KWAME NKRUMAH UNIVERSITY OF SCIENCE AND TECHNOLOGY,

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COLLEGE OF AGRICULTURE AND NATURAL RESOURCES FACULTY OF

AGRICULTURE, DEPARTMENT OF CROP AND SOIL SCIENCE

GENOTYPE BY ENVIRONMENT INTERACTION AND GRAIN YIELD STABILITY OF SORGHUM (*Sorghum bicolor*) HYBRIDS EVALUATED AT THREE LOCATIONS IN NORTHERN GHANA

A THESIS SUBMITTED TO THE SCHOOL OF GRADUATE STUDIES,

KWAME NKRUMAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, IN PARTIAL

FULFILMENT OF THE REQUIREMENT FOR THE DEGREE OF MASTERS OF PHILOSOPHY IN AGRONOMY (PLANT BREEDING).

MUSA SWARAY

AUGUST, 2015.

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MASTERS OF PHILOSOPHY DEGREE

IN

AGRONOMY (PLANT BREEDING)

MUSA SWARAY

B.Sc. (Hons.) AGRICULTURE

AUGUST, 2015

DECLARATITION

I hereby declare that this submission is my own work towards the M.Phil. Agronomy (Plant Breeding) and that to the best of my knowledge, it contains neither material previously published by another person nor material which have been accepted for the award of any other degree of the university, except where due acknowledgement has been made in the text.

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(HEAD OF DEPARTMENT)

DEDICATION

This work is dedicated to my father Mr Gassimu Swaray and mother Mrs Jenneh Swaray in their relentless effort in encouraging me through the length of this course. Also dedicated to my beloved wife Alima Swaray and son Gassimu Ezikel Swaray Junior and to the rest of the Swaray family.

ACKNOWLEDGEMENT

My greatest gratitude goes to the Almighty God for his guidance, strength and protection from the start to the completion of this study. Without Him, all my effort and that of all the people mentioned hereunder would have been in vain. My sincere appreciation and deep gratitude goes to my principal Supervisor Professor Richard Akromah, the Provost of the College of Agriculture and Natural Resources, Kwame Nkrumah University of Science and technology (KNUST), Kumasi and the Coordinator of the AGRA MSc. Programme. I am also greatful to my co-supervisor, Dr Ibrahim Dzido Kwasi Atokple a Senior Research Officer and the head of the sorghum improvement programme, CSIR-Savana Agricultural Research Institute, Tamale, for their constructive criticisms that contributed to improving the quality of this piece of work. Without their advice, criticism and direction, this work would have been inconceivable. I am greatly indebted to the West African Agricultural Productivity Programme Sierra Leone (WAAPP-SL) for taking charge of my financial needs all through the course of this programme and for providing me such seasoned training opportunity. I owe special gratefulness to the practical assistance provided during the field work by Mr Kenneth Opare-Obobi from the Sorghum section CSIR-SARI, Nyankpala station, Mr Sumani Iddrissu Mohamed, Principal Research Technologist CSIRSARI, Damongo station and Mr Peter Anabire Asungre, Principal Research Technologist, CSIR-SARI, Manga station. Very special thanks to all the staff at the Savanna Agricultural Research Institute (SARI) for providing me a good working environment at the three locations, which successfully brought me to this final stage. I owe an obligation of immense gratefulness to Dr Alfred G.O. Dixon at IITA for his tireless assistance in obtaining this grant. Special appreciation to a colleague Mr Patrick Attamah for his endless effort in assisting me in my work and a brother Morlu Sylvester Koroma for his support.

ABSTRACT

Sorghum (*Sorghum bicolor* (L) Moench) is a staple food crop for millions of poor people in the semi-arid tropics and is adapted to a wide range of environmental conditions. In Ghana where there is large variation in environment it may be expected that genotype by environment interaction may also be higher. In such situation, one cultivar may have higher yield in some environments while the second cultivar may excel in the other. Variation in soil and weather condition across sorghum growing environments has led to significant genotype by environment effect on sorghum yields. Therefore, the evaluation of sorghum genotypes for stability of performance under varying environmental condition becomes an important aspect in sorghum hybrid evaluation. It was with this idea that this study was conducted to evaluate four sorghum hybrids, two commercial sorghum varieties and a local check obtained from the Savanna Agricultural Research Institute to identify stable and high yielding sorghum genotypes for commercial production during 2014 growing season in Ghana. The genotypes were evaluated at three locations in Northern

Ghana at Nyankpala, Damongo and Manga. These were significant ($P < 0.01$) genotype (G), location (L) and genotype by location interaction (GLI) effect for grain yield. The contributions of the total variance accounted for by the genotypes were highest being

(42%) for grain yield. The location effect and genotype by location (G × L) accounted for (23%) and (13%) respectively. The GGE biplot analysis showed that G1 (XSW2134) was high yielding and most stable, G2 (XSW256) was high yielding but least stable and G4 (Marcia) was low yielding and least stable. Damongo which is located in the Guinea savannah zone would be appropriate in selecting superior genotype.

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LIST OF ABBREVIATIONS

AEA	Average Environment Axis
AHI	Anthesis Heading Interval
AMMI	Additive Main Effect and Multiplicative Interaction
ANOVA	Analysis of variance
CMS	Cytoplasmic Male Sterile
CSIR	Council for Scientific and Industrial Research
DH	Days to Heading
DA	Days to Anthesis
FAO	Food and Agriculture Organisation
GEI	Genotype by Environment Interaction
GLI	Genotype by Location Interaction
GGE	Genotype main Effect plus Genotype by Environment interaction
GW	Grain Weight
Kg	Kilogram
MS	Mean Square
PC	Principal Component
PLH	Plant Height
PNL	Panicle Length
PNW	Panicle Weight
SA	Semi-Arid Tropics
SARI	Savanna Agricultural Research Institute

SS Sum of square

SVP Singular Value Partitioning

T Tons

WAAPP-SL West African Agricultural Productivity Program-Sierra Leone WAP

Weeks After Planting

CHAPTER ONE

1.0 INTRODUCTION

Sorghum (*Sorghum bicolor* (L) Moench) is a staple food crop for millions of poor people in the semi-arid tropics (SAT) and is adapted to a wide range of environmental conditions (Mehmood *et al*., 2008). It is suitable for cultivation in the semi-arid areas of the world where other cereal crops such as rice, maize and wheat are difficult to grow (Ezeaku *et al*., 1997). In Ghana it is cultivated mainly as a subsistence rain-fed crop in the Sudan, Northern and Southern Guinea savannah zones of the country, which comprises of Upper East, Upper West and Northern region. The leaves provide fodder for farm animals whilst the stalks are used in fencing, weaving basket, mats and fuel wood. Sorghum can generally be classified into two types; forage types (mainly for forage and animal consumption) and grain types (mainly for human consumption). The forage sorghum are classified into (a) hybrid forage sorghum, (b) Sudan grass, (c) sorghum x Sudan grass hybrids (also known as Sudan hybrid), and (d) sweet sorghum. The latter is used mainly for molasses but more readily for bio fuel production as well (Newmann *et al*., 2010).

Relative to other cereals, sorghum is being utilized mainly in brewing an opaque beer known as “pito”, an important cottage industry in Northern Ghana which is as old as the cultivation of sorghum itself (Atokple *et al*., 1998). The increase in the number of people consuming sorghum has assumed greater commercial proportion throughout the country.

”Pito” mash, residues from “pito” brewing is very important for pig industry in northern Ghana (Bruce and karbo, 1997). The production of sorghum has currently assumed intense commercial importance in alcoholic and non-alcoholic beverage production in Ghana

(Atokple *et al*., 1998). In addition to being an important food, feed and forage crop, sorghum also play an important role in providing raw materials for making starch, fiber and dextrose syrup. In Northern Ghana, sorghum yield ranges between 500 and 800 kg/ha, but has also been higher in the Upper East region (700 and 900 kg/ha). (Atokple *et al*., 1999). These low yields in the production of sorghum are due to the cultivation of indigenous land race varieties with inherent low yield potential and lack of improved sorghum hybrids and varieties (Schipprack and Mercer-Quashie, 1984).

Crop breeders have been striving to develop genotype with superior grain yield, quality and other desirable characteristics over a wide range of different environmental conditions. Genotype and environment interaction effect some of the main complication in the selection of broad adaptation in most breeding programmes. Genotype by environment interaction refers to the differential response of varying genotypes under changes in environment (Matter and Caligan, 1976). It refers to the instance where joint effect of genotypes and environments are significantly greater or significantly reduced than would be predicted from the sum of the separate effect (Andrew *et al*., 1998). The phenotype of an organism is determined by the combined effect of the environment and the genotype which interact with one another. Numerous studies have shown that a proper understanding of the environmental and genetic factor causing the interactions as well as an assessment of their importance in the relevant genotype by environment interaction system could have a large impact on plant breeding (Magari and Kang, 1993; Basford and Cooper, 1998). Genotype by environment interaction occurs usually when genotypes are evaluated in several different environments (Becker and Léon, 1988; Magari, 1989; Kang 1990).

When there is large variation in environment, like in Ghana, it may be expected that genotype by environment interaction will also be higher. In such situations, one cultivar may have higher yield in some environment, while the second cultivar may excel in the other. Therefore, it is important to apprehend the eminence of the interaction in genotype selection over different environments instead of just calculating the average performance of the genotype under evaluation (Fehr, 1991; Gauch and Zobel, 1997). Information on the genotype by environment interaction leads to the successful evaluation of stable genotype, which could be used for general cultivation, consequently, to select a cultivar with high yielding ability and consistency, high attention should be given to the importance of stability in performance for the genotypes under different environment and their interactions (Ghazy *et al*., 2012). Yield is a complex quantitative character and is greatly influenced by environmental fluctuations, hence, the selection of superior genotype based on yield per se at a single location in a year may not be very effective (Shrestha *et al*., 2012). Therefore, the evaluation of sorghum genotypes for stability of performance under varying environmental condition for yield has become an important aspect in sorghum hybrid evaluation. This study was conducted to evaluate four sorghum hybrids, to identify stable and high yielding hybrids with superior agronomic performance for commercial sorghum production in Ghana

The specific objectives of the study were;

(a) To evaluate the presence of genotype by environment interaction for grain yield and agronomic performance of sorghum hybrids.

(b) To assess grain yield stability and the pattern of response of the four sorghum hybrids across the three locations.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin of Sorghum

Sorghum bicolor (L) Moench is difficult to determine when and where domestication occur (De Wet *et al*., 1970). The origin and early domestication of sorghum is hypothesized to have taken place around 5000-8000 years ago in Northern Africa or at an Egyptian Sudanese boarder (Mann et al., 1983; Wendorf *et al*., 1992) with the largest diversity of cultivated and wild sorghum also found in this part of Africa (De Wet, 1977; Doggett, 1965 and Kimber 2000). The secondary centres of origin is the Indian subcontinent, with evidence of early cereal cultivation discovered at an archaeological site in western part of Rodji dating back to about 4500 before present (Vavilov, 1992;

Damania, 2002).

Sorghum is of tropical origin, but it has been adapted through selection to temperate region where mainly annual and perennial specie are found in the wild form (Onwueme and Sinha, 1999). The genetic variation in sorghum was partitioned into five basic races (bicolor, guinea, caudatum and dura) and all combinations of their hybrid derivative for a total of 15 races (Harlan and De Wet, 1972). Sorghum is cultivated in 100 countries worldwide, covering areas in the America, Africa, Asia and the pacific. In Africa, the crop is the third most important after maize and wheat. The five largest producer of sorghum in the world are the United States (25%), India (21%), Mexico (almost 11%), China (9%) and Nigeria (almost 7% (FAO, 1991). Together, these five countries account for 73% of the world sorghum production. Eighty percent (80%) of the world total land area is devoted to sorghum in developing countries. In West Africa, Nigeria is the largest sorghum producer

accounting for about 71% of the total regional sorghum output (Ogbonna, 2011). In Africa, sorghum is grown in a large belt that spread from the Atlantic coast to Ethiopia and Somalia, bordering the Sahara in the Northern and Equatorial forest in the South. This area extends through the drier part of Eastern and Southern Africa, where rainfall is too low for the successful cultivation of the crop (FAO, 1991). Sorghum is currently grown on 45 million hectares of land worldwide. The cropped area expands in Africa where it grew from 13 million to 22 million (FAO, 1991).

2.2 Sorghum Production and Uses

Sorghum bicolor (L) Moench has being an important staple food crop in northern Ghana and has helped improve the livelihood of farmers. In the country, the total area of production is 2,964,000 ha with a production levels of 2,872,000 tons and yields of 9,691 $kgha^{-1}$. Developing countries account for 90% of the world sorghum area and 70% of the total output. Asia and Africa each account for about 25-30% of global production (FAO, 1991).

Traditional food made from sorghum include unfermented and fermented bread, porridge, couscous, boiled rice resembling food, snacks as well as alcoholic beverages. Sorghum blended with wheat flower is used in the last two decades to produce baked product including yeast leavened pan, hearth and flat breads, cakes, muffins, cookies, biscuit and flower tortillas (Badi *et al*., 1990). In developing countries like Ghana, sorghum is generally used as food in the form of porridge, tuo zaafi and fried dumplings (maasa) (Obilana, 1995). The leaves provide fodder for animals, whilst the stalks are used in fencing, making mat, weaving baskets and used as fuel wood (Atokple *et al*, 1998).

2.3 The Importance of Sorghum Hybrids

Sorghum remains to be one of the most important food crops in semi-arid tropics. In Africa, low yields of sorghum have been recorded due to the predominant cultivation of low yielding sorghum varieties, low soil fertility and failure to adopt improved cultivation practices. In a bid to address the constraints embodying sorghum, and to make production a reality, National Agricultural Research Systems (NARS) in collaboration with international research centres like ICRISAT are developing and attaching valued importance to hybrid sorghum.

The numerous importance attached to sorghum hybrids stem to the fact that, there has been a yield advantage of sorghum hybrids whenever they are compared to the improved and landrace varieties, commonly in order of 20 to 60% (Atokple, 2003). Sorghum hybrids have been shown to yield 15 to 41% higher than open pollinated varieties under small holder conditions in India and West Africa (Bidinger *et al*., 2005; Toure *et al*., 2007). Reports from research has shown that sorghum hybrids holds a lot of importance and appear to be more reliable than inbred varieties in erratic environments typically of sorghum growing regions in the semi-arid tropics (Axtell *et al*., 1999). Besides yield superiority over open-pollinated varieties, hybrids are more stable across different environments (House, 1995) and more tolerant to moisture stress. Hybrid sorghum has also been proved to be early maturing than their parental lines (Tadesse *et al*., 2008).

2.4 Hybrid Seed Development of Sorghum

Hybrid vigour was first recognised in sorghum in 1927 (Karper and Conner, 1927) using hybrid seed produced by hand emasculation. In 1948, researchers initiated studies to look

for cytoplasmic male sterility (CMS) as a method for commercial hybrid seed production in sorghum. In the development of hybrid sorghum, a male sterile parent, A line, is being crossed with the male fertile pollinator parent, R line. Hybrid seed production involves two different kinds of lines. Inbred line identification and evaluation involves one of the most costly and time consuming in sorghum hybrid development. Exploitation of heterosis is an important aspect of breeders. Heterosis or hybrid vigour means that the outstanding performance of the offspring compared to the average performance of the parents, and so they are used for their superiority to open pollinated varieties. This is due to the favourable dominant gene and linkage theory developed (Daven Port, 1908) which stipulates that the improved performance of hybrids is a result of the effect of dominant favourable gene at a locus or several loci. Heterosis denotes increased vigour, speed of development, resistance to diseases and pests or climatic conditions of any kind. Improving levels for combining ability for yields, together with desired grain qualities, genotypes and wide adaptation is the key to breeding hybrids (Axtell *et al*., 1999).

2.5 Genes and the Environments

Plants are built with a particular set of genes. These genes are basically influenced by the environment in which they live. Organisms are determined neither by their genes nor by their environment; they are the consequence of the interaction of genes and environment (Suzuki *et al*., 1981). Genotype describes the complete set of genes inherited by an individual that is important for the expression of a trait under investigation. Phenotype describes all aspects of the individual‟s morphology, physiology and ecological relationships. The genotype of an organism has been essentially known to be a stable character. This is known to be fixed throughout the life of an organism and cannot be changed by the effect of the environment. The phenotype changes continually and the

direction of that change is a function of the sequence of environments that the individual experiences (Suzuki *et al*., 1981). The sum total of the effects of physical, chemical and biological factors of an individual other than its genotype is known as the environment. The individuals or populations of plants do not live in a vacuum but are surrounded and influenced by these factors. Comstock and Moll (1963) classified environments into two categories, (i) Macro-environment that is, the environment which is linked with a particular location or area at a particular period of time. (ii) Micro-environment that is, the environment where just a single organism exist contrary to that of different organism growing at the same time and in the same place. This comprises of the chemical content and the physical nature of soil, changing climatic condition, insect pest, solar radiation and disease. Macro-environments displays a number of micro-environments that is more alike in each macro-environment with the notion that macro-environments are mainly different from each other.

The terms „predictable and unpredictable environments" were coined by Allard and Bradshaw (1964) to define and classify environments. The predictable environment relates to an environment which approximately exhibit frequent and permanent features of the environment including day length, rainfall, soil type and climate which is determined by longitude and latitude. These factors are also referred to as controllable variables (Perkins and Jinks, 1971) for example, the amount of artificial irrigation practiced, planting density, sowing date and the level of fertilizer applied. The term uncontrollable or unpredictable environment, on the other hand, include fluctuations in weather conditions, some of which are the differences between seasons with reference to the distribution and amount of rainfall and the prevailing temperature in the course of the crop life cycle. The absence or low level of interaction will be useful for uncontrollable variables, whereas for the controllable

variables a high level of interaction in the favourable direction is desirable to obtain maximal performance (Chahal and Gosal, 2002).

2.5.1 Genotype by Environment Interaction

Exploitation of genetic variability is the most important tool in plant breeding especially in sorghum breeding and this has to be inferred by phenotypic expression. The consequence of the phenotypic variation depends largely on the environment. The variation is further complicated by the fact that all the genotypes do not react in a similar way to change in environment and no two environments are exactly the same. Genotype by environment interaction is the differential response of varying genotype to changes in the environment (Matter and Caligari, 1976). It is an important consideration in plant breeding programs because it impedes progress from selection in any given environment (Yau, 1995). The phenotype of an individual is determined by the effect of the genotype and the environment surrounding it. Mean yield across environment indicator of genetic performance only in the absence of genotype by environment interaction. Therefore, it is important for plant breeders to identify specific genotype adapted or stable to environments, thereby achieving quick genetic gain through screening of genotypes for high adaptation and stability under varying environmental condition prior to their release as cultivars (Ariyo, 1989; Flores *et al*., 1998; Showemimo *et al*., 2000; Mustapha et al 2001; Yan and Kang, 2003). An understanding of the environmental and genotypic causes of genotype by environment interaction is important at all stages in plant breeding, including the design of ideotypes, selection of parents based on traits and selection based on yield (Jackson *et al*., 1998). In a situation where genotype by environment is large, it might be necessary to establish multiple testing locations, thereby augmenting the cost of developing commercially relevant varieties (Kang, 1996). In genotype by environment interaction, by minimizing the association

between genotypic and phenotypic value (Van Oosterom *et al*., 1993) also reduces the genetic progress expected.

2.5.2 Implications of Genotype by Environment interaction

Genotype by environment interaction has heavy implication on the evolution of specie. Lande and Shannon, (1996) suggested that in constant or unpredictable environment, genetic variance reduce population mean fitness and increases the risk of extension. The rate of evolution in mean phenotype in response to selection is proportional to the additive genetic variance in the character and the intensity of directional selection. In short term, genetic variability is often less critical than other determinant. But over time, it can play the decisive role in allowing a population to persist and adapt in a changing environment (Lande and Shannon, 1996).

2.5.3 Categories of Genotype by Environment Interaction

Developing high yielding and adaptation of sorghum hybrids is one approach of cereal grain deficits. The success of hybrids depends as much on it stable performance across varied environment as well as it inherent yielding ability. The desired hybrid is one that will be adapted to a wide range of growing conditions in a given production area with above average yields and below average variances in a given environment. That is to say, sorghum growers need cultivar that is dependable and consistent across wide array of stress condition and yet have high yielding potential that may be expressed when production conditions become favourable. Dividing areas into region that are in the first place different based on climatic and soil condition is one method to find out compromising solution for these various interest (Babic *et al*., 2010). For breeding to be successful in targeted growing areas, it may depend

on identification of the main source of phenotypic genotype by environment interaction of phenotypic variation in that region. To obtain varieties promising diminished genotype by environment interaction for the predominant source of variation means good ratio between the stable and high yielding (Petrovic *et al*., 2009)

Different interest of breeders as well as seed producers and distributors including farmers always come up with a very important question. That is, how well can a variety be adapted and at the same time be able to have high yield in a given location? In the case of farmers, they always want small genotype by year interaction, while breeders and seed produces and distributors want a broadly adapted genotype that will earn a great success across a great area. Genotype by environment interaction occurs when the differences between genotypes are not the same. It is the inconsistency of relative performance of genotypes over environments (Hill *et al*., 1998). If the two genotypes "A" and "B" are evaluated in two environments; E1 and E2, genotype by environment interaction occurs when;

$$A1 - B2 \neq A2\text{-}B2 \text{ or } A1\text{-}B1\text{-}(A2\text{-}B2) \neq 0$$

Where A1, is the performance of genotype A in environment 1, A2, is the performance of genotype A in environment 2, B1, is the performance of genotype B in environment 1, B2, is the performance of genotype B in environment 2.

Allard and Bradshaw (1964) suggested that when two genotype A and B are grown in two different environments E1 and E2, six types of interaction occurs, some of which are cross over and the others non cross-over are possible. The two varieties may show similar behaviour showing parallel lines when grown in two environments as shown in (a) which

indicates independence in the performance of genotype and the environment. The presence of genotype by environment

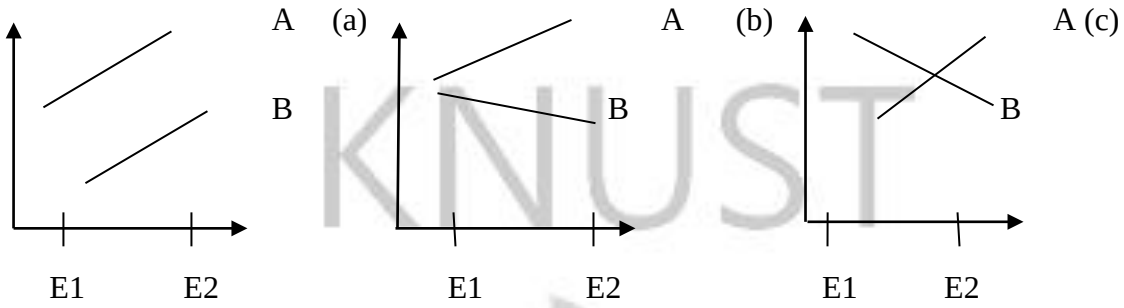


Figure 2.1. Different types of G × E interactions shown by two varieties grown in two environments

Interaction leads to non-parallel response curve of varieties without intersecting each other (b) or with intersection (c). the existence of non-intersecting but non-parallel lines suggest the relative ranking of varieties remains the same, though their absolute difference vary with the environment. The genotype by environment remains as cross over or qualitative if it leads to change in relative ranking of genotypes in different environment. The non-cross over quantitative genotype by environment interaction on the other hand results in the differential change of mean but not of ranking of different genotype.

Cross over interactions is very important in plant breeding because they affect the genotypes to be selected in a given environment. Such interactions also suggested that genotypes are specifically adapted to environments. The non-cross over interaction on the other hand influences the nature and magnitude of components of genetic variance and other related parameters like heritability and genetic advance.

The Changes that occur in relative ranking emerges to be the unavoidable consequence of growing a considerable number of plant genotype in a few location and season. This stands

to be authentic especially in the tropics where environmental variations are not only prominent, but crops rather lack the protection conferred by purchased inputs. Consequently, for plant breeders, vast genotype by environment interaction obstruct progress from selection and therefore has important implications for testing and release of cultivar (Smithson and Grisely, 1992). According to Ramagosa and Fox (1993), genotype by environment interaction generally decreases the association between phenotypic values and can justify promising selection from one location to perform poorly in another, so that plant breeders are compelled to investigate genotypic adaptation. The measurement of genotype by environment interaction is also relevant in determining ideal breeding plan for releasing genotypes with adaptation to the target environment.

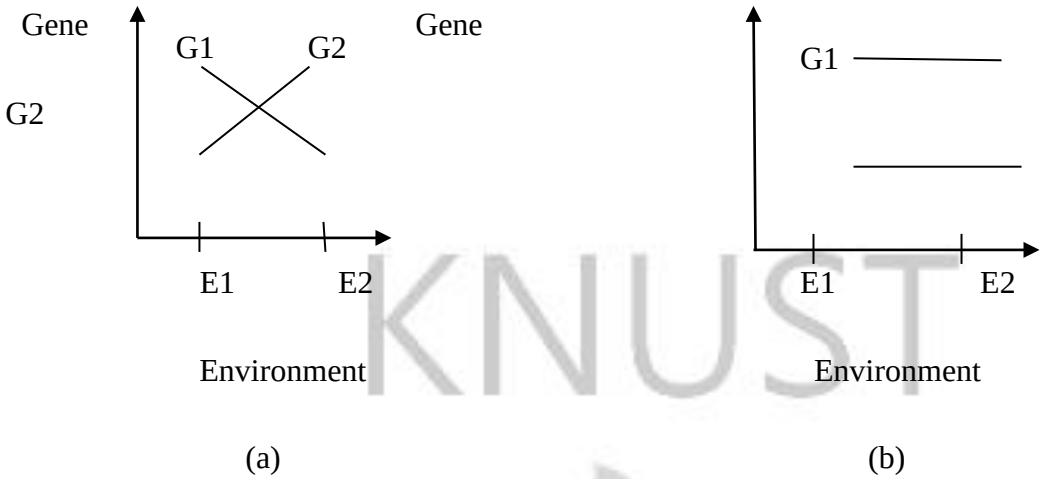
2.5.4 Computations of Genotype by Environment interaction

The occurrence of genotype by environment interaction effect is further complicated by the fact that selection of superior genotypes has to be based on a target population of environment. In situations where there are no genotype by environment, the genotypes that are known to be superior in one environment may be considered as the superior genotype in all other environment, considering that the presence of genotype by environment interaction confirms a particular genotype being superior in particular environment. A variety of statistical procedures are available to analyze the result of multi environment trials, for example, combined ANOVA, stability analysis and multivariate method. Combined ANOVA is most commonly used to identify the existence of genotype by environment interaction in multi-environmental trials. On the other hand, the major setback of this analysis is the assumption of the homogeneity of variance among environments required to determine genotype difference. Although this analysis requires the determination of component of variance arising from the genotype and the environment. It does not allow

exploring the response of genotypes in the non-additive term, which is the genotype by environment interaction (Zobel *et al*., 1998).

Several SAS programs related to the analysis of genotype by environment interaction have been developed (Kang, 1989; Fernandez, 1991; Shaffi and Price, 1998). Comstock and Moll (1963) considered environmental effect and their interaction with genotype random. However, Funnah and Mark (1980) assumed both genotype and environment (season and location) as random effect in their analysis. There are also other methods for evaluating the performance of hybrids and their genetic interaction with the environment (Cornelius *et al*., 1996). These methods differ in the parameter used in the assessment, the biometric procedure employed, and the analysis. The sites regression (SREG) (Crossa and Cornelius, 1996) has long been indicated that it is a very important model for analysing multi environmental trials when large yield variation is due to environment (Yan *et al*., 2000). The SREG method supplies a graphical display called genotype plus genotype by environment interaction (GGE) biplot that identify cultivars that are superior in different environment.

Statistically, genotype by environment interaction occurs if the performance of genotypes varies significantly across environment. Assuming two genotypes (G1 and G2) tested in two environments (E1 and E2) as shown (figure 1.1a) below



(a) (b)

Figure 2.2. Presence and Absence of G × E interaction

The presence of genotype by environment interaction since G1 is phenotypically superior to G2 in environment 1(E1) but inferior to G2 in E2 (fig 2.2a). The phenotypic difference between G1 and G2 remains the same in two environments representing no interaction between the genotype and environment in (figure 2.2b).

Finlay and Wilkinson (1963) also indicated that in handling genotype by environment interaction, regression on the environmental mean can be used. Pattern analysis method (Byth *et al*., 1976), principal coordinates analysis (Eisemann, 1981), canonical variate analysis and principal component analysis (Zobel *et al*., 1998) with each proving victorious in the analysis of univariate genotype by environment data in certain situations.

Among the statistical methods of analysing genotype by environment interaction with regards to the use of biplot, the additive main effect and the multiplicative interaction, AMMI, model becomes obvious because of the largest group of technological explanations available (Duarte and Vencovsky, 1999). The additive main effect and the multiplicative interaction interpret the result of genotype, (G), and environment, (E), as additive effect including the genotype by environment interaction as a multiplicative component and

submit it to the principal component analysis. This biplot was recognised as GE biplot (Yan *et al*., 2000). Yan *et al*., 2000 recommended an adjustment of the conventional AMMI analysis known as genotype main effect and genotype by environment interaction (GGE), which has been used for genotype by environment interaction analysis. The GGE analysis pool genotype effect (G) with GE (multiplicative effect) and subject these effect to principal component analysis. The GGE biplot has long been recognised as a refinement in biplot graphic analysis method to be applied in plant breeding. This two components (AMMI and GGE) analysis were argued out concerning the graphic accuracy it portrayed. Gauch *et al*., (2008) cross-examined the GGE analysis in relation to the fraction of the G + GE that is retained in the biplot. In prior assessment the authors insisted that GGE biplot always explained less G + GE than the AMMI2 mega environmental analysis and most of the time when GGE2 is suppressed in noise, the GGE biplot is even less accurate than AMMI1 analysis. However, Yan *et al*., (2007) stated that GGE2 always explains more of the G + GE than AMMI1 display, resulting in large graphic accuracy.

2.6 The Concept of Stability

The concept of genotype by environment in yield stability has been a concern to plant breeders for quite a long time. An informative genotype by environment interaction for a trait that is said to be quantitative is known to decrease the usefulness of genotypic means over all environments or locations, in a bid to select and advance superior genotypes to the next phase of selection (Pham and Kang, 1988). If there were no genotype by environment association with genotype by environmental structures which is important to the breeding objectives, selection will be considerably amplified because genotype that stand to be the best in one environment will also be the best genotype for all target environments (Gauch and Zobel 1997).

The term “yield stability” is crucial to all types of analysis of genotype by environment interaction especially with reference to the plant breeding. Yield stability has been reported in diverse ways over the years and there has been different concept of stability (Lin *et al*., 1986). The term adaptation, phenotypic stability and yield stability has been used by scientists in different ways (Becker and Léon, 1988). Stability in common usage connotes uniformity in performance of the genotype which explain minimum variation among environments for particular genotypes (Chahal and Gosal, 2002).

If the variation in the environment is small, a genotype is considered to be stable. This is called a biological concept of stability or stability statistics. A genotype that is stable cannot change in performance no matter the variation in environmental conditions. The concept of stability is very important for the assessment of quality traits, stress characters and for disease resistance (Baker and Léon, 1988). Caccarelli (1989) in his suggestion pointed out two main approaches for selection when significant genotypes by environment interaction were present. The first involved selection for low genotype by environment interaction and high mean yields. This approach recognizes genotypes that are widely adapted to all but most severe stress environment. The second approach is based on the use of genotype by environment interaction by breeding for maximum yields and stability within specific macro-environment (Backer and Léon, 1988). Eskridge (1990) concluded that selection based on these stability parameters most include mean yield, yet more of these methods have clearly illustrated it use. Although the stability concept is extensively not clear in plant breeding literature partly due to the myraid of definitions that has been used to represent this concept (Basford and Cooper, 1998), it is an important tool to partition genotype by environment interaction into mean square responsible for it occurrence. High yield stability usually refers to the genotypes ability to perform consistently whether at high or low yield

levels across a wide range of environment (Anniccliarico, 2002). The ultimate reason for differential stability among genotypes and differential results from various test environments is non repeatable genotype by environment (Yang and Hunt, 2002). Stability analysis provides a general result for the response of the genotype to environmental change. In this way, Yates and Cochram (1938) proposed linear regression analysis which has been widely used as proposed by a number of Authors (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Lin and Thompson, 1975). Stability studies have allowed researchers to identify broadly adapted cultivar for use in breeding programmes and have assisted to advance suggestions to farmers (Yayeh and Bosland, 2000). There are four models of stability namely, Type 1, 2, 3 and 4. Lin *et al*. (1986) established Type 1, 2 and 3, while Lin and Binns (1988) established a fourth type (Type 4). However, nearly all stability procedures relate to either of two divergent models of stability i.e. Type 1 (static) and Type 2 (dynamic) (Becker and Léon, 1988; Lin *et al.*, 1986).

Type 1 (static) model of stability is similar to the biological concept of homeostasis wherein a stable cultivar has a tendency to retain a steady yield across locations (Dyke *et al.*, 1995). Type 2 (dynamic) model of stability for a stable cultivar entails a yield response in every location that is constantly comparable to the mean response of the tested cultivar, i.e. zero GE interaction.

Type 3 is referred to as a fraction of the changing or agronomic stability model (Becker and Léon, 1988). The regression co-efficient and deviation from regression are schemes used to explained Type 3 stability model. Type 4 stability model is firmly related to the static model in that it relates to consistency of yield exclusively in time i.e. across years within locations, while Type 1 stability relates to consistency both in time and in space,

i.e. across locations belonging to the same or different sites (Lin and Binns, 1991).

2.7 The Concept of Adaptability

Byth (1981) and Clement *et al*., (1983) argued that the term adaptation applied to both a "condition" and a "process". The interpretation of their definition requires further considerations. The condition or level of adaptation possessed by individual or a population refers to the genetic constitution and how these match the plant and the environment it occupies. Ultimately, this is the function of the gene possessed by the plant, the regulation of biochemical and physiological processes by these genes during growth and development and how well these matches with the available environmental resources and possible hazards (Bindiger *et al*., 1987)., therefore, a difference in "condition" of adaptation between individual result from genetic difference which influences the matching of their growth and development process with the environment. Following 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 with populations which better match growth and development with the environment.

A variety that is adaptable over diverse environment is normally tested by the extent of how well they interact with different growing environment. A genotype or variety is considered to be more stable or adaptive if it has a high mean yield but low degree of fluctuation in yielding ability when grown over diverse environment (Falconer, 1981). Living organisms in their own way are able to undergo physiological adjustment enabling them to dispatch changes in their immediate environment. These adjustment themselves are known as adaptation. A genotype that allow its survival under selection is said to be fully adapted.

Genotypic population or adaptation is the one which performs better than the standard under comparison (Dabholkar, 1999). 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 aim of a breeding programme is to identify genotypes which are widely adapted. Ramagosa and Fox (1993) concluded that if a genotype maintains high yield over diverse environments, it is said to have wider or general adaptation. Moreover, if this notion stands to be true only for a limited environments, that genotype is said to have narrow or specific adaptation.

Further, the stability concept by Becker and Léon (1988), Lin *et al.* (1986) categorized stability into three types:

I. If the among-environment variance of a genotype is small, the genotype is considered to be stable. This concept is applicable for assessment of stress estimation, disease resistance and for quality traits. According to this concept a genotype performs the same in different environments or under different environmental conditions. This

II. Stability can be static or biological (Becker and Léon, 1988). Genotypic variances across environments (Si_2) and the coefficient of variability (CV_i) are used as parameters to describe this type of stability (Francis and Kannenburg, 1978).

III. A genotype is considered to be stable if its response to environments is parallel to the mean response of all genotypes in the trial. According to Becker and Léon (1988) this concept is called the dynamic or agronomic concept of stability. In this case, a stable genotype has no deviations from the general response to environments and creates a possible way of predicting the response of a genotype to a certain environment. Parameters used to describe this type of stability are regression coefficients (b_i) (Finlay and Wilkinson, 1963) and Shukla‟s (1972) stability variance ($_{2i}$). III. A genotype is said to be stable if the residual mean square from the regression model on an environmental index is small. The environmental index is the mean yield of all the genotypes in each location minus the grand mean of all the genotypes in all locations. The method of Eberhart and Russell (1966) and Tai (1971) can be used for estimating type

III stability.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental materials

Entries evaluated were made up of four hybrids, two commercial varieties and a local check. All entries were obtained from Savana Agricultural Research Institute (SARI).

Table 3.1: Descriptions of experimental entries.

Description of genotype	Name of Variety
Pioneer Hybrid line 1	XSW2134
Pioneer Hybrid line 2	XSW256
Wienco Hybrid line 1	Pan606
Wienco Hybrid line 2	MARCIA
Commercial variety 1 (OPV) Commercial	Kapaala
variety 2 (OPV)	Dorado
Check	Kadaga

3.2. Description of the Evaluation sites

The evaluation of genotypes were done in three locations, namely, Nyankpala, Damongo and Manga. Nyankpala is located in the Northern region in the Tolon-Kumbuya district, Damango in the West Gonja district also in the Northern region and Manga in the Bawku Municipal district, upper East region. All these areas are part of the major sorghum producing areas in Ghana.

Table 3.2: Description of evaluation sites

location	latitude	longitude	Altitude (mASL)	Mean seasonal Rainfall (mm)	Agro ecological zone	Soil type
Damongo	0º011´N	01º36´W	260	692.3	Guinea savannah	Ferric lexisol
Nyankpala	09º25´N	00º55´w	183	878.1	Guinea savannah	Haplic lexisols
Manga	11º11´N	0º61´E	135	620.9	Sudan savannah	Gleyic alfisols

3.2.2 Crop Husbandry

The genotypes were planted in 6-row plots of 5m long with an inter-row spacing of 75 cm and between plants in a row of 30 cm. Four sorghum seeds were planted per hole and were later thinned to one at two weeks after planting (WAP). Pre-emergence chemical weed control was practiced using Atrazine at a rate of 2.0 Lha^{-1}, followed by hand weeding at three and five weeks after planting. Compound fertilizer, NPK 15:15:15 was applied by digging and burying in holes at a distance of 5cm from hills and at a rate of 250kg/ha, with each plot receiving 562.5g as a basal fertilizer at two weeks after planting. Top dressing was done with sulphate of Ammonia with each plot receiving 281.25g per plot at four weeks after planting. The trials were conducted under rain-fed condition and all pre and post-management practices were essentially followed in the three locations.

Table 3.3. Planting dates of the trials at three locations

Location	**Date of planting**
Nyankpala	14 June 2014
Damongo	3 June 2014

3.2.3 Experimental Design and data collection

The genotypes were planted in a Randomized Complete Block Design (RCBD) with four replications in each location during the 2014 growing season. In the field, data was collected on the four middle rows of the six row plot and a total of ten plant was sampled for data collection. The following data were collected;

1. **Heading dates** (50% heading): dates when 50% of the plant in the net plot have panicles emergence from the boot.
2. **Anthesis dates** (50%): dates when 50% of the plants in the net plot have panicles flowered.
3. **Anthesis heading interval**: the day interval between anthesis and the date when the panicle emerged from the boot.
4. **Plant height** (at physiological maturity): average height of the sorghum plant from the base of the plant to the tip of the panicle (average of 10 plants).
5. **Panicle length**: measure of the panicle from the flag leaf to the tip of the panicle.
6. **Panicle weight**: total panicle weight per net plot
7. **Harvest index**: the weight of the harvested product as a percentage of the total plant weight of the crop.
8. **100-grain weight:** the weight of 100 grain per net plot

The heading and flowering interval was computed as the difference between days to heading and day to flowering. The plant height per net plot was obtained by taking an average of 10 plants per plot. The grain yield in kilogram per plot was converted to tons per hectare.

In a bid to estimate the variance component, the analysis of variance (ANOVA) method was used for estimating the variance component. The variance component consisted of equating

mean squares to their expectations and further solving the required result by simultaneous equation as shown in the table below:

Table 3.4. Form of variance analysis and expected mean squares for combined data over locations.

Source	Df	Mean Square	Expected Mean Squares
Location (β)	β-1 β(r-1)	M1	$\sigma_e^2 + r\sigma^2g\beta + r\beta\sigma^2g+ rg\sigma^2\beta\ \sigma_e^2 + g\sigma^2r\beta\ \sigma_e^2 + r\sigma^2g\beta + r\beta\sigma^2g\ \sigma_e^2 + r\sigma^2g\beta\ \sigma_{e2}$
Rep. in Location r(β)	g-1	M2	
Genotype (G)	(g-1)(β-1) r(g-1)(β-1)	M3	
Genotype × Location		M4	
Error (e)		M5	

Where β = number of locations, g = genotypes and r = replications, σ_e^2 = plot error Variance, σ^2g = genotype variance and $\sigma^2g\beta$ = genotype by environment interaction Variance.

Two set of statistical analysis was performed to test the significance level of grain yield of the genotype, locations and their interactions. Analysis was done separately for each trial location. Combined analysis was done in order to determine the differences between genotype across locations during 2014 growing season.

3.4 Identification of Superior Hybrids

In as much as the superiority of the sorghum hybrids will be based on commercialization, ranking was done using rank sum which rank hybrids performance in days to heading and flowering, panicle length, panicle weight, grain yield, harvest index, anthesis heading interval. The five best genotypes were selected based on rank sum values calculated by summing the ranks of each of the five genotypes

3.5 The GGE Biplot Model

Since the observed phenotypic value (P) consist of variances of the environment (E), genotype (G) and genotype and environment interaction (GE).

$$P = G + GE + E \text{ or } P - E = G + GE$$

The above formulas were in terms of variance components, when presented as effects which have the unit of originally measured values, they become (Yan *et al*., 2003).

$$Y_{ij} = \mu + \alpha_j + \beta_j + Ø_{ij}$$

$$Y_{ij} - \mu - \beta_j = \alpha_j + Ø_{ij}$$

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

μ = the grand mean of all observations α_j = the main effect of genotype j β_j = the main effect of environment j

$Ø_{ij}$ = the interaction between genotype i and environment j

Instead of trying to separate G and GE, GGE biplot keeps G and GE together and partition this mixture GGE into two multiplicative terms.

$$Y_{ij} - \mu - \beta_j = g_{i1}e_{i1} + g_{i2}e_{2i} + Ø_{ij} + \varepsilon_{ij}$$

Where e_{i1} and e_{1j} are called the primary score of genotype i and environment j, respectively; g_{i2} and e_{2j} the secondary score for genotype i and environment j, respectively; ε_{ij} is the residue not explained by the primary and secondary effect. Actually, a GGE biplot is constructed by plotting gi1 against gi2 and e1i against ej2 in a single scatter plots. The most common way to implement the above formula is by subjecting the

GGE data to singular variance decomposition (SVD) as shown below;

$$Y_{ij} - \mu - \beta_j = \lambda_i\xi_{i1}\eta_{1j} + \lambda_2\xi_{i2}\eta_{2i} + \xi_{ij}$$

Where $\lambda 1$ and $\lambda 2$ are the singular values of the first and second largest principal component, PC1 and PC2, respectively; $\xi 1$ and $\xi 2$ are the eigenvectors of genotype I for PC1 and PC2, respectively, and $\eta 1$ and $\eta 2$ are the eigenvectors of environment j for PC1 and PC2 respectively.

CHAPTER FOUR

4.0 RESULT

4.1.1 Trial at Nyankpala

Table 4.1 shows that percentage sum of squares. The genotypes contribution were the highest (78.97%) superseded by other factors under error (14.55%) and blocks (6.48%). Consequently, the genotypes contributed very much to the variations. This specifies the prevalence of fairly optimum environmental condition during the growing period throughout the crop life cycle. The lowest and highest yield recorded ranged between 6.61t/ha and 17.67t/ha respectively and the mean grain yield was 12.2t/ha. Among the accession XSW2134 showed good performance and appears as the best hybrid with an average yield of 17.67t/ha. XSW2134 (17.67t/ha), XSW256 (17t/ha), Kapaala (13.57t/ha), were the three best genotypes whereas Dorado (11.37t/ha) and Pan606 (11.29t/ha) were among the accessions that showed relatively correspondingly lower yield (appendix 1). Among the testing environments, the general performance of the genotypes was low in Manga compared to the other two locations as shown in Figure 4.2.

Table 4.1. Mean square values and the percentage of variance component for grain yield of four sorghum hybrids and two commercial varieties evaluated at three locations in Ghana during the 2014 growing season.

Sources of variation	DF	Locations					
		Nyankpala		Damongo		Manga	
		% SS	MS	% SS	MS	% SS	MS
Block	3	6.48	11.625	15.09	24.572	5.04	5.754
Genotype	6	78.97	70.823**	68.14	55.460**	63.34	36.173**
Error	18	14.55	4.350	16.77	4.549	31.62	6.018
Total	27	100		100		100	
CV %			17.1		14.3		25.7

**P < 0.01

4.1.2 Trial at Damongo

In this trial the result obtained showed that the variations among the genotypes were highly significant (P < 0.01) for grain yield. . Viewing the values of the percentage sum of squares the genotypes contribution were the highest (68.14%) superseded by other factors under error (16.77%) and blocks (15.09%) as shown in table 4.1. This essentially earnest the fact that the genotypes contributed significantly to the variations. The range in the grain yield obtained was 20.26 t/ha and 9.31t/ha. Mean grain yield obtained was 14.93t/ha. In relation to the grain yield the genotype XSW2134 (20.26t/ha) was ranked first followed by Dorado (19.22t/ha) and Marcia (14.62t/ha) whereas Kapaala (13.97t/ha), Pan606 (13.86t/ha) and XSW256 (13.3t/ha) appeared as the low yielding genotypes. The check kadaga was ranked seventh with a yield of 9.31t/ha and appeared as the lowest (appendix 1).

4.1.3 Trial at Manga

The result in this trial showed that the difference among the genotypes were highly significant (P < 0.01) for grain yield. Viewing the values of the percentage sum of squares the genotypes contribution were the highest (63.34%) superseded by other factors under error (31.62%) and blocks (5.04%) as shown in Table 4.1. Hence, the result indicated strongly that the genotypes contributed significantly to the variation that occurred. The grain yield ranged between 5.52t/ha to 15.13t/ha and the mean grain yield was 9.56t/ha. In this trial the genotype that obtained the highest was XSW2134 (15.13t/ha). In relation to their grain yield the genotype XSW2134 (15.13t/ha), Dorado (10.92t/ha) and XSW256 (10.12t/ha) were the third best grain yielders respectively whereas Pan606 (9.01t/ha), Marcia (8.34t/ha) and Kapaala (7.84t/ha) were essentially low yielding. The check Kadaga

relatively obtained low yield with 5.52t/ha (appendix 1). The individual performance of the genotypes in the three locations is shown in figure 4.1.

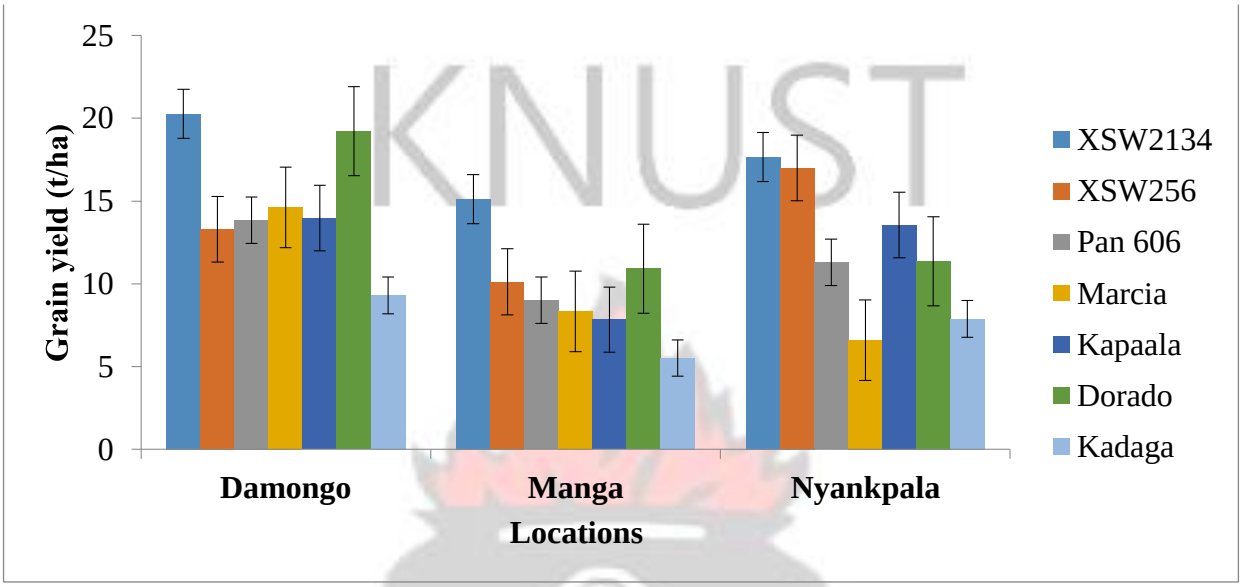


Figure 4.1. The grain yield (t/ha) of the sorghum genotypes in the three locations in Northern Ghana during 2014 growing season.

4.2 Growth and yield characters and their means across locations

4.2.1 Grain yield

From table 4.2, the combined analysis of variance (ANOVA) showed that the differences that occurred among the genotype (G), location (L) and the interaction that occurred between them, genotype by location interaction (GLI) were highly significant ($P<0.01$). The distribution of the total variance available to the genotypes were the highest (42.03%) superseded by other factors under location (22.82%), error (17.68%), Genotype by Location (12.92%) and block (4.55%) respectively as shown in table 4.2. In the combined ANOVA, the mean grain yield obtained by the genotypes at the three locations was 12.23 t/ha as shown in appendix 2. The grain yield ranges between 21.87t/ha and 4.44t/ha. The best high yielding genotype XSW2134 (17.69t/ha) out-yielded the local check kadaga (7.57t/ha).

However, XSW2134 (17.61t/ha) out-yielded the rest of the genotypes. All the genotypes out-yielded the local check Kadaga (appendix 2).

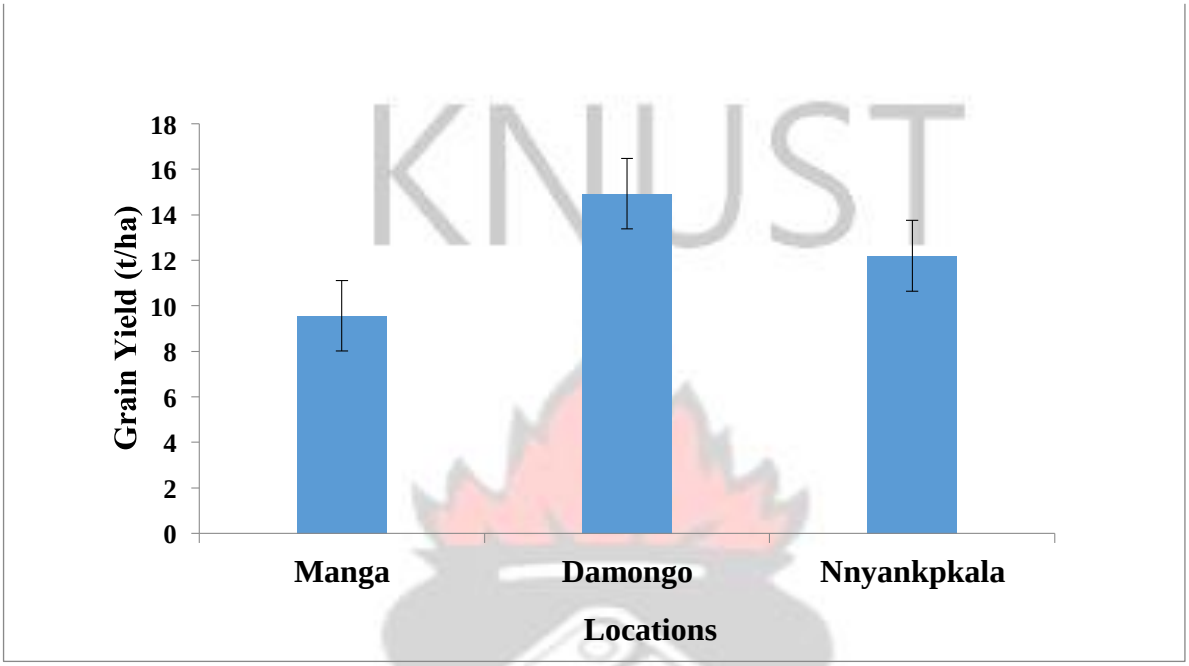


Figure 4.2. Mean grain yield (t/ha) of the sorghum genotype evaluated at three locations in northern Ghana during the 2014 growing season

Table 4.2. Combined analysis of variance and the distribution of the total variance available to the source of variation for grain yield of the sorghum genotypes evaluated in three locations in Ghana during the 2014 growing season.

SOURCES OF VARIATION	DF	SS%	MS
Block	3	4.55	26.900
Genotype	6	42.03	124.254**
Location	2	22.82	202.346**
Genotype × Location	12	12.92	19.101**
Error	60	17.68	5.228
Total	83	100	
CV %	18.7		

**P < 0.01

4.2.2 Days to Heading

From Table 4.3, the combined analysis of variance depict that there was highly significant differences ($P < 0.01$) between genotype (G), location (L) and their interactions genotype by location interaction (GLI) for days to heading. In the table, the mean square values were high for location followed by genotype and their interaction GLI. Days to heading of the genotypes ranges between 55 to 89 days and the mean days to heading obtained was 65.38 days as shown in appendix 2 .The lowest number of days to heading was recorded by XSW256.

Table 4.3. Mean square values of the combined analyses of variance for growth parameters of the sorghum genotypes evaluated at three locations in Ghana during the 2014 growing season.

		Mean squares			
sources of variation	DF	DH	DA	AHI	PLHT
Block	3	3.397	3.663	0.039	52.300
Genotype	6	251.440**	266.956**	0.367**	69265.080**
Location	2	1047.369**	558.464**	3.188**	16421.570**
Genotype × Location	12	123.952**	129.700**	0.154*	1020.020**
Error	60	3.180	2.671	0.068	31.520
CV %	83	2.7	2.3	10.4	3.4

**P < 0.01, *P < 0.05, DA: days to anthesis, DH: days to heading, AHI: anthesis heading interval, PLHT: plant height.

4.2.3 Days to Anthesis

Table 4.3 clearly shows that highly significant difference ($P < 0.01$) was observed among genotypes (G), location (L), and their interaction genotype by location interaction (GLI).

Existing range between days to anthesis for the sorghum genotypes were 62 to 94 days and the mean days to anthesis was observed to be 71.32 days (Appendix 2).

4.2.4 Anthesis Heading Interval

The combined analysis of variance in table 4.3 shows that highly significant difference ($P < 0.01$) existed between genotype (G) and location (L), but only significant ($P < 0.05$) for their interaction, genotype by location interaction (GLI) for anthesis heading interval. The mean square values among genotypes, location and genotype by location interaction was observed to be higher for the locations as compared to genotypes and their interaction (GLI). The range that existed between anthesis heading interval (AHI) was 0 to 12 days and the mean days for anthesis heading interval was 5.94 days as shown in appendix 2.

4.2.5 Plant Height

The combined analysis of variance showed that there was highly significant difference ($P < 0.01$) between genotype (G), location (L) and genotype by location interaction (GLI) for plant height. The mean square values for plant height was higher for the location as shown in table 4.3. Plant height for the genotypes ranged between 103 to 396cm and the mean plant height was 166.6cm as shown in appendix 2.

4.2.6 Panicle Length

There was highly significant difference ($P < 0.01$) between genotype (G), location (L) and their interaction genotype by location interaction (GLI) for panicle length. Viewing from

Table 4.4, the mean square values for genotype was the highest followed by location and then genotype by location interaction (GLI). The panicle length ranged between 19 to 37 cm and mean panicle length for the genotypes was 28.21cm (appendix 2).

Table 4.4. Mean square values of the combined analysis of variance for panicle length (PNL), panicle weight (PNW), harvest index (HI) and 100 grain weight (100GW) of the sorghum genotype evaluated at three locations in 2014 growing season in Ghana.

Sources of variation	DF	Mean squares			
		PNL	PNW	HI	100 GW
Block	3	2.365	2.558	43.650	0.051
Genotype	6	224.024**	6.731**	140.370**	1.945**
Location	2	34.321**	49.703**	18.720*	4.213**
Genotype × Location	12	9.988**	2.362**	49.970**	0.184**
Error	60	1.94	0.625	12.170	0.019

**P < 0.01,*P < 0.05, PNL: panicle length, PNW: panicle weight, HI: harvest index, GW: grain weight.

4.2.7 Panicle weight

As viewed by the combined analysis of variance (ANOVA) in table 4.4, there was highly significant difference (P < 0.01) between the genotype (G), location (L) and genotype by location interaction (GLI) for panicle weight. From the table, the mean square value for location appears as the highest followed by genotype and GLI. Panicle weight ranged between 1.4 to 7.6 kg and the mean panicle weight was 3.896kg (appendix 2).

4.2.8 Harvest Index

For harvest index, the combined analysis of variance (ANOVA) depict that highly significant difference (P < 0.01) existed between genotype (G), and their interactions,

genotype by location interaction (GLI) but was only significant ($P < 0.05$) for locations (L) (Table 4.4). The mean square value was highest for genotype superseded by their interaction, GLI, and then location. Average harvest index were 14.54% and the minimum and maximum harvest index accrued were 4.76 and 29.94% respectively.

4.2.9 100 Grain Weight

From Table 4.4, the combined analysis of variance (ANOVA) showed that there were highly significant ($P < 0.01$) difference was recorded between genotype (G), location (L) and their interaction, genotype by location interaction (GLI). The mean square values for 100 grain weight essentially showed high value for location followed by genotype and then their interaction, GLI. The average 100 grain weight was 2.3g, maximum 3.72g and minimum 1.45g.

4.3 Correlation among Parameters

Correlated parameters from table 4.5 affirm that grain yield was positively correlated with days to flowering, harvest index and panicle weight. Days to heading (DH) and days to flowering (DF), 100 grain weight (100GW) and anthesis head (AHI), plant height (PHLT) and 100 grain weight correlated positively and were at the same time significant ($P < 0.01$); $r = 0.972$, $r = 0.599$, $r = 0.601$ accordingly from table 4.5. Conforming to the association among grain yield and other measured parameters, the association between grain yield and days to heading was weakly negative but highly significant ($P < 0.01$) and also weakly negative for plant height but significant ($P < 0.05$); $r = -0.631$ and $r = -0.296$ respectively. Anthesis heading interval and 100 grain weight were weakly positive in association with grain yield and both were significant ($P < 0.05$) as viewed from table 4.5.

Table 4.5. Correlation coefficient among agronomic parameters of sorghum genotype evaluated at three locations in Ghana in 2014 growing season.

	AHI	DF	DH	100GW	HI	PLHT	PNL	PNW
DF	-0.231*							
DH	-0.452**	0.972**						
100GW	0.599**	0.412**	-0.522**					
HI	-0.228*	0.433**	-0.342*	-0.095 ns				
PHT	0.495**	0.157ns	0.024ns	0.601**	-0.458**			
PNL	0.211ns	0.102ns	0.043ns	0.051ns	0.177ns	0.476**		
PNW	0.464**	0.473**	-0.546**	0.295*	0.194ns	-0.136ns	0.022ns	
YIELD	0.239*	0.626**	-0.631**	0.240*	0.578**	-0.296*	-0.18 ns	0.786**

**P≤ 0.01 *P≤ 0.05 ns= not significant

4.4 Identification of Superior Genotype

4.4.1 Selection Based on Ranking

The performance of the genotypes based on grain yield (t/ha), days to heading, days to anthesis, anthesis heading interval panicle length, panicle weight, plant height and harvest index were computed using rank sum values as presented in appendix 2. The rank sum values depicted that G1 (XSW2134) G6 (Dorado) and G2 (XSW256) were the best three genotypes whereas G5 (Kapaala), G3 (Pan606) and G4 (Marcia) were essentially low yielding.

4.5 GGE biplot analysis based on grain yield and stability of sorghum genotypes

Determination of grain yield and stability in GGE biplot can be visualized in figure 4.3, 4.4, 4.5 and 4.6 which were based on environment focused singular value partitioning

(where SVP = 2) and genotype focussed singular value portioning (where SVP = 1). The SVP = 2 visualizes the relationship among test environments (figure 4.3, 4.4 and 4.6) while the SVP = 1 indicates the relationship among genotypes. The principal component axis (PC1) explained 85.4% of the total variation; while the principal component 2 (PC2) explained 13.4%. Ultimately, these two principal components summed up to 98.8% which accounted for the total variation in grain yield (figure 4.3, 4.4, 4.5 and 4.6). The result obtained in this section can be put into four categories. Category one indicates "whichwon-where" biplot for yield which explains which genotype is the best for which location; category two relationships among test environment; category three genotype performances and stability across environment and category four, discrimination and representativeness of test environment.

4.5.1. The which won- where-biplot for yield

One of the most attractive features of GGE biplot is its ability to show the which-wonwhere or which is the best for what of genotype by environment interaction data set. The which-won-where function is an extended use of pair wise comparism and an important visual tool in mega environment analysis (Yan *et al*., 2007). A polygon is first drawn from the genotypes that is furthest from the biplot origin so that all the other genotype are contained within the polygon, then the perpendicular lines to the end of the polygon are drawn. Mega environment analysis defines the portioning of the crop growing region into different target zones (Gauch and Zobel, 1997). The equality line divide the biplot into sectors and the winning genotype is the one located at their respective vertex. Therefore, in figure 4.3, five rays divide the biplot into five sectors. G1 was the vertex angle where Damongo, Manga and Nyankpala fell and thus G1 was the winning genotype for the three locations. This pattern suggest that G1 being the winning genotype, it would be selected for proper

exploitation of resources in the three environment. No environment fell into a sector where the vertex genotype G6, G4, G7 and G2 were, indicating that they were low yielding genotypes as compared to G1. Genotypes within the polygon such as G3 and G5 were less responsive than the vertex genotype.

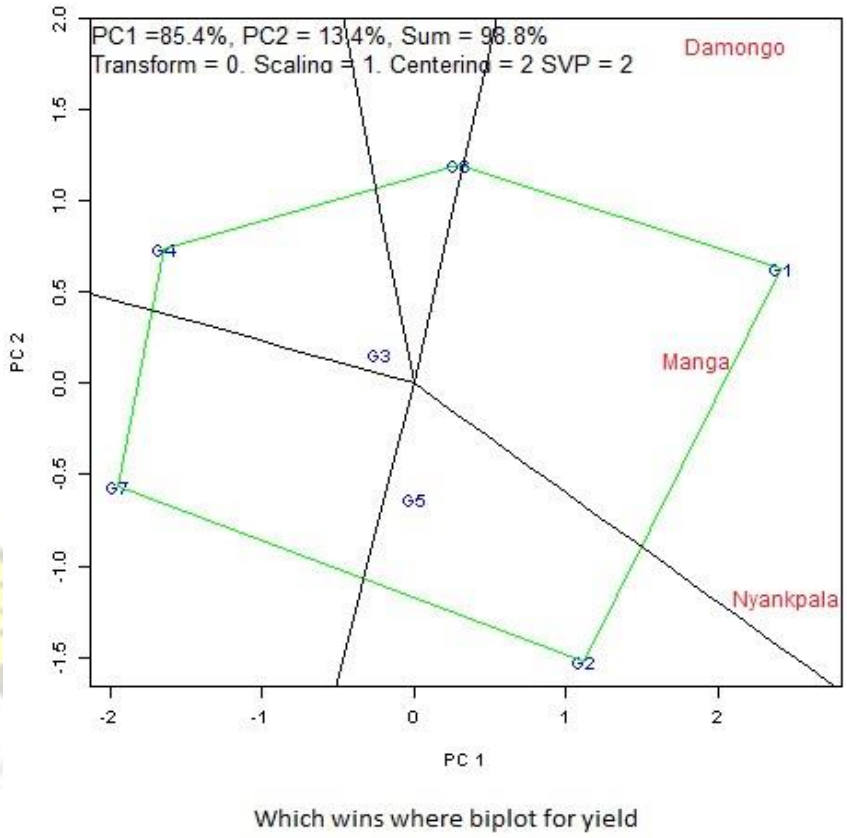


Figure 4.3. Polygon view of GGE biplot for which-won-where pattern of genotype by environment yield data of sorghum genotypes evaluated at three locations in 2014 growing season.

4.5.2. Relationship among Test Environments

Figure 4.4 is the environment vector of GGE biplot and gives the summary of the interrelationship among test environments in the study. The biplot describes the first two principal components and accounted for 98.8% of the total variation in grain yield. The lines

that connect the test environment to the biplot origin are called environment vectors. The angles between the vectors of the two environments approximate the correlation coefficient between them (Kroonenberg, 1995; Yan 2002). Therefore, in figure 4.4, the angle between Damongo and Manga, Manga and Nyankpala and Damongo and Nyankpala were all less than 90^{o}. Thus the three environments are said to be positively correlated to one another.

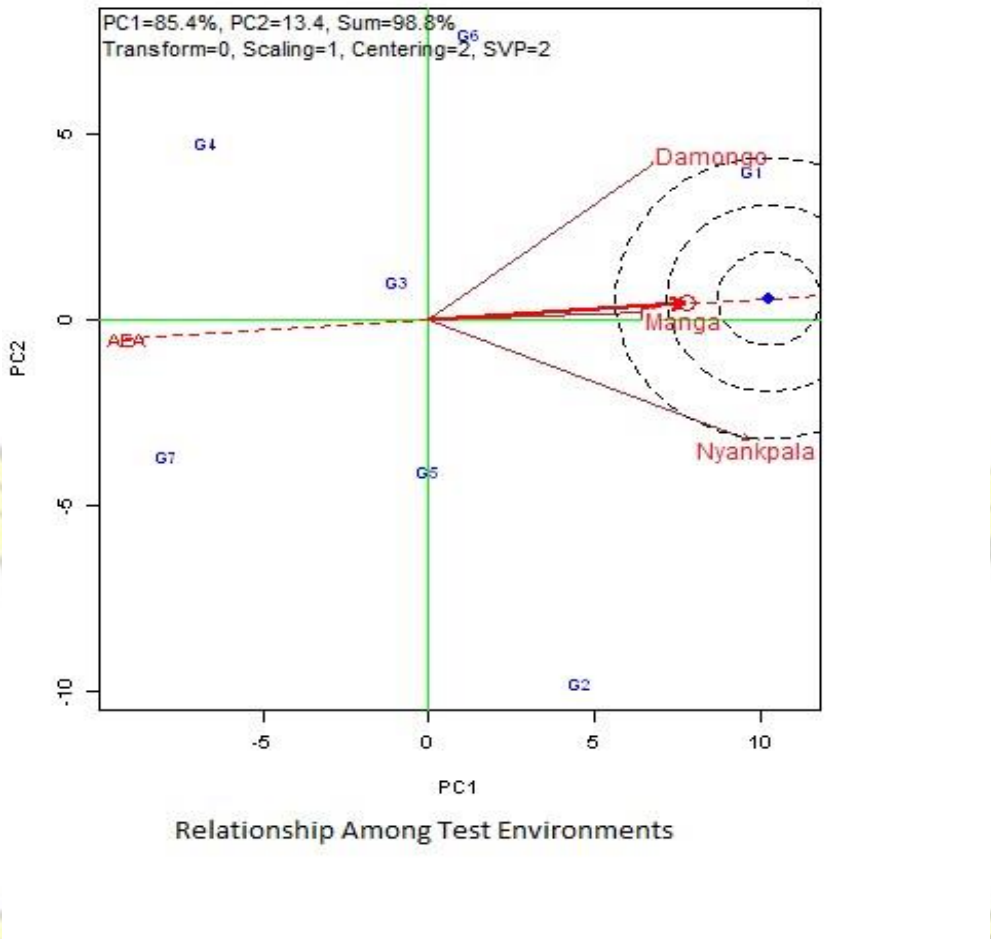
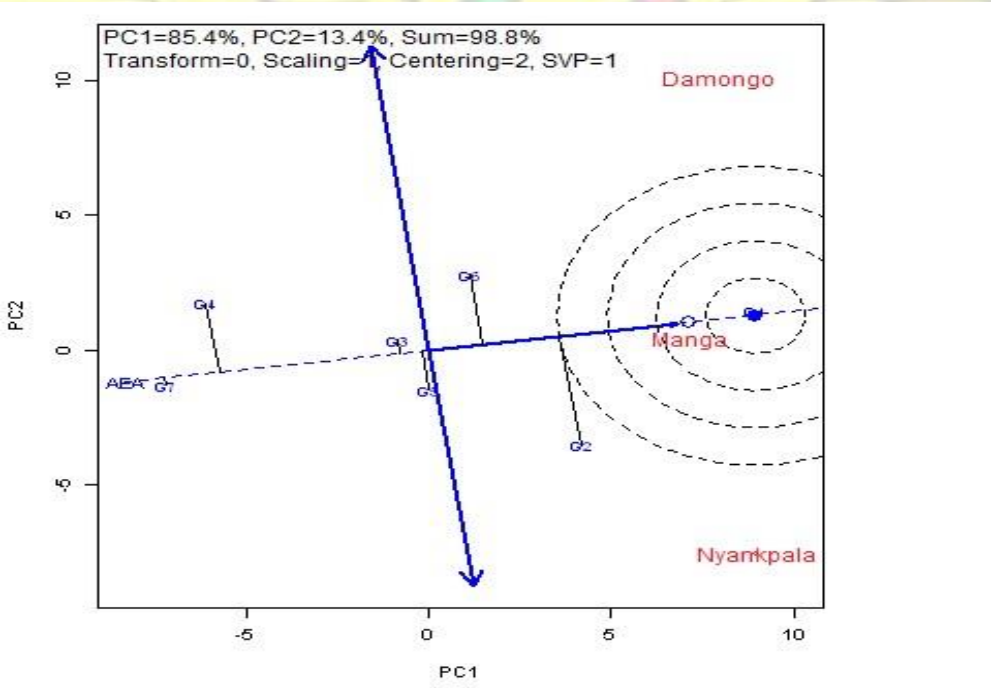


Figure 4.4. The GGE biplot view of the relationship among the three environments where the sorghum genotypes were evaluated in Ghana in the 2014 growing season

4.5.3. Genotype Performances and stability across environment

Performance and stability of genotype were visualized graphically through GGE biplot

(figure 4.5). This can be evaluated by average environment axis (AEA) method (Yan 2001, 2002). The line with single arrow head is the AEA abscissa. AEA abscissa passes through the biplot origin and a marker for average environment which point towards higher mean values. Based on this, from figure 4.5, G1 had the highest mean yield and was the best performer while G7 had the lowest mean yield and was the worst performer in relation to grain yield. The average environment has average PC1 and PC2 scores over all environments (Yan, 2001). AEA ordinate is the perpendicular lines to the AEA abscissa passing through the biplot origin. These ordinate is explained as double arrowed line. The greater the length of the projection of the genotype the less stable it is (Yan *et al*., 2000). In relation to this, G1, G5, G3 and G7 were the most stable and had a near zero projection on to the AEA ordinate. G2, G6 and G4 were the least stable genotype. G1 was high yielding and at the same time most stable while G7 was low yielding but most stable.

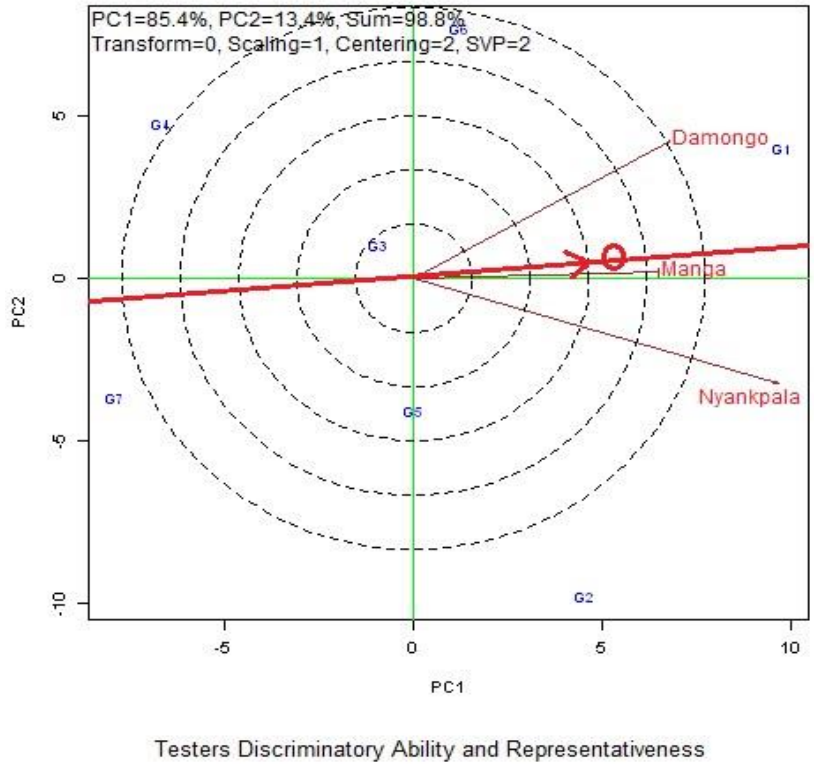


The Average Tester Coordinate for entry evaluation

Figure 4.5. The stability view of GGE biplot based on genotype by environment yield data of sorghum genotype evaluated at three locations in Ghana in the 2014 growing season.

4.5.4. Discrimination and representativeness among test environments

The biplot presented in figure 4.6 represent the discriminatory ability and representativeness of the test environments used in the study. The test environments used in the study were Damongo, Manga and Nyankpala. The reason for test environment evaluation is to identify environment that effectively identify superior genotypes in mega environment. The discriminatory power of an environment refers to the ability of an environment to identify an ideal test environment, while the representativeness refers to the ability of the test locations to represent the mega environment (Badu-apraku *et al*., 2011a). The concentric cycles of the biplot help to visualize the length of the environment vector and are the measure of the discriminatory ability of the environment. Nyankpala had the longest vector followed by Damongo while Manga had the shortest. Thus in figure
4.6, among the three environments, Damongo and Manga were most discriminating and Nyankpala least discriminating. Damongo had PC1 score of 0.51 and PC2 -0.80, Manga had PC1 score of -0.41 and PC2 -0.04 and Nyankpala had PC1 score of -0.71 and PC2 0.60.



Testers Discriminatory Ability and Representativeness

Figure 4.6. The discriminatory ability and representativeness view of GGE biplot yield data of sorghum genotypes evaluated at three locations in Ghana in the 2014 growing season

CHAPTER FIVE

5.0 DISCUSSION

5.1 Performance of sorghum genotypes evaluated at three locations in Ghana in 2014 growing season

Result from the trial at the three locations clearly shows the contributions of the genotypes with respect to their percentage sum of squares computed. The values obtained from the percentage sum of square depicted that the contribution of the genotype were highest at Nyankpala followed by Damongo and Manga respectively (Table 4.1). Results of this nature are a clear indication that the weather and climatic conditions were essentially different in the three environments. This fact can also be explained based on the result obtained in table 3.2, which indicated that soil type and the mean seasonal rainfall for the three environments were relatively different. Among the three environments, Damongo was the highest grain yielding environment followed by Nyankpala and Manga (Figure 4.2). Similar result of this nature was reported by Abdulai *et al*., (2007). In view of the causes of genotype by environment interaction, report by Langridge and Griffing (1959) showed that GEI is caused by difference in biochemical pathway of certain physiological process that takes place in plant. Although genotype may be similar phenotypically, they may still differ by a few nucleotide sequences. This phenomenon results in different expression of genes in different environments. Genotype by environment interaction which is the differential response of genotype tested in a number of locations has long been noted (Lin *et al*., 1986). Information on this current study revealed that most of the genotypes involved in the trial across the three environments showed performance based on their differential ranking (appendix 1). Thus, in the ranking across the three environments, it was shown that G1 (XSW2134) was the best hybrid rank first in the three environments. The top three high yielding genotypes

in Damongo, were G1 (XSW2134), G6 (Dorado) and G4 (Marcia) respectively. No significant difference was recorded between G2, G3 and G5. The check G7 (Kadaga) was the lowest yielding genotype. In Manga, the first three top high yielding genotypes were G1 (XSW2134), G6 (Dorado), and G2 (XSW256) respectively. Also in this environment the check G7 (Kadaga) was the lowest yielding genotype. Among these three high yielding genotypes in Manga, the commercial variety G6 (Dorado) yielded more than the hybrid G2 (XSW256). In

Nyankpala, the first top three high yielding genotypes were G1 (XSW2134), G2 (XSW256) and G5 (Kapaala) respectively. Among these top three high yielding genotypes, the hybrid G1 (XSW2134) and G2 (XSW256) yielded more than the rest of the commercial varieties. The differences that occurred in the ranking of the hybrids and commercial varieties across the three environments showed the existence of unstable genotype. This harness a close evaluation of genotype based on their interaction with the environments.

The results obtained from the combined analysis of variance depicted that the genotype contributed 42.03% sum of square value of the total variation for grain yield, while locations had 22.82% and G×L 12.92% (Table 4.2). This result is not in agreement with (Mohebodini *et al*., 2006; Sabaghina *et al*., 2008a and Mohammadi *et al*., 2009) that in their report stated that the largest proportion of the total variation in multi-environment trial is attributed to locations whereas L and G×L sources of variation are relatively smaller. Badu-apraku *et al*., (2012) reported that the presence of large genetic variability is of utmost importance for progress from selection for grain yield tested in different environment in multi environment trials. Therefore, from this trial, the large sum of square values of genotype for grain yield is a clear indication that selecting a cultivar for grain yield in different environments clearly manifested that very good progress can be made.

The mean square value that was shown significant for location showed that the effect of the genes were influenced by the environments which inhibit environmental diversity. Similar work was reported by Butron *et al*., (2002) in which they pointed out that genotype by location effect on grain yield were as a result of environment yield limiting factor such as relative humidity and temperature.

5.2 Correlation Among measured Parameters

The phenotypic correlation coefficient presented in table 4.5 Showed that anthesis heading interval (AHI) and 100 grain weight (100GW) had a positive and significant ($P<0.05$) direct contribution to yield whereas, days to flowering (DF), harvest index (HI) and panicle weight (PNW) showed positive and highly significant ($P<0.01$) direct contribution to yield.

Anthesis heading interval (AHI) had highly significant ($P<0.01$) indirect effect on yield through 100 grain weight (100GW), plant height (PHLT) and panicle weight (PNW) with the highest effect through 100GW ($r = 0.599$). Days to flowering (DF) had highly significant indirect effect on yield through DH, 100GW, HI and panicle weight the highest effect through DH ($r = 0.972$) and plant height (PHLT) only had highly significant indirect contribution on yield through panicle length (PNL). These findings were in agreement with Asthana *et al*., (1997).

The negative phenotypic correlation coefficient that existed between grain yield and days to heading (DH), plant height (PHT) is a clear indication that grain yield may be reduced by a relative increase in these two parameters. 100GW reduced yield indirectly in harvest index, HI, ($r = -0.095$) but increasing anthesis heading interval (AHI) and days to flowering (DF) with the highest effect on AHI ($r = 0.599$). The observed strong phenotypic correlation coefficient between grain yield and panicle weight (PNW) is attributed to the sufficient

supply of moisture during the reproductive phase of the genotypes (table 3.2). The result of the above study is in agreement with Sankarapandian *et al*., (1996) in their sorghum yield trial report. This correlation measurement revealed that anthesis heading interval (AHI), 100 grain weight (100GW), days to flowering (DF) and harvest index (HI) that showed significant direct contribution to yield showed that these secondary traits can also be taken into consideration in selecting for superior genotype instead of gain yield alone.

5.3 Identification of superior genotype

Measure in identifying superior genotype has to be linked with both primary trait (grain yield) and secondary parameters. The primary trait is described as a quantitative trait with low heritability. Studies in most research have indicated that highly significant phenotypic correlation between yield and many secondary parameters can be found. Edmeades *et al*., (1997) reported that the use of secondary trait in breeding significantly increase breeding progress. Superiority in hybrid sorghum or commercial sorghum varieties must be based on the fact that the hybrids or commercial varieties must be high yielding and at the same time possess desirable agronomic and end user characteristic which may be measured by selection index. If the hybrid sorghum or commercial sorghum varieties fail to meet the high yielding and end user preferred qualities, it will lead to the non-adoption of these genotypes by farmers. Since the primary and secondary traits are both part of identifying superior genotypes, result from the phenotypic correlation coefficient revealed that grain yield was positively and highly significantly ($P < 0.01$) related to days to anthesis, harvest index and panicle weight. This is a clear indication that one of these traits can be used to select for the other. Evidence from days to flowering had indicated that genotypes with shorter period for days to flowering are better placed than those with longer period. Thus, G2 (64.33days), G1

(66.42days) and G5 (69.75days) had shorter period as shown in appendix 2. Similarly, genotypes that showed high harvest index values were G1 (18.39%), G2 (17.87%) and G6 (17.45%). In the hybrid G1 (XSW2134), grain yield increased with harvest index and panicle weight and therefore were ranked first (appendix 2). Therefore, selecting for superior genotype has to go with considering the above parameters.

On the basis of these observations, G1 (XSW2134) and G2 (XSW256) has been identified as superior hybrids whereas G5 (Kapaala) and G6 (Dorado) being superior commercial varieties. From this study, these two set of hybrids and commercial varieties can be considered for large scale sorghum production.

5.4 Yield and stability performance of sorghum genotypes

In GGE biplot analysis, the complex genotype by environment interaction is simplified in different principal component and the data are presented graphically against various principal components (Yan and Tinker, 2006). Environmental PC1 and PC2 scores were obtained in positive and negative scores. If the first two principal component explain more than 60% of the genotype and genotype by environment variability in the data, and the combined genotype and genotype by environment effect account for more than 10% of the total variability, then the biplot adequately approximates the variability in genotype by environment data (Yang *et al*., 2009; Yan *et al*., 2010). In this study, the first two principal components explained 98.8% of the total variation, which is more than the 70% stated.

Thus, the biplot may be safely interpreted as effective graphical representation of the total variability in this trial. Report by Yan *et al*., (2007) has shown that the presence of two or more environment within a sector indicate that a single genotype has the highest yield in those environment. If the environments fall into different sectors, it means that the different

genotype fall in different environment. Evidence of the above report is shown in figure 4.3. G1 (XSW2134) is the vertex genotype and had the highest yield at Damongo, Manga and Nyankpala and therefore emerges as the winning genotype at the three environments (figure 4.3). This cross over genotype by environment suggests that the target environments may be divided into different mega environment. From figure 4.3, G6 was the vertex genotype that exactly fall on the rays that divide the sector where the three environment fell and was close to Damongo and Manga indicating that G6 had high yield in these two environments. Similar result can be shown in appendix 1. From the result of the relationship among test environments (figure 4.4), the angles between the three environments Damongo, Manga and Nyankpala were less than 90^{o} and imply that they are positively correlated to one another. Similar result was reported by Naroui Rad *et al*., (2013) in their genotype by environment interaction trial in wheat. Viewing from figure 4.5, which explains the performance and stability of the genotypes, it shows that G1 (XSW2134) was high yielding and most stable, G2 (XSW256) was high yielding but least stable and G4 (Marcia) was low yielding and least stable. This shows that the hybrids G2 and G4 most not be considered in terms of production in the three environments. The discriminatory ability and representativeness view of GGE biplot is presented in figure 4.6. Since the AEC abscissa is the average environment axis, test environments at smaller angles to the average environment are more representative of the mega environment than those at larger angles to it. The cosine of the angles between any environment vector and the average environment axis approximate the correlation coefficient between the genotype value in the environment and the genotype mean across the environment (Yan *et al*., 2007). The small cycle is the average environment and the arrow pointing to it is used to indicate the direction of the AEA. The absolute length of the projection on to the ATC Y-axis indicates it representativeness; hence the shorter the projection the more representative the environment. In contrast, the absolute length of the

projection from the marker of an ATC x-axis indicate it discriminative ability; the longer the projection, the more discriminative the environment. In relation to these concerns Manga was most representative but not discriminating, Nyankpala was more representative and more discriminating (far away from the origin) but least representative of the test environment since it was at largest angle to AEA. It connote that Nyankpala which had longest vector and largest angle with AEA cannot be used in selecting superior genotype but can be effectively used in culling unstable genotype (figure 4.6). An ideal test environment should effectively discriminate genotype and represent their mega environment (Yan and Rajcan, 2002). This indicated from figure 4.6 that Damongo which is located in the Guinea savannah zone would be appropriate in selecting superior genotype. The environments that have shorter vector are less informative than those with longer vector and provide little or no information on the genotype and could therefore be excluded when choosing test environment. Therefore, in figure 4.6, the shorter vector environment was Manga. Manga could be regarded as independent research environment and is supposed to be treated as unique and essential research environment.

CHAPTER SIX

6.0 CONCLUSION AND RECOMMENDATION

6.1 CONCLUSION

Scientific experimentation of genotype by environment interaction in sorghum trial has been carried out by a number of researchers (Sunjay *et al*., 2012; Itai Makanda *et al*., 2012). The procedures in the selection of good performing and stable genotypes are complicated by the phenomenon of genotype by environment interaction. The large variation in environmental factor causes the relative ranking of the genotype to change from location to location and from year to year. Therefore, it is important to have prior knowledge on the effect of genotype by environment interaction on genotype evaluation in order to help in making decision in recommending cultivars to farmers and consumers. This reason was enough to conduct a research in different locations in northern Ghana to identify high yielding sorghum genotype with superior agronomic performance during the 2014 growing season.

A total of four (4) sorghum hybrids, two (2) commercial varieties and a local check were evaluated across the three locations with the view to comparing their relative yielding ability and stability. This study revealed that the sorghum genotypes were found to be significant for grain yield and is an indication that there were large genetic variations in grain yield. This reason supported the fact that good progress can be achieved in selecting for grain yield under different environments. Despite the fact that variations among the genotype were highly significant within and among the three locations, location generally contributed immensely to the variation that occurred in the genotype performance. This depicted that the fluctuating environmental condition will be of major concern in selecting superior sorghum genotype under Ghanaian condition. The significant genotype by location

interaction that was obtained for grain yield depicted that the locations where the genotypes were tested consist of a number of special environments. Therefore the sorghum genotypes selected should be ideally adapted to the different environment.

Indications from the mean square tables showing significant genotypic mean square for grain yield, DYH, DA, AHI, PLHT, PNL, PNW, HI and 100GW emphasizes on the fact that multiple trait selection method can be used to identify reasonably best performing genotype for commercial sorghum production. Therefore, among the genotypes evaluated, the sorghum hybrid XSW2134 and a commercial variety Dorado obtained the highest yield and will be considered for commercial sorghum production. Contrarily, the hybrid Pan 606 and a commercial variety Kapaala obtained low yield and are therefore not good representatives for commercial sorghum production.

Results from the GGE biplot analysis explains the stability and performance component of the sorghum genotype used in the study. In relation to this study, the GGE biplot depicted that G1 (XSW2134) was high yielding and most stable and was considered as the best hybrid. This hybrid have the potential for production in Nyankpala, Damongo, and Manga. G3 (Pan 606) was low yielding but most stable. This shows that the performance of Pan 606 would be predictable in less favourable environment. The commercial variety Dorado was identified for production in Damongo and Manga.

6.2 RECOMMENDATIONS

Based on the results obtained in this study, more sorghum hybrids and or commercial sorghum varieties should be evaluated in subsequent research and have them repeated in

more than three locations in other sorghum producing areas in order to confirm their yield stability and the pattern of response of the sorghum genotypes across locations.

G1 (XSW2134) which was high yielding and most stable across the three locations should be tested on farmers field for more exploitation of resources whereas those low yielding genotypes such as G3 (Pan606) should be re tested in a close research environment in order to confirm their performance before taking them to farmers field.

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APPENDICES

Appendix 1. Mean grain yield (t/ha) and ranking of sorghum genotypes evaluated in three locations in Ghana during the 2014 growing season.

		Damongo		Nyankpala		Manga	
Treatment	Name	Yield	Rank	Yield	Rank	Yield	Rank
G1	XSW2134	20.26	1	17.67	1	15.13	1
G2	XSW256	13.3	6	17.00	2	10.12	3
G3	Pan 606	13.86	5	11.29	5	9.01	4
G4	Marcia	14.62	3	6.61	7	8.34	5
G5	Kapaala	13.97	4	13.57	3	7.84	6

G6	Dorado	19.22	2	11.37	4	10.92	2					
G7	Kadaga	9.31	7	7.88	6	5.52	7					
l.s.d.		3.169		3.098		3.644						
Cv		14.3		17.1		25.7						

Appendix 2. Means of grain yield (t/ha), anthesis heading interval (AHI), days to anthesis (DA), days to heading (DH), 100 grain weight (100GW) (g), harvest index (HI) (%),plant height (cm), panicle length (PNL)(cm) and panicle weight (PNW)(kg) of sorghum genotypes evaluated at three locations in northern Ghana during 2014 growing season.

Treatment	Name	Yield	AHI	DA	DH	100 GW	HI	PLHT	PNL	PNW
							9.98	331.8	34.83	2.796
							14.54	166.61	28.21	3.896
G1	XSW2134	17.69	6.0833	66.42	60.33	2.112	18.39	132.9	27.42	5.146
G2	XSW256	13.47	5.667	64.33	58.67	2.468	17.87	118.9	28.25	4.088
G3	Pan 606	11.39	4.917	72.58	67.67	1.76	14.35	126.9	33.33	4.108
G4	Marcia	9.86	5.417	76.33	70.92	1.86	6.00	139	24.92	3.258
G5	Kapaala	11.79	5.917	69.75	63.83	2.732	12.44	185.2	23.67	3.713
G6	Dorado	13.84	6.0833	73.25	67.17	2.41	17.45	131.4	25.08	4.163
		7.57	7.5	76.58	69.08	G7				
		12.23	5.94	71.32	65.38	kadaga				
2.775 grand mean			2.302							
l.s.d. 1.867		0.872	1.335	1.456	0.1133	2.849	4.585	1.137	0.6454	
cv 18.7		18	2.3	2.7	6	24	3.4	4.9	20.3	

Appendix 3. Rank sum values of genotypes based on performance of genotype using grain yield, anthesis heading interval (AHI), days to anthesis (DA), days to heading (DH) and 100 grain weight (100GW) evaluated at three locations in northern Ghana during 2014 growing season.

Treatment	Name	Yield	Rank	AHI	Rank	DA	Rank	DH	Rank	100 GW	Rank	Rank Sum
G1	XSW2134	17.69	1	6.08	5	66.42	2	60.33	2	2.11	3	13
G2	XSW256	13.47	3	5.67	3	64.33	1	58.67	1	2.47	4	12

G3	Pan606	11.39	5	4.92	1	72.58	4	67.67	5	1.76	1	16
G4	Marcia	9.86	6	5.42	2	76.33	6	70.92	6	1.86	2	22
G5	Kapaala	11.79	4	5.92	4	69.75	3	63.83	3	2.73	6	20
G6	Dorado	13.84	2	6.08	5	73.25	5	67.17	4	2.41	5	21
G7	kadaga	7.57	7	7.5	6	76.58	7	69.08	7	2.78	7	34

Appendix 4. Rank sum values of genotype based on the performance of genotype for harvest index (HI), plant height (PLHT), panicle length (PNL) and panicle weight (PNW) evaluated at three locations in northern Ghana during 2014 growing season.

Treatment	Name	HI	Rank	PLHT	Rank	PNL	Rank	PNW	Rank	Rank Sum
G1	XSW2134	18.39	1	132.9	4	27.42	4	5.15	7	16
G2	XSW256	17.87	2	118.9	1	28.25	3	4.09	4	10
G3	Pan606	14.35	4	126.9	2	33.33	2	4.11	5	13
G4	Marcia	6.00	7	139.0	5	24.92	6	3.26	2	20
G5	Kapaala	12.44	5	185.2	6	23.67	7	3.71	3	21
G6	Dorado	17.45	3	131.4	3	25.08	5	4.16	6	17
G7	kadaga	9.98	6	331.8	7	34.83	1	2.80	1	15