or stable. Therefore, a smaller the distance from genotypes to the virtual ideal genotype represents an ideal genotype. Therefore, genotype “wacci-m-1212”, “wacci-m-1208” and “wacci-m-1204” were ideal genotypes in terms of higher yield ability and stability, compared with rest of the genotypes (fig 2). In addition, genotypes “wacci-m-1209”, “wacci-m-1206” and “wacci-m-1210’, “wacci-m-1220”, “wacci-m-1205”, and “wacci-m-1207” located in the next concentric circles may be considered as desirable genotypes (fig 2).

CHAPTER FIVE

5.0. DISCUSSION

5.1. Grain yield and other agronomic traits

Seven agronomic characters across the three locations were studied. Highly significant ($P<0.01$) differences were observed among the three trial locations for all the traits studied. Analysis for grain yield showed highly significant differences among the genotypes across the three locations. Highly significant differences among locations were observed for the 23 genotypes for grain yield, days to tasseling, days to silking, plant height, field weight, ear height. For genotypes, variations were highly significant for grain yield, field weight, plant height, days to anthesis and silking. However, there were no significant differences among the genotypes for ear height, ear harvest and plant stand. Apart from grain yield and field weight, differences due to the interaction (genotype x location) were not significant for all the traits studied.

Differences due to location influences were similarly noted by Sallah *et al*. (2004) when they studied genotype by environment interaction effects of three maturity groups of maize at the same sites. Differences among locations may also be because the genotypes used were from parents of diverse genetic backgrounds, Obi (1991), Uguru (2005) and Akande and Lamidi (2006) reported similar results stating that diverse agronomic characteristics are controlled by diverse genetic factors and so genotypes perform differently in a given location.

Highly significant or significant differences due to genotypes were noted among the entries for grain yield and most of the agronomic characters evaluated. The genotypic variations found were due to the diverse backgrounds from which the genotypes used in the study were developed. This result was in agreement with findings by Sallah *et al*. (2001) and Soza *et al*. (1996), and these authors also used hybrids together with open pollinated varieties. The high yields could be due to the effects of dominant genes, which are perceived as favorable source of alleles for the development of selected maize population. Trifunovi *et al*. (1998) and Meghji et al., (1984), reported similar results. Moreover, the observed lack of significant means squares for G x E of plant height, ear height, days to silking, days to tasseling amongst others showed that these parameters were stable across the three sites used for the study. Genotype x location interaction has, over the years, continued to cause setback for researchers which necessitate the need to carry out multi-location yield trials to enable plant breeders to categorize and select genotypes that are high yielding with specific or wide-ranging adaptation to diverse agro-ecological zones, prior to variety release. Information generated from these multi-location trials could be useful for state-run breeding programmes by identifying the appropriate breeding materials with advantageous agronomic qualities at test sites (Badu-Apraku *et al*., 2010).

5.2. Yield performance and stability

The magnitude and nature of genotype by environment (GE) effect was significant according to additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield showed in Table 23. The main effects also were highly significant. Further analysis showed that the genotypes significantly contributed more than the environments in these effects. This is contrary to Easwari and Sheela (1998), and Cach *et al.* (2006) as cited by Ssemakula *et al.* (2007), Fakorede & Adeyemo (1986), Badu-Apraku *et al*.,(1995, 2003) and Mohammadi *et al*., (2009), who reported that the largest proportion of total variation in multi-environment trials is attributed to locations, whereas Genotypes and Genotype × Location sources of variation are relatively smaller based on the fact that yield is a polygenic trait and, therefore, subject to much influence from the environment. The presence of large genetic variability is of the utmost importance for progress from selection for grain yield tested in different environments in multi-environment trials (Badu-Apraku *et al*., 2012). Thus, the observed large sum of square of genotypes for grain yield indicated that good progress can be made in selecting for grain yield under the different environments. The significant mean square for location showed that genetic effects were influenced by the environments, which is a consequence of environmental diversity. Similar observations were reported by Butron *et al*., (2002) in which they indicated that Genotype x Location effects for grain yield in maize was mainly due to environmental yield limiting factors such as the mean minimum temperature and relative humidity. The observed Significant G x L mean square for grain yield suggested that the locations for which the hybrids were tested comprise a number of special environments. Hence, hybrids selected should be specifically adapted to the different environments.

Environmental PC1 scores were obtained in both positive and negative scores. This case exhibited that PC1 scores represent proportional genotype yield differences across environments which were caused by both crossover and non-crossover GEI. Similar to PC1, environmental PC2 scores had both positive and negative scores. Kaya *et al.* (2006) and Emre *et al.* (2009) reported similar results. In the polygon view of the GGE biplot, the presence of two or more environments within a sector indicates that a single genotype has the highest yield in those environments. If environments fall into different sectors, it means that different genotypes won in different environments (Yan *et al*., 2007). As observed in Figure 1, the variety “waci-m-1207” had the highest yield at Tamale and Legon, while the winning hybrid at Wenchi was “wacci-m-

1212”. This crossover G × E indicated that the target environment could be divided into different target zones.

For selection for broad adaptation in maize production, an ideal genotype should have both high mean performance and high stability within a mega-environment (Badu-Apraku *et al*, 2011a). Thus, “wacci-m-1212”, “wacci-m-1204”, “wacci-m-1208”, “wacci-m-1209”, “wacci-m-1206”, “wacci-m-1220”, “wacci-m-1205” and “wacci-m-1207” were the highest yielding and most stable hybrids. This implies that their rankings were highly consistent across locations. They were closest to the ideal genotype and may be considered as best hybrids (fig 2).

5.3. Correlations between grain yield and other agronomic traits

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

There was strong positive correlation between days to silking and days to anthesis. This suggests that the two traits may be controlled either by the same gene or by similar gene or may have pleiotropic effect on each other or may have linkage genes (Brown and Caligari, 2008). However, both traits exhibited negative highly significant correlation with grain yield, plant height, ear height and field weight. Hence, the flowering days seem undesirable for indirect selection for these traits. The negative significant association between days to flowering and grain yield agrees with Jayakumar *et al*., (2007).

There was strong significant positive association between plant height and ear height. Similarly, both plant height and ear height had significant positive relationship with field weight. Plant height, number of ears harvested, field weight had a positive and significant direct contribution to yield. Afzal *et al*., (1997) reported similar results. The negative phenotypic correlations between grain yield and days to silking, suggested that grain yield may be reduced by a relative increase in this trait. There was positive significant inter-correlation among grain yield, plant height, field weight, number of plants harvested, number of ears harvested, and plant stand suggesting the usefulness of indirect selection.

CHAPTER SIX

6.0. CONCLUSIONS AND RECOMMENDATIONS

6.1. CONCLUSIONS

A total of 23 genotypes made –up of 19 single crosses, 1 three-way cross and 3 locally released hybrids used as checks were evaluated across three locations with a view to comparing their relative yielding abilities and stability. Strong positive correlations were observed between grain yield and field weight (0.9921), grain yield and plant height (0.3789) and grain yield and ear height (0.3687). These traits possessing high correlations with grain yield can be used as superior characters to help improve maize grain yield. It is important to identify a variety of traits largely correlated to grain yield, which is the ultimate goal in most breeding programs.

The significant genotype - environment interaction revealed by AMMI suggests that the relative performance of the genotypes changed for grain yield across all environments. The study also identified Tamale as environment recording low grain yield in both seasons compared to Legon and Wenchi.

The study identified eight promising hybrids, which out yielded the check varieties used in the study. This support general opinion held by many stakeholders that use of hybrids hold the future of Ghana’s agriculture and that serious effort must be made to encourage the adoption and use of superior hybrid maize varieties in Ghana as a means of increasing maize productivity and production in the country. The use of hybrid seed will also mean that farmers will always need to obtain quality seed from the right source and reduce the use of grain as seed, as is the common practice when farmers plant OPVs and select their own seed from the grain harvested.

6.2. RECOMMENDATIONS

Supplementary testing should be carried out on the eight hybrids that performed well in terms of grain yield in order to generate data to support on-farm testing of these hybrids for possible release in Ghana. Large quantities of hybrid seeds should be produced by seed companies to bring down the unit price of hybrid seed, to make it affordable to farmers. Farmers should be encouraged to buy and use hybrid seeds to take advantage of their high yields. The use of hybrid seed must be supported with timely supply of fertilizers at subsidized prices for the desired output in higher yields.

REFERNCES

Abdulai M. S., Sallah P.Y.K. and Safo-Kantanka O. (2007). Maize Grain Yield Stability Analysis in Full Season Lowland Maize in Ghana. *Int. J. Agri. Biol., Vol. 9*, No. 1, 2007.

Acquaah, G. (2007). Principles of Plant Genetics and Breeding. Blackwell Publishing, USA.

Afzal, M., Sharif M. and Chaudhry M.H., (1997). Genetic and path coefficient analysis studies in maize. *Pak. J. Agric. Res*., 35: 360-368

Agribusiness Trade Project (2008) Maize Value Chain Assessment for West Africa, Draft 2007.

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

Al- Swailem, A. M., Shehata, M.M., Shair O.H., Sabaan, S.A., Al-Anazi, I.O. and Al-Shammari, T. A. (2005). An efficient method for identification and qualification of Genetic modification of local, improved and food products of maize in Saudi Arabia using PCR-based markers and real time PCR. *Journal of Food, Agriculture and and Environment.* 3(2): 14 -19.

Annicchiarico, P., (1997). Joint regression vs. AMMI analysis of genotype-environment interactions for cereals in Italy. *Euphytica* 94: 5362.

Asenso- Okyere, (2001). Transforming agricultural production and productivity for sustained rapid growth and development. Ghana in 21st century. ISSER Seminar series.

No.4. Institute of Statistical, Social and Econmic Research, Legon.

Badu-Apraku, B., Fajemisin, J.M. & Diallo, A.O. (1995). The performance of early and extra-early varieties across environments in West and Central Africa. In Contributing to Food Self-sufficiency: Maize Research and Development in West and Central Africa. Proceedings of a Regional Maize Workshop, 29 May–2 June 1995 (Eds B. Badu-Apraku, M. O. Akoroda, M. Ouedraogo & F. M. Quin). pp. 149–159. Cotonou, Benin Republic: IITA.

Badu-Apraku, B., Abamu, F. J., Menkir, A., Fakorede, M. A. B., Obeng-Antwi, K. & The, C. (2003). Genotype by environment interactions in the regional early variety trials in West and Central Africa. *Maydica* 48, 93–104.

Badu-Apraku, B., Akinwale, R.O., Fakorede, M.A.B., (2010). Selection of early maturing maize inbred lines for hybrids production using multiple traits under striga infested and striga free environments *Maydica* 55 261-274.

Badu-Apraku, B., R. O. Akinwale, J. Franco and M. Oyekunle (2012); Assessment of reliability of secondary traits in selecting for improved grain yield in drought and low-nitrogen environments. Crop Sci.: doi: 10.2135/cropsci2011.12.0629.

Becker, H.C. and Léon, J., (1988). Stability analysis in plant breeding. *Plant Breeding* 101: 1-23.

Benz, B.F.(2001). Archaeological evidence of teosinte domestication from Guila Naquitz, Oaxaca. *Pro. Natl. Acad. Sci*. USA 98: 2104 – 2106.

Bidinger, F.R., Mahalakshmi, V. and Rao, G.D.P. (1987) Assessment of drought resistance in pearl millet [Pennisetum americanum (L.) Leeke]. II. Estimation of genotype response to stress. Australian *Journal of Agricultural Research* 38:49-59.

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

Butron, A., Widstrom, N., Snook, M. and Wiseman, B. (2002). Recurrent selection for corn earworm (Lepidoptera: Noctuidae) resistance in three closely related corn southern synthetics. *Journal of Economic Entomology* 95: 458-462.

Byth D.E., Eisemann R.L., and Delacy I.H. (1976): Two way pattern analysis of large data set to evaluate genotypic adaptation. *Heredity* 37: 215-230.

Byth, D.E. (1981) Genotype x environment interaction and environmental adaptation in plant improvement - an overview. In: Byth, D.E. and Mungomery, V.E. (eds) *Interpretation of Plant Response and Adaptation to Agricultural Environments*. *Australian Institute of Agricultural Science*, Queensland Branch, pp. 2-10.

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

Carter, G. (1945). Plant geography and cultural history in the American Southwest. *Viking fund Publications in Anthropology*, No. 5.

Ceccarelli, S. (1989) Wide adaptation. How wide? *Euphytica* 40, 197-205.

CGIAR. (2002). Maize (Zea mays L.).Areas of research. http://www.cgiar.org/research/res_maize.html.

Clements, R.J., Hayward, M.D. and Byth, D.E. (1983) Genetic adaptation in pasture plants. In: McIvor, J.G. and Bray, R.A. (eds) *Genetic Resources of Forage Plants*. CSIRO, East Melbourne, pp. 101-115.

Cornelius, P.L., Crossa J & Seyedsadr M.S. (1996). Statistical test and estimators of multiplicative models for genotype-by-environment interaction. In: Kang, M.S. and Gauch, H.G. (eds.). Genotype by environment interaction. Boca Raton, FL, CRC Press. pp 199- 234. *Crop Sci*., 26: 894900.

Correjado, V.M. and Magulama, E.E. (2008). Usefulness of improved open- pollinated varieties in the development of top-cross white maize hybrids. *USM RD J*., 16(2), 97-103.

Crossa, J., (1990). Statistical analysis of multilocation trials. *Advances in Agronomy* 44:85.

Crossa, J. & Cornelius P.L. (1997). Sites regression and shifted multiplicative model clustering of cultivar trials sites under heterogeneity of variances. *Crop Sci* 37: 406-415.

Crossa, J., Fox, P.N., Pfeiffer, Rajaram W.H., and Gauch, H.G. (1990). AMMI adjustment for statistical analysis of an international wheat yield trial. *Theoretical and Applied Genetics*. 81:27–37.

Dabholkar, A.R., 1999. *Elements of biometrical genetics*. Concept Publishing Company. New Delhi, India.

Dankyi, A.A., Anchirinah, V.M. and Apau, A.O. (1997). Maize technology adoption in Ghana. NARP Maize Technical Report, May 1996-August 1997. National

Agricultural Research Project, Crops Research Institute, Kumasi. P. 100-103.

Deininger.K., and Byerlee.D. (2011) cited by Melinda.S., Berek.B., Thom.J., 2011 In: Maize revolution in sub-saharan Africa. *Word Bank Policy. Research working paper* N° 5659.

Deitos A, Arnhold E, Miranda GV (2006). Yield and combining ability of maize cultivars under different eco-geographic conditions. *Crop Breeding and Applied Biotechnology* 6: 222-227.

De Vries, J. and Toenniessen. (2001). Securing the harvest: Biotechnology, breeding and seed system for Africa crops CAB International. Walling food .UK.

Doebley, J. (1992). Mapping the genes that made maize. TIG 8(9): 302 – 307.

Doebley, J., Goodman, M.M., and Stuber, C.W. (1987). Pattern of isozymes variation between maize and Mexican annual teosinte. *Econ. Bot.* 41(2): 234 – 246.

Duarte JB and Vencovsky R (1999). Interação Genótipos x Ambientes. *Uma Introdução à Análise* AMMI. ESALQ/USP, Ribeirão Preto.

Eberhart S, Russell W (1966). Stability parameters for comparing varieties. *Crop Sci*. 6: 36-40.

Ewool, M.B. (2004). Estimation of genetic improvement of maize in Ghana under three levels of nitrogen application. Msc. Thesis. KNUST, Kumasi, Ghana.

Fagan, B.M.(1995). Ancient North American: the archaeology of a continent. 2nd edition. Thames and Hudson, New York. N.Y.

Fakorede, M.A.B. & Adeyemo, M.O. (1986). Genotype × environment components of variance for three types of maize varieties in the rainforest zone of S.W. Nigeria. *Nigerian Journal of Agronomy* 1, 43–46.

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

FAO (1992). Maize in human nutrition. FAO Food and Nutrition series, No. 25. Rome.

FAO (2010). http://www.fao.org/inpho/maize (Internet Information Accessed on 10 July, 2010).

FASDEP, (2002). Food and Agriculture Sector Development Policy, Ministry Of Food and Agriculture, Ghana.

Fehr, W.R. (1991). *Principles of cultivar development*. Macmillan publishing company. A division of Macmillan Inc. New York, 1: 1-465.

Fernadez, G.C.J. (1991). Analysis of genotype x environment interaction by stability estimates cited by Ogunbodede, B.A., Ajibade, S.R. and Olakojo, S.A (2001) Grain yield stability of new maize varieties in Nigeria. *African Crop Science Journal* 9: 685- 691.

Finlay, K.W. and Wilkinson G.N., (1963). The analysis of adaptation in a plant breeding programme. *Australian Journal of Agricultural Research*, 14: 742-754.

Francis, T.R. and Kannenberg, L.W. (1978) Yield stability studies in short-season maize. 1.. A descriptive method for grouping genotype. *Canadian journal of plant Science* 58:1029-34.

Freeman, G.H. and J.M. Perkins (1971). Environmental and genotype-environmental components of variability. VIII. Relation between genotypes grown at different environments and measures of these environments. *Heredity* 27: 15-23.

Gabriel, K.R. (1971). The biplot graphic display of matrices with application to principal component analysis, *Biometrika*, 58:453-467.Cited by Yan, W and Kang, M. (2003).

Gauch, H.G. (1992). Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Elsevier, Amsterdam, Netherlands. pp. 53–110.

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

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

Gauch, H.G. and Zobel, R.W. (1996). AMMI analysis of yield trials. In: Kang, M.S. and Gauch, H.G. (editions) genotype by environment interaction. CRC Press. Boca Raton, FL

Gauch H. G. Jr, Piepho H. P. and Annicchiarico P (2008). Statistical analysis of yield trials by AMMI and GGE: further considerations. *Crop Sci*. 48: 866-889.

GGDP (Ghana Grains Development Project). (1991). Maize improvement, 1992 Annual Report. Ghana Grains Development Project, Crops Research Institute, Kumasi, Ghana 146.

Global Agricultural Information Network (GAIN). (2003). USDA Foreign Agricultural

Service. gain.fas.usda.gov/Recent Gain Publications/2011 Grain and Feed Annual_Accra_Ghana_4-11-2011.pdf

GNA (2007) CSIR-CRI develops four maize varieties. http://www.ghanaweb.com/GhanaHomePage/NewsArchive/artikel.php?ID=129075.

Grobman, A., Salhuanna, W. and Sevilla R. (1961). Races of maize in Peru, their origin, evolution and classification. *Natl. Acad. Sci. Natl. Research Council Publication* 915: 1- 374, Washington, USA.

Hernandez- Xolocotiz, E. (1985). Maize and man in the greater Southwest. *Economics Botany* 39(4): 416 – 430.

Hernandez – Xolocotzi, E. and Alanis Flores, G. (1970). Estudio morfologico de cinco nueva razas de maize de la sierra madre occidental de Mexico. *Agrociencia* 5(1): 3 – 30. Hill, J., Heikoc. B., Peter, M.A and Tigerstedt (1998): Stability, adaptability and adaption Chapman Hall *Plant Breeding Series* 4(1):87-209.

IItis, H.H and Doebley, J.F.(980). *Taxonomy of zea mays*. II. Subspecific categories in the *zea mays* complex and a generic synopsis. *Amer. J.Bot*.67(6): 994 – 1004.

ISSER, (2007). The state of the Ghanaian economy 2006. Institute of Statistical, Social and Economic Research, Legon.

Jayakumar J., Sundaram T., Arun P. D. and Ragu R. R.A. (2007). Correlation studies in maize (*Zea mays* L.) evaluated for grain yield and other yield attributes. *Internat. J. Agric. Sci*. 3(2): 57-60

Jugendheimer, R.W. 1958. *Crop improvement, seed production and uses*. Janick J. (Ed.) New

York. John wiley. pp 224.

Kandus M, Almorza D, Boggio Ronceros R, Salerno JC. (2010). Statistical models for evaluating the genotype - environment interaction in maize (*Zea mays* L.). *International Journal of Experimental Botany*. YTON ISSN 0031 9457, (2010) 79: 39-46.

Kang M. S., Macus, S. Z; and Gary, F. K. (2004). Path coefficient analysis of grain yield and harvest grain moisture in maize. *Tropical Agric*. (Trinidad) 60:253-256.

Kato, Y.T.A.(1984). Chromosomes morphology and the origin of maize and its races. *Evol. Bol*.17: 219 – 253.

Kato, Y.T.A.(1976). Cytological studies of maize and teosinte in relation to their origin and evolution. Massachusetts *Agric. Expt*. Sta. Bull. 635

Langer, S., Frey, K.J. and Bailey, T. (1989). Associations among productivity, production response and stability indexes in oat varieties. *Euphytica* 28:17-21.

Lin, C.S., Binns, M.R., Lefkovitch L.P., 1986. Stability analysis: Where do we stand? *Crop Sci* 26, 894-900.

Lin, C.S., Binns, M.R. (1991) Genetic properties of four stability parameters. Theoretical Applied Genetics. 82: 205–509.

Lin, C.S. & Thompson B. (1975). An empirical method of grouping genotypes based on a linear function of the genotype-environment interaction. *Heredity* 34: 255-263.

Mangelsdorf, P.C. and Reeves, R.G. (1945). The origin of Indian corn and its relatives. Texas *Agric. Expt. Stat. Bull. 574*.

Matsuoka, Y., Vigouroux, Y., Goodman, M.M., Sanchez, J., Buckler, G.E. and Doebley J., (2002). A single domestication for maize shown by multi-locus microsatellite genotyping. *Proc.Natl. Acad. Sci*. USA 99: 6080 – 6084.

McClintock, B.(1959). Genetic and Cytological studies of maize. *Carnegies Inst. Washinton. Year book* 58: 452 – 456.

McClintock, B. (1978). Significance of chromosomes constitution intracing origin and Migration of traces of maize in the America. In: D.B. Walden (eds*). Maize Breeding and genetics*. J.Wiley, New York. Pp 159 -184.

MCclintock, B., Kato, T.A., and Blumenschieu, A. (1981). Chromosomes constitutions of Races of maize. Its significance in the interpretation of relationship between races and varieties in the America. Colego de Postgraduados, Mexico.

Meghji, M. R., Dudley, J.W., Lambert, R.Z. and Sprague, G.F. (1984). Inbreeding depression, inbred and hybrid grain yield and other traits of maize genotypes representing three eras. *Crop Science* 24: 545-549.

Melinda, S., Berek, B., Thom, J., (2011). Maize revolution in sub-Saharan Africa. World Bank Policy. Research working paper N° 5659.

Mercer- Quarshie, H., Amankwatia, Y.O., Twumasi – Afriyie, S. and Marfo, K.O. (1993).. Crops Research Institute Medium Term Research Plan 1993 – 1997. Crop Research Insititute, Kumasi.

MiDA, 2010. www.mida.gov.gh

Miranda G.V., Souza L.V., Guimarães L.J.M., Namorato H., Oliveira L.R. and Soares M.O. (2009). Multivariate analyses of genotype x environment interaction of popcorn. *Pesquisa Agropecuária Brasileira*: 44: 45-50.

MoFA (Ministry of Food and Agriculture) (2012). Agriculture in Ghana: Facts and Figures. Statistical Research and Information Directorate (SRID).

Mohammadi, R., Abdulahi, A., Haghparast, R. and Armion, M. (2009). Interpreting genotype by environment interactions for durum wheat grain yields using non-parametric methods. *Euphytica* 157: 239–251.

Morris, M.L., R. Tripp, and A.A. Dankyi. (1999). Adoption and Impacts of Improved Maize Production Technology: A Case Study of the Ghana Grains Development Project. Economics Programme Paper 99-01. Mexico, D.F.: CIMMYT pp 3-7, 13-14.

Obi, I.U. (1991). Maize: It's agronomy, diseases, pest and food values. Optimal Computer Solutions Limited. Enugu, publishers. 76 Agbani Road Enugu, Nigeria, XXVIII + 206 pp.

Oteng, J.W. (1998). Rice production and development in Ghana. Faculty of Agriculture, University of Ghana, Legon.

Paliwal, R. L. (2000) Breeding special purpose maize. In: R. L. Paliwal, (ed.), Tropical maize improvement and production. FAO Plant Production and Protection series No 28 Rome Italy, pp. 211-223.

Perkins, J.M. and Jinks, J.L. (1968). Environmental and genotype-environmental components of variability. III. Multiple lines and crosses. *Heredity*, 23: 339-56.

Plaised, R.I. (1960). A shorter method for evaluation of the ability of selection to yield consistently in different locations or seasons. *American Potato Journal* 36: 381-385.

Piperno, D. R. and Flannery, K. V. (2001). The earliest archaeological maize from highland Mexico: new accelerator mass spectrometry dates and their implications. *Proc. Natl. Acad. Sci*. USA 98: 2101 -2103.

Piperno, D. R. and Pearsall, D. M. (1998). The origins of agriculture in the lowland neo-tropics. Academic, San Diego.

Rahman, H., Khalil, I. H., Noor Islam, Durrishahwar and Rafi, A. (2007). Comparison of original and selected maize population for grain yield traits: Sarhad Journal of Agriculture Volume 23: No. 3

Romagosa I., Fox P.N., Garcia Del Moral L.F., Ramos J.M., Roca De Togores F. and Molina Cano J.L. (1993): Integration of statistical and physiological analyses of adaptation of near-isogenic barley lines. *Theor. Appl. Genet*. 86, 822-826.

Sallah, P. Y. K., Abdulai, M. S. and Obeng-Antwi, K. (2004). Genotype x environment interactions in three maturity groups of maize cultivars: *African Crop Science Journal*, Volume 12: No. 2, pp. 95-104.

SAS Institute, (2002). Statistical Analysis Software (SAS) user's guide Version 9.2. SAS Institute, Inc., Cary, NC, USA.

Shukla, G.K., (1972). Some statistical aspects of partitioning genotype-environment components of variability. *Heredity*, 29: 237-245.

Simmonds, N.W., 1962. Variability in crop plants, its use and conservation. *Biol. Rev*. 37: 422-465.

Smith, J., Barau, A.D., Goldman, A. and Mareck, J.H. (1994). The role of technology in

Agricultural intensification: the evolution of maize production in the northern Guinea Savannah of Nigeria. *Economic Development and Cultural* 42: 537 – 554.

Smith, J., Weber G., Manyong, V. M and Fakorede, M.A.B. (1997). Fostering sustainable increase in maize productivity in Nigeria. Chapter 8 in *Africa's emerging maize revolution*, edited by D. Byerlee, and C.K. Eicher, lynne Rienner Publishers, London, UK. Pp 107 -124.

Smith, B.D. (1998). *The emergence of Agriculture*. Scientific American Library, New York. Pp 231.

Smith, B.D. (2001). Documenting plant domestication: the consilience of biological and *Archaeological approaches. Proc. Natl. Acad. Sci*. USA 98 :1324 -1326.

Smith A, Cullis B and Gilmour A (2001a). The analysis of crop variety evaluation data in Australia. Austr. N. Z. J. Stat. 43: 129-145.

Smith A, Cullis B and Thompson R (2001b). Analyzing variety by environment data using multiplicative mixed models and adjustments for spatial field trend. *Biometrics* 57: 1138-1147.

Souza A.R.R., Miranda G.V., Pereira M.G. and Souza L.V. (2009) Predicting the genetic gain in the Brazilian white maize landrace. *Ciência Rural* 39: 19-24.

Souza L.V, Miranda G.V, Galvão J.C.C., Eckert F.R., Mantovani E.E., Lima R.O. and Guimarães L.J.M. (2008). Genetic control of grain yield and nitrogen use efficiency in tropical maize. *Pesquisa Agropecuária Brasileira* 43: 1517-1523.

Ssemakula G., Dixon A.G.O. and Maziya-Dixon B. (2009). Stabiltiy of total carotenoid concentration and fresh yield of selected yellow-fleshed cassava (*Manihot esculenta* Crantz). *Journal of Tropical Agriculture* 45 (1-2): 14-20.

Taba, S. (1997). Maize. In: D. Fuccillo, L. Sears and P. Stapleon (eds.). *Biodiversity in trust*. Cambridge University Press. Cambridge, UK, 213 – 226.

Trifunovi, S., Husi, I. and Ivanovi, M. (1998). Generation means analysis for grain yield from RCBD and new experimental design in maize (*Zea mays* L.), 2nd Balkan symposium on Field Crops, 16-20 June, Novi Sad, Yugoslavia.

Tweneboah, C.K. (2000). Modern Agriculture in Food Crops. Co – Wood Publishers pp 30-46.

Twumasi–Afriyie S., Badu–Apraku B., Sallah P.Y.K, and Dzah B.D. (1992). The potential of maize as a source of quality protein for Ghana. Paper presented at the twelfth National Maize and Legumes Workshop organized by Ghana Grains Development Project, Crops Research Institute, March 1992, pp 9.

Uguru, M.I. (2005). Crop Genetics and Breeding. (Revised) Epharata Press, Nsukka, Enugu State, Nigeria. 113 pp.

Van Eeuwijk FA, Keizeir LCP and Bakker JJ (1995). Linear and bilinear models for the analysis of multi-environment trials. II: An application to data from the Dutch Maize Variety Trials. *Euphytica* 84: 9-22.

Wang, R.L., Stec, A., Hey, J., Lukens, L., and Doebley, J. (1999). The limit of selection during maize domestication. *Nature* 398: 236 – 239.

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

White TL and Hodge GR (1989). Predicting Breeding Values with Applications in Forest Tree Improvement. Kluwer Academic, Dordrecht.

Whitt, S.R., Wilson L.M., Tenaillon, M.I., Gaut, B.S, Buckler IV ES (2000). Genetic diversity and Selection in the maize starch pathway. *Proceedings of the National Academy of Sciences* USA. 12959 – 12962.

Wricke, G. (1962). Uber eine Methode zur Erfassung der okologischen Streubreite in Feldversuchen. *Zeitschrist fur pflanzenzuchtung*, 47, 92-6 cited by Hill, J., Heikoc.

Yan W, Kang MS, Ma B, Woods S (2007). GGE biplot vs. AMMI analysis of Genotype-by-environment data. *Crop Sci*. 47: 643-653.

Yan, W., L.A. Hunt, Q. Sheng & Z. Szlavnics (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci., 40: 597-605.

Yan, W. (2001). Methodology of cultivar evaluation based on yield trial data-with special reference to winter wheat in Ontario. Ph. D Dissert. Univ. of Guelph, Ontario, Canada.

Yates, F. & W.G. Cochran (1938). The analysis of groups of experiments. *Journal of Agricultural Sci.,* 28: 556-580.

Zobel, R.W., Wright M.J., & Gauch H.G (1998). Statistical analysis of a yield trial. *Agron. J.* 80: 388-393.

APPENDICES

APPENDIX 1: Analysis of variance for yield

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Block	2	12.137	6.069	1.68	
GENOTYPES	22	939.559	42.707	11.79	<.001
Error	389	1409.339	3.623		
Total	413	2361.035			

APPENDIX 2: Analysis of variance for field weight

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Block	2	26.700	13.350	1.76	
GENOTYPES	22	1794.411	81.564	10.74	<.001
Error	389	2952.977	7.591		
Total	413	4774.088			

APPENDIX 3: Analysis of variance of number of days to anthesis

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Block	2	2.087	1.043	0.15	
GENOTYPES	22	297.406	13.518	1.94	0.007
Residual	389	2707.746	6.961		
Total	413	3007.239			

APPENDIX 4: Analysis of variance for days to silking

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Block	2	1.773	0.886	0.10	
GENOTYPES	22	255.536	11.615	1.34	0.144
Error	389	3384.449	8.700		
Total	413	3641.758			

APPENDIX 5: Analysis for variance foe ear height

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Block	2	1902.	951.	0.41	
GENOTYPES	22	70133.	3188.	1.36	0.129
Error	389	911618.	2343.		
Total	413	983653.			

APPENDIX 6: Analysis of variance for number of eras harvested (EHA)

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Block	2	3.71	1.86	0.14	
GENOTYPES	22	858.62	39.03	2.84	<.001
Error	389	5343.67	13.74		
Total	413	6206.01			

APPENDIX 7: Analysis for variance for plant height

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Block	2	2162.8	1081.4	1.90	
GENOTYPES	22	29816.2	1355.3	2.38	<.001
Error	389	221375.4	569.1		
Total	413	253354.4			

APPENDIX 8: Analysis of variance for number of plants harvested

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Block	2	367.4	183.7	0.62	

GENOTYPES	22	8094.2	367.9	1.25	0.201
Error	389	114430.0	294.2		
Total	413	122891.5			

APPENDIX 9: Analysis of variance for plant stand

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
BLOCK stratum	2	17.715	8.857	1.13	
GENOTYPES	22	247.826	11.265	1.44	0.091
Residual	389	3042.507	7.821		
Total	413	3308.048			